

DnaSP v5: a software for comprehensive analysis of DN

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Citation Report

#	ARTICLE	IF	CITATIONS
2	Inhibition of the Extracellular Signal-regulated Kinase/Mitogen-activated Protein Kinase Pathway Decreases DNA Methylation in Colon Cancer Cells. <i>Journal of Biological Chemistry</i> , 2007, 282, 12249-12259.	1.6	91
3	Immunogenicity Characterization of Two Ancient Wheat α -Gliadin Peptides Related to Coeliac Disease. <i>Nutrients</i> , 2009, 1, 276-290.	1.7	30
4	Haplotype Distribution and Evolutionary Pattern of miR-17 and miR-124 Families Based on Population Analysis. <i>PLoS ONE</i> , 2009, 4, e7944.	1.1	25
5	Processing and population genetic analysis of multigenic datasets with ProSeq3 software. <i>Bioinformatics</i> , 2009, 25, 3189-3190.	1.8	83
6	Sharp Phylogeographic Breaks and Patterns of Genealogical Concordance in the Brine Shrimp <i>Artemia franciscana</i> . <i>International Journal of Molecular Sciences</i> , 2009, 10, 5455-5470.	1.8	25
7	Candidate genes revealed by a genome scan for mosquito resistance to a bacterial insecticide: sequence and gene expression variations. <i>BMC Genomics</i> , 2009, 10, 551.	1.2	32
8	A recent duplication revisited: phylogenetic analysis reveals an ancestral duplication highly-conserved throughout the <i>Oryza</i> genus and beyond. <i>BMC Plant Biology</i> , 2009, 9, 146.	1.6	41
9	Recombination, selection and clock-like evolution of Rice yellow mottle virus. <i>Virology</i> , 2009, 394, 164-172.	1.1	21
10	Development of primers for amplification and further research on the D-loop control region for the Common Spadefoot toad, <i>Pelobates fuscus</i> (Amphibia). <i>Conservation Genetics Resources</i> , 2009, 1, 495-499.	0.4	2
11	Implications of isolation and low genetic diversity in peripheral populations of an amphipod Atlantic coral. <i>Molecular Ecology</i> , 2009, 18, 4283-4297.	2.0	70
12	Complete mitochondrial DNA replacement in a Lake Tanganyika cichlid fish. <i>Molecular Ecology</i> , 2009, 18, 4240-4255.	2.0	82
13	Contrasting mtDNA diversity and population structure in a direct-developing marine gastropod and its trematode parasites. <i>Molecular Ecology</i> , 2009, 18, 4591-4603.	2.0	61
14	Evolution of serum albumin intron-1 is shaped by a 5' truncated non-long terminal repeat retrotransposon in western Palearctic water frogs (<i>Neobatrachia</i>). <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 784-791.	1.2	29
15	MLST scheme of <i>Ehrlichia ruminantium</i> : Genomic stasis and recombination in strains from Burkina-Faso. <i>Infection, Genetics and Evolution</i> , 2009, 9, 1320-1328.	1.0	24
16	Mitochondrial DNA of <i>Anisakis simplex</i> S.S. as a Potential Tool for Differentiating Populations. <i>Journal of Parasitology</i> , 2009, 95, 1364-1370.	0.3	11
17	Population Genetics of the Eastern Oyster <i>Crassostrea virginica</i> (Gmelin, 1791) in the Gulf of Mexico. <i>Journal of Shellfish Research</i> , 2009, 28, 855-864.	0.3	34
18	Bat Activity and Genetic Diversity at Long Point, Ontario, an Important Bird Stopover Site. <i>Acta Chiropterologica</i> , 2009, 11, 307-315.	0.2	23
19	Convergently Recruited Nuclear Transport Retrogenes Are Male Biased in Expression and Evolving Under Positive Selection in <i>Drosophila</i> . <i>Genetics</i> , 2010, 184, 1067-1076.	1.2	21

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20	Genetic variation in senescence marker protein-30 is associated with natural variation in cold tolerance in <i>Drosophila</i> . <i>Genetical Research</i> , 2010, 92, 103-113.	0.3	21
21	CYP1A2 is more variable than previously thought: a genomic biography of the gene behind the human drug-metabolizing enzyme. <i>Pharmacogenetics and Genomics</i> , 2010, 20, 647-664.	0.7	27
22	High Level of Structural Polymorphism Driven by Mobile Elements in the Hox Genomic Region of the <i>Chaetognath Spadella cephaloptera</i> . <i>Genome Biology and Evolution</i> , 2010, 2, 665-667.	1.1	3
23	Genetic heritage in the Darling River Aboriginal peoples captures ancient presence and post-contact survival. <i>Before Farming</i> , 2010, 2010, 1-17.	0.2	1
24	Mitochondrial Haplotype Analysis as a Tool for Differentiating Isolates of <i>Verticillium dahliae</i> . <i>Phytopathology</i> , 2010, 100, 1231-1239.	1.1	9
25	Analysis of three multigene families as useful tools in species characterization of two closely-related species, <i>Dicentrarchus labrax</i> , <i>Dicentrarchus punctatus</i> and their hybrids. <i>Genes and Genetic Systems</i> , 2010, 85, 341-349.	0.2	31
26	<i>Trichuris vulpis</i> and <i>T. trichiura</i> infections among schoolchildren of a rural community in northwestern Thailand: the possible role of dogs in disease transmission. <i>Asian Biomedicine</i> , 2010, 4, 49-60.	0.2	63
27	ALTER: program-oriented conversion of DNA and protein alignments. <i>Nucleic Acids Research</i> , 2010, 38, W14-W18.	6.5	367
28	Population-based resequencing analysis of improved wheat germplasm at wheat leaf rust resistance locus Lr21. <i>Theoretical and Applied Genetics</i> , 2010, 121, 271-281.	1.8	11
29	Allelic variation of the $\hat{\Gamma}^2$ -, $\hat{\Gamma}^3$ - and $\hat{\Gamma}^4$ -kafrin genes in diverse <i>Sorghum</i> genotypes. <i>Theoretical and Applied Genetics</i> , 2010, 121, 1227-1237.	1.8	39
30	Evolutionary Dynamics of the 5S rDNA Gene Family in the Mussel <i>Mytilus</i> : Mixed Effects of Birth-and-Death and Concerted Evolution. <i>Journal of Molecular Evolution</i> , 2010, 70, 413-426.	0.8	35
31	Allelic Variation in Malawi Cichlid Opsins: A Tale of Two Genera. <i>Journal of Molecular Evolution</i> , 2010, 70, 593-604.	0.8	11
32	MHC evolution in three salmonid species: a comparison between class II alpha and beta genes. <i>Immunogenetics</i> , 2010, 62, 531-542.	1.2	31
33	MHC class I and MHC class II DRB gene variability in wild and captive Bengal tigers (<i>Panthera tigris</i>) Tj ETQq1 1 0.784314 rgBTj/Overlo	1.2	31
34	B chromosome ancestry revealed by histone genes in the migratory locust. <i>Chromosoma</i> , 2010, 119, 217-225.	1.0	65
35	Molecular and experimental evidence refuse the life cycle of <i>Proctoeces lintoni</i> (Fellodistomidae) in Chile. <i>Parasitology Research</i> , 2010, 106, 737-740.	0.6	17
36	Haplotype diversity and molecular evolution of the rice <i>Pikm</i> locus for blast resistance. <i>Journal of General Plant Pathology</i> , 2010, 76, 37-42.	0.6	9
37	Comparative Phylogeography of North American Atlantic Salt Marsh Communities. <i>Estuaries and Coasts</i> , 2010, 33, 828-839.	1.0	31

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38	Development of microsatellite markers from four Hawaiian corals: <i>Acropora cytherea</i> , <i>Fungia scutaria</i> , <i>Montipora capitata</i> and <i>Porites lobata</i> . <i>Conservation Genetics Resources</i> , 2010, 2, 11-15.	0.4	21
39	New primers for the amplification and sequencing of nuclear loci in a taxonomically wide set of reptiles and amphibians. <i>Conservation Genetics Resources</i> , 2010, 2, 181-185.	0.4	57
40	Genetic diversity and population structure of Marsh Grassbird (<i>Locustella pryeri sinensis</i>) in China. <i>Journal of Forestry Research</i> , 2010, 21, 361-366.	1.7	0
41	Mitochondrial DNA analysis reveals genetic structure in two New Zealand Cook's petrel (<i>Pterodroma</i>) Tj ETQq1_1_0.784314 rgBT (0.8)	0.8	19
42	Cryptic diversity and conservation units in the Bahama parrot. <i>Conservation Genetics</i> , 2010, 11, 1809-1821.	0.8	19
43	Conservation genetic inferences in the carnivorous pitcher plant <i>Sarracenia alata</i> (Sarraceniaceae). <i>Conservation Genetics</i> , 2010, 11, 2027-2038.	0.8	32
44	East-west genetic differentiation in Musk Ducks (<i>Biziura lobata</i>) of Australia suggests late Pleistocene divergence at the Nullarbor Plain. <i>Conservation Genetics</i> , 2010, 11, 2105-2120.	0.8	15
45	Mitochondrial DNA suggests independent evolutionary history and population decline of the Menzies's pipit (<i>Anthus [gustavi] menziesii</i>). <i>Conservation Genetics</i> , 2010, 11, 2419-2423.	0.8	0
46	Comparative analysis of iol clusters in <i>Lactobacillus casei</i> strains. <i>World Journal of Microbiology and Biotechnology</i> , 2010, 26, 1949-1955.	1.7	5
47	Nucleotide diversity of a ND5 fragment confirms that population expansion is the most suitable explanation for the mtDNA haplotype polymorphism of <i>Drosophila subobscura</i> . <i>Genetica</i> , 2010, 138, 819-829.	0.5	9
48	Genetic evidence of recent population contraction in the southernmost population of giant pandas. <i>Genetica</i> , 2010, 138, 1297-1306.	0.5	61
49	Phylogenetic network of <i>Linum</i> species as revealed by non-coding chloroplast DNA sequences. <i>Genetic Resources and Crop Evolution</i> , 2010, 57, 667-677.	0.8	60
50	A $\Delta 11$ desaturase gene genealogy reveals two divergent allelic classes within the European corn borer (<i>Ostrinia nubilalis</i>). <i>BMC Evolutionary Biology</i> , 2010, 10, 112.	3.2	6
51	Cryptic diversity of the bent-wing bat, <i>Miniopterus schreibersii</i> (Chiroptera: Vespertilionidae), in Asia Minor. <i>BMC Evolutionary Biology</i> , 2010, 10, 121.	3.2	31
52	Historical spatial range expansion and a very recent bottleneck of <i>Cinnamomum kanehirae</i> Hay. (Lauraceae) in Taiwan inferred from nuclear genes. <i>BMC Evolutionary Biology</i> , 2010, 10, 124.	3.2	60
53	The gene transformer-2 of <i>Anastrepha</i> fruit flies (Diptera, Tephritidae) and its evolution in insects. <i>BMC Evolutionary Biology</i> , 2010, 10, 140.	3.2	63
54	High amino acid diversity and positive selection at a putative coral immunity gene (tachylectin-2). <i>BMC Evolutionary Biology</i> , 2010, 10, 150.	3.2	31
55	Analysis of <i>Canis</i> mitochondrial DNA demonstrates high concordance between the control region and ATPase genes. <i>BMC Evolutionary Biology</i> , 2010, 10, 215.	3.2	23

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56	Phylogeography and population structure of the grape powdery mildew fungus, <i>Erysiphe necator</i> , from diverse <i>Vitis</i> species. <i>BMC Evolutionary Biology</i> , 2010, 10, 268.	3.2	117
57	Evidence for positive selection in the gene <i>fruitless</i> in <i>Anastrepha</i> fruit flies. <i>BMC Evolutionary Biology</i> , 2010, 10, 293.	3.2	16
58	When environmental changes do not cause geographic separation of fauna: differential responses of Baikalian invertebrates. <i>BMC Evolutionary Biology</i> , 2010, 10, 320.	3.2	11
59	Mito-nuclear genetic comparison in a <i>Wolbachia</i> infected weevil: insights on reproductive mode, infection age and evolutionary forces shaping genetic variation. <i>BMC Evolutionary Biology</i> , 2010, 10, 340.	3.2	27
60	Evolutionary history and molecular epidemiology of rabbit haemorrhagic disease virus in the Iberian Peninsula and Western Europe. <i>BMC Evolutionary Biology</i> , 2010, 10, 347.	3.2	45
61	Haplowebs as a graphical tool for delimiting species: a revival of Doyle's "field for recombination" approach and its application to the coral genus <i>Pocillopora</i> in Clipperton. <i>BMC Evolutionary Biology</i> , 2010, 10, 372.	3.2	123
62	Fine-scale genetic mapping of a hybrid sterility factor between <i>Drosophila simulans</i> and <i>D. mauritiana</i> : The varied and elusive functions of "speciation genes".. <i>BMC Evolutionary Biology</i> , 2010, 10, 385.	3.2	19
63	Two <i>Frequenins</i> in <i>Drosophila</i> : unveiling the evolutionary history of an unusual Neuronal Calcium Sensor (NCS) duplication. <i>BMC Evolutionary Biology</i> , 2010, 10, 54.	3.2	14
64	Genetic diversity, molecular phylogeny and selection evidence of the silkworm mitochondria implicated by complete resequencing of 41 genomes. <i>BMC Evolutionary Biology</i> , 2010, 10, 81.	3.2	40
65	Burst expansion, distribution and diversification of MITEs in the silkworm genome. <i>BMC Genomics</i> , 2010, 11, 520.	1.2	31
66	Duplication, divergence and persistence in the Phytochrome photoreceptor gene family of cottons (<i>Gossypium</i> spp.). <i>BMC Plant Biology</i> , 2010, 10, 119.	1.6	11
67	Genetic diversity in Tunisian rosy garlic populations (<i>Allium roseum</i> L.) as evidenced by chloroplastic DNA analysis: Sequence variation of non-coding region and intergenic spacers. <i>Biochemical Systematics and Ecology</i> , 2010, 38, 502-509.	0.6	4
68	Homogeneity of Powassan virus populations in naturally infected <i>Ixodes scapularis</i> . <i>Virology</i> , 2010, 402, 366-371.	1.1	26
69	Population genetics of <i>Homalodisca vitripennis</i> reovirus validates timing and limited introduction to California of its invasive insect host, the glassy-winged sharpshooter. <i>Virology</i> , 2010, 407, 53-59.	1.1	43
70	Alternative processing of scrambled genes generates protein diversity in the ciliate <i>Chilodonella uncinata</i> . <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2010, 314B, 480-488.	0.6	51
71	Limited genetic polymorphism of the <i>Plasmodium vivax</i> low molecular weight rhoptry protein complex in the Colombian population. <i>Infection, Genetics and Evolution</i> , 2010, 10, 261-267.	1.0	24
72	Lovesongs and period gene polymorphisms indicate <i>Lutzomyia cruzi</i> (Mangabeira, 1938) as a sibling species of the <i>Lutzomyia longipalpis</i> (Lutz and Neiva, 1912) complex. <i>Infection, Genetics and Evolution</i> , 2010, 10, 734-739.	1.0	37
73	Clonal origin of emerging populations of <i>Ehrlichia ruminantium</i> in Burkina Faso. <i>Infection, Genetics and Evolution</i> , 2010, 10, 903-912.	1.0	19

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74	Relating the liver damage with hepatitis C virus polymorphism in core region and human variables in HIV-1-coinfected patients. <i>Infection, Genetics and Evolution</i> , 2010, 10, 1252-1261.	1.0	3
75	A multiplex-PCR assay for the authentication of mackerels of the genus <i>Scomber</i> in processed fish products. <i>Food Chemistry</i> , 2010, 122, 319-326.	4.2	29
76	Molecular identification and pathology of <i>Anisakis pegreffii</i> (Nematoda: Anisakidae) infection in the Mediterranean loggerhead sea turtle (<i>Caretta caretta</i>). <i>Veterinary Parasitology</i> , 2010, 174, 65-71.	0.7	20
77	Mitochondrial DNA evidence for deep genetic divergences in allopatric populations of the rocky intertidal isopod <i>Ligia occidentalis</i> from the eastern Pacific. <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 468-473.	1.2	28
78	Slow worm, <i>Anguis fragilis</i> (Reptilia: Anguidae) as a species complex: Genetic structure reveals deep divergences. <i>Molecular Phylogenetics and Evolution</i> , 2010, 55, 460-472.	1.2	75
79	A molecular phylogenetic framework for the Muricidae, a diverse family of carnivorous gastropods. <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 1025-1039.	1.2	71
80	Phylogeography of the Middle Eastern tree frogs (<i>Hyla</i> , Hylidae, Amphibia) as inferred from nuclear and mitochondrial DNA variation, with a description of a new species. <i>Molecular Phylogenetics and Evolution</i> , 2010, 55, 1146-1166.	1.2	92
81	Phylogeography and molecular adaptation of Siberian salamander <i>Salamandrella keyserlingii</i> based on mitochondrial DNA variation. <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 562-571.	1.2	18
82	Conflicting patterns of nucleotide diversity between mtDNA and nDNA in the Moorish gecko, <i>Tarentola mauritanica</i> . <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 962-971.	1.2	64
83	Phylogeny and species boundaries of the endemic species complex, <i>Eliurus antsingy</i> and <i>E. carletoni</i> (Rodentia: Muridae: Nesomyidae), in Madagascar using mitochondrial and nuclear DNA sequence data. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 11-22.	1.2	6
84	Reticulate evolution, cryptic species, and character convergence in the core East Asian clade of <i>Gaultheria</i> (Ericaceae). <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 364-379.	1.2	35
85	Mitochondrial DNA structure of the Iberian populations of the white-clawed crayfish, <i>Austropotamobius italicus italicus</i> (Faxon, 1914). <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 327-342.	1.2	37
86	The differential effect of lowlands on the phylogeographic pattern of a Mesoamerican montane species (<i>Lepidocolaptes affinis</i> , Aves: Furnariidae). <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 658-668.	1.2	50
87	Lack of genetic structure in the jellyfish <i>Pelagia noctiluca</i> (Cnidaria: Scyphozoa: Semaestomeae) across European seas. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 417-428.	1.2	56
88	Inferring the demographic history of the Adriatic <i>Flexopecten</i> complex. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 942-947.	1.2	17
89	Species delimitation in the Central African herbs <i>Haumania</i> (Marantaceae) using georeferenced nuclear and chloroplastic DNA sequences. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 859-867.	1.2	20
90	Toward a resolution of a taxonomic enigma: First genetic analyses of <i>Paradoxornis webbianus</i> and <i>Paradoxornis alphonisianus</i> (Aves: Paradoxornithidae) from China and Italy. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 1312-1318.	1.2	7
91	Analysis of <i>vkorc1</i> polymorphisms in Norway rats using the roof rat as outgroup. <i>BMC Genetics</i> , 2010, 11, 43.	2.7	23

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92	Low linkage disequilibrium in wild <i>Anopheles gambiae</i> s.l. populations. <i>BMC Genetics</i> , 2010, 11, 81.	2.7	18
93	Contrasting population genetic patterns within the white-throated sparrow genome (<i>Zonotrichia</i>) Tj ETQq1 1 0.784314 rgBT/Overlo	2.7	27
94	Radiative evolution of polyploid races of the Iberian carnation <i>Dianthus broteri</i> (Caryophyllaceae). <i>New Phytologist</i> , 2010, 187, 542-551.	3.5	51
95	A Test of Seven Candidate Barcode Regions from the Plastome in <i>Picea</i> (Pinaceae). <i>Journal of Integrative Plant Biology</i> , 2010, 52, 1109-1126.	4.1	42
96	ELUCIDATION OF CRYPTIC DIVERSITY IN A WIDESPREAD NEARCTIC TREEFROG REVEALS EPISODES OF MITOCHONDRIAL GENE CAPTURE AS FROGS DIVERSIFIED ACROSS A DYNAMIC LANDSCAPE. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, no-no.	1.1	52
97	NUCLEAR AND MITOCHONDRIAL SEQUENCE DATA REVEAL AND CONCEAL DIFFERENT DEMOGRAPHIC HISTORIES AND POPULATION GENETIC PROCESSES IN CARIBBEAN REEF FISHES. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, 3380-3397.	1.1	65
98	RECONSTRUCTING ORIGINS OF LOSS OF SELF-INCOMPATIBILITY AND SELFING IN NORTH AMERICAN <i>ARABIDOPSIS LYRATA</i> : A POPULATION GENETIC CONTEXT. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, 3495-3510.	1.1	101
99	GENETIC ARCHITECTURE OF METABOLIC RATE: ENVIRONMENT SPECIFIC EPISTASIS BETWEEN MITOCHONDRIAL AND NUCLEAR GENES IN AN INSECT. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, 3354-3363.	1.1	146
100	Population mixing of <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> nodulating <i>Vicia faba</i> : the role of recombination and lateral gene transfer. <i>FEMS Microbiology Ecology</i> , 2010, 73, no-no.	1.3	65
101	Discovery of a breeding area of the enigmatic large-billed reed warbler <i>Acrocephalus orinus</i> . <i>Journal of Avian Biology</i> , 2010, 41, 452-459.	0.6	9
102	Northern glacial refugia for the pygmy shrew <i>Sorex minutus</i> in Europe revealed by phylogeographic analyses and species distribution modelling. <i>Ecography</i> , 2010, 33, 260-271.	2.1	24
103	High mitochondrial differentiation levels between wild and domestic Bactrian camels: a basis for rapid detection of maternal hybridization. <i>Animal Genetics</i> , 2010, 41, 315-318.	0.6	45
104	Analysis of the non-recombining Y chromosome defines polymorphisms in domestic pig breeds: ancestral bases identified by comparative sequencing. <i>Animal Genetics</i> , 2010, 41, 619-629.	0.6	16
105	Population genomic analysis of Tunisian <i>Medicago truncatula</i> reveals candidates for local adaptation. <i>Plant Journal</i> , 2010, 63, 623-635.	2.8	33
106	Cytoplasmic phylogeny and evidence of cyto-nuclear co-adaptation in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2010, 63, 728-738.	2.8	63
107	Ancient DNA reveals traces of Iberian Neolithic and Bronze Age lineages in modern Iberian horses. <i>Molecular Ecology</i> , 2010, 19, 64-78.	2.0	56
108	Nuclear gene phylogeography reveals the historical legacy of an ancient inland sea on lineages of the western pond turtle, <i>Emys marmorata</i> in California. <i>Molecular Ecology</i> , 2010, 19, 542-556.	2.0	44
109	Ultrassequencing of the meiofaunal biosphere: practice, pitfalls and promises. <i>Molecular Ecology</i> , 2010, 19, 4-20.	2.0	309

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110	Rejecting strictly allopatric speciation on a continental island: prolonged postdivergence gene flow between Taiwan (<i>Leucodioptron taewanus</i>), Passeriformes Timaliidae) and Chinese (<i>L. Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 7</i>)	2.0	10
111	Genomic diversity, population structure, and migration following rapid range expansion in the Balsam Poplar, <i>Populus balsamifera</i> . <i>Molecular Ecology</i> , 2010, 19, 1212-1226.	2.0	101
112	Ecological rather than geographical isolation dominates Quaternary formation of Mediterranean <i>Cistus</i> species. <i>Molecular Ecology</i> , 2010, 19, 1381-1395.	2.0	65
113	Population demography influences climatic niche evolution: evidence from diploid American <i>Hordeum</i> species (Poaceae). <i>Molecular Ecology</i> , 2010, 19, 1423-1438.	2.0	57
114	Molecular phylogeography of <i>Carapichea ipecacuanha</i> , an amphitropical shrub that occurs in the understory of both semideciduous and evergreen forests. <i>Molecular Ecology</i> , 2010, 19, 1410-1422.	2.0	15
115	Global population structure of the spiny dogfish <i>Squalus acanthias</i> , a temperate shark with an antitropical distribution. <i>Molecular Ecology</i> , 2010, 19, 1651-1662.	2.0	71
116	Phylogeography of Douglas-fir based on mitochondrial and chloroplast DNA sequences: testing hypotheses from the fossil record. <i>Molecular Ecology</i> , 2010, 19, 1877-1897.	2.0	83
117	Differential introgression causes genealogical discordance in host races of <i>Acrocercops transecta</i> (Insecta: Lepidoptera). <i>Molecular Ecology</i> , 2010, 19, 2106-2119.	2.0	17
118	Inter-specific gene flow dynamics during the Pleistocene-dated speciation of forest-dependent mosquitoes in Southeast Asia. <i>Molecular Ecology</i> , 2010, 19, 2269-2285.	2.0	44
119	Detection of recombinant haplotypes in wild mice (<i>Mus musculus</i>) provides new insights into the origin of Japanese mice. <i>Molecular Ecology</i> , 2010, 19, no-no.	2.0	31
120	The divergence of two independent lineages of an endemic Chinese gecko, <i>Gekko swinhonis</i> , launched by the Qinling orogenic belt. <i>Molecular Ecology</i> , 2010, 19, 2490-2500.	2.0	33
121	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. <i>Molecular Ecology</i> , 2010, 19, 3139-3156.	2.0	40
122	Seeing red: the origin of grain pigmentation in US weedy rice. <i>Molecular Ecology</i> , 2010, 19, 3380-3393.	2.0	79
123	Multilocus analysis of honeyeaters (Aves: Meliphagidae) highlights spatio-temporal heterogeneity in the influence of biogeographic barriers in the Australian monsoonal zone. <i>Molecular Ecology</i> , 2010, 19, 2980-2994.	2.0	76
124	Genetic diversity and differentiation at MHC genes in island populations of tuatara (<i>Sphenodon</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.0	114
125	Evidence for range stasis during the latter Pleistocene for the Atlantic Coastal Plain endemic genus, <i>Pyxidanthera Michaux</i> . <i>Molecular Ecology</i> , 2010, 19, 4302-4314.	2.0	13
126	Multiple hybridization events between <i>Drosophila simulans</i> and <i>Drosophila mauritiana</i> are supported by mtDNA introgression. <i>Molecular Ecology</i> , 2010, 19, 4695-4707.	2.0	37
127	Range-wide population genetic structure of the European bitterling (<i>Rhodeus amarus</i>) based on microsatellite and mitochondrial DNA analysis. <i>Molecular Ecology</i> , 2010, 19, 4708-4722.	2.0	54

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128	Plio-Pleistocene history of West African Sudanian savanna and the phylogeography of the <i>Praomys daltoni</i> complex (Rodentia): the environment/geography/genetic interplay. <i>Molecular Ecology</i> , 2010, 19, 4783-4799.	2.0	50
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488	Fitness effects of derived deleterious mutations in four closely related wild tomato species with spatial structure. <i>Heredity</i> , 2011, 107, 189-199.	1.2	30
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500	New universal <i>matK</i> primers for DNA barcoding angiosperms. <i>Journal of Systematics and Evolution</i> , 2011, 49, 176-181.	1.6	145
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797	Presence of Torque teno sus virus in porcine circovirus type 2 associated disease in Croatia. <i>Veterinary Record</i> , 2012, 171, 529-529.	0.2	5
798	Trans-Species Polymorphism and Allele-Specific Expression in the CBF Gene Family of Wild Tomatoes. <i>Molecular Biology and Evolution</i> , 2012, 29, 3641-3652.	3.5	40
799	Impact of Sampling Schemes on Demographic Inference: An Empirical Study in Two Species with Different Mating Systems and Demographic Histories. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 803-814.	0.8	10
800	Evidence for Population-Specific Positive Selection on Immune Genes of <i>Anopheles gambiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1505-1519.	0.8	18
802	Variation in Migratory Behavior Influences Regional Genetic Diversity and Structure among American Kestrel Populations (<i>Falco sparverius</i>) in North America. <i>Journal of Heredity</i> , 2012, 103, 503-514.	1.0	37
803	Distinctive Epstein-Barr Virus Variants Associated with Benign and Malignant Pediatric Pathologies: LMP1 Sequence Characterization and Linkage with Other Viral Gene Polymorphisms. <i>Journal of Clinical Microbiology</i> , 2012, 50, 609-618.	1.8	22
804	Genome-Wide Survey of Mutual Homologous Recombination in a Highly Sexual Bacterial Species. <i>Genome Biology and Evolution</i> , 2012, 4, 628-640.	1.1	34
805	Chromosomal Organization and Sequence Diversity of Genes Encoding Lachrymatory Factor Synthase in <i>Allium cepa</i> L.. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 643-651.	0.8	16
806	Diversity of the Cronobacter Genus as Revealed by Multilocus Sequence Typing. <i>Journal of Clinical Microbiology</i> , 2012, 50, 3031-3039.	1.8	171
807	Neutrality Tests for Sequences with Missing Data. <i>Genetics</i> , 2012, 191, 1397-1401.	1.2	38
808	Mitochondrial Gene Diversity Associated with the atp9 Stop Codon in Natural Populations of Wild Carrot (<i>Daucus carota</i> ssp. <i>carota</i>). <i>Journal of Heredity</i> , 2012, 103, 418-425.	1.0	21
809	Evolution of limpet assemblages driven by environmental changes and harvesting in North Iberia. <i>Marine Ecology - Progress Series</i> , 2012, 466, 121-131.	0.9	14
810	The Complete Mitochondrial Genome and Novel Gene Arrangement of the Unique-Headed Bug <i>Stenopirates</i> sp. (Hemiptera: Enicocephalidae). <i>PLoS ONE</i> , 2012, 7, e29419.	1.1	100
811	Alp, an Arthropod-Associated Outer Membrane Protein of <i>Borrelia</i> Species That Cause Relapsing Fever. <i>Infection and Immunity</i> , 2012, 80, 1881-1890.	1.0	14
812	Identification and Characterization of Psychrotolerant Sporeformers Associated with Fluid Milk Production and Processing. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1853-1864.	1.4	160
813	Differentiation of <i>Xylella fastidiosa</i> Strains via Multilocus Sequence Analysis of Environmentally Mediated Genes (MLSA-E). <i>Applied and Environmental Microbiology</i> , 2012, 78, 1385-1396.	1.4	28
814	Evolutionary and Functional Evidence for Positive Selection at the Human CD5 Immune Receptor Gene. <i>Molecular Biology and Evolution</i> , 2012, 29, 811-823.	3.5	20

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815	Population Structure and Genetic Diversity of the Boll Weevil (Coleoptera: Curculionidae) on <i>Gossypium</i> in North America. <i>Annals of the Entomological Society of America</i> , 2012, 105, 902-916.	1.3	17
816	Use of Massively Parallel Pyrosequencing to Evaluate the Diversity of and Selection on <i>Plasmodium falciparum</i> csp T-Cell Epitopes in Lilongwe, Malawi. <i>Journal of Infectious Diseases</i> , 2012, 206, 580-587.	1.9	51
817	Single-Nucleotide Polymorphisms for High-Throughput Genotyping of <i>Anopheles arabiensis</i> in East and Southern Africa. <i>Journal of Medical Entomology</i> , 2012, 49, 307-315.	0.9	10
818	Impact of pyrethroid resistance on operational malaria control in Malawi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19063-19070.	3.3	104
819	The heterogeneous levels of linkage disequilibrium in white spruce genes and comparative analysis with other conifers. <i>Heredity</i> , 2012, 108, 273-284.	1.2	61
820	mtDNA haplotypes differ in their probability of being eliminated by a mass die-off in an abundant seabird. <i>Heredity</i> , 2012, 109, 29-33.	1.2	9
821	Genetic Diversity within <i>Schistosoma haematobium</i> : DNA Barcoding Reveals Two Distinct Groups. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1882.	1.3	55
822	Genetic Structure of <i>Culex erraticus</i> Populations Across the Americas. <i>Journal of Medical Entomology</i> , 2012, 49, 522-534.	0.9	9
823	First Complete Mitochondrial Genome Sequence from a Box Jellyfish Reveals a Highly Fragmented Linear Architecture and Insights into Telomere Evolution. <i>Genome Biology and Evolution</i> , 2012, 4, 52-58.	1.1	57
824	Genetic evidence for glacial refugia of the temperate tree <i>Eucryphia cordifolia</i> (Cunoniaceae) in southern South America. <i>American Journal of Botany</i> , 2012, 99, 121-129.	0.8	23
825	Genetic diversity in human erythrocyte pyruvate kinase. <i>Genes and Immunity</i> , 2012, 13, 98-102.	2.2	23
826	Genetic diversity analysis of <i>Arius manillensis</i> (Siluriformes: Ariidae) using the mitochondrial control region. <i>Mitochondrial DNA</i> , 2012, 23, 45-52.	0.6	6
827	Population-based resequencing analysis of wild and cultivated barley revealed weak domestication signal of selection and bottleneck in the <i>Rrs2</i> scald resistance gene region. <i>Genome</i> , 2012, 55, 93-104.	0.9	23
828	Are the Great Plains wildrye (<i>Elymus canadensis</i>) and the Siberian wildrye (<i>Elymus sibiricus</i>) conspecific? A study based on the nuclear 5S rDNA sequences. <i>Botany</i> , 2012, 90, 407-421.	0.5	8
829	The importance of <i>Helicobacter pylori</i> 's genetic variability for the construction of an efficient vaccine. , 2012, , .		0
830	Investigation into genetic variability of Hazel Grouse <i>Bonasa bonasia</i> (= <i>Tetrastes bonasia</i>) population in Lithuania using non-invasive sampling. <i>Zoology and Ecology</i> , 2012, 22, 150-159.	0.2	0
831	Is There any Genetic Variation among Native Mexican and Argentinian Populations of <i>Dalbulus maidis</i> (Hemiptera: Cicadellidae)? <i>Florida Entomologist</i> , 2012, 95, 150-155.	0.2	18
832	Flowering Time in Maize: Linkage and Epistasis at a Major Effect Locus. <i>Genetics</i> , 2012, 190, 1547-1562.	1.2	75

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833	Phylogenetic and Coalescent Strategies of Species Delimitation in Snubnose Darters (Percidae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74	2.7	74
834	Impaired Auxin Biosynthesis in the <i>defective endosperm18</i> Mutant Is Due to Mutational Loss of Expression in the <i>ZmYuc1</i> Gene Encoding Endosperm-Specific YUCCA1 Protein in Maize Â Â Â. Plant Physiology, 2012, 160, 1318-1328.	2.3	128
835	Genetic Structure of <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> Populations in Michigan Commercial Tomato Fields. Plant Disease, 2012, 96, 788-796.	0.7	18
836	Conserved KIR allele-level haplotypes are altered by microvariation in individuals with European ancestry. Genes and Immunity, 2012, 13, 47-58.	2.2	25
837	Phylogeographic structure, outbreeding depression, and reluctant virgin oviposition in the bean thrips, <i>Caliothrips fasciatus</i> (Pergande) (Thysanoptera: Thripidae), in California. Bulletin of Entomological Research, 2012, 102, 698-709.	0.5	19
838	Tibet is one of the centers of domestication of cultivated barley. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16969-16973.	3.3	221
839	Population Genomics and Phylogeography of an Australian Dairy Factory Derived Lytic Bacteriophage. Genome Biology and Evolution, 2012, 4, 382-393.	1.1	36
840	Phylogeography and Demographic History of the Neotropical Otter (<i>Lontra longicaudis</i>). Journal of Heredity, 2012, 103, 479-492.	1.0	22
841	Phylogenetics inferred from mitogenome and control region of Silver Sillago, <i>Sillago sihama</i> . Mitochondrial DNA, 2012, 23, 255-263.	0.6	5
842	Phylogeny Estimation of the Radiation of Western North American Chipmunks (<i>Tamias</i>) in the Face of Introgression Using Reproductive Protein Genes. Systematic Biology, 2012, 61, 44.	2.7	55
843	Population Expanding with the Phalanx Model and Lineages Split by Environmental Heterogeneity: A Case Study of <i>Primula obconica</i> in Subtropical China. PLoS ONE, 2012, 7, e41315.	1.1	49
844	Genetic signatures of rafting dispersal in algal-dwelling brooders <i>Limnoria</i> spp. (Isopoda) along the SE Pacific (Chile). Marine Ecology - Progress Series, 2012, 455, 111-122.	0.9	29
845	Genetic variability and demographic history of <i>Heliiothis virescens</i> (Lepidoptera: Noctuidae) populations from Brazil inferred by mtDNA sequences. Bulletin of Entomological Research, 2012, 102, 333-343.	0.5	22
846	Recent Gene Duplication and Subfunctionalization Produced a Mitochondrial GrpE, the Nucleotide Exchange Factor of the Hsp70 Complex, Specialized in Thermotolerance to Chronic Heat Stress in <i>Arabidopsis</i> Â Â. Plant Physiology, 2012, 158, 747-758.	2.3	83
847	Character of chicken polymorphic major histocompatibility complex class II alleles of 3 Chinese local breeds. Poultry Science, 2012, 91, 1097-1104.	1.5	12
848	Inter- and Intraspecific Variation in <i>Drosophila</i> Genes with Sex-Biased Expression. International Journal of Evolutionary Biology, 2012, 2012, 1-10.	1.0	13
849	Glaciation Effects on the Phylogeographic Structure of <i>Oligoryzomys longicaudatus</i> (Rodentia: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 10	1.1	26
850	Differences in Selection Drive Olfactory Receptor Genes in Different Directions in Dogs and Wolf. Molecular Biology and Evolution, 2012, 29, 3475-3484.	3.5	30

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851	Extreme phenotypic variation in <i>Cetraria aculeata</i> (lichenized Ascomycota): adaptation or incidental modification?. <i>Annals of Botany</i> , 2012, 109, 1133-1148.	1.4	40
852	SAFE Software and FED Database to Uncover Protein-Protein Interactions using Gene Fusion Analysis. <i>Evolutionary Bioinformatics</i> , 2012, 8, EBO.S8018.	0.6	6
853	Evolution of the RALF Gene Family in Plants: Gene Duplication and Selection Patterns. <i>Evolutionary Bioinformatics</i> , 2012, 8, EBO.S9652.	0.6	70
854	Population genetic structure of golden pheasant <i>Chrysolophus pictus</i> in the Qinling Mountains, China. <i>Animal Biology</i> , 2012, 62, 231-243.	0.6	2
855	Investigating the Relationship between Topology and Evolution in a Dynamic Nematode Odor Genetic Network. <i>International Journal of Evolutionary Biology</i> , 2012, 2012, 1-8.	1.0	2
856	Selective Sweep of a cis-Regulatory Sequence in a Non-African Population of <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2012, 29, 1167-1174.	3.5	25
857	Rapid divergence and expansion of the X chromosome in papaya. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13716-13721.	3.3	52
858	Contrasting recombination patterns and demographic histories of the plant pathogen <i>Ralstonia solanacearum</i> inferred from MLSA. <i>ISME Journal</i> , 2012, 6, 961-974.	4.4	180
859	(Lack of) Genetic Diversity in Immune Genes Predates Glacial Isolation in the North American Mountain Goat (<i>Oreamnos americanus</i>). <i>Journal of Heredity</i> , 2012, 103, 371-379.	1.0	21
860	Comparative Genomics Reveals Adaptive Protein Evolution and a Possible Cytonuclear Incompatibility between European and American Eels. <i>Molecular Biology and Evolution</i> , 2012, 29, 2909-2919.	3.5	64
861	Host and Bacterial Phenotype Variation in Adhesion of <i>Streptococcus mutans</i> to Matched Human Hosts. <i>Infection and Immunity</i> , 2012, 80, 3869-3879.	1.0	22
862	Evolution of a Complex Disease Resistance Gene Cluster in Diploid and Tetraploid <i>Glycine</i> . <i>Plant Physiology</i> , 2012, 159, 336-354.	2.3	76
863	West-Central African Pleistocene lowland forest evolution revealed by the phylogeography of <i>Misonne</i> 's soft-furred mouse. <i>African Zoology</i> , 2012, 47, 100-112.	0.2	11
864	Hog-Nosed Skunks (<i>Conepatus leuconotus</i>) Along the Gulf of Mexico: Population Status and Genetic Diversity. <i>Southwestern Naturalist</i> , 2012, 57, 223-225.	0.1	0
865	New penicillin-producing <i>Penicillium</i> species and an overview of section <i>Chrysogena</i> . <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2012, 29, 78-100.	1.6	123
866	Genetic diversity of <i>Monoporeia affinis</i> in relationship to environmental and spatial factors in Sweden's largest lakes. <i>Fundamental and Applied Limnology</i> , 2012, 181, 183-195.	0.4	6
867	ADOPS - Automatic Detection Of Positively Selected Sites. <i>Journal of Integrative Bioinformatics</i> , 2012, 9, 18-32.	1.0	17
868	Genetic Diversity of <i>Lymantria Dispar</i> Linnaeus (Lepidoptera: Lymantriidae) in Northern Greece and Evaluation of the Effectiveness of Novel Insecticides. <i>Biotechnology and Biotechnological Equipment</i> , 2012, 26, 2976-2980.	0.5	3

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869	DNA Barcodes and Insights into the Relationships and Systematics of Buckeye Butterflies (Nymphalidae): Tj ETQq0 0 0 rgBT /Qverlock 10	0.0	20
870	Cryptic diversity of the acrothoracican barnacle <i>Armatoglyptes taiwanus</i> in the Indo-Pacific waters, with description of a new species from the Mozambique Channel collected from the MAINBAZA cruise. <i>Zoosystema</i> , 2012, 34, 5-20.	0.2	6
871	Statistical phylogeographic tests of competing 'Lake Carpentaria hypotheses' in the mouth-brooding freshwater fish, <i>Glossamia aprion</i> (Apogonidae). <i>Marine and Freshwater Research</i> , 2012, 63, 450.	0.7	12
872	Population genetic structure, coloration, and morphometrics of yellowhead jawfish <i>Opistognathus aurifrons</i> (Perciformes: Opistognathidae) in the Caribbean region. <i>Marine Ecology - Progress Series</i> , 2012, 444, 275-287.	0.9	8
873	Genetic differentiation of the neon flying squid <i>Ommastrephes bartramii</i> between North Pacific and South Atlantic populations. <i>Nippon Suisan Gakkaishi</i> , 2012, 78, 198-203.	0.0	4
874	Little gene flow between domestic silkmoth <i>Bombyx mori</i> and its wild relative <i>Bombyx mandarina</i> in Japan, and possible artificial selection on the <i>CAD</i> gene of <i>B. mori</i>. <i>Genes and Genetic Systems</i> , 2012, 87, 331-340.	0.2	9
875	Cloning and Sequence Analysis of the Circadian Clock Genes <i>period</i> and <i>timeless</i> in <i>Aedes albopictus</i> (Diptera: Culicidae). <i>Journal of Medical Entomology</i> , 2012, 49, 777-782.	0.9	11
876	Extensive variation in surface lipoprotein gene content and genomic changes associated with virulence during evolution of a novel North American house finch epizootic strain of <i>Mycoplasma gallisepticum</i> . <i>Microbiology (United Kingdom)</i> , 2012, 158, 2073-2088.	0.7	43
877	A Remarkable Case of Micro-Endemism in <i>Laonastes aenigmamus</i> (Diatomyidae, Rodentia) Revealed by Nuclear and Mitochondrial DNA Sequence Data. <i>PLoS ONE</i> , 2012, 7, e48145.	1.1	15
878	CONCORDANCE BETWEEN GENETIC AND SPECIES DIVERSITY IN CORAL REEF FISHES ACROSS THE PACIFIC OCEAN BIODIVERSITY GRADIENT. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 3902-3917.	1.1	29
879	Phylogenetics and population genetics of the Eurasian parasitoid <i>M</i><i>acrocentrus cingulum</i> based on mitochondrial and nuclear loci. <i>Entomologia Experimentalis Et Applicata</i> , 2012, 145, 1-14.	0.7	4
880	Two genetically distinct stocks in Baird's beaked whale (Cetacea: Ziphiidae). <i>Marine Mammal Science</i> , 2013, 29, 755-766.	0.9	9
881	Re-examination of Population Structure and Phylogeography of Hawksbill Turtles in the Wider Caribbean Using Longer mtDNA Sequences. <i>Journal of Heredity</i> , 2012, 103, 806-820.	1.0	58
882	Life history and biogeographic diversification of an endemic western North American freshwater fish clade using a comparative species tree approach. <i>Molecular Phylogenetics and Evolution</i> , 2012, 65, 940-952.	1.2	15
883	Patterns of Molecular Evolution of an Avian Neo-sex Chromosome. <i>Molecular Biology and Evolution</i> , 2012, 29, 3741-3754.	3.5	26
884	Refugia within refugia as a key to disentangle the genetic pattern of a highly variable species: The case of <i>Rana temporaria</i> Linnaeus, 1758 (Anura, Ranidae). <i>Molecular Phylogenetics and Evolution</i> , 2012, 65, 718-726.	1.2	21
885	Selected mitochondrial genes as species markers of the Arctic <i>Contracecum osculatum</i> complex. <i>Journal of Helminthology</i> , 2012, 86, 252-258.	0.4	7
886	Mitochondrial genome variability within the <i>Candida parapsilosis</i> species complex. <i>Mitochondrion</i> , 2012, 12, 514-519.	1.6	20

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887	Phylogeographic Study of <i>Apodemus ilex</i> (Rodentia: Muridae) in Southwest China. PLoS ONE, 2012, 7, e31453.	1.1	39
888	Genetic characterization of the endangered and endemic anchialine squat lobster <i>Munidopsis polymorpha</i> from Lanzarote (Canary Islands): management implications. ICES Journal of Marine Science, 2012, 69, 1030-1037.	1.2	10
889	Genetic structure and connectivity patterns of two Caribbean rocky-intertidal gastropods. Journal of Molluscan Studies, 2012, 78, 112-118.	0.4	16
890	High Degree of Mitochondrial Haplotype Diversity in the Japanese Common Toad <i>Bufo japonicus</i> in Urban Tokyo. Zoological Science, 2012, 29, 702.	0.3	10
891	Comparative Phylogeography of Direct-Developing Frogs (Anura: Craugastoridae: Pristimantis) in the Southern Andes of Colombia. PLoS ONE, 2012, 7, e46077.	1.1	27
892	A Genetic Approach to Spanish Populations of the Threatened <i>Austropotamobius italicus</i> Located at Three Different Scenarios. Scientific World Journal, The, 2012, 2012, 1-9.	0.8	5
893	Maternal Lineages in Native Canadian Equine Populations and Their Relationship to the Nordic and Mountain and Moorland Pony Breeds. Journal of Heredity, 2012, 103, 380-390.	1.0	19
894	Biogeographically dynamic genetic structure bridging two continents in the monotypic Central American rodent <i>Ototylomys phyllotis</i> . Biological Journal of the Linnean Society, 2012, 107, 593-610.	0.7	39
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896	Comparative biogeography reveals differences in population genetic structure of five species of stream fishes. Biological Journal of the Linnean Society, 2012, 107, 867-885.	0.7	38
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898	Cryptic species in <i>Iphisa elegans</i> Gray, 1851 (Squamata: Gymnophthalmidae) revealed by hemipenial morphology and molecular data. Zoological Journal of the Linnean Society, 2012, 166, 361-376.	1.0	70
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900	Population genetic structure and its implications for adaptive variation in memory and the hippocampus on a continental scale in food-eating black-capped chickadees. Molecular Ecology, 2012, 21, 4486-4497.	2.0	17
901	Genetic isolation within the malaria mosquito <i>Anopheles melas</i> . Molecular Ecology, 2012, 21, 4498-4513.	2.0	17
902	Functional diversity of Teleost arylalkylamine N-acetyltransferase: is the enzyme evolution driven by habitat temperature?. Molecular Ecology, 2012, 21, 5027-5041.	2.0	13
903	Speciation history of three closely related oak gall wasps, <i>Andricus mukaigawae</i> , <i>A. kashiwaphilus</i> , and <i>A. pseudoflos</i> (Hymenoptera: Cynipidae) inferred from nuclear and mitochondrial DNA sequences. Molecular Ecology, 2012, 21, 4681-4694.	2.0	5
904	Influences of past climatic changes on historical population structure and demography of a cosmopolitan marine predator, the common dolphin (genus <i>Delphinus</i>). Molecular Ecology, 2012, 21, 4854-4871.	2.0	43

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906	Small body size increases the regional differentiation of populations of tropical mantellid frogs (<i>Aurelia antellidae</i>). <i>Journal of Evolutionary Biology</i> , 2012, 25, 2310-2324.	0.8	58
907	The Genetic Structure of Populations of <i>Potato virus Y</i> in Japan; Based on the Analysis of 20 Full Genomic Sequences. <i>Journal of Phytopathology</i> , 2012, 160, 661-673.	0.5	42
908	Molecular substitution rate increases in myrmecophilous lycaenid butterflies (Lepidoptera). <i>Zoologica Scripta</i> , 2012, 41, 651-658.	0.7	17
909	Intraspecific variation in mitochondrial genome sequence, structure, and gene content in <i>Silene vulgaris</i> , an angiosperm with pervasive cytoplasmic male sterility. <i>New Phytologist</i> , 2012, 196, 1228-1239.	3.5	108
910	Testing for hybridization and assessing genetic diversity in Morelet's crocodile (<i>Crocodylus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 15	0.8	15
911	<i>Colpomenia durvillei</i> (Scytosiphonaceae, Phaeophyceae): its distribution and relationships with other elongate species of the genus. <i>Botanica Marina</i> , 2012, 55, 367-375.	0.6	4
912	Characterization of West Nile Viruses Isolated from Captive American Flamingoes (<i>Phoenicopterus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 21	0.6	21
913	Diversity and linkage disequilibrium features in a composite public/private dent maize panel: consequences for association genetics as evaluated from a case study using flowering time. <i>Theoretical and Applied Genetics</i> , 2012, 125, 731-747.	1.8	13
914	Comparing apples with apples: clarifying the identities of two highly invasive Neotropical Ampullariidae (Caenogastropoda). <i>Zoological Journal of the Linnean Society</i> , 2012, 166, 723-753.	1.0	147
915	High divergence levels of <i>Panonychus citri</i> populations on Rutaceae and Oleaceae as indicated by internal transcribed spacer 1 (ITS1) sequences. <i>International Journal of Acarology</i> , 2012, 38, 66-73.	0.3	0
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917	Contrasting Patterns of X/Y Polymorphism Distinguish <i>Carica papaya</i> from Other Sex Chromosome Systems. <i>Molecular Biology and Evolution</i> , 2012, 29, 3909-3920.	3.5	16
918	Miocene and Pliocene dominated diversification of the lichen-forming fungal genus <i>Melanohalea</i> (Parmeliaceae, Ascomycota) and Pleistocene population expansions. <i>BMC Evolutionary Biology</i> , 2012, 12, 176.	3.2	62
919	Phylogenetic footprints of an Antarctic radiation: The Trematominae (Notothenioidei, Teleostei). <i>Molecular Phylogenetics and Evolution</i> , 2012, 65, 87-101.	1.2	31
920	Cryptic speciation in the field vole: a multilocus approach confirms three highly divergent lineages in <i>Eurostoma</i> . <i>Molecular Ecology</i> , 2012, 21, 6015-6032.	2.0	59
921	Genetic and Reproductive Evidence of Natural Hybridization between the Sister Species <i>Rhinella atacamensis</i> and <i>Rhinella arunco</i> (Anura, Bufonidae). <i>Journal of Herpetology</i> , 2012, 46, 568-577.	0.2	5
922	Does high intraspecific variability of two genome fragments indicate a recent speciation process of <i>Paramecium dodecaurelia</i> (<i>P. aurelia</i>) species complex, Ciliophora, Protozoa?. <i>Systematics and Biodiversity</i> , 2012, 10, 289-304.	0.5	4

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924	Congruence Between Acoustic Traits and Genealogical History Reveals a New Species of <i>Dendropsophus</i> (Anura: Hylidae) in the High Andes of Colombia. <i>Herpetologica</i> , 2012, 68, 523-540.	0.2	22
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1054	Conservation genetics of harvested river turtles, <i>Podocnemis expansa</i> and <i>Podocnemis unifilis</i> , in the Peruvian Amazon: All roads lead to Iquitos. <i>Mitochondrial DNA</i> , 2012, 23, 230-238.	0.6	9
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1056	Pronounced genetic structure and low genetic diversity in European red-billed chough (<i>Pyrrhocorax</i>)	0.8	25
1057	Glacial refugium versus range limit: Conservation genetics of <i>Macoma balthica</i> , a key species in the Bay of Biscay (France). <i>Journal of Experimental Marine Biology and Ecology</i> , 2012, 432-433, 73-82.	0.7	18
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1059	Geographic variation and molecular evidence of the Blackish Deer Mouse complex (<i>Peromyscus</i>)	0.8	9
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1084	Population structure of <i>Bactrocera dorsalis</i> s.s., <i>B. papayae</i> and <i>B. philippinensis</i> (Diptera: Tephritidae) in southeast Asia: evidence for a single species hypothesis using mitochondrial DNA and wing-shape data. <i>BMC Evolutionary Biology</i> , 2012, 12, 130.	3.2	75

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1089	Phylogenetic relationships among <i>Staphylococcus</i> species and refinement of cluster groups based on multilocus data. <i>BMC Evolutionary Biology</i> , 2012, 12, 171.	3.2	88
1090	Population-genetic analysis of HvABCG31 promoter sequence in wild barley (<i>Hordeum vulgare</i> ssp.) Tj ETQq1 1 0.784314 rgBT /Overl	3.2	11
1091	Evidence for 5S rDNA Horizontal Transfer in the toadfish <i>Halobatrachus didactylus</i> (Schneider, 1801) based on the analysis of three multigene families. <i>BMC Evolutionary Biology</i> , 2012, 12, 201.	3.2	27
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1105	DNA variation in the phenotypically-diverse brown alga <i>Saccharina japonica</i> . <i>BMC Plant Biology</i> , 2012, 12, 108.	1.6	25
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1113	Comparison of intraspecific genetic structure among related chironomids (Diptera) from New Zealand and Patagonia: disparity between potential and realized dispersal. <i>Freshwater Science</i> , 2012, 31, 1105-1120.	0.9	4
1114	Highly conserved d-loop sequences in woolly mouse opossums <i>Marmosa</i> (<i>Micoureus</i>). <i>Mitochondrial DNA</i> , 2012, 23, 77-83.	0.6	1
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1116	Biogeographical Study of Plateau Pikas <i>Ochotona curzoniae</i> (<i>Lagomorpha</i> , <i>Ochotonidae</i>). <i>Zoological Science</i> , 2012, 29, 518-526.	0.3	15
1117	Genetic divergence, range expansion and possible homoploid hybrid speciation among pine species in Northeast China. <i>Heredity</i> , 2012, 108, 552-562.	1.2	46
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1155	MHC polymorphism and disease-resistance to <i>Edwardsiella tarda</i> in six turbot (<i>Scophthalmus</i>) Tj ETQq1 1 0.784314 1.7 BT /Ovrlock 10		
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1160	High Degree of Single Nucleotide Polymorphisms in California <i>Culex pipiens</i> (Diptera: Culicidae) sensu lato. <i>Journal of Medical Entomology</i> , 2012, 49, 299-306.	0.9	15
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1170	The origin and genetic variability of the Czech sika deer population. <i>Ecological Research</i> , 2012, 27, 991-1003.	0.7	17
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1176	Natural Variation in a Chloride Channel Subunit Confers Avermectin Resistance in <i>C. elegans</i> . <i>Science</i> , 2012, 335, 574-578.	6.0	160
1177	Mitochondrial and nuclear markers reveal a lack of genetic structure in the entocommensal nemertean <i>Malacobdella arrokeana</i> in the Patagonian gulfs. <i>Helgoland Marine Research</i> , 2013, 67, 407-412.	1.3	7
1178	Molecular Signatures Identify a Candidate Target of Balancing Selection in an <i>arcD</i> -Like Gene of <i>Staphylococcus epidermidis</i> . <i>Journal of Molecular Evolution</i> , 2012, 75, 43-54.	0.8	10
1179	Comparative Nucleotide Diversity Across North American and European <i>Populus</i> Species. <i>Journal of Molecular Evolution</i> , 2012, 74, 257-272.	0.8	25
1180	Delimiting genetic units in Neotropical toads under incomplete lineage sorting and hybridization. <i>BMC Evolutionary Biology</i> , 2012, 12, 242.	3.2	31
1181	MHC class II DQB diversity in the Japanese black bear, <i>Ursus thibetanus japonicus</i> . <i>BMC Evolutionary Biology</i> , 2012, 12, 230.	3.2	17
1182	Molecular evolution and phylogenetics of rodent malaria parasites. <i>BMC Evolutionary Biology</i> , 2012, 12, 219.	3.2	33
1183	Male-killing <i>Wolbachia</i> and mitochondrial selective sweep in a migratory African insect. <i>BMC Evolutionary Biology</i> , 2012, 12, 204.	3.2	33
1184	Phylogenetic analysis of a gene cluster encoding an additional, rhizobial-like type III secretion system that is narrowly distributed among <i>Pseudomonas syringae</i> strains. <i>BMC Microbiology</i> , 2012, 12, 188.	1.3	49
1185	Genetic polymorphism and natural selection in the C-terminal 42 kDa region of merozoite surface protein-1 among <i>Plasmodium vivax</i> Korean isolates. <i>Malaria Journal</i> , 2012, 11, 206.	0.8	26
1186	Genetic population structure of the malaria vector <i>Anopheles baimaii</i> in north-east India using mitochondrial DNA. <i>Malaria Journal</i> , 2012, 11, 76.	0.8	21
1187	Genetic diversity and population structure of genes encoding vaccine candidate antigens of <i>Plasmodium vivax</i> . <i>Malaria Journal</i> , 2012, 11, 68.	0.8	46
1188	Genetic polymorphism and natural selection of Duffy binding protein of <i>Plasmodium vivax</i> Myanmar isolates. <i>Malaria Journal</i> , 2012, 11, 60.	0.8	29
1189	Deep evolutionary lineages in a Western Mediterranean snake (<i>Vipera latastei/monticola</i> group) and high genetic structuring in Southern Iberian populations. <i>Molecular Phylogenetics and Evolution</i> , 2012, 65, 965-973.	1.2	39
1190	Genetic characterization of Chikungunya virus from New Delhi reveal emergence of a new molecular signature in Indian isolates. <i>Virology Journal</i> , 2012, 9, 100.	1.4	77
1191	Rapid Evolution of Enormous, Multichromosomal Genomes in Flowering Plant Mitochondria with Exceptionally High Mutation Rates. <i>PLoS Biology</i> , 2012, 10, e1001241.	2.6	480
1192	A Role in Immunity for <i>Arabidopsis</i> Cysteine Protease RD21, the Ortholog of the Tomato Immune Protease C14. <i>PLoS ONE</i> , 2012, 7, e29317.	1.1	120
1193	A Dig into the Past Mitochondrial Diversity of Corsican Goats Reveals the Influence of Secular Herding Practices. <i>PLoS ONE</i> , 2012, 7, e30272.	1.1	10

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1194	Sequence Polymorphism, Segmental Recombination and Toggling Amino Acid Residues within the DBL3X Domain of the VAR2CSA Placental Malaria Antigen. <i>PLoS ONE</i> , 2012, 7, e31565.	1.1	12
1195	Phylogeography of Sardinian Cave Salamanders (Genus <i>Hydromantes</i>) Is Mainly Determined by Geomorphology. <i>PLoS ONE</i> , 2012, 7, e32332.	1.1	37
1196	Invasion Genetics of the Western Flower Thrips in China: Evidence for Genetic Bottleneck, Hybridization and Bridgehead Effect. <i>PLoS ONE</i> , 2012, 7, e34567.	1.1	55
1197	Complete Mitochondrial Genome Sequencing Reveals Novel Haplotypes in a Polynesian Population. <i>PLoS ONE</i> , 2012, 7, e35026.	1.1	23
1198	Molecular Systematic of Three Species of <i>Oithona</i> (Copepoda, Cyclopoida) from the Atlantic Ocean: Comparative Analysis Using 28S rDNA. <i>PLoS ONE</i> , 2012, 7, e35861.	1.1	27
1199	The Origin of the "Mycoplasma mycoides Cluster" Coincides with Domestication of Ruminants. <i>PLoS ONE</i> , 2012, 7, e36150.	1.1	76
1200	Evolution of Neutral and Flowering Genes along Pearl Millet (<i>Pennisetum glaucum</i>) Domestication. <i>PLoS ONE</i> , 2012, 7, e36642.	1.1	11
1201	Selective Enrichment and Sequencing of Whole Mitochondrial Genomes in the Presence of Nuclear Encoded Mitochondrial Pseudogenes (Numts). <i>PLoS ONE</i> , 2012, 7, e37142.	1.1	31
1202	Great Genetic Differentiation among Populations of <i>Meconopsis integrifolia</i> and Its Implication for Plant Speciation in the Qinghai-Tibetan Plateau. <i>PLoS ONE</i> , 2012, 7, e37196.	1.1	77
1203	Population Structure and Gene Flow of the Yellow Anaconda (<i>Eunectes notaeus</i>) in Northern Argentina. <i>PLoS ONE</i> , 2012, 7, e37473.	1.1	10
1204	Is Promiscuity Associated with Enhanced Selection on MHC-DQ α in Mice (genus <i>Peromyscus</i>)?. <i>PLoS ONE</i> , 2012, 7, e37562.	1.1	12
1205	Phylogeography of the South China Field Mouse (<i>Apodemus draco</i>) on the Southeastern Tibetan Plateau Reveals High Genetic Diversity and Glacial Refugia. <i>PLoS ONE</i> , 2012, 7, e38184.	1.1	35
1206	Molecular Phylogeny and Phylogeography of the Australian Freshwater Fish Genus <i>Galaxiella</i> , with an Emphasis on Dwarf <i>Galaxias</i> (<i>G. pusilla</i>). <i>PLoS ONE</i> , 2012, 7, e38433.	1.1	39
1207	Multi-Locus Phylogeographic and Population Genetic Analysis of <i>Anolis carolinensis</i> : Historical Demography of a Genomic Model Species. <i>PLoS ONE</i> , 2012, 7, e38474.	1.1	40
1208	Genetic Connectivity between North and South Mid-Atlantic Ridge Chemosynthetic Bivalves and Their Symbionts. <i>PLoS ONE</i> , 2012, 7, e39994.	1.1	31
1209	A Genomic Island in <i>Salmonella enterica</i> ssp. <i>salamae</i> Provides New Insights on the Genealogy of the Locus of Enterocyte Effacement. <i>PLoS ONE</i> , 2012, 7, e41615.	1.1	14
1210	Multiple SNP Markers Reveal Fine-Scale Population and Deep Phylogeographic Structure in European Anchovy (<i>Engraulis encrasicolus</i> L.). <i>PLoS ONE</i> , 2012, 7, e42201.	1.1	60
1211	Fixed Differences in the paralytic Gene Define Two Lineages within the <i>Lutzomyia longipalpis</i> Complex Producing Different Types of Courtship Songs. <i>PLoS ONE</i> , 2012, 7, e44323.	1.1	18

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1212	A European Melting Pot of Harbour Porpoise in the French Atlantic Coasts Inferred from Mitochondrial and Nuclear Data. <i>PLoS ONE</i> , 2012, 7, e44425.	1.1	20
1213	Variation at Innate Immunity Toll-Like Receptor Genes in a Bottlenecked Population of a New Zealand Robin. <i>PLoS ONE</i> , 2012, 7, e45011.	1.1	62
1214	Natural or Naturalized? Phylogeography Suggests That the Abundant Sea Urchin <i>Arbacia lixula</i> Is a Recent Colonizer of the Mediterranean. <i>PLoS ONE</i> , 2012, 7, e45067.	1.1	45
1215	Reconstruction of the Evolutionary History of <i>Saccharomyces cerevisiae</i> x <i>S. kudriavzevii</i> Hybrids Based on Multilocus Sequence Analysis. <i>PLoS ONE</i> , 2012, 7, e45527.	1.1	28
1216	Multi-Gene Analysis Reveals a Lack of Genetic Divergence between <i>Calanus agulhensis</i> and <i>C. sinicus</i> (Copepoda; Calanoida). <i>PLoS ONE</i> , 2012, 7, e45710.	1.1	18
1217	Genome Sequencing and Phylogenetic Analysis of 39 Human Parainfluenza Virus Type 1 Strains Isolated from 1997a€“2010. <i>PLoS ONE</i> , 2012, 7, e46048.	1.1	20
1218	Tough Adults, Frail Babies: An Analysis of Stress Sensitivity across Early Life-History Stages of Widely Introduced Marine Invertebrates. <i>PLoS ONE</i> , 2012, 7, e46672.	1.1	84
1219	Interpreting the Process behind Endemism in China by Integrating the Phylogeography and Ecological Niche Models of the <i>Stachyridopsis ruficeps</i> . <i>PLoS ONE</i> , 2012, 7, e46761.	1.1	29
1220	The Roles of Gene Duplication, Gene Conversion and Positive Selection in Rodent <i>Esp</i> and <i>Mup</i> Pheromone Gene Families with Comparison to the <i>Abp</i> Family. <i>PLoS ONE</i> , 2012, 7, e47697.	1.1	13
1221	Patterns of Deep-Sea Genetic Connectivity in the New Zealand Region: Implications for Management of Benthic Ecosystems. <i>PLoS ONE</i> , 2012, 7, e49474.	1.1	36
1222	Phylogeography of Bivalve <i>Cyclina sinensis</i> : Testing the Historical Glaciations and Changjiang River Outflow Hypotheses in Northwestern Pacific. <i>PLoS ONE</i> , 2012, 7, e49487.	1.1	59
1223	Assessing the Genetic Influence of Ancient Sociopolitical Structure: Micro-differentiation Patterns in the Population of Asturias (Northern Spain). <i>PLoS ONE</i> , 2012, 7, e50206.	1.1	9
1224	<i>Desmophyllum dianthus</i> (Esper, 1794) in the Scleractinian Phylogeny and Its Intraspecific Diversity. <i>PLoS ONE</i> , 2012, 7, e50215.	1.1	30
1225	Untangling Nucleotide Diversity and Evolution of the H Genome in Polyploid <i>Hordeum</i> and <i>Elymus</i> Species Based on the Single Copy of Nuclear Gene <i>DMC1</i> . <i>PLoS ONE</i> , 2012, 7, e50369.	1.1	9
1226	Evolutionary Genomics of Transposable Elements in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2012, 7, e50978.	1.1	91
1227	Mitochondrial DNA Evidence Indicates the Local Origin of Domestic Pigs in the Upstream Region of the Yangtze River. <i>PLoS ONE</i> , 2012, 7, e51649.	1.1	21
1228	Impact of Vector Dispersal and Host-Plant Fidelity on the Dissemination of an Emerging Plant Pathogen. <i>PLoS ONE</i> , 2012, 7, e51809.	1.1	53
1229	Unusual Symbiotic Cyanobacteria Association in the Genetically Diverse Intertidal Marine Sponge <i>Hymeniacidon perlevis</i> (Demospongiae, Halichondrida). <i>PLoS ONE</i> , 2012, 7, e51834.	1.1	34

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1230	Phylogeographical Analysis of mtDNA Data Indicates Postglacial Expansion from Multiple Glacial Refugia in Woodland Caribou (<i>Rangifer tarandus caribou</i>). <i>PLoS ONE</i> , 2012, 7, e52661.	1.1	40
1231	Variable Regions of PI4P 5-Kinases Direct PtdIns(4,5)P ₂ Toward Alternative Regulatory Functions in Tobacco Pollen Tubes. <i>Frontiers in Plant Science</i> , 2011, 2, 114.	1.7	38
1232	Effects of <i>Wolbachia</i> on rDNA-ITS2 variation and evolution in natural populations of <i>Tetranychus urticae</i> Koch. <i>Systematic and Applied Acarology</i> , 2012, 17, .	0.5	0
1234	Distribution, Abundance, and Diversity Patterns of the Thermoacidophilic Deep-Sea Hydrothermal Vent Euryarchaeota. <i>Frontiers in Microbiology</i> , 2012, 3, 47.	1.5	32
1235	Linkage disequilibrium approaches for detecting hybrid zone movement. , 0, , 504-518.		0
1236	Pattern of Genetic Divergence of Mitochondrial DNA Sequences in <i>Biomphalaria tenagophila</i> Complex Species Based on Barcode and Morphological Analysis. , 2012, , .		10
1237	Phylogenetic position and taxonomy of <i>Cycloseris explanulata</i> and <i>C. wellsii</i> (Scleractinia: Fungiidae): lost mushroom corals find their way home. <i>Contributions To Zoology</i> , 2012, 81, 125-146.	0.2	84
1238	Revision of the little brown frogs in the <i>Gephyromantis decaryi</i> complex with description of a new species. <i>Zootaxa</i> , 2012, 3421, 32.	0.2	5
1239	Detection of <i>Crocodylus mindorensis</i> x <i>Crocodylus porosus</i> (Crocodylidae) hybrids in a Philippine crocodile systematics analysis. <i>Zootaxa</i> , 2012, 3560, 1.	0.2	5
1240	<i>Hydrophis donaldi</i> (Elapidae, Hydrophiinae), a highly distinctive new species of sea snake from northern Australia. <i>Zootaxa</i> , 2012, 3201, 45.	0.2	10
1241	Molecular phylogeny of Asiatic Short-Tailed Shrews, genus <i>Blarinella</i> Thomas, 1911 (Mammalia: Sorex). <i>Journal of Biogeography</i> , 2012, 39, 1015-1023.	0.2	18
1242	Genetic and shell-shape analyses of <i>Orlitia borneensis</i> (Testudines: Geoemydidae) reveal limited divergence among founders of the European zoo population. <i>Zootaxa</i> , 2012, 3280, 56.	0.2	1
1243	<i>Anterastes davrazensis</i> sp. n. (Orthoptera, Tettigoniidae): morphology, song and 16S rDNA phylogeny. <i>Zootaxa</i> , 2012, 3401, 49.	0.2	4
1244	A new species of <i>Crinia</i> (Anura: Myobatrachidae) from the Flinders Ranges, South Australia. <i>Zootaxa</i> , 2012, 3499, 1.	0.2	1
1245	<i>Aipysurus mosaicus</i> , a new species of egg-eating sea snake (Elapidae: Hydrophiinae), with a redescription of <i>Aipysurus eydouxii</i> (Gray, 1849). <i>Zootaxa</i> , 2012, 3431, 1.	0.2	9
1246	Nucleotide variation in the mitochondrial genome provides evidence for dual routes of postglacial recolonization and genetic recombination in the northeastern brook trout (<i>Salvelinus fontinalis</i>). <i>Genetics and Molecular Research</i> , 2012, 11, 3466-3481.	0.3	7
1247	Genetic diversity of ITS sequences of <i>Bursaphelenchus xylophilus</i> . <i>Genetics and Molecular Research</i> , 2012, 11, 4508-4515.	0.3	13
1248	Genetic structure of a Brazilian population of the begomovirus Tomato severe rugose virus (ToSRV). <i>Tropical Plant Pathology</i> , 2012, 37, 346-353.	0.8	13

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1249	Restricted geographic distribution and low genetic diversity of the brooding sea urchin <i>Abatus agassizii</i> (Spatangoidea: Schizasteridae) in the South Shetland Islands: A bridgehead population before the spread to the northern Antarctic Peninsula?. <i>Revista Chilena De Historia Natural</i> , 2012, 85, 457-468.	0.5	13
1250	Levels and patterns of genetic diversity in wild <i>Chrysichthys nigrodigitatus</i> in the Lagos Lagoon complex. <i>African Journal of Biotechnology</i> , 2012, 11, 15748-15754.	0.3	7
1251	Genetic variability in mitochondrial and nuclear genes of <i>Larus dominicanus</i> (Charadriiformes). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662</i>	0.6	8
1252	Population Structure of <i>Lutjanus purpureus</i> (Lutjanidae - Perciformes) on the Brazilian coast: further existence evidence of a single species of red snapper in the western Atlantic. <i>Anais Da Academia Brasileira De Ciencias</i> , 2012, 84, 979-999.	0.3	29
1253	Divergence time estimations and contrasting patterns of genetic diversity between Antarctic and southern South America benthic invertebrates. <i>Revista Chilena De Historia Natural</i> , 2012, 85, 445-456.	0.5	31
1254	Sequence variation in the melanocortin-1 receptor (MC1R) pigmentation gene and its role in the cryptic coloration of two South American sand lizards. <i>Genetics and Molecular Biology</i> , 2012, 35, 81-87.	0.6	19
1255	Inclusion of South American samples reveals new population structuring of the blacktip shark (<i>Carcharhinus limbatus</i>) in the western Atlantic. <i>Genetics and Molecular Biology</i> , 2012, 35, 752-760.	0.6	21
1256	Identification of the e allele at the Extension locus (MC1R) in Brazilian Creole sheep and its role in wool color variation. <i>Genetics and Molecular Research</i> , 2012, 11, 2997-3006.	0.3	15
1257	Mitochondrial genetic variability of <i>Didelphis albiventris</i> (Didelphimorphia, Didelphidae) in Brazilian localities. <i>Genetics and Molecular Biology</i> , 2012, 35, 522-529.	0.6	10
1258	Characterization of 10 tobacco vein banding mosaic virus isolates from China. <i>Acta Virologica</i> , 2012, 56, 19-24.	0.3	1
1259	Molecular barcoding for central-eastern European <i>Crioceris</i> leaf-beetles (Coleoptera:). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342 Td (Chry</i>	0.6	9
1260	Phylogenetic clustering of <i>Bradyrhizobium</i> symbionts on legumes indigenous to North America. <i>Microbiology (United Kingdom)</i> , 2012, 158, 2050-2059.	0.7	29
1261	Do the European Great Reed Warblers (<i>Acrocephalus arundinaceus</i>) reach South Africa during wintering?. <i>Journal of Ornithology</i> , 2012, 153, 579-583.	0.5	2
1262	Mitochondrial phylogeography of the Holarctic <i>Parnassius phoebus</i> complex supports a recent refugial model for alpine butterflies. <i>Journal of Biogeography</i> , 2012, 39, 1058-1072.	1.4	36
1263	Development of PCR primer sets for intron 1 of the low-copy gene LEAFY in Davalliaceae. <i>American Journal of Botany</i> , 2012, 99, e223-e225.	0.8	11
1264	Genetic diversity of flat-headed vole (<i>Alticola strelzowi</i> (Kastschenko, 1899)) inferred from cytochrome b variation. <i>Russian Journal of Genetics</i> , 2012, 48, 302-309.	0.2	2
1265	Nuclear Genomic Sequences Reveal that Polar Bears Are an Old and Distinct Bear Lineage. <i>Science</i> , 2012, 336, 344-347.	6.0	238
1266	Characterization of the Complete Mitochondrial Genome Sequence of <i>Spirometra erinaceieuropaei</i> (Cestoda: Diphyllobothriidae) from China. <i>International Journal of Biological Sciences</i> , 2012, 8, 640-649.	2.6	34

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1268	Opsin gene sequence variation across phylogenetic and population histories in <i>Mysis</i> (Crustacea: Mysida) does not match current light environments or visual pigment absorbance spectra. <i>Molecular Ecology</i> , 2012, 21, 2176-2196.	2.0	9
1269	Geographic Selection in the Small Heat Shock Gene Complex Differentiating Populations of <i>Drosophila pseudoobscura</i> . <i>Journal of Heredity</i> , 2012, 103, 400-407.	1.0	8
1270	High latitudes and high genetic diversity: Phylogeography of a widespread boreal bird, the gray jay (<i>Perisoreus canadensis</i>). <i>Molecular Phylogenetics and Evolution</i> , 2012, 63, 456-465.	1.2	56
1271	Multiple Quaternary Refugia in the Eastern Guiana Shield Revealed by Comparative Phylogeography of 12 Frog Species. <i>Systematic Biology</i> , 2012, 61, 461.	2.7	113
1272	Structural diversity and African origin of the 17q21.31 inversion polymorphism. <i>Nature Genetics</i> , 2012, 44, 872-880.	9.4	129
1273	Cryptic species in a Neotropical parrot: genetic variation within the <i>Amazona farinosa</i> species complex and its conservation implications. <i>Conservation Genetics</i> , 2012, 13, 1427-1432.	0.8	17
1274	Morphological, demographic and genetic traces of Upper Palaeolithic human impact on limpet assemblages in North Iberia. <i>Journal of Quaternary Science</i> , 2012, 27, 244-253.	1.1	15
1275	Genetic structure of red deer population in northeastern Poland in relation to the history of human interventions. <i>Journal of Wildlife Management</i> , 2012, 76, 1264-1276.	0.7	40
1276	Population-based resequencing revealed an ancestral winter group of cultivated flax: implication for flax domestication processes. <i>Ecology and Evolution</i> , 2012, 2, 622-635.	0.8	11
1277	Phylogeographic insights into an irruptive pest outbreak. <i>Ecology and Evolution</i> , 2012, 2, 908-919.	0.8	25
1278	Hiding deep in the trees: discovery of divergent mitochondrial lineages in Malagasy chameleons of the <i>Calumma nasutum</i> group. <i>Ecology and Evolution</i> , 2012, 2, 1468-1479.	0.8	23
1279	Sequence polymorphisms in wild, weedy, and cultivated rice suggest seed shattering locus <i>sh4</i> played a minor role in Asian rice domestication. <i>Ecology and Evolution</i> , 2012, 2, 2106-2113.	0.8	54
1280	Locus-specific view of flax domestication history. <i>Ecology and Evolution</i> , 2012, 2, 139-152.	0.8	53
1281	Role of recent and old riverine barriers in fine-scale population genetic structure of Geoffroy's tamarin (<i>Saguinus geoffroyi</i>) in the Panama Canal watershed. <i>Ecology and Evolution</i> , 2012, 2, 298-309.	0.8	20
1282	Phylogeography of the prehensile-tailed skink <i>Corucia zebrata</i> on the Solomon Archipelago. <i>Ecology and Evolution</i> , 2012, 2, 1220-1234.	0.8	16
1283	A species assemblage approach to comparative phylogeography of birds in southern Australia. <i>Ecology and Evolution</i> , 2012, 2, 354-369.	0.8	52
1284	Increased divergence but reduced variation on the Z chromosome relative to autosomes in <i>Ficedula</i> flycatchers: differential introgression or the faster-Z effect?. <i>Ecology and Evolution</i> , 2012, 2, 379-396.	0.8	29

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1285	Genetic signatures of a demographic collapse in a large-bodied forest dwelling primate (<i>Mandrillus</i>). <i>Trends in Ecology and Evolution</i> , 2012, 27, 100-108.	0.8	16
1286	Comparative phylogeography of meroplanktonic species, <i>Aurelia</i> spp. and <i>Rhizostoma pulmo</i> (Cnidaria). <i>Journal of Biogeography</i> , 2012, 39, 1074-1084.	1.0	34
1287	Deleterious Mutation Accumulation in Asexual <i>Timema</i> Stick Insects. <i>Molecular Biology and Evolution</i> , 2012, 29, 401-408.	3.5	65
1288	On the comparison of population-level estimates of haplotype and nucleotide diversity: a case study using the gene <i>cox1</i> in animals. <i>Heredity</i> , 2012, 109, 50-56.	1.2	130
1289	Phylogeography of an invasive land snail: natural range expansion versus anthropogenic dispersal in <i>Theba pisana</i> . <i>Biological Invasions</i> , 2012, 14, 1665-1682.	1.2	36
1290	Quantifying the Elevation of Mitochondrial DNA Evolutionary Substitution Rates Over Nuclear Rates in the Intertidal Copepod <i>Tigriopus californicus</i> . <i>Journal of Molecular Evolution</i> , 2012, 74, 310-318.	0.8	28
1291	Comparative Phylogeography of Two Crow Species: Jungle Crow <i>Corvus macrorhynchos</i> and Carrion Crow <i>Corvus corone</i> . <i>Zoological Science</i> , 2012, 29, 484.	0.3	12
1292	Genetic variation and recombination in Aichi virus. <i>Journal of General Virology</i> , 2012, 93, 1226-1235.	1.3	19
1293	A Species Tree for the Australo-Papuan Fairy-wrens and Allies (Aves: Maluridae). <i>Systematic Biology</i> , 2012, 61, 253.	2.7	55
1294	Coalescent-Based Analysis Distinguishes between Allo- and Autopolyploid Origin in Shepherd's Purse (<i>Capsella bursa-pastoris</i>). <i>Molecular Biology and Evolution</i> , 2012, 29, 1721-1733.	3.5	29
1295	Greater flamingo colonies around the Mediterranean form a single interbreeding population and share a common history. <i>Journal of Avian Biology</i> , 2012, 43, 341-354.	0.6	36
1296	Species delimitations in the <i>Cladonia cariosa</i> group (Cladoniaceae, Ascomycota). <i>Lichenologist</i> , 2012, 44, 121-135.	0.5	35
1297	Genetic Structure and the North American Postglacial Expansion of the Barnacle, <i>Semibalanus balanoides</i> . <i>Journal of Heredity</i> , 2012, 103, 153-165.	1.0	21
1298	Use of molecular genetics for understanding seabird evolution, ecology and conservation. <i>Marine Ecology - Progress Series</i> , 2012, 451, 285-304.	0.9	25
1299	Anonymous single-copy nuclear DNA (scnDNA) markers for Grey-cheeked Fulvetta (<i>Alcippe morrisonia</i>) and Rufous-capped Babbler (<i>Stachyridopsis ruficeps</i>). <i>Conservation Genetics Resources</i> , 2012, 4, 777-781.	0.4	4
1300	The spatial distribution does not affect host-parasite coevolution in <i>Rossomyrmex</i> ants. <i>Insectes Sociaux</i> , 2012, 59, 361-368.	0.7	4
1301	Patterns of linkage disequilibrium and association mapping in diploid alfalfa (<i>M. sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2012, 125, 577-590.	1.8	41
1302	Evidence for evolutionary distinctiveness of a newly discovered population of sooglossid frogs on Praslin Island, Seychelles. <i>Conservation Genetics</i> , 2012, 13, 557-566.	0.8	9

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1303	Evaluating the genetic status of a Great Basin endemic minnow: the relict dace (<i>Relictus solitarius</i>). <i>Conservation Genetics</i> , 2012, 13, 727-742.	0.8	6
1304	Habitat connectivity, more than speciesâ€™ biology, influences genetic differentiation in a habitat specialist, the short-eared rock-wallaby (<i>Petrogale brachyotis</i>). <i>Conservation Genetics</i> , 2012, 13, 937-952.	0.8	18
1305	Evaluation of genetic structure across freshwater mussel community (genus <i>Elliptio</i>) in the Altamaha River basin. <i>Conservation Genetics</i> , 2012, 13, 965-975.	0.8	1
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1314	The Pleistocene glacial cycles shaped the historical demography and phylogeography of a pine fungal endophyte. <i>Mycological Progress</i> , 2012, 11, 569-581.	0.5	20
1315	Sequence conservation and divergence in miR164C1 and its target, CUC1, in Brassica species. <i>Plant Biotechnology Reports</i> , 2012, 6, 149-163.	0.9	13
1316	Molecular species diagnosis confirmed the occurrence of Kumamoto oyster <i>Crassostrea sikamea</i> in Korean waters. <i>Fisheries Science</i> , 2012, 78, 259-267.	0.7	24
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1329	Population genetics of cucumber mosaic virus infecting medicinal, aromatic and ornamental plants from northern Italy. <i>Archives of Virology</i> , 2012, 157, 739-745.	0.9	41
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1332	Comparative phylogeography of four component species of deciduous broad-leaved forests in Japan based on chloroplast DNA variation. <i>Journal of Plant Research</i> , 2012, 125, 207-221.	1.2	66
1333	Population fragmentation causes randomly fixed genotypes in populations of <i>Arabidopsis kamchatica</i> in the Japanese Archipelago. <i>Journal of Plant Research</i> , 2012, 125, 223-233.	1.2	14
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1335	Phylogeography and population structure of <i>Crataegus</i> Nuthatch <i>Sitta krueperi</i> from Turkey based on microsatellites and mitochondrial DNA. <i>Journal of Ornithology</i> , 2012, 153, 405-411.	0.5	14
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1337	Patterns of genetic variation of a Lessepsian parasite. <i>Biological Invasions</i> , 2012, 14, 1725-1736.	1.2	7
1338	Physiological implications of genomic state in parthenogenetic lizards of reciprocal hybrid origin. <i>Journal of Evolutionary Biology</i> , 2012, 25, 252-263.	0.8	10

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1353	MOLECULAR SIGNATURES OF SELECTION ON REPRODUCTIVE CHARACTER DISPLACEMENT OF FLOWER COLOR IN <i>PHLOX DRUMMONDII</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 469-485.	1.1	50
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1356	The Parasite that Causes Whirling Disease, <i>Myxobolus cerebralis</i> , is Genetically Variable Within and Across Spatial Scales. <i>Journal of Eukaryotic Microbiology</i> , 2012, 59, 80-87.	0.8	9

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1362	Population structure of adult female Australian sea lions is driven by fine-scale foraging site fidelity. <i>Animal Behaviour</i> , 2012, 83, 691-701.	0.8	63
1363	Genetic diversity patterns of <i>Haemonchus placei</i> and <i>Haemonchus contortus</i> populations isolated from domestic ruminants in Brazil. <i>International Journal for Parasitology</i> , 2012, 42, 469-479.	1.3	82
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1365	The Balkans and the colonization of Europe: the post-glacial range expansion of the wild boar, <i>Sus scrofa</i> . <i>Journal of Biogeography</i> , 2012, 39, 713-723.	1.4	64
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1369	Phylogeography and palaeodistribution modelling in the Patagonian steppe: the case of <i>Mulinum spinosum</i> (Apiaceae). <i>Journal of Biogeography</i> , 2012, 39, 1041-1057.	1.4	30
1370	Phylogeography of the medically important mosquito <i>Aedes</i> (<i>Ochlerotatus</i>) <i>vigilax</i> (Diptera: Culicidae) in Australasia. <i>Journal of Biogeography</i> , 2012, 39, 1333-1346.	1.4	14
1371	Trapped in desert springs: phylogeography of Australian desert spring snails. <i>Journal of Biogeography</i> , 2012, 39, 1573-1582.	1.4	47
1372	Phylogeography of the cold-water barnacle <i>Chthamalus challengerii</i> in the northwestern Pacific: effect of past population expansion and contemporary gene flow. <i>Journal of Biogeography</i> , 2012, 39, 1819-1835.	1.4	47
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1374	Gene flow networks among American <i>Aedes aegypti</i> populations. <i>Evolutionary Applications</i> , 2012, 5, 664-676.	1.5	38

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1376	DNA barcoding for identification of sand flies (Diptera: Psychodidae) in India. <i>Molecular Ecology Resources</i> , 2012, 12, 414-420.	2.2	74
1377	Demographic History of <i>Shorea curtisii</i> (Dipterocarpaceae) Inferred from Chloroplast DNA Sequence Variations. <i>Biotropica</i> , 2012, 44, 577-585.	0.8	22
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1380	TEMPO AND MODE OF MATING SYSTEM EVOLUTION BETWEEN INCIPIENT CLARKIA SPECIES. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 1210-1225.	1.1	50
1381	DYNAMICS OF DRIFT, GENE FLOW, AND SELECTION DURING SPECIATION IN <i>SILENE</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 1447-1458.	1.1	26
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1385	MULTILOCUS COALESCENCE ANALYSES SUPPORT A mtDNA-BASED PHYLOGEOGRAPHIC HISTORY FOR A WIDESPREAD PALEARCTIC PASSERINE BIRD, <i>SITTA EUROPAEA</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 2850-2864.	1.1	45
1386	GENOME SIZE IS NOT CORRELATED WITH EFFECTIVE POPULATION SIZE IN THE <i>ORYZA</i> SPECIES. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 3302-3310.	1.1	20
1387	Lichen myco- and photobiont diversity and their relationships at the edge of life (McMurdo Dry) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 26 1.3 66	1.3	66
1388	The molecular basis of the plumage colour polymorphism in the Tahiti reed warbler <i>Acrocephalus caffer</i> . <i>Journal of Avian Biology</i> , 2012, 43, 3-8.	0.6	23
1389	Maintenance of MHC Class IIB diversity in a recently established songbird population. <i>Journal of Avian Biology</i> , 2012, 43, 109-118.	0.6	14
1390	Molecular markers provide insights into contemporary and historic gene flow for a non-migratory species. <i>Journal of Avian Biology</i> , 2012, 43, 198-214.	0.6	25
1391	Phylogeography of <i>Cyananthus delavayi</i> (Campanulaceae) in Hengduan Mountains inferred from variation in nuclear and chloroplast DNA sequences. <i>Journal of Systematics and Evolution</i> , 2012, 50, 305-315.	1.6	18
1392	Response of a desert shrub to past geological and climatic change: A phylogeographic study of <i>Reaumuria soongarica</i> (Tamaricaceae) in western China. <i>Journal of Systematics and Evolution</i> , 2012, 50, 351-361.	1.6	44

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1394	Novel coding genetic variants of the GBP1 gene in wild and domestic pigs (<i>Sus scrofa</i>). <i>Livestock Science</i> , 2012, 146, 1-4.	0.6	0
1395	Inferring the demographic history of a highly endangered goat breed through the analysis of nuclear and mitochondrial genetic signatures. <i>Small Ruminant Research</i> , 2012, 104, 78-84.	0.6	9
1396	Levels of genetic diversity vary dramatically between <i>Blastocystis</i> subtypes. <i>Infection, Genetics and Evolution</i> , 2012, 12, 263-273.	1.0	157
1397	High evolutionary rate of human astrovirus. <i>Infection, Genetics and Evolution</i> , 2012, 12, 435-442.	1.0	32
1398	Polymorphisms at MHC class II DRB1 exon 2 locus in Pyrenean chamois (<i>Rupicapra pyrenaica pyrenaica</i>). <i>Infection, Genetics and Evolution</i> , 2012, 12, 1020-1026.	1.0	12
1399	Phylogenetic evidence based on <i>Trypanosoma cruzi</i> nuclear gene sequences and information entropy suggest that inter-strain intragenic recombination is a basic mechanism underlying the allele diversity of hybrid strains. <i>Infection, Genetics and Evolution</i> , 2012, 12, 1064-1071.	1.0	19
1400	The complete mitochondrial genome sequence of the filarial nematode <i>Wuchereria bancrofti</i> from three geographic isolates provides evidence of complex demographic history. <i>Molecular and Biochemical Parasitology</i> , 2012, 183, 32-41.	0.5	52
1401	A Two-locus Molecular Characterization of <i>Paramecium calkinsi</i> . <i>Protist</i> , 2012, 163, 263-273.	0.6	21
1402	Identification of <i>Paramecium bursaria</i> Syngens through Molecular Markers – Comparative Analysis of Three Loci in the Nuclear and Mitochondrial DNA. <i>Protist</i> , 2012, 163, 671-685.	0.6	33
1403	Population genetic structure and phylogeography of <i>Mesokallapseudes macsweenyi</i> (Crustacea: Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 and Ecology, 2012, 412, 58-65.	0.7	16
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1406	Genetic divergence among invasive and native populations of <i>Plagioscion squamosissimus</i> (Perciformes, Sciaenidae) in Neotropical regions. <i>Journal of Fish Biology</i> , 2012, 80, 2434-2447.	0.7	13
1407	Mitochondrial DNA differentiation between the antitropical blue whiting species <i>Micromesistius poutassou</i> and <i>Micromesistius australis</i> . <i>Journal of Fish Biology</i> , 2012, 81, 253-269.	0.7	3
1408	Pseudocryptic speciation of <i>Chrysochroa fulgidissima</i> (Coleoptera: Buprestidae) with two new species from Korea, China and Vietnam. <i>Zoological Journal of the Linnean Society</i> , 2012, 164, 71-98.	1.0	12
1409	Multilocus sequence analysis and type III effector repertoire mining provide new insights into the evolutionary history and virulence of <i>Xanthomonas oryzae</i> . <i>Molecular Plant Pathology</i> , 2012, 13, 288-302.	2.0	56
1410	The evolution of the <i>Gpâ€Rbpâ€1</i> gene in <i>Globodera pallida</i> includes multiple selective replacements. <i>Molecular Plant Pathology</i> , 2012, 13, 546-555.	2.0	19

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1412	Genetic structure of Eurasian and North American mallard ducks based on mtDNA data. <i>Animal Genetics</i> , 2012, 43, 352-355.	0.6	11
1413	High microsatellite and mitochondrial diversity in Anatolian native horse breeds shows Anatolia as a genetic conduit between Europe and Asia. <i>Animal Genetics</i> , 2012, 43, 401-409.	0.6	8
1414	Effects of stocking on the genetic structure of brown trout, <i>Salmo trutta</i> , in Central Europe inferred from mitochondrial and nuclear DNA markers. <i>Fisheries Management and Ecology</i> , 2012, 19, 252-263.	1.0	41
1415	Multiple refugia and barriers explain the phylogeography of the Valais shrew, <i>Sorex antinorii</i> (Mammalia: Soricomorpha). <i>Biological Journal of the Linnean Society</i> , 2012, 105, 864-880.	0.7	21
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1417	Climate and refugial origin influence the mitochondrial lineage distribution of weasels (<i>Mustela</i>). <i>Journal of Biogeography</i> , 2012, 39, 1075-1085.	0.7	53
1418	Divergence between passerine populations from the Malvinas - Falkland Islands and their continental counterparts: a comparative phylogeographical study. <i>Biological Journal of the Linnean Society</i> , 2012, 106, 865-879.	0.7	32
1419	Genetic structure of Eurasian badgers <i>Meles meles</i> (Carnivora: Mustelidae) and the colonization history of Ireland. <i>Biological Journal of the Linnean Society</i> , 2012, 106, 893-909.	0.7	21
1420	The role of niche divergence and phenotypic adaptation in promoting lineage diversification in the Sage Sparrow (<i>Artemisospiza belli</i> , Aves: Emberizidae). <i>Biological Journal of the Linnean Society</i> , 2012, 107, 332-354.	0.7	27
1421	Molecular phylogeography of the Japanese weasel, <i>Mustela itatsi</i> (Carnivora: Mustelidae), endemic to the Japanese islands, revealed by mitochondrial DNA analysis. <i>Biological Journal of the Linnean Society</i> , 2012, 107, 307-321.	0.7	12
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1423	Speciation in the White-breasted Nuthatch (<i>Sitta carolinensis</i>): a multilocus perspective. <i>Molecular Ecology</i> , 2012, 21, 907-920.	2.0	33
1424	Cryptic lineages and Pleistocene population expansion in a Brazilian Cerrado frog. <i>Molecular Ecology</i> , 2012, 21, 921-941.	2.0	64
1425	Speciation in the <i>Rana chensinensis</i> species complex and its relationship to the uplift of the Qinghai-Tibetan Plateau. <i>Molecular Ecology</i> , 2012, 21, 960-973.	2.0	72
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1427	Spatially structured populations with a low level of cryptic diversity in European marine Gastrotricha. <i>Molecular Ecology</i> , 2012, 21, 1239-1254.	2.0	60
1428	Integration of molecular, ecological, morphological and endosymbiont data for species delimitation within the <i>Pnigalio soemius</i> complex (Hymenoptera: Eulophidae). <i>Molecular Ecology</i> , 2012, 21, 1190-1208.	2.0	52

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1429	Contrasting introduction scenarios among continents in the worldwide invasion of the banana fungal pathogen <i>Mycosphaerella fijiensis</i> . <i>Molecular Ecology</i> , 2012, 21, 1098-1114.	2.0	47
1430	Disentangling the effects of breakdown of self-incompatibility and transition to selfing in North American <i>Arabidopsis lyrata</i> . <i>Molecular Ecology</i> , 2012, 21, 1130-1142.	2.0	8
1431	Influence of finite-sites mutation, population subdivision and sampling schemes on patterns of nucleotide polymorphism for species with molecular hyperdiversity. <i>Molecular Ecology</i> , 2012, 21, 1345-1359.	2.0	24
1432	Inferring the evolutionary history of Indian <i>Plasmodium vivax</i> from population genetic analyses of multilocus nuclear DNA fragments. <i>Molecular Ecology</i> , 2012, 21, 1597-1616.	2.0	27
1433	Fig trees at the northern limit of their range: the distributions of cryptic pollinators indicate multiple glacial refugia. <i>Molecular Ecology</i> , 2012, 21, 1687-1701.	2.0	62
1434	Divergence and biogeography of the recently evolved Macaronesian red <i>Festuca</i> (Gramineae) species inferred from coalescence-based analyses. <i>Molecular Ecology</i> , 2012, 21, 1702-1726.	2.0	10
1435	Legumes select symbiosis island sequence variants in <i>Bradyrhizobium</i> . <i>Molecular Ecology</i> , 2012, 21, 1769-1778.	2.0	60
1436	Identifying insecticide resistance genes in mosquito by combining AFLP genome scans and 454 pyrosequencing. <i>Molecular Ecology</i> , 2012, 21, 1672-1686.	2.0	28
1437	Evidence for selection at cytokine loci in a natural population of field voles (<i>Microtus</i>). <i>Molecular Ecology</i> , 2012, 21, 1702-1726.	2.0	44
1438	Comprehensive sampling reveals circumpolarity and sympatry in seven mitochondrial lineages of the Southern Ocean crinoid species <i>Promachocrinus kerguelensis</i> (Echinodermata). <i>Molecular Ecology</i> , 2012, 21, 2502-2518.	2.0	73
1439	Russian wheat aphids (<i>Diuraphis noxia</i>) in China: native range expansion or recent introduction?. <i>Molecular Ecology</i> , 2012, 21, 2130-2144.	2.0	34
1440	Multiple biogeographical barriers identified across the monsoon tropics of northern Australia: phylogeographic analysis of the <i>brachyotis</i> group of rock-wallabies. <i>Molecular Ecology</i> , 2012, 21, 2254-2269.	2.0	67
1441	Extensive sympatry, cryptic diversity and introgression throughout the geographic distribution of two coral species complexes. <i>Molecular Ecology</i> , 2012, 21, 2224-2238.	2.0	139
1442	Recent population decline and selection shape diversity of taxol-related genes. <i>Molecular Ecology</i> , 2012, 21, 3006-3021.	2.0	24
1443	Mitogenome sequencing reveals shallow evolutionary histories and recent divergence time between morphologically and ecologically distinct European whitefish (<i>Coregonus</i> spp.). <i>Molecular Ecology</i> , 2012, 21, 2727-2742.	2.0	83
1444	Postglacial colonization of Europe by the barbastelle bat: agreement between molecular data and past predictive modelling. <i>Molecular Ecology</i> , 2012, 21, 2761-2774.	2.0	37
1445	A phylogeographic investigation of the hybrid origin of a species of swordtail fish from Mexico. <i>Molecular Ecology</i> , 2012, 21, 2692-2712.	2.0	17
1446	Cultivation shapes genetic novelty in a globally important invader. <i>Molecular Ecology</i> , 2012, 21, 3187-3199.	2.0	34

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1447	Model-based comparisons of phylogeographic scenarios resolve the intraspecific divergence of cactophilic <i>Drosophila mojavensis</i> . <i>Molecular Ecology</i> , 2012, 21, 3293-3307.	2.0	36
1448	Coalescence patterns of endemic Tibetan species of stream salamanders (Hynobiidae). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 70</i>	2.0	35
1449	Parentage-based pedigree reconstruction reveals female matrilineal clusters and male-biased dispersal in nongregarious Asian great apes, the Bornean orangutans (<i>Pongo pygmaeus</i>). <i>Molecular Ecology</i> , 2012, 21, 3352-3362.	2.0	51
1450	Management increases genetic diversity of honey bees via admixture. <i>Molecular Ecology</i> , 2012, 21, 4414-4421.	2.0	128
1451	Diversification and phylogeographic structure in widespread <i>Azteca</i> plants from the northern Neotropics. <i>Molecular Ecology</i> , 2012, 21, 3576-3592.	2.0	24
1452	Reconstruction of caribou evolutionary history in Western North America and its implications for conservation. <i>Molecular Ecology</i> , 2012, 21, 3610-3624.	2.0	54
1453	Phylogeography of Asian wild rice, <i>Oryza rufipogon</i> : a genome-wide view. <i>Molecular Ecology</i> , 2012, 21, 4593-4604.	2.0	79
1454	Effects of vicariant barriers, habitat stability, population isolation and environmental features on species divergence in the southwestern Australian coastal reptile community. <i>Molecular Ecology</i> , 2012, 21, 3809-3822.	2.0	34
1455	Appearances can be deceptive: different diversification patterns within a group of Mediterranean earthworms (Oligochaeta, Hormogastridae). <i>Molecular Ecology</i> , 2012, 21, 3776-3793.	2.0	35
1456	Climate oscillation during the Quaternary associated with landscape heterogeneity promoted allopatric lineage divergence of a temperate tree <i>Kalopanax septemlobus</i> (Araliaceae) in East Asia. <i>Molecular Ecology</i> , 2012, 21, 3823-3838.	2.0	113
1457	Pleistocene speciation with and without gene flow in <i>Euphaea</i> damselflies of subtropical and tropical East Asian islands. <i>Molecular Ecology</i> , 2012, 21, 3739-3756.	2.0	17
1458	Origin and in situ diversification in <i>Hemidactylus</i> geckos of the Socotra Archipelago. <i>Molecular Ecology</i> , 2012, 21, 4074-4092.	2.0	35
1459	Mitochondrial genomes reveal the global phylogeography and dispersal routes of the migratory locust. <i>Molecular Ecology</i> , 2012, 21, 4344-4358.	2.0	171
1460	Rapid genetic assimilation of native wall lizard populations (<i>Podarcis muralis</i>) through extensive hybridization with introduced lineages. <i>Molecular Ecology</i> , 2012, 21, 4313-4326.	2.0	50
1461	Symbiont communities and host genetic structure of the brain coral <i>Platygyra verweyi</i> , at the outlet of a nuclear power plant and adjacent areas. <i>Molecular Ecology</i> , 2012, 21, 4393-4407.	2.0	51
1462	Allotetraploid <i>Mimulus sookensis</i> are highly interfertile despite independent origins. <i>Molecular Ecology</i> , 2012, 21, 5280-5298.	2.0	23
1463	Genetic diversity of <i>Philaenus spumarius</i> and <i>P. tessellatus</i> (Hemiptera, Aphrophoridae): implications for evolution and taxonomy. <i>Systematic Entomology</i> , 2012, 37, 55-64.	1.7	18
1464	<i>Plasmodium vivax</i> Duffy binding protein: baseline antibody responses and parasite polymorphisms in a well-consolidated settlement of the Amazon Region. <i>Tropical Medicine and International Health</i> , 2012, 17, 989-1000.	1.0	30

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1465	Multilocus analysis of nucleotide variation in <i>Drosophila madeirensis</i> , an endemic species of the Laurisilva forest in Madeira. <i>Journal of Evolutionary Biology</i> , 2012, 25, 726-739.	0.8	2
1466	Single origin of human commensalism in the house sparrow. <i>Journal of Evolutionary Biology</i> , 2012, 25, 788-796.	0.8	72
1467	Detecting cryptic speciation in the widespread and morphologically conservative carpet chameleon (<i>Furcifer lateralis</i>) of Madagascar. <i>Journal of Evolutionary Biology</i> , 2012, 25, 1399-1414.	0.8	45
1468	Molecular phylogeny of <i>Ganoderma lucidum</i> isolates collected from northern India. <i>Forest Pathology</i> , 2012, 42, 429-436.	0.5	1
1469	Genetic Structure and Variability of East Asian <i>Passiflora virus</i> Population in Amami-Oshima, Japan. <i>Journal of Phytopathology</i> , 2012, 160, 404-411.	0.5	5
1470	Rapid chromosomal evolution in the mesic four-striped grass rat <i>Rhabdomys dilectus</i> (Rodentia). <i>Evolutionary Research</i> , 2012, 50, 165-172.	0.6	34
1471	Phylogeography of the poison frog <i>Mantella viridis</i> (Amphibia: Mantellidae) reveals chromatic and genetic differentiation across ecotones in northern Madagascar. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2012, 50, 305-314.	0.6	10
1472	Differential mRNA Expression and Promoter Methylation Status of SYCP3 Gene in Testes of Yaks and Cattle. <i>Reproduction in Domestic Animals</i> , 2012, 47, 455-462.	0.6	31
1473	Molecular evolution of key genes for type II secretion in <i>Legionella pneumophila</i> . <i>Environmental Microbiology</i> , 2012, 14, 2017-2033.	1.8	17
1474	Mitochondrial capture and incomplete lineage sorting in the diversification of balitorine loaches (Cypriniformes, Balitoridae) revealed by mitochondrial and nuclear genes. <i>Zoologica Scripta</i> , 2012, 41, 233-247.	0.7	42
1475	Northern genetic richness and southern purity, but just one species in the <i>Chelonoidis chilensis</i> complex. <i>Zoologica Scripta</i> , 2012, 41, 220-232.	0.7	31
1476	Phylogenetic analysis of the north-east Atlantic and Mediterranean species of the genus <i>Stenosoma</i> (Isopoda, Valvifera, Idoteidae). <i>Zoologica Scripta</i> , 2012, 41, 386-399.	0.7	8
1477	Phylogeny of woodcreepers of the genus <i>Lepidocolaptes</i> (Aves, Furnariidae), a widespread Neotropical taxon. <i>Zoologica Scripta</i> , 2012, 41, 363-373.	0.7	3
1478	Phylogenetic analyses of band-winged grasshoppers (Orthoptera, Acrididae, Oedipodinae) reveal convergence of wing morphology. <i>Zoologica Scripta</i> , 2012, 41, 515-526.	0.7	21
1479	Cenozoic evolution of Muricidae (Mollusca, Neogastropoda) in the Southern Ocean, with the description of a new subfamily. <i>Zoologica Scripta</i> , 2012, 41, 596-616.	0.7	21
1480	Gene conversion in the mitochondrial genome on interspecific hybridization in voles of the <i>Clethrionomys</i> genus. <i>Biochemistry (Moscow)</i> , 2012, 77, 518-523.	0.7	2
1481	<i>Plasmodium vivax</i> populations revisited: mitochondrial genomes of temperate strains in Asia suggest ancient population expansion. <i>BMC Evolutionary Biology</i> , 2012, 12, 22.	3.2	19
1482	Watershed boundaries and geographic isolation: patterns of diversification in cutthroat trout from western North America. <i>BMC Evolutionary Biology</i> , 2012, 12, 38.	3.2	32

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1483	Nucleotide and phylogenetic analyses of the <i>Chlamydia trachomatis</i> ompA gene indicates it is a hotspot for mutation. BMC Research Notes, 2012, 5, 53.	0.6	11
1484	Historical geographic dispersal of the golden snub-nosed monkey (<i>Rhinopithecus roxellana</i>) and the influence of climatic oscillations. American Journal of Primatology, 2012, 74, 91-101.	0.8	24
1485	Population genetic structure of Guizhou snub-nosed monkeys (<i>Rhinopithecus brelichi</i>) as inferred from mitochondrial control region sequences, and comparison with <i>R. roxellana</i> and <i>R. bieti</i> . American Journal of Physical Anthropology, 2012, 147, 1-10.	2.1	28
1486	The population genetics of quechuas, the largest native south american group: Autosomal sequences, SNPs, and microsatellites evidence high level of diversity. American Journal of Physical Anthropology, 2012, 147, 443-451.	2.1	11
1487	Population Genetic Structure of the New Zealand Estuarine Clam <i>Austrovenus stutchburyi</i> (Bivalvia: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Estuaries and Coasts, 2012, 35, 143-154.	1.0	27
1488	Time and space: genetic structure of the cohorts of the common sea urchin <i>Paracentrotus lividus</i> in Western Mediterranean. Marine Biology, 2012, 159, 187-197.	0.7	37
1489	Phylogeography of the sub-Antarctic notothenioid fish <i>Eleginops maclovinus</i> : evidence of population expansion. Marine Biology, 2012, 159, 499-505.	0.7	34
1490	Population genetic structure of protected allis shad (<i>Alosa alosa</i>) and twaite shad (<i>Alosa fallax</i>). Marine Biology, 2012, 159, 675-687.	0.7	39
1491	Positive selection of Toll-like receptor 2 polymorphisms in two closely related old world monkey species, rhesus and Japanese macaques. Immunogenetics, 2012, 64, 15-29.	1.2	6
1492	Molecular Characterization and Comparative Analysis of Six Durum Wheat Accessions Including Graziella Ra. Plant Molecular Biology Reporter, 2012, 30, 168-175.	1.0	6
1493	The complete phylogeny of <i>Pseudobulweria</i> , the most endangered seabird genus: systematics, species status and conservation implications. Conservation Genetics, 2012, 13, 39-52.	0.8	16
1494	Remaining genetic diversity in Brazilian Merganser (<i>Mergus octosetaceus</i>). Conservation Genetics, 2012, 13, 293-298.	0.8	8
1495	Extremely low genetic diversity and weak population differentiation in the endangered Colombian river turtle <i>Podocnemis lewyana</i> (Testudines: Podocnemididae). Conservation Genetics, 2012, 13, 65-77.	0.8	25
1496	Inferring the ancient population structure of the vulnerable albatross <i>Phoebastria albatrus</i> , combining ancient DNA, stable isotope, and morphometric analyses of archaeological samples. Conservation Genetics, 2012, 13, 143-151.	0.8	19
1497	The role of genes in understanding the evolutionary ecology of reef building corals. Evolutionary Ecology, 2012, 26, 317-335.	0.5	28
1498	Study of polymorphisms in the promoter region of ovine β -lactoglobulin gene and phylogenetic analysis among the Valle del Belice breed and other sheep breeds considered as ancestors. Molecular Biology Reports, 2012, 39, 745-751.	1.0	14
1499	DNA barcoding of nymphalid butterflies (Nymphalidae: Lepidoptera) from Western Ghats of India. Molecular Biology Reports, 2012, 39, 2375-2383.	1.0	21
1500	Polymorphism analysis of <i>csd</i> gene in six <i>Apis mellifera</i> subspecies. Molecular Biology Reports, 2012, 39, 3067-3071.	1.0	15

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1501	Polymorphisms of beta-lactoglobulin promoter region in three Sicilian goat breeds. <i>Molecular Biology Reports</i> , 2012, 39, 3203-3210.	1.0	10
1502	Differences between sympatric populations of <i>Eotetranychus carpini</i> collected from <i>Vitis vinifera</i> and <i>Carpinus betulus</i> : insights from host-switch experiments and molecular data. <i>Experimental and Applied Acarology</i> , 2012, 56, 209-219.	0.7	3
1503	The Iberian endemic species <i>Ranunculus cabrerensis</i> Rothm.: an intricate history in the <i>Ranunculus parnassifolius</i> L. polyploid complex. <i>Plant Systematics and Evolution</i> , 2012, 298, 121-138.	0.3	11
1504	Phylogeography of <i>Anguilla marmorata</i> (Teleostei: Anguilliformes) from the eastern Caroline Islands. <i>Ichthyological Research</i> , 2012, 59, 70-76.	0.5	9
1505	Recurrent gene deletions and the evolution of adaptive cyanogenesis polymorphisms in white clover (<i>Trifolium repens</i> L.). <i>Molecular Ecology</i> , 2013, 22, 724-738.	2.0	37
1506	Population structure of <i>Sclerotinia sclerotiorum</i> in crop and wild hosts in the UK. <i>Plant Pathology</i> , 2013, 62, 309-324.	1.2	45
1507	Molecular and morphological support for a Florida origin of the Cuban oak. <i>Journal of Biogeography</i> , 2013, 40, 632-645.	1.4	42
1508	STRUCTURE AND POPULATION GENETICS OF THE BREAKPOINTS OF A POLYMORPHIC INVERSION IN <i>INDROSOPHILA SUBOBSCURA</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 66-79.	1.1	20
1509	Mitochondrial DNA D-loop sequence variation in maternal lineages of Iberian native horses. <i>Animal Genetics</i> , 2013, 44, 209-213.	0.6	22
1510	Population connectivity buffers genetic diversity loss in a seabird. <i>Frontiers in Zoology</i> , 2013, 10, 28.	0.9	20
1511	Molecular investigation of Torque teno sus virus in geographically distinct porcine breeding herds of Sichuan, China. <i>Virology Journal</i> , 2013, 10, 161.	1.4	7
1512	Phylogeography of the neotropical <i>Anopheles triannulatus</i> complex (Diptera: Culicidae) supports deep structure and complex patterns. <i>Parasites and Vectors</i> , 2013, 6, 47.	1.0	21
1513	Intraspecific sequence variation and differential expression in starch synthase genes of <i>Arabidopsis thaliana</i> . <i>BMC Research Notes</i> , 2013, 6, 84.	0.6	20
1514	Polyporales genomes reveal the genetic architecture underlying tetrapolar and bipolar mating systems. <i>Mycologia</i> , 2013, 105, 1374-1390.	0.8	42
1515	Molecular characterization of novel haplotypes of eIF4E family in Chinese cabbage (<i>Brassica rapa</i> L.). <i>Trends in Plant Science</i> , 2013, 18, 100-105.	0.5	10
1516	Genome-wide identification of the class III aminotransferase gene family in rice and expression analysis under abiotic stress. <i>Genes and Genomics</i> , 2013, 35, 597-608.	0.5	5
1517	Nucleotide diversity of the upstream region of the putative MADS-box gene controlling soybean maturity. <i>Genes and Genomics</i> , 2013, 35, 159-166.	0.5	0
1518	Characterization and evolutionary analysis of <i>Brassica</i> species-diverged sequences containing simple repeat units. <i>Genes and Genomics</i> , 2013, 35, 167-175.	0.5	1

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1519	Genetic variation of two apterous wasps <i>Haplogonatopus apicalis</i> and <i>H. oratorius</i> (Hymenoptera: Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	0.6	10
1520	Complex patterns of population genetic structure of moose, <i>Alces alces</i> , after recent spatial expansion in Poland revealed by sex-linked markers. <i>Acta Theriologica</i> , 2013, 58, 367-378.	1.1	21
1521	Cytochrome b gene (<i>cytb</i>) sequence diversity in a <i>Microtus oeconomus</i> population from Bialowieza Primeval Forest. <i>Acta Theriologica</i> , 2013, 58, 119-126.	1.1	7
1522	Evidence of recombination and genetic diversity in southern rice black-streaked dwarf virus. <i>Archives of Virology</i> , 2013, 158, 2147-2151.	0.9	15
1523	Range-wide conservation genetics of Buff-breasted Sandpipers (<i>Tryngites subruficollis</i>). <i>Auk</i> , 2013, 130, 429-439.	0.7	5
1524	Multiple cases of asymmetric introgression among horseshoe bats detected by phylogenetic conflicts across loci. <i>Biological Journal of the Linnean Society</i> , 2013, 110, 346-361.	0.7	18
1525	Genetic diversity and maternal origin of Bangladeshi chicken. <i>Molecular Biology Reports</i> , 2013, 40, 4123-4128.	1.0	20
1526	Diversity and selection of MHC class IIb gene exon3 in Chinese alligator. <i>Molecular Biology Reports</i> , 2013, 40, 295-301.	1.0	4
1527	Exploring the pattern of phenotypic and genetic polymorphism in the arsenic hyperaccumulator <i>Pteris vittata</i> L. (Chinese brake fern). <i>Plant and Soil</i> , 2013, 373, 471-483.	1.8	2
1528	Complete Chloroplast Genome of <i>Chionographis japonica</i> (Willd.) Maxim. (Melanthiaceae): Comparative Genomics and Evaluation of Universal Primers for Liliales. <i>Plant Molecular Biology Reporter</i> , 2013, 31, 1407-1421.	1.0	26
1529	Phylogenetic Analyses of Teleki Grapevine Rootstocks Using Three Chloroplast DNA Markers. <i>Plant Molecular Biology Reporter</i> , 2013, 31, 371-386.	1.0	12
1530	Molecular population genetics of male and female mitochondrial genomes in subarctic <i>Mytilus trossulus</i> . <i>Marine Biology</i> , 2013, 160, 1709-1721.	0.7	40
1531	Complex genetic patterns and a phylogeographic disjunction among New Zealand mud snails <i>Zeacumantus subcarinatus</i> and <i>Z. lutulentus</i> . <i>Marine Biology</i> , 2013, 160, 1477-1488.	0.7	12
1532	Hydrology influences population genetic structure and connectivity of the intertidal amphipod <i>Corophium volutator</i> in the northwest Atlantic. <i>Marine Biology</i> , 2013, 160, 1015-1027.	0.7	11
1533	Rapid Evolution of a Few Members of Nasuta-Albomicans Complex of <i>Drosophila</i> : Study on Two Candidate Genes, <i>Sod1</i> and <i>Rpd3</i> . <i>Journal of Molecular Evolution</i> , 2013, 76, 311-323.	0.8	4
1534	Evolution of an Ancient Microsatellite Hotspot in the Conifer Mitochondrial Genome and Comparison with Other Plants. <i>Journal of Molecular Evolution</i> , 2013, 76, 146-157.	0.8	16
1535	Diversity of <i>Wolbachia</i> in Natural Populations of Spider Mites (genus <i>Tetranychus</i>): Evidence for Complex Infection History and Disequilibrium Distribution. <i>Microbial Ecology</i> , 2013, 65, 731-739.	1.4	31
1536	<i>Campylobacter</i> spp. Recovered from the Upper Oconee River Watershed, Georgia in a 4-Year Study. <i>Microbial Ecology</i> , 2013, 65, 22-27.	1.4	10

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1537	Influence of late Quaternary climate change on present patterns of genetic variation in valley oak, <i>Quercus lobata</i> Née. <i>Molecular Ecology</i> , 2013, 22, 3598-3612.	2.0	127
1538	The Southwestern Indian Ocean as a potential marine evolutionary hotspot: perspectives from comparative phylogeography of reef brittlestars. <i>Journal of Biogeography</i> , 2013, 40, 2167-2179.	1.4	55
1539	The 5S rDNA High Dynamism in <i>Diplodus sargus</i> is a Transposon-Mediated Mechanism. Comparison with Other Multigene Families and Sparidae Species. <i>Journal of Molecular Evolution</i> , 2013, 76, 83-97.	0.8	26
1540	Comparative genome characterization of <i>Achromobacter</i> members reveals potential genetic determinants facilitating the adaptation to a pathogenic lifestyle. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 6413-6425.	1.7	45
1541	Hidden species diversity of Australian burrowing snakes (Ramphotyphlops). <i>Biological Journal of the Linnean Society</i> , 2013, 110, 427-441.	0.7	38
1542	Phylogeography of two closely related species of <i>Nolana</i> from the coastal Atacama Desert of Chile: post-glacial population expansions in response to climate fluctuations. <i>Journal of Biogeography</i> , 2013, 40, 2191-2203.	1.4	29
1543	Stable Pleistocene-Era Populations of <i>Chaerephon pumilus</i> (Chiroptera: Molossidae) in Southeastern Africa do not use Different Echolocation Calls. <i>African Zoology</i> , 2013, 48, 125-142.	0.2	1
1544	<i>Burkholderia pseudomultivorans</i> sp. nov., a novel <i>Burkholderia cepacia</i> complex species from human respiratory samples and the rhizosphere. <i>Systematic and Applied Microbiology</i> , 2013, 36, 483-489.	1.2	128
1545	Cryptic diversity in <i>Brevipalpus</i> mites (Tenuipalpidae). <i>Zoologica Scripta</i> , 2013, 42, 406-426.	0.7	39
1546	Left-right dewlap asymmetry and phylogeography of <i>Anolis lineatus</i> on Aruba and Curaçao. <i>Biological Journal of the Linnean Society</i> , 2013, 110, 409-426.	0.7	17
1547	Comparison of <i>Botrytis cinerea</i> populations isolated from two open-field cultivated host plants. <i>Microbiological Research</i> , 2013, 168, 379-388.	2.5	27
1548	An extensive candidate gene approach to speciation: diversity, divergence and linkage disequilibrium in candidate pigmentation genes across the European crow hybrid zone. <i>Heredity</i> , 2013, 111, 467-473.	1.2	30
1549	Phylogenetic Relationship of the Greater White-Fronted Goose <i>Anser albifrons</i> Subspecies Wintering in the Palearctic Region. <i>Ornithological Science</i> , 2013, 12, 35-42.	0.3	3
1550	Population genetics of <i>Wolbachia</i> -infected, parthenogenetic and uninfected, sexual populations of <i>Trastichus coeruleus</i> (Hymenoptera: Tj ETQq1 1 0.784314 rgBT Overlock 10 Tf 50 21		
1551	Molecular characterization of trophic ecology within an island radiation of insect herbivores (Curculionidae: Entiminae: <i>Ceratopus</i>). <i>Molecular Ecology</i> , 2013, 22, 5441-5455.	2.0	32
1552	Multilocus phylogeographic assessment of the California Mountain Kingsnake (<i>Lampropeltis zonata</i>) suggests alternative patterns of diversification for the California Floristic Province. <i>Molecular Ecology</i> , 2013, 22, 5418-5429.	2.0	45
1553	Phylogeography of the heathers <i>Erica arborea</i> and <i>E. trimera</i> in the afro-alpine "sky islands" inferred from AFLPs and plastid DNA sequences. <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2013, 208, 453-463.	0.6	29
1554	Genetic structure of an endangered raptor at individual and population levels. <i>Conservation Genetics</i> , 2013, 14, 1135-1147.	0.8	16

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1555	A novel <i>hAT</i> element in <i>Bombyx mori</i> and <i>Rhodnius prolixus</i> : its relationship with miniature inverted repeat transposable elements (MITEs) and horizontal transfer. <i>Insect Molecular Biology</i> , 2013, 22, 584-596.	1.0	15
1556	Molecular phylogeny of an ancient rodent family (Aplodontiidae). <i>Journal of Mammalogy</i> , 2013, 94, 529-543.	0.6	8
1557	Complex dynamic of dengue virus serotypes 2 and 3 in Cambodia following series of climate disasters. <i>Infection, Genetics and Evolution</i> , 2013, 15, 77-86.	1.0	11
1558	Evolutionary and dispersal history of Eurasian house mice <i>Mus musculus</i> clarified by more extensive geographic sampling of mitochondrial DNA. <i>Heredity</i> , 2013, 111, 375-390.	1.2	113
1559	Mining of rice blast resistance gene Pi54 shows effect of single nucleotide polymorphisms on phenotypic expression of the alleles. <i>European Journal of Plant Pathology</i> , 2013, 137, 55-65.	0.8	35
1560	A population genetics-based approach reveals candidate gene regions important in the determination of resistance specificity for the Pik family of rice blast resistance genes. <i>Journal of General Plant Pathology</i> , 2013, 79, 178-181.	0.6	3
1561	Spatial spread and demographic expansion of Lyme borreliosis spirochaetes in Eurasia. <i>Infection, Genetics and Evolution</i> , 2013, 14, 147-155.	1.0	43
1562	From southern refugia to the northern range margin: genetic population structure of the common wall lizard, <i>Podarcis muralis</i> . <i>Journal of Biogeography</i> , 2013, 40, 1475-1489.	1.4	40
1563	Diversity of Endosymbiotic <i>Nostoc</i> in <i>Gunnera magellanica</i> (L) from Tierra del Fuego, Chile. <i>Microbial Ecology</i> , 2013, 66, 335-350.	1.4	20
1564	A Late Holocene Population Bottleneck in California Tule Elk (<i>Cervus elaphus nannodes</i>): Provisional Support from Ancient DNA. <i>Journal of Archaeological Method and Theory</i> , 2013, 20, 495-524.	1.4	15
1565	Molecular diversity of Rice grassy stunt virus in Vietnam. <i>Virus Genes</i> , 2013, 46, 383-386.	0.7	9
1566	Late-Pleistocene Phylogeography and Demographic History of Two Evolutionary Lineages of <i>Artibeus jamaicensis</i> (Chiroptera: Phyllostomidae) in Mexico. <i>Acta Chiropterologica</i> , 2013, 15, 19-33.	0.2	9
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1582	Molecular diversity and population structure at the Cytochrome P450 3A5 gene in Africa. <i>BMC Genetics</i> , 2013, 14, 34.	2.7	49
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1589	Multilocus sequence analysis of <i>Treponema denticola</i> strains of diverse origin. <i>BMC Microbiology</i> , 2013, 13, 24.	1.3	13
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1601	Phylogeography in the northern Andes: Complex history and cryptic diversity in a cloud forest frog, <i>Pristimantis w-nigrum</i> (Craugastoridae). <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 417-429.	1.2	24
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1610	Molecular characterisation of the amino- and carboxyl-domains in different Glu-A1x alleles of <i>Triticum urartu</i> Thum. ex Gandil.. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1703-1711.	1.8	8
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1614	Phylogeography of <i>Quercus phillyraeoides</i> (Fagaceae) in Japan as revealed by chloroplast DNA variation. <i>Journal of Forest Research</i> , 2013, 18, 361-370.	0.7	11
1615	Phylogeographical Features of <i>Octopus vulgaris</i> and <i>Octopus insularis</i> in the Southeastern Atlantic Based on the Analysis of Mitochondrial Markers. <i>Journal of Shellfish Research</i> , 2013, 32, 325-339.	0.3	24
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1618	Population genetic data of a model symbiotic cnidarian system reveal remarkable symbiotic specificity and vectored introductions across ocean basins. <i>Molecular Ecology</i> , 2013, 22, 4499-4515.	2.0	119
1619	Unique arylalkylamine <i>N</i> -acetyltransferase-2 polymorphism in Salmonids and profound variations in thermal stability and catalytic efficiency conferred by two residues. <i>Journal of Experimental Biology</i> , 2013, 216, 1938-48.	0.8	16
1620	Dispersal patterns and population structuring among platypuses, <i>Ornithorhynchus anatinus</i> , throughout south-eastern Australia. <i>Conservation Genetics</i> , 2013, 14, 837-853.	0.8	14
1621	Phylogenetic structure among pocket gopher populations, genus <i>Thomomys</i> (Rodentia): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 873-891.	1.0	4
1622	A multigene phylogeny demonstrates that <i>Tuber aestivum</i> and <i>Tuber uncinatum</i> are conspecific. <i>Organisms Diversity and Evolution</i> , 2013, 13, 503-512.	0.7	17
1623	Natural variation and artificial selection in four genes determine grain shape in rice. <i>New Phytologist</i> , 2013, 200, 1269-1280.	3.5	70
1624	The role of <i>Bh4</i> in parallel evolution of hull colour in domesticated and weedy rice. <i>Journal of Evolutionary Biology</i> , 2013, 26, 1738-1749.	0.8	40
1625	Characterization of MHC class II B polymorphism in bottlenecked New Zealand saddlebacks reveals low levels of genetic diversity. <i>Immunogenetics</i> , 2013, 65, 619-633.	1.2	21
1626	Peculiarities of phosphoglycerate kinase-1 pseudogene evolution in Schrenck salamander (<i>Salamandrella schrenckii</i> Strauch 1870). <i>Russian Journal of Genetics</i> , 2013, 49, 722-729.	0.2	1

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1628	Molecular genetic identification and phylogeny of <i>Daphnia</i> species (Crustacea, Cladocera) from water bodies of the Lake Chany basin. <i>Russian Journal of Genetics</i> , 2013, 49, 206-213.	0.2	15
1629	No reproductive character displacement in male advertisement signals of <i>Hyla japonica</i> in relation to the sympatric <i>H. suweonensis</i> . <i>Behavioral Ecology and Sociobiology</i> , 2013, 67, 1345-1355.	0.6	25
1630	Differentiation in the Atlantic Forest: phylogeography of <i>Akodon montensis</i> (Rodentia). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10</i> 94, 911-922.	0.6	35
1631	Genetic phylogeography and maternal lineages of 18 Chinese black goat breeds. <i>Tropical Animal Health and Production</i> , 2013, 45, 1833-1837.	0.5	8
1632	Nucleotide sequence analysis of two lignin genes in <i>Acacia auriculiformis</i> × <i>Acacia mangium</i> hybrid for enhancement of wood pulp quality. <i>Tree Genetics and Genomes</i> , 2013, 9, 1369-1381.	0.6	2
1633	Insights into drought adaptation of two European oak species revealed by nucleotide diversity of candidate genes. <i>Tree Genetics and Genomes</i> , 2013, 9, 1179-1192.	0.6	24
1634	Molecular identification of natural mangrove hybrids of <i>Rhizophora</i> in Peninsular Malaysia. <i>Tree Genetics and Genomes</i> , 2013, 9, 1151-1160.	0.6	16
1635	Genetic structure and different color morphotypes suggest the occurrence and bathymetric segregation of two incipient species of <i>Sebastes</i> off Argentina. <i>Die Naturwissenschaften</i> , 2013, 100, 645-658.	0.6	13
1636	Extraordinary micro-endemism in Australian desert spring amphipods. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 645-653.	1.2	54
1637	The phylogenetic status of typical Chinese native pigs: analyzed by Asian and European pig mitochondrial genome sequences. <i>Journal of Animal Science and Biotechnology</i> , 2013, 4, 9.	2.1	19
1638	MHC II DRB variation and trans-species polymorphism in the golden snub-nosed monkey (<i>Rhinopithecus</i>). <i>Tj ETQq1 1 0.784314 rgBT /Ov</i> 1,7 9	1.7	9
1639	Molecular demographic history of the Hainan Peacock Pheasant (<i>Polyplectron katsumatae</i>) and its conservation implications. <i>Science Bulletin</i> , 2013, 58, 2185-2190.	1.7	6
1640	Comparative genomics of four Liliales families inferred from the complete chloroplast genome sequence of <i>Veratrum patulum</i> O. Loes. (Melanthiaceae). <i>Gene</i> , 2013, 530, 229-235.	1.0	47
1641	Molecular phylogeny, population genetics, and evolution of heterocystous cyanobacteria using <i>nifH</i> gene sequences. <i>Protoplasma</i> , 2013, 250, 751-764.	1.0	31
1642	Reflects the coat protein variability of apple mosaic virus host preference?. <i>Virus Genes</i> , 2013, 47, 119-125.	0.7	13
1643	Genetic diversity and population structure of the endangered ripon barbel, <i>Barbus altianalis</i> (Boulenger, 1900) in Lake Victoria catchment, Kenya based on mitochondrial DNA sequences. <i>Journal of Applied Ichthyology</i> , 2013, 29, 1225-1233.	0.3	9
1644	Contemporary genetic structure reflects historical drainage isolation in an Australian snapping turtle, <i>Elseya albagula</i> . <i>Zoological Journal of the Linnean Society</i> , 2013, 169, 200-214.	1.0	9

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1646	Phylogeography and genetic diversity of the Robin (<i>Erithacus rubecula</i>) in the Azores Islands: Evidence of a recent colonisation. <i>Journal of Ornithology</i> , 2013, 154, 889-900.	0.5	15
1647	A golden jackal (<i>Canis aureus</i>) from Austria bearing <i>Hepatozoon canis</i> import due to immigration into a non-endemic area?. <i>Ticks and Tick-borne Diseases</i> , 2013, 4, 133-137.	1.1	37
1648	Reproductive Cycle and Strategy of <i>Anodonta anatina</i> (L., 1758): Notes on Hermaphroditism. <i>Journal of Experimental Zoology</i> , 2013, 319, 378-390.	1.2	39
1649	Evolution of Functional Genes in Cetaceans Driven by Natural Selection on a Phylogenetic and Population Level. <i>Evolutionary Biology</i> , 2013, 40, 341-354.	0.5	2
1650	Genetic diversity and phylogeny of the family Osteoglossidae by the nuclear 18S ribosomal RNA and implications for its conservation. <i>Biochemical Systematics and Ecology</i> , 2013, 51, 280-287.	0.6	4
1651	Mitochondrial phylogeography of the red-tailed knobby newt (<i>Tylototriton kweichowensis</i>). <i>Biochemical Systematics and Ecology</i> , 2013, 51, 195-202.	0.6	1
1652	Population deviation of piggery-associated methicillin-resistant <i>Staphylococcus aureus</i> based on <i>mec</i> -associated direct repeat unit analysis. <i>Infection, Genetics and Evolution</i> , 2013, 16, 349-354.	1.0	2
1653	Multilocus population genetic analysis of the Southwest Pacific malaria vector <i>Anopheles punctulatus</i> . <i>International Journal for Parasitology</i> , 2013, 43, 825-835.	1.3	8
1654	Occurrence, sequence polymorphism and population structure of <i>Circulifer tenellus</i> virus 1 in a field population of the beet leafhopper. <i>Virus Research</i> , 2013, 176, 307-311.	1.1	2
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1656	Analysis of mitochondrial genome diversity identifies new and ancient maternal lineages in Cambodian aborigines. <i>Nature Communications</i> , 2013, 4, 2599.	5.8	37
1657	Differential spreading of <i>Hinfl</i> satellite DNA variants during radiation in Centaureinae. <i>Annals of Botany</i> , 2013, 112, 1793-1802.	1.4	11
1658	Isolation of the MAT1-1 mating type idiomorph and evidence for selfing in the Chinese medicinal fungus <i>Ophiocordyceps sinensis</i> . <i>Fungal Biology</i> , 2013, 117, 599-610.	1.1	42
1659	Quantitation of HIV-1 DNA with a sensitive TaqMan assay that has broad subtype specificity. <i>Journal of Virological Methods</i> , 2013, 187, 94-102.	1.0	15
1660	<i>Pseudoplusia includens</i> single nucleopolyhedrovirus: Genetic diversity, phylogeny and hypervariability of the <i>pif-2</i> gene. <i>Journal of Invertebrate Pathology</i> , 2013, 114, 258-267.	1.5	19
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1664	<i>Plasmodium falciparum</i> mitochondrial genetic diversity exhibits isolation-by-distance patterns supporting a sub-Saharan African origin. <i>Mitochondrion</i> , 2013, 13, 630-636.	1.6	15
1665	Biogeographic Determinants of Genetic Diversification in the Mouse Opossum <i>Gracilinanus agilis</i> (Didelphimorphia: Didelphidae). <i>Journal of Heredity</i> , 2013, 104, 613-626.	1.0	36
1666	Simultaneous Purifying Selection on the Ancestral MC1R Allele and Positive Selection on the Melanoma-Risk Allele V60L in South Europeans. <i>Molecular Biology and Evolution</i> , 2013, 30, 2654-2665.	3.5	30
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1671	Relative importance of pollen and seed dispersal across a <sc>N</sc>eotropical mountain landscape for an epiphytic orchid. <i>Molecular Ecology</i> , 2013, 22, 6048-6059.	2.0	29
1672	Genetic Diversity and Natal Origins of Green Turtles (<i>Chelonia mydas</i>) in the Western Gulf of Mexico. <i>Journal of Herpetology</i> , 2013, 47, 251-257.	0.2	16
1673	Global spread and genetic variants of the two CYP9M10 haplotype forms associated with insecticide resistance in <i>Culex quinquefasciatus</i> Say. <i>Heredity</i> , 2013, 111, 216-226.	1.2	19
1674	Mitochondrial DNA polymorphisms shared between modern humans and neanderthals: Adaptive convergence or evidence for interspecific hybridization?. <i>Russian Journal of Genetics</i> , 2013, 49, 975-978.	0.2	1
1675	Whole-genome sequencing of two <sc>N</sc>orth <sc>A</sc>merican <sc>D</sc>rosophila melanogaster</i> populations reveals genetic differentiation and positive selection. <i>Molecular Ecology</i> , 2013, 22, 5084-5097.	2.0	47
1676	Rye <sc>P</sc>m8</i> and wheat <sc>P</sc>m3</i> are orthologous genes and show evolutionary conservation of resistance function against powdery mildew. <i>Plant Journal</i> , 2013, 76, 957-969.	2.8	178
1677	Identification of the <i>Daphnia</i> species (Crustacea: Cladocera) in the lakes of the Ob and Yenisei River basins: morphological and molecular phylogenetic approaches. <i>Hydrobiologia</i> , 2013, 715, 135-150.	1.0	20
1678	Multi-locus typing scheme for <i>Babesia bovis</i> and <i>Babesia bigemina</i> reveals high levels of genetic variability in strains from Northern Argentina. <i>Infection, Genetics and Evolution</i> , 2013, 14, 214-222.	1.0	12
1679	OUTBREEDING DEPRESSION WITH LOW GENETIC VARIATION IN SELFING<i>CAENORHABDITIS</i>NEMATODES. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 3087-3101.	1.1	55
1680	Complete mitochondrial genomes from four subspecies of common chaffinch (<i>Fringilla coelebs</i>): New inferences about mitochondrial rate heterogeneity, neutral theory, and phylogenetic relationships within the order Passeriformes. <i>Gene</i> , 2013, 517, 37-45.	1.0	13

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1682	Impact of an intragenic retrotransposon on the structural integrity and evolution of a major isoprenoid biosynthesis pathway gene in <i>Hevea brasiliensis</i> . <i>Plant Physiology and Biochemistry</i> , 2013, 73, 176-188.	2.8	32
1683	Complete Mitochondrial Genomes of Ancient Canids Suggest a European Origin of Domestic Dogs. <i>Science</i> , 2013, 342, 871-874.	6.0	438
1684	Molecular and morphological evidence of hybridization between native <i>Ruditapes philippinarum</i> and the introduced <i>Ruditapes</i> form in Japan. <i>Conservation Genetics</i> , 2013, 14, 717-733.	0.8	22
1685	Mitochondrial cytochrome b gene variation in brown bear (<i>Ursus arctos</i> Linnaeus, 1758) from southern part of Russian Far East. <i>Russian Journal of Genetics</i> , 2013, 49, 1213-1218.	0.2	9
1686	Allelic diversity and molecular characterization of puroindoline genes in five diploid species of the <i>Aegilops</i> genus. <i>Journal of Experimental Botany</i> , 2013, 64, 5133-5143.	2.4	14
1687	Multiple gene genealogical analyses of a nematophagous fungus <i>Paecilomyces lilacinus</i> from China. <i>Journal of Microbiology</i> , 2013, 51, 423-429.	1.3	5
1688	Extremely High Copy Numbers and Polymorphisms of the rDNA Operon Estimated from Single Cell Analysis of <i>Oligotrich</i> and <i>Peritrich</i> Ciliates. <i>Protist</i> , 2013, 164, 369-379.	0.6	259
1689	Genetic variability and evolution of rice stripe virus. <i>Journal of Zhejiang University: Science B</i> , 2013, 14, 875-885.	1.3	11
1690	Corolla morphology influences diversification rates in bifid toadflaxes (<i>Linaria</i> sect. <i>Versicolores</i>). <i>Annals of Botany</i> , 2013, 112, 1705-1722.	1.4	43
1691	Polymorphism at genes involved in salt tolerance in <i>Arabidopsis thaliana</i> (Brassicaceae). <i>American Journal of Botany</i> , 2013, 100, 384-390.	0.8	4
1692	Continent-wide panmixia of an African fruit bat facilitates transmission of potentially zoonotic viruses. <i>Nature Communications</i> , 2013, 4, 2770.	5.8	105
1693	Self-maintaining or continuously refreshed? The genetic structure of <i>Euphausia lucens</i> populations in the Benguela upwelling ecosystem. <i>Journal of Plankton Research</i> , 2013, 35, 982-992.	0.8	5
1694	Congruence between <i>mcy</i> based genetic type and microcystin composition within the populations of toxic <i>Microcystis</i> in a plateau lake, China. <i>Environmental Microbiology Reports</i> , 2013, 5, 637-647.	1.0	3
1695	Evolutionary perspective on hepatitis B virus with an expanded sampling strategy. <i>Virus Research</i> , 2013, 178, 525-529.	1.1	0
1696	The Function and Evolution of Closely Related COR/LEA (Cold-Regulated/Late Embryogenesis Abundant) Proteins in <i>Arabidopsis thaliana</i> . , 2013, , 89-105.		5
1697	Diversity and endemism of Murinae rodents in Thai limestone karsts. <i>Systematics and Biodiversity</i> , 2013, 11, 323-344.	0.5	28
1698	Concordant mitochondrial and microsatellite DNA structuring between Polish lowland and Carpathian Mountain wolves. <i>Conservation Genetics</i> , 2013, 14, 573-588.	0.8	58

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1700	Hybridization may facilitate in situ survival of endemic species through periods of climate change. <i>Nature Climate Change</i> , 2013, 3, 1039-1043.	8.1	94
1701	Genetic Evidence of Paleolithic Colonization and Neolithic Expansion of Modern Humans on the Tibetan Plateau. <i>Molecular Biology and Evolution</i> , 2013, 30, 1761-1778.	3.5	194
1702	Human Genetic Data Reveal Contrasting Demographic Patterns between Sedentary and Nomadic Populations That Predate the Emergence of Farming. <i>Molecular Biology and Evolution</i> , 2013, 30, 2629-2644.	3.5	40
1703	Elucidating the native sources of an invasive tree species, <i>Acacia pycnantha</i> , reveals unexpected native range diversity and structure. <i>Annals of Botany</i> , 2013, 111, 895-904.	1.4	19
1704	Assessment of drug resistance related genes as candidate markers for treatment outcome prediction of cutaneous leishmaniasis in Brazil. <i>Acta Tropica</i> , 2013, 126, 132-141.	0.9	18
1705	Eco-geographical differentiation among Colombian populations of the Chagas disease vector <i>Triatoma dimidiata</i> (Hemiptera: Reduviidae). <i>Infection, Genetics and Evolution</i> , 2013, 20, 352-361.	1.0	29
1706	Comparative phylogeography of the <i>Smilax hispida</i> group (Smilacaceae) in eastern Asia and North America – Implications for allopatric speciation, causes of diversity disparity, and origins of temperate elements in Mexico. <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 300-311.	1.2	35
1707	Genetic variability within and among <i>Haemonchus contortus</i> isolates from goats and sheep in China. <i>Parasites and Vectors</i> , 2013, 6, 279.	1.0	41
1708	Virulence and Molecular Diversity of <i>Venturia inaequalis</i> in Commercial Apple Growing Regions in Kashmir. <i>Journal of Phytopathology</i> , 2013, 161, 271-279.	0.5	15
1709	Phylogeography of the Indo-West Pacific maskrays (Dasyatidae, <i>Neotrygon</i>): a complex example of chondrichthyan radiation in the Cenozoic. <i>Ecology and Evolution</i> , 2013, 3, 217-232.	0.8	51
1710	Phylogeny and Classification of <i>Prunus sensu lato</i> (Rosaceae). <i>Journal of Integrative Plant Biology</i> , 2013, 55, 1069-1079.	4.1	124
1711	RECENT ECOLOGICAL SELECTION ON REGULATORY DIVERGENCE IS SHAPING CLINAL VARIATION IN <i>Senecio</i> ON MOUNT ETNA. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, n/a-n/a.	1.1	16
1712	Frequent recombination shapes the epidemic population structure of <i>Pseudomonas</i> (<i>Cyanoprokaryota</i>) in Italian subalpine lakes. <i>Journal of Phycology</i> , 2013, 49, 1107-1117.	1.0	26
1713	Genetic variation of the Turnip mosaic virus population of Vietnam: A case study of founder, regional and local influences. <i>Virus Research</i> , 2013, 171, 138-149.	1.1	44
1714	Biogeography and host-related factors trump parasite life history: limited congruence among the genetic structures of specific ectoparasitic lice and their rodent hosts. <i>Molecular Ecology</i> , 2013, 22, 5185-5204.	2.0	50
1715	On the reliability of DNA sequences of <i>Ophiocordyceps sinensis</i> in public databases. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2013, 40, 365-378.	1.4	11
1716	Nocturnal Light Environments Influence Color Vision and Signatures of Selection on the OPN1SW Opsin Gene in Nocturnal Lemurs. <i>Molecular Biology and Evolution</i> , 2013, 30, 1420-1437.	3.5	96

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1718	Pliocene intraspecific divergence and Pliocene range expansions within <i>Picea likiangensis</i> (Lijiang spruce), a dominant forest tree of the Qinghai-Tibet Plateau. <i>Molecular Ecology</i> , 2013, 22, 5237-5255.	2.0	112
1719	Genetic Diversity of Fluorescent Proteins in Caribbean Agariciid Corals. <i>Journal of Heredity</i> , 2013, 104, 572-577.	1.0	2
1720	Inferences of evolutionary history of a widely distributed mangrove species, <i>Bruguiera gymnorrhiza</i> , in the Indo-West Pacific region. <i>Ecology and Evolution</i> , 2013, 3, 2251-2261.	0.8	35
1721	Genome-wide identification and characterisation of F-box family in maize. <i>Molecular Genetics and Genomics</i> , 2013, 288, 559-577.	1.0	63
1722	Phylogeography and historical demography of <i>Sicydium salvini</i> in the eastern Pacific. <i>Ichthyological Research</i> , 2013, 60, 353-362.	0.5	8
1723	Molecular identification and morphological description of totoaba <i>Totoaba macdonaldi</i> and <i>curvina Cynoscion reticulatus</i> preflexion larvae (Perciformes: Sciaenidae). <i>Ichthyological Research</i> , 2013, 60, 390-395.	0.5	9
1724	Mitochondrial DNA diversity of mud crab <i>Scylla olivacea</i> (Portunidae) in Peninsular Malaysia: a preliminary assessment. <i>Molecular Biology Reports</i> , 2013, 40, 6407-6418.	1.0	6
1725	Molecular phylogeny of Indian horse breeds with special reference to Manipuri pony based on mitochondrial D-loop. <i>Molecular Biology Reports</i> , 2013, 40, 5861-5867.	1.0	7
1726	Paleoclimatic modeling and phylogeography of least killifish, <i>Heterandria formosa</i> : insights into Pleistocene expansion-contraction dynamics and evolutionary history of North American Coastal Plain freshwater biota. <i>BMC Evolutionary Biology</i> , 2013, 13, 223.	3.2	29
1727	Positive selection in glycolysis among Australasian stick insects. <i>BMC Evolutionary Biology</i> , 2013, 13, 215.	3.2	25
1728	Molecular taxonomy of the two <i>Leishmania</i> vectors <i>Lutzomyia umbratilis</i> and <i>Lutzomyia anduzei</i> (Diptera: Psychodidae) from the Brazilian Amazon. <i>Parasites and Vectors</i> , 2013, 6, 258.	1.0	31
1729	Contrasted evolutionary histories of two Toll-like receptors (Tlr4 and Tlr7) in wild rodents (MURINAE). <i>BMC Evolutionary Biology</i> , 2013, 13, 194.	3.2	58
1730	Strong population genetic structuring in an annual fish, <i>Nothobranchius furzeri</i> , suggests multiple savannah refugia in southern Mozambique. <i>BMC Evolutionary Biology</i> , 2013, 13, 196.	3.2	62
1731	Maternal phylogenetic relationships and genetic variation among Arabian horse populations using whole mitochondrial DNA D-loop sequencing. <i>BMC Genetics</i> , 2013, 14, 83.	2.7	33
1732	Nucleotide diversity and linkage disequilibrium of adaptive significant genes in <i>Larix</i> (Pinaceae). <i>Russian Journal of Genetics</i> , 2013, 49, 915-923.	0.2	7
1733	Molecular characterization and identification of members of the <i>Anopheles subpictus</i> complex in Sri Lanka. <i>Malaria Journal</i> , 2013, 12, 304.	0.8	43
1734	Insights into the European rabbit (<i>Oryctolagus cuniculus</i>) innate immune system: genetic diversity of the toll-like receptor 3 (TLR3) in wild populations and domestic breeds. <i>BMC Genetics</i> , 2013, 14, 73.	2.7	25

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1736	Effect of malaria transmission reduction by insecticide-treated bed nets (ITNs) on the genetic diversity of <i>Plasmodium falciparum</i> merozoite surface protein (MSP-1) and circumsporozoite (CSP) in western Kenya. <i>Malaria Journal</i> , 2013, 12, 295.	0.8	8
1737	Merozoite surface protein-3 alpha as a genetic marker for epidemiologic studies in <i>Plasmodium vivax</i> : a cautionary note. <i>Malaria Journal</i> , 2013, 12, 288.	0.8	22
1738	High levels of variation in <i>Salix lignocellulose</i> genes revealed using poplar genomic resources. <i>Biotechnology for Biofuels</i> , 2013, 6, 114.	6.2	6
1739	Twenty-one new sequence markers for population genetics, species delimitation and phylogenetics in wall lizards (<i>Podarcis</i> spp.). <i>BMC Research Notes</i> , 2013, 6, 299.	0.6	4
1740	Gene conversion yields novel gene combinations in paralogs of GOT1 in the copepod <i>Tigriopus californicus</i> . <i>BMC Evolutionary Biology</i> , 2013, 13, 148.	3.2	1
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1742	Molecular evidence supports hypervariability in <i>Phytophthora colocasiae</i> associated with leaf blight of taro. <i>European Journal of Plant Pathology</i> , 2013, 136, 483-494.	0.8	4
1743	Mitochondrial DNA and microsatellite markers evidence a different pattern of hybridization in red-legged partridge (<i>Alectoris rufa</i>) populations from NW Italy. <i>European Journal of Wildlife Research</i> , 2013, 59, 407-419.	0.7	21
1744	Genotypic and phenotypic diversity of <i>Pediococcus pentosaceus</i> strains isolated from food matrices and characterisation of the penocin operon. <i>Antonie Van Leeuwenhoek</i> , 2013, 103, 1149-1163.	0.7	26
1745	A study on the phylogeny and phylogeography of a marine cosmopolite diatom from the southern Black Sea. <i>Oceanological and Hydrobiological Studies</i> , 2013, 42, 406-411.	0.3	2
1746	<i>Amblyomma cajennense</i> (Fabricius, 1787) (Acari: Ixodidae), the Cayenne tick: phylogeography and evidence for allopatric speciation. <i>BMC Evolutionary Biology</i> , 2013, 13, 267.	3.2	117
1747	Evolutionary history of Nile perch <i>Lates</i> sp. inferred from mitochondrial DNA variation analyses. <i>Zoological Studies</i> , 2013, 52, .	0.3	3
1748	Association of microsatellite pairs with segmental duplications in insect genomes. <i>BMC Genomics</i> , 2013, 14, 907.	1.2	6
1749	Molecular and genetic variability in populations of <i>Syngnathus nigrolineatus</i> Eichwald 1831 and ways of expansion in the Volga River basins on the basis of mitochondrial DNA sequence analysis. <i>Russian Journal of Biological Invasions</i> , 2013, 4, 249-254.	0.2	8
1750	A widespread distribution for <i>Arostrilepis tenuicirrosa</i> (Eucestoda: Hymenolepididae) in <i>Myodes voles</i> (Cricetidae: Arvicolinae) from the Palearctic based on molecular and morphological evidence: historical and biogeographic implications. <i>Acta Parasitologica</i> , 2013, 58, 441-52.	0.4	10
1751	Isolation with differentiation followed by expansion with admixture in the tunicate <i>Pyura chilensis</i> . <i>BMC Evolutionary Biology</i> , 2013, 13, 252.	3.2	21
1752	Two Rapidly Evolving Genes Contribute to Male Fitness in <i>Drosophila</i> . <i>Journal of Molecular Evolution</i> , 2013, 77, 246-259.	0.8	6

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1754	Comprehensive analysis of medaka major histocompatibility complex (MHC) class II genes: Implications for evolution in teleosts. <i>Immunogenetics</i> , 2013, 65, 883-895.	1.2	13
1755	Multilocus phylogeny and cryptic diversity in Asian shrew-like moles (<i>Uropsilus</i> , Talpidae): implications for taxonomy and conservation. <i>BMC Evolutionary Biology</i> , 2013, 13, 232.	3.2	28
1756	Molecular identification of a cryptic species in the Amazonian predatory catfish genus <i>Pseudoplatystoma</i> (Bleeker, 1962) from Peru. <i>Genetica</i> , 2013, 141, 347-358.	0.5	19
1757	Cryptic diversity within and amongst spring-associated <i>Stygobromus</i> amphipods (Amphipoda: Tj ETQq0 0 0 rBT /Overlock 10 Tf	1.0	14
1758	Phylogeography of the western jumping mouse (<i>Zapus princeps</i>) detects deep and persistent allopatry with expansion. <i>Journal of Mammalogy</i> , 2013, 94, 1016-1029.	0.6	17
1759	Conservation phylogeography: does historical diversity contribute to regional vulnerability in European tree frogs (<i>Hyla arborea</i>)?. <i>Molecular Ecology</i> , 2013, 22, 5669-5684.	2.0	45
1760	A population genetic model to infer allotetraploid speciation and long-term evolution applied to two yarrow species. <i>New Phytologist</i> , 2013, 199, 609-621.	3.5	17
1761	Population genetic patterns among social groups of the endangered Central American spider monkey (<i>Ateles geoffroyi</i>) in a human-dominated landscape. <i>Ecology and Evolution</i> , 2013, 3, 1388-1399.	0.8	22
1762	Genetics at the verge of extinction: insights from the Iberian lynx. <i>Molecular Ecology</i> , 2013, 22, 5503-5515.	2.0	48
1763	Identification of <i>Channa</i> species using the partial cytochrome c oxidase subunit I (COI) gene as a DNA barcoding marker. <i>Biochemical Systematics and Ecology</i> , 2013, 51, 117-122.	0.6	27
1764	A new species of Brush-Finch (Arremon; Emberizidae) from western Mexico. <i>Wilson Journal of Ornithology</i> , 2013, 125, 443-453.	0.1	11
1765	Genetic differentiation between migratory and sedentary populations of the Northern Boobook (<i>Ninox japonica</i>), with the discovery of a novel cryptic sedentary lineage. <i>Journal of Ornithology</i> , 2013, 154, 987-994.	0.5	4
1766	Speciation Dynamics of the Fruit-Eating Bats (Genus <i>Artibeus</i>): With Evidence of Ecological Divergence in Central American Populations. , 2013, , 315-339.		15
1767	Cytosuclear discordance among Southeast Asian black rats (<i>Rattus rattus</i> complex). <i>Molecular Ecology</i> , 2013, 22, 1019-1034.	2.0	71
1768	Integrated systematics of the <i>Poecilimon luschanis</i> species group (Orthoptera, Tettigoniidae): radiation as a chain of populations in a small heterogeneous area. <i>Zoological Journal of the Linnean Society</i> , 2013, 169, 43-69.	1.0	11
1769	Analyses of the Population Structure in a Global Collection of <i>Phytophthora nicotianae</i> Isolates Inferred from Mitochondrial and Nuclear DNA Sequences. <i>Phytopathology</i> , 2013, 103, 610-622.	1.1	35
1770	Genetic divergence of insular marsh rice rats in subtropical Florida. <i>Journal of Mammalogy</i> , 2013, 94, 897-910.	0.6	6

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1772	Genetic population structure in <i>Siniperca scherzeri</i> (Perciformes: Siniperca) in China inferred from mitochondrial DNA sequences and microsatellite loci. <i>Biochemical Systematics and Ecology</i> , 2013, 51, 160-170.	0.6	4
1773	Extinction and recolonization of maritime Antarctic in the limpet <i>Nacella concinna</i> (Strebel, 1908) during the last glacial cycle: toward a model of Quaternary biogeography in shallow Antarctic invertebrates. <i>Molecular Ecology</i> , 2013, 22, 5221-5236.	2.0	45
1774	Population genetic structure of the <i>Plasmodium vivax</i> circumsporozoite protein (Pvcsp) in Sri Lanka. <i>Gene</i> , 2013, 518, 381-387.	1.0	24
1775	Multilocus genetic diversity and historical biogeography of the endemic wall lizard from <i>Lepidochelys olivacea</i> and <i>Furcifer ormeroti</i> , <i>Pseudis odarctis pityusensis</i> (<i>Squamata: Lacertidae</i>). <i>Molecular Ecology</i> , 2013, 22, 4829-4841.	2.0	23
1776	An empirical comparison of character-based and coalescent-based approaches to species delimitation in a young avian complex. <i>Molecular Ecology</i> , 2013, 22, 4943-4957.	2.0	63
1777	Identification and antiviral activity of common polymorphisms in the APOBEC3 locus in human populations. <i>Virology</i> , 2013, 443, 329-337.	1.1	36
1778	Integrating multiple lines of evidence to better understand the evolutionary divergence of humpback dolphins along their entire distribution range: a new dolphin species in Australian waters?. <i>Molecular Ecology</i> , 2013, 22, 5936-5948.	2.0	67
1779	Genetic differentiation, speciation, and phylogeography of cactus flies (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 427 Td (Neriidae: Linnean Society, 2013, 110, 245-256.	0.7	12
1780	Population genetics and phylogenetic relationships of beetles (Coleoptera: Histeridae and) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 427 Td (Neriidae: Phylogenetics and Evolution, 2013, 69, 491-501.	1.2	15
1781	Phylogeography of Beck's Desert Scorpion, <i>Paruroctonus becki</i> , reveals Pliocene diversification in the Eastern California Shear Zone and postglacial expansion in the Great Basin Desert. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 502-513.	1.2	25
1782	Haplotype variation at <i>Badh2</i> , the gene determining fragrance in rice. <i>Genomics</i> , 2013, 101, 157-162.	1.3	54
1783	A link between historical population decline in the threatened great bustard and human expansion in Iberia: evidence from genetic and demographic data. <i>Biological Journal of the Linnean Society</i> , 2013, 110, 518-527.	0.7	10
1784	Molecular divergence in tropical tree populations occupying environmental mosaics. <i>Journal of Evolutionary Biology</i> , 2013, 26, 529-544.	0.8	37
1785	Taxonomic Clarification in the Genus <i>Elysia</i> (Gastropoda: Sacoglossa): <i>E. atroviridis</i> and <i>E. setoensis</i> . <i>American Malacological Bulletin</i> , 2013, 31, 25-37.	0.2	10
1786	Molecules and morphology suggest cryptic species diversity and an overall complex taxonomy of fish scale geckos, genus <i>Geckolepis</i> . <i>Organisms Diversity and Evolution</i> , 2013, 13, 87-95.	0.7	11
1787	High-latitude connectivity of the scleractinian coral <i>Acropora tenuis</i> in the south-western Indian Ocean, identified using nuclear intron and mitochondrial sequence data. <i>African Journal of Marine Science</i> , 2013, 35, 233-241.	0.4	5
1788	Migration route estimation of the Jeju striped field mouse <i>Apodemus agrarius chejuensis</i> (Rodentia, Muridae). <i>Mitochondrial DNA</i> , 2013, 24, 137-144.	0.6	11

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1789	Nucleotide diversity of vernalization and flowering time-related genes in a germplasm collection of meadow fescue (<i>Festuca pratensis</i> Huds. syn. <i>Festuca ovina</i>)	0.8	10
1790	Colonization of islands in the Mona Passage by endemic dwarf geckoes (genus <i>Sphaerodactylus</i>)	0.8	10
1791	Is population structure in the European white stork determined by flyway permeability rather than translocation history?. <i>Ecology and Evolution</i> , 2013, 3, 4881-4895.	0.8	19
1792	Natural Genome Diversity of AI-2 Quorum Sensing in <i>Escherichia coli</i> : Conserved Signal Production but Labile Signal Reception. <i>Genome Biology and Evolution</i> , 2013, 5, 16-30.	1.1	26
1793	Long-Distance Movement in a Dusky Great Horned Owl and Limits to Phylogeography for Establishing Provenance. <i>Western North American Naturalist</i> , 2013, 73, 401-408.	0.2	2
1794	Delimiting shades of gray: phylogeography of the Northern Fulmar, <i>Fulmarus glacialis</i> .	0.8	14
1795	Mitochondrial genome diversity and population structure of the giant squid <i>Architeuthis</i> : genetics sheds new light on one of the most enigmatic marine species. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20130273.	1.2	57
1796	Impact of Livestock Grazing on Plant and Small Mammal Communities in the Ruby Mountains, Northeastern Nevada. <i>Western North American Naturalist</i> , 2013, 73, 505-515.	0.2	28
1797	Population Stability of the Northern Desert Nightsnake (<i>Hypsiglena chlorophaea deserticola</i>) during the Pleistocene. <i>Journal of Herpetology</i> , 2013, 47, 432-439.	0.2	7
1798	Estimating the Nucleotide Diversity in <i>Ceratodon purpureus</i> (Ditrichaceae) from 218 Conserved Exon-Primed, Intron-Spanning Nuclear Loci. <i>Applications in Plant Sciences</i> , 2013, 1, 1200387.	0.8	17
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1800	Genetic Diversity and Inferences on Potential Source Areas of Adventive <i>Frankliniella occidentalis</i> (Thysanoptera: Thripidae) in Shandong, China Based on Mitochondrial and Microsatellite Markers. <i>Florida Entomologist</i> , 2013, 96, 964-973.	0.2	16
1801	Use of Morphology and CO1 Barcoding to Test the Validity of <i>Tetraopes huetheri</i> Skillman (Coleoptera: Tenebrionidae)	0.15	3
1802	A novel taxonomic marker that discriminates between morphologically complex actinomycetes. <i>Open Biology</i> , 2013, 3, 130073.	1.5	66
1803	The phylogenetic position of Turkish populations within the European Bitterling, <i>Rhodeus amarus</i> (Osteichthyes: Cyprinidae). <i>Zoology in the Middle East</i> , 2013, 59, 39-50.	0.2	9
1804	Gene Amplification and Functional Diversification of Melanocortin 4 Receptor at an Extremely Polymorphic Locus Controlling Sexual Maturation in the Platyfish. <i>Genetics</i> , 2013, 195, 1337-1352.	1.2	22
1805	Differentiation in neutral genes and a candidate gene in the pied flycatcher: using biological archives to track global climate change. <i>Ecology and Evolution</i> , 2013, 3, 4799-4814.	0.8	17
1806	Barcoding stingless bees: genetic diversity of the economically important genus <i>Scaptotrigona</i> in Mesoamerica. <i>Apidologie</i> , 2013, 44, 1-10.	0.9	27

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1807	Loss of Genetic Variability Induced by Agroecosystems: <i>Chrysoperla externa</i> (Hagen) (Neuroptera: Tj ETQq0 0 0 rgBTJ/Overlock 10 Tf 50	0.5	4
1808	Exploring phylogeography and species limits in the Altai vole (Rodentia: Cricetidae). <i>Biological Journal of the Linnean Society</i> , 2013, 108, 434-452.	0.7	38
1809	Evolutionary history of the sable (<i>Martes zibellina brachyura</i>) on Hokkaido inferred from mitochondrial Cytb and nuclear Mc1r and Tcf25 gene sequences. <i>Acta Theriologica</i> , 2013, 58, 13-24.	1.1	17
1810	Molecular systematics and evolution of the <i>Synallaxis ruficapilla</i> complex (Aves: Furnariidae) in the Atlantic Forest. <i>Molecular Phylogenetics and Evolution</i> , 2013, 67, 86-94.	1.2	24
1811	The uncertainty of Late Pleistocene range expansions in the western Mediterranean: a case study of the colonization of south-eastern Spain by the spur-thighed tortoise, <i>Testudo graeca</i> . <i>Journal of Biogeography</i> , 2013, 40, 323-334.	1.4	25
1812	Hidden diversity in bent-winged bats (Chiroptera: Miniopteridae) of the Western Palearctic and adjacent regions: implications for taxonomy. <i>Zoological Journal of the Linnean Society</i> , 2013, 167, 165-190.	1.0	19
1813	Genetic Variation of <i>Wheat streak mosaic virus</i> in the United States Pacific Northwest. <i>Phytopathology</i> , 2013, 103, 98-104.	1.1	19
1814	Amazon diversification and cross-Andean dispersal of the widespread Neotropical tree species <i>Jacaranda copaia</i> (Bignoniaceae). <i>Journal of Biogeography</i> , 2013, 40, 707-719.	1.4	25
1815	Demographic expansions in South America: Enlightening a complex scenario with genetic and linguistic data. <i>American Journal of Physical Anthropology</i> , 2013, 150, 453-463.	2.1	31
1816	Colonization of vegetation-rich moraines and inference of multiple sources of colonization in the High Arctic for <i>Salix arctica</i> . <i>Conservation Genetics</i> , 2013, 14, 223-229.	0.8	2
1817	Effects of species biology on the historical demography of sharks and their implications for likely consequences of contemporary climate change. <i>Conservation Genetics</i> , 2013, 14, 125-144.	0.8	30
1818	Polymorphism pattern at a miniature inverted-repeat transposable element locus downstream of the domestication gene <i>Teosinte-branched1</i> in wild and domesticated pearl millet. <i>Molecular Ecology</i> , 2013, 22, 327-340.	2.0	7
1819	A geographic mosaic of evolutionary lineages within the insular endemic newt <i>Uroproctus montanus</i> . <i>Molecular Ecology</i> , 2013, 22, 143-156.	2.0	19
1820	Phylogeography of the large <i>Myotis</i> bats (Chiroptera: Vespertilionidae) in Europe, Asia Minor, and Transcaucasia. <i>Biological Journal of the Linnean Society</i> , 2013, 108, 189-209.	0.7	16
1821	Are Ring Ouzel (<i>Turdus torquatus</i>) populations of the low mountain ranges remnants of a broader distribution in the past?. <i>Journal of Ornithology</i> , 2013, 154, 231-237.	0.5	1
1822	Isolation and Characterization of Nucleotide-Binding Site Resistance Gene Homologues in Common Bean (<i>Phaseolus vulgaris</i>). <i>Phytopathology</i> , 2013, 103, 156-168.	1.1	9
1823	The Early Stages of Speciation in Amazonian Forest Frogs: Phenotypic Conservatism Despite Strong Genetic Structure. <i>Evolutionary Biology</i> , 2013, 40, 228-245.	0.5	43
1824	Comparative phylogeography reveals distinct colonization patterns of <i>Crotalus</i> snakes. <i>Journal of Biogeography</i> , 2013, 40, 1143-1155.	1.4	34

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1825	Northern richness and southern poverty: contrasting genetic footprints of glacial refugia in the relictual tree <i>Sciadopitys verticillata</i> (Coniferales: Sciadopityaceae). <i>Biological Journal of the Linnean Society</i> , 2013, 108, 263-277.	0.7	16
1826	Divergent introduction histories among invasive populations of the delicate skink (<i>Lampropholis delicata</i>): has the importance of genetic admixture in the success of biological invasions been overemphasized?. <i>Diversity and Distributions</i> , 2013, 19, 134-146.	1.9	53
1827	New insights into the intricate taxonomy and phylogeny of the <i>Sylvia curruca</i> complex. <i>Molecular Phylogenetics and Evolution</i> , 2013, 67, 72-85.	1.2	17
1828	Intraspecific comparative genomics of <i>Candida albicans</i> mitochondria reveals non-coding regions under neutral evolution. <i>Infection, Genetics and Evolution</i> , 2013, 14, 302-312.	1.0	19
1829	High SNP density in the blacklegged tick, <i>Ixodes scapularis</i> , the principal vector of Lyme disease spirochetes. <i>Ticks and Tick-borne Diseases</i> , 2013, 4, 63-71.	1.1	22
1830	Multilocus phylogeography (mitochondrial, autosomal and Z-chromosomal loci) and genetic consequence of long-distance male dispersal in Black-throated tits (<i>Aegithalos concinnus</i>). <i>Heredity</i> , 2013, 110, 457-465.	1.2	22
1831	A mitochondrial phylogeographic scenario for the most widespread African rodent, <i>Mastomys natalensis</i> . <i>Biological Journal of the Linnean Society</i> , 2013, 108, 901-916.	0.7	58
1832	FEMALE PROMISCUITY IS POSITIVELY ASSOCIATED WITH NEUTRAL AND SELECTED GENETIC DIVERSITY IN PASSERINE BIRDS. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, no-no.	1.1	30
1833	Genetic evidence for multiple introduction events of raccoons (<i>Procyon lotor</i>) in Spain. <i>Biological Invasions</i> , 2013, 15, 687-698.	1.2	30
1834	Earthworms, good indicators for palaeogeographical studies? Testing the genetic structure and demographic history in the peregrine earthworm <i>Aporrectodea trapezoides</i> (Dugès, 1828) in southern Europe. <i>Soil Biology and Biochemistry</i> , 2013, 58, 127-135.	4.2	25
1835	Rapid Hepatitis C Virus Divergence among Chronically Infected Individuals. <i>Journal of Clinical Microbiology</i> , 2013, 51, 629-632.	1.8	16
1836	Quaternary climate and environmental changes have shaped genetic differentiation in a Chinese pheasant endemic to the eastern margin of the Qinghai-Tibetan Plateau. <i>Molecular Phylogenetics and Evolution</i> , 2013, 67, 129-139.	1.2	26
1837	Biosecurity interceptions of an invasive lizard: origin of stowaways and human-assisted spread within New Zealand. <i>Evolutionary Applications</i> , 2013, 6, 324-339.	1.5	30
1838	Assessing model fit in phylogeographical investigations: an example from the North American sandbar willow <i>Salix melanopsis</i> . <i>Journal of Biogeography</i> , 2013, 40, 131-141.	1.4	35
1839	Post-glacial dispersal, rather than in situ glacial survival, best explains the disjunct distribution of the Lusitanian plant species <i>Daboecia cantabrica</i> (Ericaceae). <i>Journal of Biogeography</i> , 2013, 40, 335-344.	1.4	39
1840	Phylogenetic relationships among North Atlantic redfish (genus <i>Sebastes</i>) as revealed by mitochondrial DNA sequence analyses. <i>Journal of Applied Ichthyology</i> , 2013, 29, 82-92.	0.3	6
1841	Codon usage bias: causative factors, quantification methods and genome-wide patterns: with emphasis on insect genomes. <i>Biological Reviews</i> , 2013, 88, 49-61.	4.7	174
1842	RIBOSOMAL RNA GENE DIVERSITY, EFFECTIVE POPULATION SIZE, AND EVOLUTIONARY LONGEVITY IN ASEXUAL GLOMEROMYCOTA. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 207-224.	1.1	24

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1844	The genetic structure of the cosmopolitan three-partner lichen <i>Ramalina farinacea</i> evidences the concerted diversification of symbionts. FEMS Microbiology Ecology, 2013, 83, 310-323.	1.3	64
1845	Distributional records of Tor mahseer <i>Tor tor</i> (Hamilton, 1822) from Southern India. Journal of Applied Ichthyology, 2013, 29, 1086-1090.	0.3	7
1846	Molecular evidence that the deadliest sea snake <i>Enhydrina schistosa</i> (Elapidae: Hydrophiinae) consists of two convergent species. Molecular Phylogenetics and Evolution, 2013, 66, 262-269.	1.2	21
1847	Molecular systematics and phylogeography of the tribe Myonycterini (Mammalia, Pteropodidae) inferred from mitochondrial and nuclear markers. Molecular Phylogenetics and Evolution, 2013, 66, 126-137.	1.2	48
1848	Significance of pre-Quaternary climate change for montane species diversity: Insights from Asian salamanders (Salamandridae: Pachytriton). Molecular Phylogenetics and Evolution, 2013, 66, 380-390.	1.2	36
1849	Genetic diversity and natural selection of Duffy binding protein of <i>Plasmodium vivax</i> Korean isolates. Acta Tropica, 2013, 125, 67-74.	0.9	32
1850	Genealogy and Demographic History of a Widespread Amphibian throughout Indochina. Journal of Heredity, 2013, 104, 72-85.	1.0	23
1851	Positive selection drives rapid evolution of certain amino acid residues in an evolutionarily highly conserved interferon-inducible antiviral protein of fishes. Immunogenetics, 2013, 65, 75-81.	1.2	13
1852	Greater prairie chickens have a compact MHC-B with a single class IA locus. Immunogenetics, 2013, 65, 133-144.	1.2	20
1853	Anti-microbial peptide (AMP): nucleotide variation, gene expression, and host resistance in the white pine blister rust (WPBR) pathosystem. Planta, 2013, 237, 43-54.	1.6	14
1854	Genetic diversity in <i>Artemisia halodendron</i> (Asteraceae) based on chloroplast DNA <i>psbA-trnH</i> region from different hydrothermal conditions in Horqin sandy land, northern China. Plant Systematics and Evolution, 2013, 299, 107-113.	0.3	3
1855	Reticulate evolution of the critical Mediterranean <i>Gagea</i> sect. <i>Didymobulbos</i> (Liliaceae) and its taxonomic implications. Plant Systematics and Evolution, 2013, 299, 413-438.	0.3	27
1856	<i>Onychostoma minnanensis</i> , a new cyprinid species (Teleostei: Cyprinidae) from Fujian, southern mainland China, with comments on the mitogenetic differentiation among related species. Ichthyological Research, 2013, 60, 62-74.	0.5	7
1857	Subspecies of the Central American Squirrel Monkey (<i>Saimiri oerstedii</i>) as Units for Conservation. International Journal of Primatology, 2013, 34, 86-98.	0.9	8
1858	Conservation genetics of endangered leaf-beetle <i>Cheilotoma musciformis</i> populations in Poland. Journal of Insect Conservation, 2013, 17, 67-77.	0.8	16
1859	New nuclear primers for molecular studies of Epinephelidae fishes. Conservation Genetics Resources, 2013, 5, 165-168.	0.4	9
1860	Phylogeography of the garden dormouse <i>Eliomys quercinus</i> in the western Palearctic region. Journal of Mammalogy, 2013, 94, 202-217.	0.6	17

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1861	Effects of late quaternary climate change on Palearctic shrews. <i>Global Change Biology</i> , 2013, 19, 1865-1874.	4.2	24
1862	Extending ecological niche models to the past 120,000 years corroborates the lack of strong phylogeographic structure in the Crested Drongo (<i>Dicrurus forficatus forficatus</i>) on Madagascar. <i>Biological Journal of the Linnean Society</i> , 2013, 108, 658-676.	0.7	20
1863	Genetic structure of the Peruvian scallop <i>Argopecten purpuratus</i> inferred from mitochondrial and nuclear DNA variation. <i>Marine Genomics</i> , 2013, 9, 1-8.	0.4	17
1864	Phylogeographic structure is strong in the Atlantic Forest; predictive power of correlative paleodistribution models, not always. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2013, 51, 114-121.	0.6	34
1865	Predation drives interpopulation differences in parental care expression. <i>Journal of Animal Ecology</i> , 2013, 82, 429-437.	1.3	18
1866	The EU protected taxon <i>Morimus funereus</i> Mulsant, 1862 (Coleoptera: Cerambycidae) and its western Palaearctic allies: systematics and conservation outcomes. <i>Conservation Genetics</i> , 2013, 14, 683-694.	0.8	37
1867	Deep sympatric mtDNA divergence in the autumnal moth (<i>Epirrita autumnata</i>). <i>Ecology and Evolution</i> , 2013, 3, 126-144.	0.8	28
1868	Phylogeny and genetic history of the Siberian salamander (<i>Salamandrella keyserlingii</i> , Dybowski, 1870) inferred from complete mitochondrial genomes. <i>Molecular Phylogenetics and Evolution</i> , 2013, 67, 348-357.	1.2	17
1869	DNA barcoding™ of <i>Schistosoma mansoni</i> across sub-Saharan Africa supports substantial within locality diversity and geographical separation of genotypes. <i>Acta Tropica</i> , 2013, 128, 250-260.	0.9	28
1870	Genome-scale evolution and phylodynamics of H5N1 influenza virus in China during 1996–2012. <i>Veterinary Microbiology</i> , 2013, 167, 383-393.	0.8	16
1871	Dynamic of H5N1 virus in Cambodia and emergence of a novel endemic sub-clade. <i>Infection, Genetics and Evolution</i> , 2013, 15, 87-94.	1.0	27
1872	Differential sequence diversity at merozoite surface protein-1 locus of <i>Plasmodium knowlesi</i> from humans and macaques in Thailand. <i>Infection, Genetics and Evolution</i> , 2013, 18, 213-219.	1.0	24
1873	Identification of a new species of <i>Cercospora</i> causing leaf spot disease in <i>Capsicum assamicum</i> in northeastern India. <i>Research in Microbiology</i> , 2013, 164, 894-902.	1.0	8
1874	Low heterogeneity in populations of the terrestrial earthworm, <i>Metaphire peguana</i> (Rosa, 1890), in Thailand, as revealed by analysis of mitochondrial DNA COI sequences and nuclear allozymes. <i>Biochemical Systematics and Ecology</i> , 2013, 51, 8-15.	0.6	11
1875	Toll like receptor 2 and 4 polymorphisms in malaria endemic populations of India. <i>Human Immunology</i> , 2013, 74, 223-229.	1.2	10
1876	The evolution and diversity of a low complexity vaccine candidate, merozoite surface protein 9 (MSP-9), in <i>Plasmodium vivax</i> and closely related species. <i>Infection, Genetics and Evolution</i> , 2013, 20, 239-248.	1.0	18
1877	The mRNAs of maternally and paternally inherited mtDNAs of the mussel <i>Mytilus galloprovincialis</i> : Start/end points and polycistronic transcripts. <i>Gene</i> , 2013, 520, 156-165.	1.0	8
1878	Diversity of <i>Orientia tsutsugamushi</i> clinical isolates in Cambodia reveals active selection and recombination process. <i>Infection, Genetics and Evolution</i> , 2013, 15, 25-34.	1.0	26

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1879	Comparative and evolutionary analysis of mitochondrial genes in Indian major carps. <i>Biochemical Systematics and Ecology</i> , 2013, 47, 56-73.	0.6	2
1880	Characteristics and virulence factors of livestock associated ST9 methicillin-resistant <i>Staphylococcus aureus</i> with a novel recombinant staphylocoagulase type. <i>Veterinary Microbiology</i> , 2013, 162, 779-784.	0.8	41
1881	Phylogeography of <i>Aedes aegypti</i> (Yellow Fever Mosquito) in South Florida: mtDNA Evidence for Human-Aided Dispersal. <i>American Journal of Tropical Medicine and Hygiene</i> , 2013, 89, 482-488.	0.6	27
1882	Population Genetics and Evaluation of Genetic Evidence for Subspecies in the Semipalmated Sandpiper (<i>Calidris pusilla</i>). <i>Waterbirds</i> , 2013, 36, 166-178.	0.2	7
1883	Multilocus sequence analysis of <i>Aspergillus Sect. Nigri</i> in dried vine fruits of worldwide origin. <i>International Journal of Food Microbiology</i> , 2013, 165, 163-168.	2.1	12
1884	Non-neutral evolution in non-LEE-encoded type III effectors of attaching and effacing <i>Escherichia coli</i> . <i>Microbes and Infection</i> , 2013, 15, 147-151.	1.0	3
1885	Rapid and sustained autologous neutralizing response leading to early spontaneous recovery after HCV infection. <i>Virology</i> , 2013, 444, 90-99.	1.1	16
1886	Association between MT-CO3 haplotypes and high-altitude adaptation in Tibetan chicken. <i>Gene</i> , 2013, 529, 131-137.	1.0	28
1887	Population genetics, sequence diversity and selection in the gene encoding the <i>Plasmodium falciparum</i> apical membrane antigen 1 in clinical isolates from the south-east of Iran. <i>Infection, Genetics and Evolution</i> , 2013, 17, 51-61.	1.0	13
1888	Intraspecific differentiation of <i>Paramecium novaurelia</i> strains (Ciliophora, Protozoa) inferred from phylogenetic analysis of ribosomal and mitochondrial DNA variation. <i>European Journal of Protistology</i> , 2013, 49, 50-61.	0.5	10
1889	Molecular evolution of a polymorphic HSP40-like protein encoded in the histocompatibility locus of an invertebrate chordate. <i>Developmental and Comparative Immunology</i> , 2013, 41, 128-136.	1.0	12
1890	Genetic variation in codons 167, 198 and 200 of the beta-tubulin gene in whipworms (<i>Trichuris</i> spp.) from a range of domestic animals and wildlife. <i>Veterinary Parasitology</i> , 2013, 193, 141-149.	0.7	20
1891	Molecular characterisation and infection dynamics of <i>Dentitruncus truttae</i> from trout (<i>Salmo</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262	0.7	18
1892	Adaptive radiation within the vaccine target tetraspanin-23 across nine <i>Schistosoma</i> species from Africa. <i>International Journal for Parasitology</i> , 2013, 43, 95-103.	1.3	11
1893	Genetic structure and divergence in populations of <i>Lutzomyia cruciata</i> , a phlebotomine sand fly (Diptera: Psychodidae) vector of <i>Leishmania mexicana</i> in southeastern Mexico. <i>Infection, Genetics and Evolution</i> , 2013, 16, 254-262.	1.0	30
1894	Mitochondrial DNA reveals Pleistocenic colonisation of the Mediterranean by loggerhead turtles (<i>Caretta caretta</i>). <i>Journal of Experimental Marine Biology and Ecology</i> , 2013, 439, 15-24.	0.7	42
1895	Variations and evolution of polyubiquitin genes from ciliates. <i>European Journal of Protistology</i> , 2013, 49, 40-49.	0.5	1
1896	Single-nucleotide polymorphisms and association analysis of drought-resistance gene TaSnRK2.8 in common wheat. <i>Plant Physiology and Biochemistry</i> , 2013, 70, 174-181.	2.8	28

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1897	Genetic diversity of hydrothermal-vent barnacles in Manus Basin. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2013, 82, 73-79.	0.6	13
1898	Among population differentiation at nuclear genes in native Scots pine (<i>Pinus sylvestris</i> L.) in Scotland. <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2013, 208, 79-86.	0.6	11
1899	Extensively variable surface antigens of <i>Sarcocystis</i> spp. infecting Brazilian marsupials in the genus <i>Didelphis</i> occur in myriad allelic combinations, suggesting sexual recombination has aided their diversification. <i>Veterinary Parasitology</i> , 2013, 196, 64-70.	0.7	18
1900	Isolation and expression analysis of miR165a and REVOLUTA from Brassica species. <i>Acta Physiologiae Plantarum</i> , 2013, 35, 399-410.	1.0	14
1901	Mitochondrial DNA barcoding for Okinawan oysters: a cryptic population of the Portuguese oyster <i>Crassostrea angulata</i> in Japanese waters. <i>Fisheries Science</i> , 2013, 79, 61-76.	0.7	25
1902	Cryptic speciation and genetic structure of widely distributed brittle stars (Ophiuroidea) in Europe. <i>Zoologica Scripta</i> , 2013, 42, 151-169.	0.7	43
1903	Genetic identification of <i>Peromyscus</i> rodent species using both mitochondrial and nuclear loci: application to noninvasive sampling. <i>Molecular Ecology Resources</i> , 2013, 13, 43-56.	2.2	55
1904	Evolutionary history of bulldog bats (genus <i>Noctilio</i>): recent diversification and the role of the Caribbean in Neotropical biogeography. <i>Biological Journal of the Linnean Society</i> , 2013, 108, 210-224.	0.7	25
1905	Genetic differentiation of island populations: geographical barrier or a host switch?. <i>Biological Journal of the Linnean Society</i> , 2013, 108, 68-78.	0.7	5
1906	Phylogenetic analysis and phylogeography of the tetraploid rodent <i>Tympanoctomys barrerae</i> (Octodontidae): insights on its origin and the impact of Quaternary climate changes on population dynamics. <i>Biological Journal of the Linnean Society</i> , 2013, 108, 453-469.	0.7	16
1907	Phylogeography of <i>Troglophilus</i> (Orthoptera: Troglophilinae) based on Anatolian members of the genus: radiation of an old lineage following the Messinian. <i>Biological Journal of the Linnean Society</i> , 2013, 108, 335-348.	0.7	21
1908	Precipitation rather than temperature influenced the phylogeography of the endemic shrub <i>Arthrophyllum desideratum</i> in the Patagonian steppe. <i>Journal of Biogeography</i> , 2013, 40, 168-182.	1.4	33
1909	Incongruence between morphological and molecular markers in the butterfly genus <i>Zizina</i> (Lepidoptera: Lycaenidae) in New Zealand. <i>Systematic Entomology</i> , 2013, 38, 151-163.	1.7	8
1910	Comparative analysis of genome composition in Triticeae reveals strong variation in transposable element dynamics and nucleotide diversity. <i>Plant Journal</i> , 2013, 73, 347-356.	2.8	43
1911	Delimiting species in recent radiations with low levels of morphological divergence: A case study in Australian <i>Gehyra</i> geckos. <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 135-143.	1.2	33
1912	Characterization of thymosin β^4 in mammals' saliva. <i>Peptides</i> , 2013, 40, 1-7.	1.2	6
1913	Assessment of genetic and pheromonal diversity of the <i>Cydia strobilella</i> species complex (Lepidoptera: Tortricidae). <i>Systematic Entomology</i> , 2013, 38, 305-315.	1.7	12
1914	Hidden diversity and cryptic speciation refute cosmopolitan distribution in <i>Caprella penantis</i> (Crustacea: Amphipoda: Caprellidae). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2013, 51, 85-99.	0.6	32

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1915	Gene flow maintains genetic diversity and colonization potential in recently range-expanded populations of an Oriental bird, the <i>Lophophanes inornatus</i> (<i>Lophophanes inornatus</i> <i>sinensis</i>). <i>Diversity and Distributions</i> , 2013, 19, 1248-1262.	1.9	28
1916	Asymmetric Functional Divergence of Young, Dispersed Gene Duplicates in <i>Arabidopsis thaliana</i> . <i>Journal of Molecular Evolution</i> , 2013, 76, 13-27.	0.8	5
1917	Sequence-based molecular phylogenetics and phylogeography of the American box turtles (<i>Terrapene</i>). <i>Trends in Ecology and Evolution</i> , 2013, 28, 107-115.	1.2	31
1918	<i>Pinus monticola</i> pathogenesis-related gene PmPR10-2 alleles as defense candidates for stem quantitative disease resistance against white pine blister rust (<i>Cronartium ribicola</i>). <i>Tree Genetics and Genomes</i> , 2013, 9, 397-408.	0.6	14
1919	Molecular analysis of the parallel domestication of the common bean (<i>Phaseolus vulgaris</i>). <i>Trends in Ecology and Evolution</i> , 2013, 28, 240-249.	3.5	240
1920	Role of vernalization and of duplicated <i>FLOWERING LOCUS C</i> in the perennial <i>Arabidopsis lyrata</i> . <i>New Phytologist</i> , 2013, 197, 323-335.	3.5	60
1921	Nuclear and chloroplast DNA phylogeography of <i>Ficus hirta</i> : obligate pollination mutualism and constraints on range expansion in response to climate change. <i>New Phytologist</i> , 2013, 197, 276-289.	3.5	31
1922	Phylogenetic lineages of <i>Monopterus albus</i> (Synbranchiformes: Synbranchidae) in China inferred from mitochondrial control region. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2013, 51, 38-44.	0.6	7
1923	The odd couple: contrasting phylogeographic patterns in two sympatric sibling species of woodlouse-hunter spiders in the Canary Islands. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2013, 51, 29-37.	0.6	10
1924	River islands, refugia and genetic structuring in the endemic brown frog <i>Rana kukunoris</i> (<i>Rana kukunoris</i> , <i>Rana kukunoris</i>) of the Qinghai-Tibetan Plateau. <i>Molecular Ecology</i> , 2013, 22, 130-142.	2.0	36
1925	The role of selection in driving landscape genomic structure of the waterflea <i>Daphnia magna</i> . <i>Molecular Ecology</i> , 2013, 22, 583-601.	2.0	74
1926	The evolution of north-east Atlantic gadfly petrels using statistical phylogeography. <i>Molecular Ecology</i> , 2013, 22, 495-507.	2.0	19
1927	Single nucleotide polymorphisms of two closely related microsporidian parasites suggest a clonal population expansion after the last glaciation. <i>Molecular Ecology</i> , 2013, 22, 314-326.	2.0	34
1928	Crossing the uncrossable: novel transvalley biogeographic patterns revealed in the genetic history of low-dispersal mygalomorph spiders (<i>Antrodiaetidae</i> , <i>Antrodiaetus</i>) from California. <i>Molecular Ecology</i> , 2013, 22, 508-526.	2.0	61
1929	An assessment of haplotype variation in ribosomal and mitochondrial DNA fragments suggests incomplete lineage sorting in some species of the <i>Paramecium aurelia</i> complex (Ciliophora, Protozoa). <i>Molecular Phylogenetics and Evolution</i> , 2013, 67, 255-265.	1.2	26
1930	New <i>Paramecium quadecaurelia</i> strains (<i>P. aurelia</i> spp. complex, Ciliophora) identified by molecular markers (rDNA and mtDNA). <i>European Journal of Protistology</i> , 2013, 49, 477-486.	0.5	19
1931	Impact of climate changes from the Middle Miocene onwards on evolutionary diversification in <i>Eurasia</i> : Insights from the mesobuthid scorpions. <i>Molecular Ecology</i> , 2013, 22, 1700-1716.	2.0	32
1932	Predominance of hybrid discrete typing units of <i>Trypanosoma cruzi</i> in domestic <i>Triatoma infestans</i> from the Bolivian Gran Chaco region. <i>Infection, Genetics and Evolution</i> , 2013, 13, 116-123.	1.0	21

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1933	Stepwise colonization of the Andes by Ruddy Ducks and the evolution of novel β -globin variants. <i>Molecular Ecology</i> , 2013, 22, 1231-1249.	2.0	12
1934	Assessing intraspecific diversity in a lichen-forming fungus and its green algal symbiont: Evaluation of eight molecular markers. <i>Fungal Ecology</i> , 2013, 6, 141-151.	0.7	18
1935	OsLG1 regulates a closed panicle trait in domesticated rice. <i>Nature Genetics</i> , 2013, 45, 462-465.	9.4	181
1936	Multilocus phylogeny and recent rapid radiation of the viviparous sea snakes (Elapidae: Hydrophiinae). <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 575-591.	1.2	105
1937	The origins of the enigmatic Falkland Islands wolf. <i>Nature Communications</i> , 2013, 4, 1552.	5.8	40
1938	Matrilineal evidence for demographic expansion, low diversity and lack of phylogeographic structure in the Atlantic forest endemic Greenish Schiffornis <i>Schiffornis virescens</i> (Aves: Tityridae). <i>Journal of Ornithology</i> , 2013, 154, 371-384.	0.5	29
1939	Using population genetic methods to identify the origin of an invasive population and to diagnose cryptic subspecies of <i>Telchin licus</i> (Lepidoptera: Castniidae). <i>Bulletin of Entomological Research</i> , 2013, 103, 89-97.	0.5	15
1940	Population genetic structure and polymorphism analysis of gene encoding apical membrane antigen-1 (AMA-1) of Iranian <i>Plasmodium vivax</i> wild isolates. <i>Acta Tropica</i> , 2013, 126, 269-279.	0.9	31
1941	Development and validation of a D-loop mtDNA SNP assay for the screening of specimens in forensic casework. <i>Forensic Science International: Genetics</i> , 2013, 7, 353-358.	1.6	13
1942	Mitochondrial <i>scp</i> DNA variability of the pipefish <i>Syngnathus abaster</i> . <i>Journal of Fish Biology</i> , 2013, 82, 856-876.	0.7	13
1943	PERCHED AT THE MITO-NUCLEAR CROSSROADS: DIVERGENT MITOCHONDRIAL LINEAGES CORRELATE WITH ENVIRONMENT IN THE FACE OF ONGOING NUCLEAR GENE FLOW IN AN AUSTRALIAN BIRD. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 3412-3428.	1.1	97
1944	Molecular hyperdiversity and evolution in very large populations. <i>Molecular Ecology</i> , 2013, 22, 2074-2095.	2.0	67
1945	Genetic variability and differentiation among polymorphic populations of the genus <i>Synoicum</i> (Tunicata, Ascidiacea) from the South Shetland Islands. <i>Polar Biology</i> , 2013, 36, 871-883.	0.5	3
1946	Genetic diversity of dairy <i>Geotrichum candidum</i> strains revealed by multilocus sequence typing. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 5907-5920.	1.7	20
1947	Accelerated gene evolution through replication-transcription conflicts. <i>Nature</i> , 2013, 495, 512-515.	13.7	120
1948	Phylogeographic Patterns of mtDNA Variation Revealed Multiple Glacial Refugia for the Frog Species <i>Feirana taihangnica</i> Endemic to the Qinling Mountains. <i>Journal of Molecular Evolution</i> , 2013, 76, 112-128.	0.8	24
1949	Phylogeography of sable (<i>Martes zibellina</i> L. 1758) in the southeast portion of its range based on mitochondrial DNA variation: highlighting the evolutionary history of the sable. <i>Acta Theriologica</i> , 2013, 58, 139-148.	1.1	16
1950	Insights from population genetics for range limits of a widely distributed native plant. <i>American Journal of Botany</i> , 2013, 100, 744-753.	0.8	12

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1951	Multilocus approach to species recognition in the <i>Cladonia humilis</i> complex (Cladoniaceae.) <i>Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50</i>	0.8	25
1952	Genetic variation and Phylogeography of <i>Sinibrama Macrops</i> (Teleostei: Cyprinidae) in Qiantang River Basin, China. <i>Biochemical Systematics and Ecology</i> , 2013, 49, 10-20.	0.6	8
1953	Nuclear and chloroplast DNA phylogeography reveals Pleistocene divergence and subsequent secondary contact of two genetic lineages of the tropical rainforest tree species <i>Syzygia leprosula</i> (Dipterocarpaceae) in Southeast Asia. <i>Molecular Ecology</i> , 2013, 22, 2264-2279.	2.0	32
1954	Molecular evolution and epidemiology of echovirus 6 in Finland. <i>Infection, Genetics and Evolution</i> , 2013, 16, 234-247.	1.0	21
1955	Pleistocene climate change and the origin of two desert plant species, <i>Pugionium cornutum</i> and <i>Pugionium Adolabratum</i> (Borraginaceae), in northwest China. <i>New Phytologist</i> , 2013, 199, 277-287.	3.5	55
1956	The genetic structure of the Lithuanian wolf population. <i>Open Life Sciences</i> , 2013, 8, 440-447.	0.6	1
1957	Mitochondrial DNA diversity in Indian sheep. <i>Livestock Science</i> , 2013, 153, 50-55.	0.6	17
1958	Characterization of Sour Cherry Isolates of <i>Plum pox virus</i> from the Volga Basin in Russia Reveals a New Cherry Strain of the Virus. <i>Phytopathology</i> , 2013, 103, 972-979.	1.1	46
1959	A freshwater fish defies ancient mountain ranges and drainage divides: extrinsic and intrinsic influences on the evolutionary history of a recently identified galaxiid. <i>Journal of Biogeography</i> , 2013, 40, 1399-1412.	1.4	18
1960	Late Quaternary climatic vegetational shifts in an ecological transition zone of northern Madagascar: insights from genetic analyses of two endemic rodent species. <i>Journal of Evolutionary Biology</i> , 2013, 26, 1019-1034.	0.8	18
1961	Herbivore host-associated genetic differentiation depends on the scale of plant genetic variation examined. <i>Evolutionary Ecology</i> , 2013, 27, 65-81.	0.5	21
1962	Genetic variability among <i>Trichuris</i> ovis isolates from different hosts in Guangdong Province, China revealed by sequences of three mitochondrial genes. <i>Mitochondrial DNA</i> , 2013, 24, 50-54.	0.6	18
1963	Phylogeography and population genetic structure of the Talas tuco-tuco (<i>Ctenomys talarum</i>): integrating demographic and habitat histories. <i>Journal of Mammalogy</i> , 2013, 94, 459-476.	0.6	30
1964	Colonization history of <i>Metrioptera roeselii</i> in northern Europe indicates human-mediated dispersal. <i>Journal of Biogeography</i> , 2013, 40, 977-987.	1.4	20
1965	Forces shaping major histocompatibility complex evolution in two hyena species. <i>Journal of Mammalogy</i> , 2013, 94, 282-294.	0.6	6
1966	Role of the Dinaric Karst (western Balkans) in shaping the phylogeographic structure of the threatened crayfish <i>Austropotamobius torrentium</i> . <i>Freshwater Biology</i> , 2013, 58, 1089-1105.	1.2	67
1967	Phylogeography of North American herbaceous <i>Smilax</i> (Smilacaceae): Combined AFLP and cpDNA data support a northern refugium in the Driftless Area. <i>American Journal of Botany</i> , 2013, 100, 801-814.	0.8	36
1968	<i>Aegilops tauschii</i> single nucleotide polymorphisms shed light on the origins of wheat genome genetic diversity and pinpoint the geographic origin of hexaploid wheat. <i>New Phytologist</i> , 2013, 198, 925-937.	3.5	243

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1969	Genetic structure and phylogeography of a European flagship species, the white-tailed sea eagle <i>Haliaeetus albicilla</i> . <i>Journal of Avian Biology</i> , 2013, 44, 263-271.	0.6	21
1970	Mitochondrial DNA and microsatellite loci data supporting a management plan for a critically endangered lizard from Brazil. <i>Conservation Genetics</i> , 2013, 14, 943-951.	0.8	8
1971	Susceptibility status of <i>Culex quinquefasciatus</i> (Diptera: Culicidae) populations to the chemical insecticide temephos in Pernambuco, Brazil. <i>Pest Management Science</i> , 2013, 69, 1307-1314.	1.7	26
1972	From widespread to microendemic: molecular and acoustic analyses show that <i>Ischnocnema guentheri</i> (Amphibia: Brachycephalidae) is endemic to Rio de Janeiro, Brazil. <i>Conservation Genetics</i> , 2013, 14, 973-982.	0.8	42
1973	Pleistocene expansion of the bipolar lichen <i>Cetraria aculeata</i> into the Southern hemisphere. <i>Molecular Ecology</i> , 2013, 22, 1961-1983.	2.0	75
1974	Northern range expansion of European populations of the wasp spider <i>Argiope bruennichi</i> is associated with global warming—correlated genetic admixture and population-specific temperature adaptations. <i>Molecular Ecology</i> , 2013, 22, 2232-2248.	2.0	117
1975	Haplotype dictionary for the Rht-1 loci in wheat. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1733-1747.	1.8	50
1976	Positive selection of protective variants for type 2 diabetes from the Neolithic onward: a case study in Central Asia. <i>European Journal of Human Genetics</i> , 2013, 21, 1146-1151.	1.4	35
1977	Phylogeography of the forest-dwelling European pine marten (<i>Martes martes</i>): new insights into cryptic northern glacial refugia. <i>Biological Journal of the Linnean Society</i> , 2013, 109, 1-18.	0.7	42
1978	Complex evolutionary pathways of the intergenic region of the mini-exon gene in <i>Trypanosoma cruzi</i> TcI: A possible ancient origin in the Gran Chaco and lack of strict genetic structuration. <i>Infection, Genetics and Evolution</i> , 2013, 16, 27-37.	1.0	19
1979	Speciation in the asexual realm: Is the parthenogenetic weevil <i>Naupactus cervinus</i> a complex of species in statu nascendi?. <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 644-656.	1.2	14
1980	Evolution of a transposon in <i>Daphnia</i> hybrid genomes. <i>Mobile DNA</i> , 2013, 4, 7.	1.3	6
1981	Recent allopatric divergence and niche evolution in a widespread Palearctic bird, the common rosefinch (<i>Carpodacus erythrinus</i>). <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 103-111.	1.2	17
1982	Comparative phylogeography of Australo-Papuan mangrove-restricted and mangrove-associated avifaunas. <i>Biological Journal of the Linnean Society</i> , 2013, 109, 574-598.	0.7	13
1983	Multiple substitutions and reduced genetic variability in sharks. <i>Biochemical Systematics and Ecology</i> , 2013, 49, 21-29.	0.6	16
1984	Long-term panmixia in a cosmopolitan Indo-Pacific coral reef fish and a nebulous genetic boundary with its broadly sympatric sister species. <i>Journal of Evolutionary Biology</i> , 2013, 26, 783-799.	0.8	15
1985	Local representation of global diversity in a cosmopolitan lichen-forming fungal species complex (<i>Rhizoplaca</i> , Ascomycota). <i>Journal of Biogeography</i> , 2013, 40, 1792-1806.	1.4	47
1986	Radically different phylogeographies and patterns of genetic variation in two European brown frogs, genus <i>Rana</i> . <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 657-670.	1.2	56

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1987	Phylogenetic relationships among <i>Sarcocystis</i> species in cervids, cattle and sheep inferred from the mitochondrial cytochrome c oxidase subunit I gene. <i>International Journal for Parasitology</i> , 2013, 43, 579-591.	1.3	184
1988	Planktonic larvae do not ensure gene flow in the edible sea urchin <i>Paracentrotus lividus</i> . <i>Marine Ecology - Progress Series</i> , 2013, 480, 155-170.	0.9	33
1989	Congruence between distribution modelling and phylogeographical analyses reveals Quaternary survival of a toadflax species (<i>Linaris elegans</i>) in oceanic climate areas of a mountain ring range. <i>New Phytologist</i> , 2013, 198, 1274-1289.	3.5	46
1990	Quaternary refugia in southwestern Iran: insights from two sympatric moth species (Insecta, Tortricidae). <i>Journal of Biogeography</i> , 2013, 40, 107-119.	0.7	39
1991	Evolutionary history of alpine and subalpine <i>Daphnia</i> in western North America. <i>Freshwater Biology</i> , 2013, 58, 1512-1522.	1.2	13
1992	Characterizing polymorphisms and allelic diversity of von Willebrand factor gene in the 1000 Genomes. <i>Journal of Thrombosis and Haemostasis</i> , 2013, 11, 261-269.	1.9	49
1993	Extensive variation at MHC DRB in the New Zealand sea lion (<i>Phocarctos hookeri</i>) provides evidence for balancing selection. <i>Heredity</i> , 2013, 111, 44-56.	1.2	28
1994	Local selection of human populations shapes complex evolution patterns of CXCL10 gene. <i>Immunogenetics</i> , 2013, 65, 635-644.	1.2	0
1995	Evolution and variability of <i>Solanum</i> RanGAP2, a cofactor in the incompatible interaction between the resistance protein GPA2 and the <i>Globodera pallida</i> effector Gp-RBP-1. <i>BMC Evolutionary Biology</i> , 2013, 13, 87.	3.2	6
1996	Comparative phylogeography reveals deep lineages and regional evolutionary hotspots in the Mojave and Sonoran Deserts. <i>Diversity and Distributions</i> , 2013, 19, 722-737.	1.9	58
1997	Positive selection along the evolution of primate mitogenomes. <i>Mitochondrion</i> , 2013, 13, 846-851.	1.6	11
1998	Historical demography and genetic differentiation inferred from the mitochondrial DNA of the silky shark (<i>Carcharhinus falciformis</i>) in the Pacific Ocean. <i>Fisheries Research</i> , 2013, 147, 36-46.	0.9	24
1999	Genetic diversity and population structure of Sugarcane mosaic virus. <i>Virus Research</i> , 2013, 171, 242-246.	1.1	36
2000	A multilocus sequencing approach reveals the cryptic phylogeographical history of <i>Phyllodoce nipponica</i> (Ericaceae). <i>Biological Journal of the Linnean Society</i> , 2013, 110, 214-226.	0.7	13
2001	The role of chromosomal rearrangements and geographical barriers in the divergence of lineages in a South American subterranean rodent (Rodentia: Ctenomyidae: <i>Ctenomys minutus</i>). <i>Heredity</i> , 2013, 111, 293-305.	1.2	40
2002	Photobiont selectivity for lichens and evidence for a possible glacial refugium in the Ross Sea Region, Antarctica. <i>Polar Biology</i> , 2013, 36, 767-774.	0.5	12
2003	Mitochondrial gene trees support persistence of cold tolerant fairy shrimp throughout the Pleistocene glaciations in both southern and more northerly refugia. <i>Hydrobiologia</i> , 2013, 714, 155-167.	1.0	27
2004	The genetic structure of crossbills suggests rapid diversification with little niche conservatism. <i>Biological Journal of the Linnean Society</i> , 2013, 109, 908-922.	0.7	11

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2005	Rapid sperm evolution in the bluethroat (<i>Luscinia svecica</i>) subspecies complex. <i>Behavioral Ecology and Sociobiology</i> , 2013, 67, 1205-1217.	0.6	29
2006	Characterization of two unrelated satellite DNA families in the Colorado potato beetle <i>Leptinotarsa decemlineata</i> (Coleoptera, Chrysomelidae). <i>Bulletin of Entomological Research</i> , 2013, 103, 538-546.	0.5	8
2007	Tracking the molecular epidemiology of Brazilian Infectious bursal disease virus (IBDV) isolates. <i>Infection, Genetics and Evolution</i> , 2013, 13, 18-26.	1.0	24
2008	DNA barcoding commercially important fish species of Turkey. <i>Molecular Ecology Resources</i> , 2013, 13, 788-797.	2.2	87
2009	Molecular Cloning and Evolutionary Analysis of the HOG-Signaling Pathway Genes from <i>Saccharomyces cerevisiae</i> Rice Wine Isolates. <i>Biochemical Genetics</i> , 2013, 51, 296-305.	0.8	4
2010	Combining phylogeography and landscape genetics of <i>Xenopipo atronitens</i> (Aves: Pipridae), a white sand <i>campina</i> specialist, to understand Pleistocene landscape evolution in Amazonia. <i>Biological Journal of the Linnean Society</i> , 2013, 110, 60-76.	0.7	56
2011	Geographical patterns of nucleotide diversity and population differentiation in three closely related European pine species in the <i>Pinus mugo</i> complex. <i>Botanical Journal of the Linnean Society</i> , 2013, 172, 225-238.	0.8	48
2012	Marine dispersal and barriers drive Atlantic seahorse diversification. <i>Journal of Biogeography</i> , 2013, 40, 1839-1849.	1.4	47
2013	Stacks: an analysis tool set for population genomics. <i>Molecular Ecology</i> , 2013, 22, 3124-3140.	2.0	3,077
2014	Mountain barriers and river conduits: phylogeographical structure in a large, mobile lizard (<i>Varanidae: Varanus varius</i>) from eastern Australia. <i>Journal of Biogeography</i> , 2013, 40, 1729-1740.	1.4	37
2015	An ancient lineage of slow worms, genus <i>Anguis</i> (Squamata: Anguidae), survived in the Italian Peninsula. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 1077-1092.	1.2	43
2016	Gene trees, species trees and Earth history combine to shed light on the evolution of migration in a model avian system. <i>Molecular Ecology</i> , 2013, 22, 3333-3344.	2.0	42
2017	Geological and ecological factors drive cryptic speciation of yews in a biodiversity hotspot. <i>New Phytologist</i> , 2013, 199, 1093-1108.	3.5	236
2018	Severe plant invasions can increase mycorrhizal fungal abundance and diversity. <i>ISME Journal</i> , 2013, 7, 1424-1433.	4.4	180
2019	Evolution of tetraploid wheat based on variations in 5' UTR regions of Ppd-A1: evidence of gene flow between emmer and timopheevi wheat. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 2143-2155.	0.8	7
2020	A skeletonless sponge of Caribbean mangroves: invasive or undescribed?. <i>Invertebrate Biology</i> , 2013, 132, 81-94.	0.3	4
2021	Single Nucleotide Polymorphisms in HSP17.8 and Their Association with Agronomic Traits in Barley. <i>PLoS ONE</i> , 2013, 8, e56816.	1.1	27
2022	Duplicated CCAAT/enhancer-binding protein β^2 (C/EBP β^2) gene: Transcription and methylation changes in response to dietary betaine in Landes goose liver. <i>Poultry Science</i> , 2013, 92, 1878-1887.	1.5	4

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2023	Multilocus tests of <i>Pleistocene refugia and ancient divergence in a pair of Atlantic forest antbirds (<i>Myciophobus nigriceps</i>). Molecular Ecology, 2013, 22, 3996-4013.</i>	2.0	85
2024	Mitochondrial DNA diversity and the origin of Chinese indigenous sheep. Tropical Animal Health and Production, 2013, 45, 1715-1722.	0.5	21
2025	When east meets west: population structure of a high-latitude resident species, the boreal chickadee (<i>Poecile hudsonicus</i>). Heredity, 2013, 111, 321-329.	1.2	33
2026	A High Load of Non-neutral Amino-Acid Polymorphisms Explains High Protein Diversity Despite Moderate Effective Population Size in a Marine Bivalve With Sweepstakes Reproduction. G3: Genes, Genomes, Genetics, 2013, 3, 333-341.	0.8	31
2027	Genetic Diversity in Introduced Golden Mussel Populations Corresponds to Vector Activity. PLoS ONE, 2013, 8, e59328.	1.1	26
2028	Three phases for the early peopling of Hainan Island viewed from mitochondrial DNA. Journal of Systematics and Evolution, 2013, 51, 671-680.	1.6	10
2029	Phylogeny and biogeography of New World Stachydeae (Lamiaceae) with emphasis on the origin and diversification of Hawaiian and South American taxa. Molecular Phylogenetics and Evolution, 2013, 69, 218-238.	1.2	37
2030	Northern origin and diversification in the central lowlands? "Complex phylogeography and taxonomy of widespread day geckos (<i>Phelsuma</i>) from Madagascar. Organisms Diversity and Evolution, 2013, 13, 605-620.	0.7	10
2031	Genetic drift or natural selection? Hybridization and asymmetric mitochondrial introgression in two Caribbean lizards (<i>Anolis pulchellus</i> and <i>Anolis krugi</i>). Journal of Evolutionary Biology, 2013, 26, 1458-1471.	0.8	20
2032	Genetic relatedness and phylogenetics of five Indian pufferfishes. Mitochondrial DNA, 2013, 24, 602-609.	0.6	6
2033	The role of local ecology during hybridization at the initial stages of ecological speciation in a marine snail. Journal of Evolutionary Biology, 2013, 26, 1472-1487.	0.8	31
2034	<i>Plasmodium vivax</i> : C-terminal diversity in the blood stage SERA genes from Indian field isolates. Experimental Parasitology, 2013, 134, 82-91.	0.5	3
2035	Genetic diversity and substantial population differentiation in <i>Crassostrea hongkongensis</i> revealed by mitochondrial DNA. Marine Genomics, 2013, 11, 31-37.	0.4	25
2036	Comparative phylogeography of the ants <i>Myrmica ruginodis</i> and <i>Myrmica rubra</i> . Journal of Biogeography, 2013, 40, 479-491.	1.4	15
2037	Distinctness, phylogenetic relations and biogeography of intertidal mussels (<i>Brachidontes</i>) in the United Kingdom, 2013, 93, 1843-1855.	0.4	30
2038	Molecular phylogenetic analysis reveals six new species of <i>Diaporthe</i> from Australia. Fungal Diversity, 2013, 61, 251-260.	4.7	44
2039	Phylogeography and postglacial expansion of the endangered semi-aquatic mammal <i>Galemys pyrenaicus</i> . BMC Evolutionary Biology, 2013, 13, 115.	3.2	33
2040	Genetic diversity and lineage dynamic of dengue virus serotype 1 (DENV-1) in Cambodia. Infection, Genetics and Evolution, 2013, 15, 59-68.	1.0	26

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2041	DNA-barcoding of sympatric species of ectoparasitic gastropods of the genus <i>Cerithiopsis</i> (Mollusca: Gastropoda: Cerithiopsidae) from Croatia. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2013, 93, 1059-1065.	0.4	10
2042	Phylogenetic and phylogeographic analysis of the genus <i>Orestias</i> (Teleostei: Cyprinodontidae) in the southern Chilean Altiplano: the relevance of ancient and recent divergence processes in speciation. <i>Journal of Fish Biology</i> , 2013, 82, 927-943.	0.7	37
2043	Molecular cloning and expression analysis of major histocompatibility complex class IIB gene of the Whitespotted bambooshark (<i>Chiloscyllium plagiosum</i>). <i>Fish Physiology and Biochemistry</i> , 2013, 39, 131-142.	0.9	12
2044	Genetic diversity, phylogeny and evolution of alkaloid sequestering in Cuban miniaturized frogs of the <i>Eleutherodactylus limbatus</i> group. <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 541-554.	1.2	7
2045	Analysis of nucleotide diversity among alleles of the major bacterial blight resistance gene Xa27 in cultivars of rice (<i>Oryza sativa</i>) and its wild relatives. <i>Planta</i> , 2013, 238, 293-305.	1.6	18
2046	Global population divergence of the sea star <i>Hippasteria phrygiana</i> corresponds to the onset of the last glacial period of the Pleistocene. <i>Marine Biology</i> , 2013, 160, 1285-1296.	0.7	18
2047	Glacial expansion and diversification of an East Asian montane bird, the green-backed tit (<i>Parus</i>). <i>Trends in Ecology and Evolution</i> , 2013, 24, 194-197.	1.4	74
2048	High phylogeographic structure in sylvatic vectors of Chagas disease of the genus <i>Mepraia</i> (Hemiptera: Reduviidae). <i>Infection, Genetics and Evolution</i> , 2013, 19, 280-286.	1.0	22
2049	Elongation factor-1 β , a putative single-copy nuclear gene, has divergent sets of paralogs in an arachnid. <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 471-481.	1.2	12
2050	Fine-scale population genetic structure in <i>Artemia urmiana</i> (G \ddot{u} nter, 1890) based on mtDNA sequences and ISSR genomic fingerprinting. <i>Organisms Diversity and Evolution</i> , 2013, 13, 531-543.	0.7	22
2051	DNA barcoding reveals cryptic diversity in the peanut worm <i>Sipunculus nudus</i> . <i>Molecular Ecology Resources</i> , 2013, 13, 596-606.	2.2	25
2052	The complete mitochondrial genome of the grey bamboo shark (<i>Chiloscyllium griseum</i>) (Orectolobiformes: Hemiscylliidae): genomic characterization and phylogenetic application. <i>Acta Oceanologica Sinica</i> , 2013, 32, 59-65.	0.4	59
2053	A foreign invader or a reclusive native? DNA bar coding reveals a distinct European lineage of the zoonotic parasite <i>Schistosoma turkestanicum</i> (syn. <i>Orientobilharzia turkestanicum</i> (Dutt and) Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 25). <i>PLoS ONE</i> , 2013, 8, e61000.	1.0	10
2054	Molecular evolution of human adenoviruses. <i>Scientific Reports</i> , 2013, 3, 1812.	1.6	198
2055	Mitochondrial and Next-Generation Sequence Data Used to Infer Phylogenetic Relationships and Species Limits in the Clapper/King Rail Complex. <i>Condor</i> , 2013, 115, 316-329.	0.7	24
2056	Uncovering cryptic evolutionary diversity in extant and extinct populations of the southern Australian arid zone Western and Thick-billed Grasswrens (Passeriformes: Maluridae: Amytornis). <i>Conservation Genetics</i> , 2013, 14, 1173-1184.	0.8	27
2057	Purifying selection after episodes of recurrent adaptive diversification in fungal pathogens. <i>Infection, Genetics and Evolution</i> , 2013, 17, 123-131.	1.0	15
2058	Assessing the genetic impact of massive restocking on wild mallard. <i>Animal Conservation</i> , 2013, 16, 295-305.	1.5	24

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2059	Influence of the geological history of the Tansâ€™Mexican volcanic belt on the diversification of <i>Nolina parviflora</i> (Asparagaceae: Nolinoideae). <i>Journal of Biogeography</i> , 2013, 40, 1336-1347.	1.4	64
2060	Mutualism and asexual reproduction influence recognition genes in a fungal symbiont. <i>Fungal Biology</i> , 2013, 117, 439-450.	1.1	2
2061	Employing 454 amplicon pyrosequencing to reveal intragenomic divergence in the internal transcribed spacer rDNA region in fungi. <i>Ecology and Evolution</i> , 2013, 3, 1751-1764.	0.8	97
2062	Evolutionary patterns of the mitochondrial genome in the Moorish gecko, <i>Tarentola mauritanica</i> . <i>Gene</i> , 2013, 512, 166-173.	1.0	7
2063	Mitochondrial DNA of seven Italian sheep breeds shows faint signatures of domestication and suggests recent breed formation. <i>Mitochondrial DNA</i> , 2013, 24, 577-583.	0.6	25
2064	Multiple origins of the western European house mouse in the Aeolian Archipelago: clues from mtDNA and chromosomes. <i>Biological Invasions</i> , 2013, 15, 729-739.	1.2	10
2065	Evolutionary rate patterns of genes involved in the <i>Drosophila</i> Toll and Imd signaling pathway. <i>BMC Evolutionary Biology</i> , 2013, 13, 245.	3.2	23
2066	Analysis of western lowland gorilla (<i>Gorilla gorilla gorilla</i>) specific Alu repeats. <i>Mobile DNA</i> , 2013, 4, 26.	1.3	13
2067	Genetic Variation and Invasion Pattern of the Arabian Rhinoceros Beetle, <i>Oryctes agamemnon arabicus</i> (Burmeister) (Coleoptera: Scarabaeidae), in Tunisia, Deduced from Mitochondrial DNA Sequences. <i>Journal of the Entomological Society of Southern Africa</i> , 2013, 21, 362-367.	0.3	7
2068	Inference of Potential Genetic Risks Associated with Large-Scale Releases of Red Sea Bream in Kanagawa Prefecture, Japan Based on Nuclear and Mitochondrial DNA Analysis. <i>Marine Biotechnology</i> , 2013, 15, 206-220.	1.1	11
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2071	Species-specific traits predict genetic structure but not genetic diversity of three fragmented Afrotropical forest butterfly species. <i>Conservation Genetics</i> , 2013, 14, 511-528.	0.8	3
2072	Genetic characterization of dengue viruses prevalent in Kerala State, India. <i>Journal of Medical Microbiology</i> , 2013, 62, 545-552.	0.7	20
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2078	Where is the line? Phylogeography and secondary contact of western Palearctic coal tits (<i>Periparus</i>) Tj ETQq1 1 0.784314 rgBT /Overl 0.4 19		
2079	Genetic diversity of the HLA-G coding region in Amerindian populations from the Brazilian Amazon: a possible role of natural selection. <i>Genes and Immunity</i> , 2013, 14, 518-526.	2.2	17
2080	Discordant Genetic Diversity and Geographic Patterns Between <i>Crassicutis cichlasomae</i> (Digenea): Tj ETQq1 1 0.784314 rgBT /Overl 0.3 14 Middle-America. <i>Journal of Parasitology</i> , 2013, 99, 978-988.		
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2085	Long-distance dispersal, low connectivity and molecular evidence of a new cryptic species in the obligate rafter <i>Caprella andreae</i> Mayer, 1890 (Crustacea: Amphipoda: Caprellidae). <i>Helgoland Marine Research</i> , 2013, 67, 483-497.	1.3	36
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2090	Biological invasions in soil: DNA barcoding as a monitoring tool in a multiple taxa survey targeting European earthworms and springtails in North America. <i>Biological Invasions</i> , 2013, 15, 899-910.	1.2	89
2091	The molecular identification and genetic diversity of economically important wireworm species (Coleoptera: Elateridae) in Canada. <i>Journal of Pest Science</i> , 2013, 86, 19-27.	1.9	33
2092	Taxonomy versus phylogeny: evolutionary history of marsh rabbits without hopping to conclusions. <i>Diversity and Distributions</i> , 2013, 19, 120-133.	1.9	6
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2098	Evolutionary Genomics of <i>Salmonella enterica</i> Subspecies. <i>MBio</i> , 2013, 4, .	1.8	106
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2104	<l> <i>Hymenoscyphus pseudoalbidus</i> </l>, the correct name for <l> <i>Lambertella albida</i> </l> reported from Japan. <i>Mycotaxon</i> , 2013, 122, 25-41.	0.1	149
2105	Stable Pleistocene-era populations of <i>Chaerephon pumilus</i> (Chiroptera: Molossidae) in southeastern Africa do not use different echolocation calls. <i>African Zoology</i> , 2013, 48, 125-142.	0.2	3
2106	Genetic Recombination Events Between Sympatric Clade A and Clade C Lice in Africa. <i>Journal of Medical Entomology</i> , 2013, 50, 1165-1168.	0.9	11
2107	Disentangling the effects of mating systems and mutation rates on cytoplasmic diversity in gynodioecious <i>Silene nutans</i> and dioecious <i>Silene otites</i> . <i>Heredity</i> , 2013, 111, 157-164.	1.2	16
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2110	High gene flow in reef fishes and its implications for ad-hoc no-take marine reserves. <i>Mitochondrial DNA</i> , 2013, 24, 584-595.	0.6	4
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2113	Mesoamerican Origin and Pre- and Post-Columbian Expansions of the Ranges of <i>Acanthoscelides obtectus</i> Say, a Cosmopolitan Insect Pest of the Common Bean. <i>PLoS ONE</i> , 2013, 8, e70039.	1.1	33

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2119	New Insights into the Molecular Epidemiology and Population Genetics of Schistosoma mansoni in Ugandan Pre-school Children and Mothers. PLoS Neglected Tropical Diseases, 2013, 7, e2561.	1.3	18
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2129	Whole Genome Sequence of the Treponema Fribourg-Blanc: Unspecified Simian Isolate Is Highly Similar to the Yaws Subspecies. PLoS Neglected Tropical Diseases, 2013, 7, e2172.	1.3	53
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2151	A Phylogeographic Study of the Endemic Rodent <i>Eliurus carletoni</i> (Rodentia: Nesomyinae) in an Ecological Transition Zone of Northern Madagascar. <i>Journal of Heredity</i> , 2013, 104, 23-35.	1.0	17
2152	In silico analysis of mt 16S rRNA sequences of ocypodid crabs. <i>International Journal of Bioinformatics Research and Applications</i> , 2013, 9, 311.	0.1	0
2153	Distribution of Long-Range Linkage Disequilibrium and Tajima's D Values in Scandinavian Populations of Norway Spruce (<i>Picea abies</i>). <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 795-806.	0.8	26
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2157	Polymorphisms at the innate immune receptor <i>TLR2</i> are associated with <i>Borrelia</i> infection in a wild rodent population. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20130364.	1.2	82
2158	Specificity of resistance to dengue virus isolates is associated with genotypes of the mosquito antiviral gene <i>Dicer-2</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20122437.	1.2	66
2159	Molecular Reconstruction of Extinct LINE-1 Elements and Their Interaction with Nonautonomous Elements. <i>Molecular Biology and Evolution</i> , 2013, 30, 88-99.	3.5	21
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2162	Adaptive Evolution of M3 Lysin A Candidate Gamete Recognition Protein in the <i>Mytilus edulis</i> Species Complex. <i>Molecular Biology and Evolution</i> , 2013, 30, 2688-2698.	3.5	14
2163	From Green to Red: Horizontal Gene Transfer of the Phycoerythrin Gene Cluster between <i>Planktothrix</i> Strains. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6803-6812.	1.4	39
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2167	Deep Divergences within Liolaemus nigroviridis (Squamata,) Tj ETQq1 1 0.784314 rgBT /Overloc 59-69.	0.2	17

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2168	trnL-F is a powerful marker for DNA identification of field vittarioid gametophytes (Pteridaceae). <i>Annals of Botany</i> , 2013, 111, 663-673.	1.4	39
2169	Biogeography and Historical Demography of the Juan Fernandez Rock Lobster, <i>Jasus frontalis</i> (Milne) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 422 T	1.0	20
2170	Identification of a Tibetan-Specific Mutation in the Hypoxic Gene EGLN1 and Its Contribution to High-Altitude Adaptation. <i>Molecular Biology and Evolution</i> , 2013, 30, 1889-1898.	3.5	151
2171	Differences in population structure estimated within maternally- and paternally-inherited forms of mitochondria in <i>Lampsilis siliquoidea</i> (Bivalvia: Unionidae). <i>Biological Journal of the Linnean Society</i> , 2013, 109, 229-240.	0.7	16
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2174	Applications of DNA barcoding to fish landings: authentication and diversity assessment. <i>ZooKeys</i> , 2013, 365, 49-65.	0.5	65
2175	Genetic consequences of historical anthropogenic and ecological events on giant pandas. <i>Ecology</i> , 2013, 94, 2346-2357.	1.5	64
2176	Vulnerability to cavitation, hydraulic efficiency, growth and survival in an insular pine (<i>Pinus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422 T	1.4	76
2177	Forensic DNA Barcoding and Bio-Response Studies of Animal Horn Products Used in Traditional Medicine. <i>PLoS ONE</i> , 2013, 8, e55854.	1.1	41
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2179	A Selective Sweep across Species Boundaries in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2013, 30, 2177-2186.	3.5	48
2180	Testing for the Footprint of Sexually Antagonistic Polymorphisms in the Pseudoautosomal Region of a Plant Sex Chromosome Pair. <i>Genetics</i> , 2013, 194, 663-672.	1.2	51
2181	Investigation of the Population Structure of the Tick Vector of Lyme Disease <i>Ixodes scapularis</i> (Acari: Ixodidae) in Canada Using Mitochondrial Cytochrome C Oxidase Subunit I Gene Sequences. <i>Journal of Medical Entomology</i> , 2013, 50, 560-570.	0.9	20
2182	Identification and characterization of anonymous nuclear markers for the double-striped cockroach, <i>Blattella bisignata</i> . <i>Bulletin of Entomological Research</i> , 2013, 103, 29-35.	0.5	1
2183	Origin and evolution of the Italian subterranean termite <i>Reticulitermes lucifugus</i> (Blattodea,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 422 T	0.5	8
2184	ZRT1 Harbors an Excess of Nonsynonymous Polymorphism and Shows Evidence of Balancing Selection in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 665-673.	0.8	7
2185	Extensive paternal mtDNA leakage in natural populations of <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2013, 22, 2106-2117.	2.0	57

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2189	Intraspecific variability and genetic structure in <i>Meloidogyne chitwoodi</i> from the USA. <i>Nematology</i> , 2013, 15, 315-327.	0.2	19
2190	Molecular Identification and Historic Demography of the Marine Tucuxi (<i>Sotalia guianensis</i>) at the Amazon River's Mouth by Means of Mitochondrial Control Region Gene Sequences and Implications for Conservation. <i>Diversity</i> , 2013, 5, 703-723.	0.7	1
2191	Observations of Migrant Exchange and Mixing in a Coral Reef Fish Metapopulation Link Scales of Marine Population Connectivity. <i>Journal of Heredity</i> , 2013, 104, 532-546.	1.0	19
2192	Endemicity in the Gulf of Gabon: the small mussel drill <i>Ocenebrina hispidula</i> is a distinct species in the <i>Ocenebrina edwardsii</i> complex (Muricidae: Ocenebrinae). <i>Journal of Molluscan Studies</i> , 2013, 79, 273-276.	0.4	4
2193	Genetic and physiological data suggest demographic and adaptive responses in complex interactions between populations of figs (<i>Ficus pumila</i>) and their pollinating wasps (<i>Wespa pumilae</i>). <i>Molecular Ecology</i> , 2013, 22, 3814-3832.	2.0	7
2194	Phylogenetic Relationships among Populations of the Vineyard Snail <i>Ceruella virgata</i> (Da Costa). <i>Trends in Ecology & Evolution</i> , 2013, 28, 1010-1015.	0.5	10
2195	The Origin and Evolution of Six Miniature Inverted-Repeat Transposable Elements in <i>Bombyx mori</i> and <i>Rhodnius prolixus</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 2020-2031.	1.1	20
2196	Gene Conversion Shapes Linear Mitochondrial Genome Architecture. <i>Genome Biology and Evolution</i> , 2013, 5, 905-912.	1.1	23
2197	Sequence variation in three mitochondrial DNA genes among isolates of <i>Ascaridia galli</i> originating from Guangdong, Hunan and Yunnan provinces, China. <i>Journal of Helminthology</i> , 2013, 87, 371-375.	0.4	7
2198	Carving out turf in a biodiversity hotspot: multiple, previously unrecognized shrew species occur on Java island, Indonesia. <i>Molecular Ecology</i> , 2013, 22, 4972-4987.	2.0	37
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2200	Population genetic evidence for speciation pattern and gene flow between <i>Picea wilsonii</i> , <i>P. morrisonicola</i> and <i>P. neoveitchii</i> . <i>Annals of Botany</i> , 2013, 112, 1829-1844.	1.4	49
2201	Sudden Widespread Distribution of <i>Frankliniella occidentalis</i> (Thysanoptera: Thripidae) in Shandong Province, China. <i>Florida Entomologist</i> , 2013, 96, 933-940.	0.2	9
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2203	A tale of time and depth: intralacustrine radiation in endemic <i>Gammarus</i> species flock from the ancient Lake Ohrid. <i>Zoological Journal of the Linnean Society</i> , 2013, 167, 345-359.	1.0	31

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2205	Temporal, spatial and ecological dynamics of speciation among amphibian small mammals. <i>Journal of Biogeography</i> , 2013, 40, 415-429.	1.4	34
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2211	Using population genetics for management of bobcats in Oregon. <i>Wildlife Society Bulletin</i> , 2013, 37, 342-351.	1.6	7
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2326	Genetic Relatedness among Hepatitis A Virus Strains Associated with Food-Borne Outbreaks. <i>PLoS ONE</i> , 2013, 8, e74546.	1.1	31
2327	Signatures of Rapid Evolution in Urban and Rural Transcriptomes of White-Footed Mice (<i>Peromyscus</i>) Tj ETQq1 1 0,784314 rgBT /Ove 1.1 88	1.1	88
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2334	The Lesser of Two Weevils: Molecular-Genetics of Pest Palm Weevil Populations Confirm <i>Rhynchophorus vulneratus</i> (Panzer 1798) as a Valid Species Distinct from <i>R. ferrugineus</i> (Olivier 1790), and Reveal the Global Extent of Both. <i>PLoS ONE</i> , 2013, 8, e78379.	1.1	87
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2342	Microbial Ecology of the Hive and Pollination Landscape: Bacterial Associates from Floral Nectar, the Alimentary Tract and Stored Food of Honey Bees (<i>Apis mellifera</i>). <i>PLoS ONE</i> , 2013, 8, e83125.	1.1	233
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2347	Taxonomic position of <i>Eothenomys wardi</i>; (Arvicolinae: Cricetidae) based on morphological and molecular analyses with a detailed description of the species. <i>Zootaxa</i> , 2013, 3682, 85-104.	0.2	6

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2388	A Snail Perspective on the Biogeography of Sulawesi, Indonesia: Origin and Intra-Island Dispersal of the Viviparous Freshwater Gastropod <i>Tylomelania</i> . PLoS ONE, 2014, 9, e98917.	1.1	28
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2400	DNA Barcodes and Species Distribution Models Evaluate Threats of Global Climate Changes to Genetic Diversity: A Case Study from <i>Nanorana parkeri</i> (Anura: Dicroglossidae). PLoS ONE, 2014, 9, e103899.	1.1	14
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2403	An Exploration of Evolution, Maturation, Expression and Function Relationships in <i>Mir-23a</i> ~ <i>1/4</i> ~ <i>27a</i> ~ <i>1/4</i> ~ <i>24</i> Cluster. <i>PLoS ONE</i> , 2014, 9, e106223.	1.1	23
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2405	The Phylogeographical Pattern and Conservation of the Chinese Cobra (<i>Naja atra</i>) across Its Range Based on Mitochondrial Control Region Sequences. <i>PLoS ONE</i> , 2014, 9, e106944.	1.1	10
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2413	Molecular Variation in <i>AVP</i> and <i>AVPR1a</i> in New World Monkeys (Primates, <i>Platyrrhini</i>): Evolution and Implications for Social Monogamy. <i>PLoS ONE</i> , 2014, 9, e111638.	1.1	19
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2422	Genetic Variability of <i>Aspergillus flavus</i> Isolates from a Mississippi Corn Field. <i>Scientific World Journal</i> , The, 2014, 2014, 1-8.	0.8	8
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2432	Research Article Quaternary origin and genetic divergence of the endemic cactus <i>Mammillaria pectinifera</i> in a changing landscape in the Tehuac�n Valley, Mexico. <i>Genetics and Molecular Research</i> , 2014, 13, 73-88.	0.3	6
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2434	Prevalence and genetic diversity of fig mosaic virus isolates infecting fig tree in Iran. <i>Acta Virologica</i> , 2014, 58, 245-252.	0.3	8
2435	Range-wide phylogeography and conservation genetics of a narrowly endemic stream salamander, <i>Pachyhynobius shangchengensis</i> (Caudata, Hynobiidae): implications for conservation. <i>Genetics and Molecular Research</i> , 2014, 13, 2873-85.	0.3	6
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2437	Population genetic structure of <i>Aedes albopictus</i> in Penang, Malaysia. <i>Genetics and Molecular Research</i> , 2014, 13, 8184-8196.	0.3	23

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2445	Nucleotide and amino acid variations of tannase gene from different <i>Aspergillus</i> strains. <i>Canadian Journal of Microbiology</i> , 2014, 60, 509-516.	0.8	6
2446	A taxonomic and phylogenetic revision of <i>Penicillium</i> section <i>Aspergilloides</i> . <i>Studies in Mycology</i> , 2014, 78, 373-451.	4.5	61
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2449	Reinforcement shapes clines in female mate discrimination in <i>Drosophila subquinaria</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 3082-3094.	1.1	25
2450	Introgression of mitochondrial DNA promoted by natural selection in the Japanese pipistrelle bat (<i>Pipistrellus abramus</i>). <i>Genetica</i> , 2014, 142, 483-494.	0.5	4
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2484	Geographical variation of <i>Plutella xylostella</i> (Lepidoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 347 Td) <i>C. hina</i> . <i>Journal of Applied Entomology</i> , 2014, 138, 692-700.	0.8	11
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2487	PsasM2I, a Type II Restriction Modification System in <i>Pseudomonas savastanoi</i> pv. <i>savastanoi</i> : Differential Distribution of Carrier Strains in the Environment and the Evolutionary History of Homologous RM Systems in the <i>Pseudomonas syringae</i> Complex. <i>Microbial Ecology</i> , 2014, 68, 842-858.	1.4	0
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2500	A bioinformatics workflow for detecting signatures of selection in genomic data. <i>Frontiers in Genetics</i> , 2014, 5, 293.	1.1	51
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2504	Cyanidiophyceae in Iceland: plastid <i>rbcL</i> gene elucidates origin and dispersal of extremophilic <i>Galdieria sulphuraria</i> and <i>G. maxima</i> (Galdieriaceae, Rhodophyta). <i>Phycologia</i> , 2014, 53, 542-551.	0.6	35
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2506	Genetic Diversity and Population Structure of the Critically Endangered Yangtze Finless Porpoise (<i>Neophocaena asiaeorientalis asiaeorientalis</i>) as Revealed by Mitochondrial and Microsatellite DNA. <i>International Journal of Molecular Sciences</i> , 2014, 15, 11307-11323.	1.8	10
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2542	Haplotype-Habitat Associations of <i>Coptotermes gestroi</i> (Termitoidea: Rhinotermitidae) From Mitochondrial Dna Genes. <i>Environmental Entomology</i> , 2014, 43, 1105-1116.	0.7	6
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2546	Genetic variation in <i>Labeo fimbriatus</i> (Cypriniformes: Cyprinidae) populations as revealed by partial cytochrome b sequences of mitochondrial DNA. <i>Mitochondrial DNA</i> , 2016, 27, 1-5.	0.6	3

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2578	Phenotypic and genetic evidence for ecological speciation of <i>Aquilegia japonica</i> and <i>A. oxysepala</i> . <i>New Phytologist</i> , 2014, 204, 1028-1040.	3.5	21
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2584	<i>Bursaphelenchus fungivorus</i> from <i>Pinus pinaster</i> bark in Portugal. <i>Forest Pathology</i> , 2014, 44, 131-136.	0.5	4
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2589	Towards the understanding of the origin of the Polish remote population of <i>Polyommatus (Agrodiaetus) ripartii</i> (Lepidoptera: Lycaenidae) based on karyology and molecular phylogeny. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2014, 52, 44-51.	0.6	28
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2597	Genetic structure and differentiation of four populations of Afghan Pika (<i>Ochotona rufescens</i>) in Iran based on mitochondrial cytochrome b gene. <i>Zoology in the Middle East</i> , 2014, 60, 288-298.	0.2	4
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2604	Speciation, population structure, and demographic history of the Mojave Fringe-toed Lizard (<i>Uma</i>)	1.0	17
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2615	Association of <i>FLOWERING LOCUS T</i> like gene expression with growth rhythm in Scots pine (<i>Pinus</i>)	0.0	0
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2618	Diploid hybrid origin of <i>Ostryopsis intermedia</i> (Betulaceae) in the Qinghai-Tibet Plateau triggered by Quaternary climate change. <i>Molecular Ecology</i> , 2014, 23, 3013-3027.	2.0	61

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2715	Cryptic speciation reversal in the <i>Etheostoma zonale</i> (Teleostei: Percidae) species group, with an examination of the effect of recombination and introgression on species tree inference. Molecular Phylogenetics and Evolution, 2014, 70, 13-28.	1.2	16
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2719	Genetic homogeneity and historical expansions of the slipper lobster, <i>Scyllarides brasiliensis</i> , in the south-west Atlantic. Marine and Freshwater Research, 2014, 65, 59.	0.7	16
2720	Contrasting genetic structure of closely related giant water bugs: Phylogeography of <i>Appasus japonicus</i> and <i>Appasus major</i> (Insecta: Heteroptera, Belostomatidae). Molecular Phylogenetics and Evolution, 2014, 72, 7-16.	1.2	43
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2723	Genetic diversity of GH1 and LEP genes in Argentine llama (<i>Lama glama</i>) populations. Small Ruminant Research, 2014, 120, 20-26.	0.6	0
2724	Evolutionary and demographic history among Maghrebian <i>Medicago</i> species (Fabaceae) based on the nucleotide sequences of the chloroplast DNA barcode <i>trnH-psbA</i> . Biochemical Systematics and Ecology, 2014, 55, 296-304.	0.6	7
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2731	Genetic factors associated with serum haptoglobin level in a Japanese population. <i>Clinica Chimica Acta</i> , 2014, 433, 54-57.	0.5	28
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2739	Diversification across the Palaearctic desert belt throughout the Pleistocene: phylogeographic history of the Houbara-Macqueen's bustard complex (<i>Otididae</i> : <i>Chlamydotis</i>) as revealed by mitochondrial DNA. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2014, 52, 65-74.	0.6	10
2740	Phylogeographic patterns of the <i>Aconitum nemorum</i> species group (Ranunculaceae) shaped by geological and climatic events in the Tianshan Mountains and their surroundings. <i>Plant Systematics and Evolution</i> , 2014, 300, 51-61.	0.3	15
2741	Molecular epidemiology and population dynamics of hepatitis B virus in Dianjiang County, Chongqing, China. <i>Archives of Virology</i> , 2014, 159, 117-124.	0.9	2
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2743	Tracing the origin of US brown marmorated stink bugs, <i>Halyomorpha halys</i> . <i>Biological Invasions</i> , 2014, 16, 153-166.	1.2	90
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2760	Temporal change in the spatial genetic structure of a sika deer population with an expanding distribution range over a 15-year period. <i>Population Ecology</i> , 2014, 56, 311-325.	0.7	12
2761	Genetic variation analysis of apple chlorotic leaf spot virus coat protein reveals a new phylogenetic type and two recombinants in China. <i>Archives of Virology</i> , 2014, 159, 1431-1438.	0.9	15
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2765	The genetic structure of raccoon introduced in Central Europe reflects multiple invasion pathways. <i>Biological Invasions</i> , 2014, 16, 1611-1625.	1.2	33
2766	Levels and distribution patterns of mitochondrial <i>cox3</i> gene variation in brown seaweed, <i>Sargassum polycystum</i> C. Agardh (Fucales, Phaeophyceae) from Southeast Asia. <i>Journal of Applied Phycology</i> , 2014, 26, 1301-1308.	1.5	21
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2771	Does the niche breadth or trade-off hypothesis explain the abundance–occupancy relationship in avian Haemosporidia?. <i>Molecular Ecology</i> , 2014, 23, 3322-3329.	2.0	92
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2776	Multilocus phylogeography and morphology give insights into the recent evolution of a Mexican endemic songbird: <i>Vireo hypochryseus</i> . <i>Journal of Avian Biology</i> , 2014, 45, 253-263.	0.6	18
2777	Phylogeography of the Australian freshwater turtle <i>Chelodina expansa</i> reveals complex relationships among inland and coastal bioregions. <i>Biological Journal of the Linnean Society</i> , 2014, 111, 789-805.	0.7	10
2778	Comparative phylogeography in marginal seas of the northwestern Pacific. <i>Molecular Ecology</i> , 2014, 23, 534-548.	2.0	149
2779	Genetic analysis on <i>Dolichospermum</i> (Cyanobacteria; sensu <i>Anabaena</i>) populations based on the culture-independent clone libraries revealed the dominant genotypes existing in Lake Taihu, China. <i>Harmful Algae</i> , 2014, 31, 76-81.	2.2	14
2780	Intraspecific lineages of the lizard <i>Phrynocephalus putjatia</i> from the Qinghai-Tibetan Plateau: Impact of physical events on divergence and discordance between morphology and molecular markers. <i>Molecular Phylogenetics and Evolution</i> , 2014, 71, 288-297.	1.2	21

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2782	Population genetics and natural selection in the gene encoding the Duffy binding protein II in Iranian <i>Plasmodium vivax</i> wild isolates. <i>Infection, Genetics and Evolution</i> , 2014, 21, 424-435.	1.0	20
2783	Triparental origin of triploid onion, <i>Allium</i> sp. (Clementi ex Visiani, 1842), as evidenced by molecular, phylogenetic and cytogenetic analyses. <i>BMC Plant Biology</i> , 2014, 14, 24.	1.6	29
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2788	Insights into the origin and distribution of biodiversity in the Brazilian Atlantic forest hot spot: a statistical phylogeographic study using a low-dispersal organism. <i>Heredity</i> , 2014, 112, 656-665.	1.2	60
2789	Fine-scale distribution of juvenile Atlantic and Mediterranean loggerhead turtles (<i>Caretta caretta</i>) in the Mediterranean Sea. <i>Marine Biology</i> , 2014, 161, 509-519.	0.7	60
2790	Mitochondrial phylogeography, intraspecific diversity and phenotypic convergence in the four-lined snake (Reptilia, Squamata). <i>Zoologica Scripta</i> , 2014, 43, 149-160.	0.7	13
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2792	Invasion history of <i>Caprella scaura</i> Templeton, 1836 (Amphipoda: Caprellidae) in the Iberian Peninsula: multiple introductions revealed by mitochondrial sequence data. <i>Biological Invasions</i> , 2014, 16, 2221-2245.	1.2	32
2793	Genomic characterization of the <i>Hordeum vulgare</i> DEP1 (HvDEP1) gene and its diversity in a collection of barley accessions. <i>Euphytica</i> , 2014, 198, 29-41.	0.6	10
2794	Mitochondrial DNA phylogeography of <i>Semisulcospira libertina</i> (Gastropoda: Cerithioidea: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 2014, 41, 3733-3743.	1.0	18
2795	Phylogeography and population dynamics of the white-sided dolphin (<i>Lagenorhynchus acutus</i>) in the North Atlantic. <i>Conservation Genetics</i> , 2014, 15, 789-802.	0.8	13
2796	Introgression of nuclear and mitochondrial DNA markers of <i>Mus musculus musculus</i> to aboriginal populations of wild mice from Central Asia (<i>M. m. wagneri</i>) and South Siberia (<i>M. m. gansuensis</i>). <i>Molecular Biology</i> , 2014, 48, 75-83.	0.4	11
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2800	A Candidate Gene Association Study for Growth Performance in an Improved Giant Freshwater Prawn (<i>Macrobrachium rosenbergii</i>) Culture Line. <i>Marine Biotechnology</i> , 2014, 16, 161-180.	1.1	27
2801	Morphological and molecular characteristics of four <i>Sarcocystis</i> spp. in Canadian moose (<i>Alces</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66	0.6	38
2802	Genetic structure of <i>Plasmodium vivax</i> using the merozoite surface protein 1 icb5-6 fragment reveals new hybrid haplotypes in southern Mexico. <i>Malaria Journal</i> , 2014, 13, 35.	0.8	7
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2804	Genetic variation in the green anole lizard (<i>Anolis carolinensis</i>) reveals island refugia and a fragmented Florida during the quaternary. <i>Genetica</i> , 2014, 142, 59-72.	0.5	32
2805	Occurrence, genetic diversity, and potential pathways of entry of <i>Halyomorpha halys</i> in newly invaded areas of Canada and Switzerland. <i>Journal of Pest Science</i> , 2014, 87, 17-28.	1.9	82
2806	Analysis of <i>pfhrp2</i> genetic diversity in Senegal and implications for use of rapid diagnostic tests. <i>Malaria Journal</i> , 2014, 13, 34.	0.8	60
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2813	Disentangling the Population Structure and Evolution of the Clam Pathogen <i>Vibrio tapetis</i> . <i>Microbial Ecology</i> , 2014, 67, 145-154.	1.4	4
2814	Weak population genetic differentiation in the most numerous Arctic seabird, the little auk. <i>Polar Biology</i> , 2014, 37, 621-630.	0.5	23
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2818	Analyses of sequence polymorphism and haplotype diversity of LEAFY genes revealed post-domestication selection in the Chinese elite maize inbred lines. <i>Molecular Biology Reports</i> , 2014, 41, 1117-1125.	1.0	6
2819	Molecular variability of Apple chlorotic leaf spot virus in Shaanxi, China. <i>Phytoparasitica</i> , 2014, 42, 445-454.	0.6	6
2820	Unregulated hunting and genetic recovery from a severe population decline: the cautionary case of Bulgarian wolves. <i>Conservation Genetics</i> , 2014, 15, 405-417.	0.8	49
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2823	Genetic diversity and structuring of the grey wolf population from the Central Balkans based on mitochondrial DNA variation. <i>Mammalian Biology</i> , 2014, 79, 277-282.	0.8	15
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2825	From ancient to contemporary molecular eco-epidemiology of Chagas disease in the Americas. <i>International Journal for Parasitology</i> , 2014, 44, 605-612.	1.3	40
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2829	Multiple transgressions of Wallace's Line explain diversity of flightless <i>Trigonopterus</i> weevils on Bali. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20132528.	1.2	42
2830	OXA ¹² -Lactamases. <i>Clinical Microbiology Reviews</i> , 2014, 27, 241-263.	5.7	641
2831	Climate, physiological tolerance and sex-biased dispersal shape genetic structure of Neotropical orchid bees. <i>Molecular Ecology</i> , 2014, 23, 1874-1890.	2.0	62
2832	Mitochondrial DNA haplotypes indicate two postglacial recolonization routes of the spruce bark beetle <i>Ips typographus</i> through northern Europe to Scandinavia. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2014, 52, 285-292.	0.6	10
2833	Diverse avian malaria and other haemosporidian parasites in Andean house wrens: evidence for regional co-diversification by host-switching. <i>Journal of Avian Biology</i> , 2014, 45, 374-386.	0.6	70
2834	The ubiquitous nature of <i>Listeria monocytogenes</i> clones: a large-scale multilocus sequence typing study. <i>Environmental Microbiology</i> , 2014, 16, 405-416.	1.8	130

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2835	Landscape evolution and phylogeography of <i>Micrablepharus atticolus</i> (Squamata). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 Td</i> 1506-1519.	1.4	36
2836	Phylogenetic relationships and population structure of <i>Ralstonia solanacearum</i> isolated from diverse origins in Taiwan. <i>Plant Pathology</i> , 2014, 63, 1395-1403.	1.2	46
2837	<i>Aeromonas</i> spp.: ubiquitous or specialized bugs?. <i>Environmental Microbiology</i> , 2014, 16, 1005-1018.	1.8	26
2838	A multilocus evaluation of ermine (<i>Mustela erminea</i>) across the Holarctic, testing hypotheses of Pleistocene diversification in response to climate change. <i>Journal of Biogeography</i> , 2014, 41, 464-475.	1.4	32
2839	Chloroplast DNA-based genetic diversity and phylogeography of <i>Pyrus betulaeifolia</i> (Rosaceae) in Northern China. <i>Tree Genetics and Genomes</i> , 2014, 10, 739-749.	0.6	30
2840	Reduced genetic variation and strong genetic population structure in the freshwater killifish <i>Valencia letourneuxi</i> (Valenciidae) based on nuclear and mitochondrial markers. <i>Biological Journal of the Linnean Society</i> , 2014, 111, 334-349.	0.7	14
2841	Phylogeography of the <i>Petunia integrifolia</i> complex in southern Brazil. <i>Botanical Journal of the Linnean Society</i> , 2014, 174, 199-213.	0.8	34
2842	Refugia, colonization and diversification of an arid-adapted bird: coincident patterns between genetic data and ecological niche modelling. <i>Molecular Ecology</i> , 2014, 23, 390-407.	2.0	20
2843	Phylogeography of the North African dipodil (Rodentia: Muridae) based on cytochrome- <i>b</i> sequences. <i>Journal of Mammalogy</i> , 2014, 95, 241-253.	0.6	17
2844	The influence of the complex topography and dynamic history of the montane Neotropics on the evolutionary differentiation of a cloud forest bird (<i>Premnoplex brunnescens</i> , Furnariidae). <i>Journal of Biogeography</i> , 2014, 41, 1533-1546.	1.4	55
2845	Tracking the blue: A MLST approach to characterise the <i>Pseudomonas fluorescens</i> group. <i>Food Microbiology</i> , 2014, 39, 116-126.	2.1	75
2846	Nuclear and mitochondrial DNA variation within threatened species and subspecies of the giant New Zealand land snail genus <i>Powelliphanta</i> : implications for classification and conservation. <i>Journal of Molluscan Studies</i> , 2014, 80, 291-302.	0.4	4
2847	Limited genetic divergence among Australian alpine <i>Poa</i> tussock grasses coupled with regional structuring points to ongoing gene flow and taxonomic challenges. <i>Annals of Botany</i> , 2014, 113, 953-965.	1.4	14
2848	Strong Population Structure and Shallow Mitochondrial Phylogeny in the Banded Guitarfish, <i>Zapteryx exasperata</i> (Jordan y Gilbert, 1880), from the Northern Mexican Pacific. <i>Journal of Heredity</i> , 2014, 105, 91-100.	1.0	25
2849	Noninvasive genetic assessment of brown bear population structure in Bulgarian mountain regions. <i>Mammalian Biology</i> , 2014, 79, 268-276.	0.8	48
2850	Positive selection and intragenic recombination contribute to high allelic diversity in effector genes of <i>Mycosphaerella fijiensis</i> , causal agent of the black leaf streak disease of banana. <i>Molecular Plant Pathology</i> , 2014, 15, 447-460.	2.0	36
2851	Evolutionary history of purple cone spruce (<i>Picea purpurea</i>) in the Qinghai-Tibet Plateau: homoploid hybrid origin and Pleistocene expansion. <i>Molecular Ecology</i> , 2014, 23, 343-359.	2.0	97
2852	Cost-effective enrichment hybridization capture of chloroplast genomes at deep multiplexing levels for population genetics and phylogeography studies. <i>Molecular Ecology Resources</i> , 2014, 14, 1103-1113.	2.2	110

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2854	Phylogeny and phylogeography of the Tuber brumale aggr.. Mycorrhiza, 2014, 24, 101-113.	1.3	22
2855	Interkingdom Transfer of the Acne-Causing Agent, Propionibacterium acnes, from Human to Grapevine. Molecular Biology and Evolution, 2014, 31, 1059-1065.	3.5	54
2856	HUMAN IMPACTS HAVE SHAPED HISTORICAL AND RECENT EVOLUTION IN <i>AEDES AEGYPTI</i> , THE DENGUE AND YELLOW FEVER MOSQUITO. Evolution; International Journal of Organic Evolution, 2014, 68, 514-525.	1.1	225
2857	GENETIC, MORPHOLOGICAL, AND ACOUSTIC EVIDENCE REVEALS LACK OF DIVERSIFICATION IN THE COLONIZATION PROCESS IN AN ISLAND BIRD. Evolution; International Journal of Organic Evolution, 2014, 68, n/a-n/a.	1.1	18
2858	Genetic diversity and historical biogeography of the Maltese wall lizard, Podarcis filfolensis (Squamata: Lacertidae). Conservation Genetics, 2014, 15, 295-304.	0.8	5
2859	Evolutionary basis of mitonuclear discordance between sister species of mole salamanders (<i>Ambystoma</i> sp.). Molecular Ecology, 2014, 23, 2811-2824.	2.0	21
2860	A phylogeographic evaluation of the Amolops mantzorum species group: Cryptic species and plateau uplift. Molecular Phylogenetics and Evolution, 2014, 73, 40-52.	1.2	35
2861	Phylogeny of the Centaurea group (Centaurea, Compositae) – Geography is a better predictor than morphology. Molecular Phylogenetics and Evolution, 2014, 77, 195-215.	1.2	59
2862	Genetic diversity of VAR2CSA ID1-DBL2Xb in worldwide Plasmodium falciparum populations: Impact on vaccine design for placental malaria. Infection, Genetics and Evolution, 2014, 25, 81-92.	1.0	20
2863	Genetic restoration of a threatened population of greater prairie-chickens. Biological Conservation, 2014, 174, 12-19.	1.9	25
2864	Does the Platanthera dilatata (Orchidaceae) complex contain cryptic species or continuously variable populations?. Plant Systematics and Evolution, 2014, 300, 1465-1476.	0.3	6
2865	Genetic Structure of Little Brown Bats (Myotis lucifugus) Corresponds with Spread of White-Nose Syndrome among Hibernacula. Journal of Heredity, 2014, 105, 354-364.	1.0	34
2866	Are mitochondrial lineages, mitochondrial lysis and respiration rate associated with phosphine susceptibility in the maize weevil <i>Sitophilus zeamais</i> ?. Annals of Applied Biology, 2014, 165, 137-146.	1.3	28
2867	The phylogeography of Eurasian Fraxinus species reveals ancient transcontinental reticulation. Molecular Phylogenetics and Evolution, 2014, 77, 223-237.	1.2	15
2868	Genetic delineation between and within the widespread coccolithophore morpho-species <i>Emiliania huxleyi</i> and <i>Gephyrocapsa oceanica</i> (Haptophyta). Journal of Phycology, 2014, 50, 140-148.	1.0	42
2869	Genetic population structure of miiuy croaker (<i>Miichthys miiuy</i>) in the Yellow and East China Seas base on mitochondrial COI sequences. Biochemical Systematics and Ecology, 2014, 54, 240-246.	0.6	13
2870	Phylogeography of <i>Peromyscus schmidlyi</i> : an endemic of the Sierra Madre Occidental, Mexico. Journal of Mammalogy, 2014, 95, 254-268.	0.6	8

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2871	Molecular data indicate the presence of a novel species of <i>Centropomus</i> (Centropomidae) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 742	1.2	19
2872	Morphometric variation between two morphotypes within the <i>Astyanax</i> Baird and Girard, 1854 (Actinopterygii: Characidae) genus, From a Mexican tropical lake. <i>Journal of Morphology</i> , 2014, 275, 721-731.	0.6	20
2873	Genetic structure of populations of whale sharks among ocean basins and evidence for their historic rise and recent decline. <i>Molecular Ecology</i> , 2014, 23, 2590-2601.	2.0	89
2874	Colonization pathways of the northeast Atlantic by northern fulmars: a test of James Fisher's "out of Iceland" hypothesis using museum collections. <i>Journal of Avian Biology</i> , 2014, 45, 209-218.	0.6	3
2875	Recent speciation and secondary contact in endemic ants. <i>Molecular Ecology</i> , 2014, 23, 2529-2542.	2.0	14
2876	Extensive gene flow characterizes the phylogeography of a North American migrant bird: Black-headed Grosbeak (<i>Pheucticus melanocephalus</i>). <i>Molecular Phylogenetics and Evolution</i> , 2014, 78, 148-159.	1.2	11
2877	Population structure and reticulate evolution of <i>Saccharomyces eubayanus</i> and its lagerbrewing hybrids. <i>Molecular Ecology</i> , 2014, 23, 2031-2045.	2.0	128
2878	Phylogeography and genetic diversity of the red squirrel (<i>Sciurus vulgaris</i>) in China: Implications for the species' postglacial expansion history. <i>Mammalian Biology</i> , 2014, 79, 247-253.	0.8	9
2879	Phylogeography of noble crayfish (<i>Astacus astacus</i>) reveals multiple refugia. <i>Freshwater Biology</i> , 2014, 59, 761-776.	1.2	44
2880	Revision and phylogeny of the European species of the <i>Eurytoma moriospecies</i> group (Hymenoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 742) 2014, 171, 370-421.	1.0	6
2881	Cryptic habitats and cryptic diversity: unexpected patterns of connectivity and phylogeographical breaks in a Mediterranean endemic marine cave mysid. <i>Molecular Ecology</i> , 2014, 23, 2825-2843.	2.0	23
2882	Identification, characterisation and discriminatory power of microsatellite markers in the parasitic weed <i>Orobancha cumana</i> . <i>Weed Research</i> , 2014, 54, 120-132.	0.8	18
2883	Genetic diversity and recombination analysis in the coat protein gene of Banana bract mosaic virus. <i>Virus Genes</i> , 2014, 48, 509-517.	0.7	18
2884	Molecular Characterization of Southern Rice Blacked Streaked Dwarf Virus (<i>SRBSDV</i>) from Vietnam. <i>Journal of Phytopathology</i> , 2014, 162, 349-358.	0.5	11
2885	Pod shattering resistance associated with domestication is mediated by a NAC gene in soybean. <i>Nature Communications</i> , 2014, 5, 3352.	5.8	177
2886	Transmission and evolution of hepatitis C virus in HCV seroconverters in HIV infected subjects. <i>Virology</i> , 2014, 449, 339-349.	1.1	12
2887	Sequencing and comparison of the mitochondrial COI gene from isolates of Arbuscular Mycorrhizal Fungi belonging to Gigasporaceae and Glomeraceae families. <i>Molecular Phylogenetics and Evolution</i> , 2014, 75, 1-10.	1.2	13
2888	Molecular polymorphism and phylogenetic relationships within Tunisian date palm (Phoenix) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 742 2014, 170, 32-38.	1.7	17

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2889	Conservation implications of the evolutionary history and genetic diversity hotspots of the snowshoe hare. <i>Molecular Ecology</i> , 2014, 23, 2929-2942.	2.0	32
2890	Phylogeography and Pleistocene refugia of the Little Owl <i>Aethes noctua</i> inferred from mtDNA sequence data. <i>Ibis</i> , 2014, 156, 639-657.	1.0	24
2891	Towards a phylogenetic approach to the composition of species complexes in the North and Central American <i>Triatoma</i> , vectors of Chagas disease. <i>Infection, Genetics and Evolution</i> , 2014, 24, 157-166.	1.0	16
2892	Species limits in avian malaria parasites (Haemosporida): how to move forward in the molecular era. <i>Parasitology</i> , 2014, 141, 1223-1232.	0.7	80
2893	Complex phylogeography and historical hybridization between sister taxa of freshwater sculpin (<i>Cottus</i>). <i>Molecular Ecology</i> , 2014, 23, 2602-2618.	2.0	14
2894	Specialist versus generalist life histories and nucleotide diversity in <i>Caenorhabditis</i> nematodes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20132858.	1.2	51
2895	Genetic Diversity of Grapevine virus A in Washington and California Vineyards. <i>Phytopathology</i> , 2014, 104, 548-560.	1.1	30
2896	The contribution of Anatolia to European phylogeography: the centre of origin of the meadow grasshopper, <i>Chorthippus parallelus</i> . <i>Journal of Biogeography</i> , 2014, 41, 1793-1805.	1.4	43
2897	Identifying <i>Neisseria</i> Species by Use of the 50S Ribosomal Protein L6 (<i>rplF</i>) Gene. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1375-1381.	1.8	55
2898	Adaptive phylogeography: functional divergence between haemoglobins derived from different glacial refugia in the bank vole. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140021.	1.2	28
2899	Evolution of methicillin-resistant <i>Staphylococcus aureus</i> towards increasing resistance. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 616-622.	1.3	50
2900	Hiding in the highlands: Evolution of a frog species complex of the genus <i>Ptychadena</i> in the Ethiopian highlands. <i>Molecular Phylogenetics and Evolution</i> , 2014, 71, 157-169.	1.2	34
2901	Coalescent Species Delimitation in Milksnakes (Genus <i>Lampropeltis</i>) and Impacts on Phylogenetic Comparative Analyses. <i>Systematic Biology</i> , 2014, 63, 231-250.	2.7	109
2902	Ain't no mountain high enough, ain't no valley low enough? Phylogeography of the rupicolous Cape girdled lizard (<i>Cordylus cordylus</i>) reveals a generalist pattern. <i>Molecular Phylogenetics and Evolution</i> , 2014, 71, 234-248.	1.2	21
2903	Molecular systematics of the world's most polytypic bird: the <i>Pachycephala pectoralis</i> / <i>melanura</i> (Aves: Pachycephalidae) species complex. <i>Zoological Journal of the Linnean Society</i> , 2014, 170, 566-588.	1.0	48
2904	Uncovering cryptic diversity and refugial persistence among small mammal lineages across the Eastern Afrotropical biodiversity hotspot. <i>Molecular Phylogenetics and Evolution</i> , 2014, 71, 41-54.	1.2	80
2905	Timeframes of Speciation, Reticulation, and Hybridization in the Bulldog Bat Explained Through Phylogenetic Analyses of All Genetic Transmission Elements. <i>Systematic Biology</i> , 2014, 63, 96-110.	2.7	28
2906	Hidden diversity in the Andes: Comparison of species delimitation methods in montane marsupials. <i>Molecular Phylogenetics and Evolution</i> , 2014, 70, 137-151.	1.2	45

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2907	Phylogenetic relationships of extant zokors (Myospalacinae) (Rodentia, Spalacidae) inferred from mitochondrial DNA sequences. <i>Mitochondrial DNA</i> , 2014, 25, 135-141.	0.6	18
2908	The significance of past interdrainage connectivity for studies of diversity, distribution and movement of freshwater-limited taxa within a catchment. <i>Journal of Biogeography</i> , 2014, 41, 536-547.	1.4	15
2909	Detection of a novel intracellular microbiome hosted in arbuscular mycorrhizal fungi. <i>ISME Journal</i> , 2014, 8, 257-270.	4.4	128
2910	Multilocus analysis of intraspecific differentiation in three endemic bird species from the northern Neotropical dry forest. <i>Molecular Phylogenetics and Evolution</i> , 2014, 70, 362-377.	1.2	32
2911	Home-loving boreal hare mitochondria survived several invasions in Iberia: the relative roles of recurrent hybridisation and allele surfing. <i>Heredity</i> , 2014, 112, 265-273.	1.2	30
2912	Mixed infection by <i>Legionella pneumophila</i> in outbreak patients. <i>International Journal of Medical Microbiology</i> , 2014, 304, 307-313.	1.5	20
2913	A panmictic fiddler crab from the coast of Brazil? Impact of divergent ocean currents and larval dispersal potential on genetic and morphological variation in <i>Uca maracoani</i> . <i>Marine Biology</i> , 2014, 161, 173-185.	0.7	33
2914	Origin and Differential Selection of Allelic Variation at TAS2R16 Associated with Salicin Bitter Taste Sensitivity in Africa. <i>Molecular Biology and Evolution</i> , 2014, 31, 288-302.	3.5	43
2915	Molecular Identification of Mullet Species of the Atlantic South Caribbean and South America and the Phylogeographic Analysis of <i>Mugil liza</i> . <i>Reviews in Fisheries Science and Aquaculture</i> , 2014, 22, 86-96.	5.1	17
2916	Cryptic genetic diversity and complex phylogeography of the boreal North American scorpion, <i>Paruroctonus boreus</i> (Vaejovidae). <i>Molecular Phylogenetics and Evolution</i> , 2014, 71, 298-307.	1.2	14
2917	Phylogeography-Based Delimitation of Subspecies Boundaries in the Common Pheasant (<i>Phasianus</i>)	0.8	11
2918	Mitochondrial phylogeography of a Beringian relict: the endemic freshwater genus of blackfish <i>Dallia</i> (Esociformes). <i>Journal of Fish Biology</i> , 2014, 84, 523-538.	0.7	21
2919	Species delimitation, patterns of diversification and historical biogeography of the Neotropical frog genus <i>Acanomera</i> (<i>Acanomera</i>)	0.8	11
2920	Partial Sequence Homogenization in the 5S Multigene Families May Generate Sequence Chimeras and Spurious Results in Phylogenetic Reconstructions. <i>Systematic Biology</i> , 2014, 63, 219-230.	2.7	8
2921	Alternative mutational pathways, outside the VPg, of rice yellow mottle virus to overcome eIF(iso)4G-mediated rice resistance under strong genetic constraints. <i>Journal of General Virology</i> , 2014, 95, 219-224.	1.3	12
2922	Disparate molecular evolution of two types of repetitive DNAs in the genome of the grasshopper <i>Eyprepocnemis plorans</i> . <i>Heredity</i> , 2014, 112, 531-542.	1.2	22
2923	Spatial genetic heterogeneity of the cosmopolitan chaetognath <i>Eukrohnia hamata</i> (Mbius, 1875) revealed by mitochondrial DNA. <i>Hydrobiologia</i> , 2014, 721, 197-207.	1.0	25
2924	Genetic and structural characterization of PvSERA4: potential implication as therapeutic target for <i>Plasmodium vivax</i> malaria. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 580-590.	2.0	7

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2925	Lineage fusion in <i>Galapagos</i> giant tortoises. <i>Molecular Ecology</i> , 2014, 23, 5276-5290.	2.0	59
2926	A Y-chromosome-encoded small RNA acts as a sex determinant in persimmons. <i>Science</i> , 2014, 346, 646-650.	6.0	330
2927	Effect of founding events on coat colour polymorphism of <i>Apodemus speciosus</i> (Rodentia). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	0.7	10
2928	Symbiosis in the green leafhopper, <i>Cicadella viridis</i> (Hemiptera, Cicadellidae). <i>Association in statu nascendi?</i> . <i>Arthropod Structure and Development</i> , 2014, 43, 579-587.	0.8	51
2929	Genetic diversity in caribou linked to past and future climate change. <i>Nature Climate Change</i> , 2014, 4, 132-137.	8.1	154
2930	Species-wide Genetic Incompatibility Analysis Identifies Immune Genes as Hot Spots of Deleterious Epistasis. <i>Cell</i> , 2014, 159, 1341-1351.	13.5	247
2931	Genetic diversity and population structure of Mongolian domestic Bactrian camels (<i>Camelus bactrianus</i>). <i>Animal Genetics</i> , 2014, 45, 550-558.	0.6	39
2932	Blacktip reef sharks, <i>Carcharhinus melanopterus</i> , have high genetic structure and varying demographic histories in their Indo-Pacific range. <i>Molecular Ecology</i> , 2014, 23, 5193-5207.	2.0	44
2933	Conservation and Management of Polyttypic Species: The Little Striped Whiptail Complex (<i>Aspidoscelis inornata</i>) as a Case Study. <i>Copeia</i> , 2014, 2014, 519-529.	1.4	13
2934	Prospects for discriminating Zingiberaceae species in India using DNA barcodes. <i>Journal of Integrative Plant Biology</i> , 2014, 56, 760-773.	4.1	21
2935	Functional characterization of sex pheromone receptors in the purple stem borer, <i>Sesamia inferens</i> (<i>Walker</i>). <i>Insect Molecular Biology</i> , 2014, 23, 611-620.	1.0	28
2936	Genetic Divergence During Long-term Isolation in Highly Diverse Populations of Tropical Trees Across the Eastern Arc Mountains of Tanzania. <i>Biotropica</i> , 2014, 46, 565-574.	0.8	6
2937	Phylogeographic evidence for two mesic refugia in a biodiversity hotspot. <i>Heredity</i> , 2014, 113, 454-463.	1.2	29
2938	Morphology and Molecular Phylogeny of <i>Apoterritricha lutea</i> n. g., n. sp. (Ciliophora). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i> <i>Afrokeronopsis</i> . <i>Journal of Eukaryotic Microbiology</i> , 2014, 61, 520-536.	0.8	22
2939	In situ glacial survival at the northern limit of tropical insular Asia by a lowland herb <i>Begonia fenicis</i> (Begoniaceae). <i>Botanical Journal of the Linnean Society</i> , 2014, 174, 305-325.	0.8	12
2940	Developing major histocompatibility markers in a species of concern: the Sacramento perch <i>Archoplites interruptus</i> . <i>Journal of Fish Biology</i> , 2014, 85, 1766-1776.	0.7	0
2941	Herbarium specimens reveal a historical shift in phylogeographic structure of common ragweed during native range disturbance. <i>Molecular Ecology</i> , 2014, 23, 1701-1716.	2.0	68
2942	The need for genetic support in restocking activities and <i>ex situ</i> conservation programmes: the case of the Adriatic sturgeon (<i>Acipenser naccarii</i> Bonaparte, 1836) in the Ticino River Park. <i>Journal of Applied Ichthyology</i> , 2014, 30, 1416-1422.	0.3	17

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2943	Molecular phylogenetics and morphological variation reveal recent speciation in freshwater mussels of the genera <i>Arcidens</i> and <i>Arkansia</i> (Bivalvia: Unionidae). <i>Biological Journal of the Linnean Society</i> , 2014, 112, 535-545.	0.7	33
2944	Flies on the move: an inherited virus mirrors <i>Drosophila melanogaster</i> 's elusive ecology and demography. <i>Molecular Ecology</i> , 2014, 23, 2093-2104.	2.0	19
2945	Historical and recent processes shaping the geographic range of a rocky intertidal gastropod: phylogeography, ecology, and habitat availability. <i>Ecology and Evolution</i> , 2014, 4, 3244-3255.	0.8	26
2946	Species delimitation in the Chinese bamboo partridge <i>Bambusicola thoracica</i> (Passeriformes: Caprimulgidae). <i>Zoologica Scripta</i> , 2014, 43, 562-575.	0.7	15
2947	Phylogenetic relationships of <i>Salix</i> L. subg. <i>Salix</i> species (Salicaceae) according to sequencing data of intergenic spacers of the chloroplast genome and ITS rDNA. <i>Russian Journal of Genetics</i> , 2014, 50, 828-837.	0.2	13
2948	Genetic uniformity and long-distance clonal dispersal in the invasive androgenetic <i>Corbicula</i> clams. <i>Molecular Ecology</i> , 2014, 23, 5102-5116.	2.0	60
2949	Characterization of wound-induced serine protease inhibitor (wip1) genes and proteins in Turkish maize varieties. <i>Biochemistry (Moscow)</i> , 2014, 79, 836-844.	0.7	3
2950	Stronger transferability but lower variability in transcriptomic than in anonymous microsatellites: evidence from <i>Hyla</i> frogs. <i>Molecular Ecology Resources</i> , 2014, 14, 716-725.	2.2	26
2951	Analysis of <i>ATP6</i> sequence diversity in the <i>Triticum</i> <i>Aegilops</i> species group reveals the crucial role of rearrangement in mitochondrial genome evolution. <i>Genome</i> , 2014, 57, 279-288.	0.9	2
2952	Interspecific variability of class II hydrophobin GEO1 in the genus <i>Geosmithia</i> . <i>Fungal Biology</i> , 2014, 118, 862-871.	1.1	4
2953	Evaluation of the relationship between <i>Chlamydia pecorum</i> sequence types and disease using a species-specific multi-locus sequence typing scheme (MLST). <i>Veterinary Microbiology</i> , 2014, 174, 214-222.	0.8	37
2954	Barriers, rather than refugia, underlie the origin of diversity in toads endemic to the Brazilian Atlantic Forest. <i>Molecular Ecology</i> , 2014, 23, 6152-6164.	2.0	77
2955	<i>Rhizopogon kretzeriae</i> sp. nov.: the rare fungal symbiont in the tripartite system with <i>Pterospora andromedea</i> and <i>Pinus strobus</i> . <i>Botany</i> , 2014, 92, 527-534.	0.5	8
2956	Evolutionary dynamics and genetic diversity from three genes of Anguillid rhabdovirus. <i>Journal of General Virology</i> , 2014, 95, 2390-2401.	1.3	6
2957	Fine-Scale Phylogeography of a Putative Secondary Contact Zone of the Land Snail <i>Cornu aspersum</i> (Gastropoda: Pulmonata: Helicidae) Along the Croatian Coast and Islands. <i>American Malacological Bulletin</i> , 2014, 32, 62-73.	0.2	0
2958	Fine-scale Morphological and Genetic Variability of <i>Geomys personatus</i> Subspecies in Southern Coastal Texas. <i>American Midland Naturalist</i> , 2014, 171, 350-364.	0.2	4
2959	Preponderant clonal evolution of <i>Trypanosoma cruzi</i> I from Argentinean Chaco revealed by Multilocus Sequence Typing (MLST). <i>Infection, Genetics and Evolution</i> , 2014, 27, 348-354.	1.0	15
2960	Population structure of root nodulating <i>Rhizobium leguminosarum</i> in <i>Vicia cracca</i> populations at local to regional geographic scales. <i>Systematic and Applied Microbiology</i> , 2014, 37, 613-621.	1.2	33

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2962	Detection of a distinct variation site for geographical classification of mitochondrial DNA haplogroup A in the domestic goat (<i>Capra hircus</i>). <i>Genes and Genomics</i> , 2014, 36, 701-709.	0.5	0
2963	Reticulate evolution in North American black-fruited hawthorns (<i>Crataegus</i> section <i>Douglasia</i>); Tj ETQq0 0 0 rgBT /Qverlock 10 Tf 50 66.	1.4	19
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2965	Genomic resources and genetic diversity of captive lesser kudu (<i>Tragelaphus imberbis</i>). <i>Zoo Biology</i> , 2014, 33, 440-445.	0.5	4
2966	Close Genetic Relationships between Two American Octopuses: <i>Octopus hubbsorum</i> Berry, 1953, and <i>Octopus mimus</i> Gould, 1852. <i>Journal of Shellfish Research</i> , 2014, 33, 293-303.	0.3	20
2967	Phylogeography and Demographic History of <i>Gotocotyla sawara</i> (Monogenea: Gotocotylidae) on Japanese Spanish Mackerel (<i>Scomberomorus niphonius</i>) Along the Coast of China. <i>Journal of Parasitology</i> , 2014, 100, 85-92.	0.3	10
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2975	The evolution of flowering strategies in US weedy rice. <i>American Journal of Botany</i> , 2014, 101, 1737-1747.	0.8	28
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2977	Sex determination in Madagascar geckos of the genus <i>Paroedura</i> (Squamata: Gekkonidae): are differentiated sex chromosomes indeed so evolutionary stable?. <i>Chromosome Research</i> , 2014, 22, 441-452.	1.0	62
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2983	Genetic diversity and haplotype distribution of <i>Pachymeniopsis garguili</i> sp. nov. and <i>P. lanceolata</i> (<i>Hyalmeniales</i> , <i>Rhodophyta</i>) in <i>Korea</i> , with notes on their non-native distributions. <i>Journal of Phycology</i> , 2014, 50, 885-896.	1.0	16
2984	MOLECULAR ASSESSMENT OF <i>HEPATOZOON</i> (APICOMPLEXA: ADELEORINA) INFECTIONS IN WILD CANIDS AND RODENTS FROM NORTH AFRICA, WITH IMPLICATIONS FOR TRANSMISSION DYNAMICS ACROSS TAXONOMIC GROUPS. <i>Journal of Wildlife Diseases</i> , 2014, 50, 837-848.	0.3	37
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2988	Natural genetic variation in MIR172 isolated from Brassica species. <i>Biologia Plantarum</i> , 2014, 58, 627-640.	1.9	12
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2994	Description of <i>Klebsiella quasipneumoniae</i> sp. nov., isolated from human infections, with two subspecies, <i>Klebsiella quasipneumoniae</i> subsp. <i>quasipneumoniae</i> subsp. nov. and <i>Klebsiella quasipneumoniae</i> subsp. <i>similipneumoniae</i> subsp. nov., and demonstration that <i>Klebsiella singaporensis</i> is a junior heterotypic synonym of <i>Klebsiella variicola</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 3146-3152.	0.8	188
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2997	Unknown Evolutionary Lineages and Population Differentiation in <i>Anolis heterodermus</i> (Squamata: Tj ETQq1 1 0.784314 rgBT /Overl South American Journal of Herpetology, 2014, 9, 131.	0.5	9

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3004	Phylogeographic structure, demographic history and morph composition in a colour polymorphic lizard. <i>Journal of Evolutionary Biology</i> , 2014, 27, 2123-2137.	0.8	31
3005	Characterization of Ancient DNA Supports Long-Term Survival of Haloarchaea. <i>Astrobiology</i> , 2014, 14, 553-560.	1.5	22
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3011	Population Genetic Analysis of <i>Blumeria graminis</i> f. sp. <i>tritici</i> in Qinghai Province, China. <i>Journal of Integrative Agriculture</i> , 2014, 13, 1952-1961.	1.7	6
3012	Genetic diversity and natural selection of three blood-stage 6-Cys proteins in <i>Plasmodium vivax</i> populations from the China-Myanmar endemic border. <i>Infection, Genetics and Evolution</i> , 2014, 28, 167-174.	1.0	18
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3018	Species delimitation and phylogeny in the genus <i><sc>N</sc>asutitermes</i> (<sc>T</sc>ermitidae: <sc>N</sc>asutitermitinae) in <sc>F</sc>rench <sc>G</sc>uiana. <i>Molecular Ecology</i> , 2014, 23, 902-920.	2.0	19
3019	Interglacial genetic diversification of <i>Moussonia deppeana</i> (<sc>G</sc>esneriaceae), a hummingbirdâ€pollinated, cloud forest shrub in northern <sc>M</sc>esoamerica. <i>Molecular Ecology</i> , 2014, 23, 4119-4136.	2.0	25
3020	Phylogeny and evolutionary histories of <i>Pyrus</i> L. revealed by phylogenetic trees and networks based on data from multiple DNA sequences. <i>Molecular Phylogenetics and Evolution</i> , 2014, 80, 54-65.	1.2	58
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3022	<i>Drosophila suzukii</i> : The Genetic Footprint of a Recent, Worldwide Invasion. <i>Molecular Biology and Evolution</i> , 2014, 31, 3148-3163.	3.5	70
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3026	A Few Decades of Habitat Fragmentation has Reduced Population Genetic Diversity: A Case Study of Landscape Genetics of the Large Japanese Field Mouse, <i>Apodemus speciosus</i>. <i>Mammal Study</i> , 2014, 39, 1-10.	0.2	18
3027	Global analysis of population structure, spatial and temporal dynamics of genetic diversity, and evolutionary lineages of Iris yellow spot virus (Tospovirus: Bunyaviridae). <i>Gene</i> , 2014, 547, 111-118.	1.0	8
3028	How many genera and species of woolly monkeys (Atelidae, Platyrrhine, Primates) are there? The first molecular analysis of <i>Lagothrix flavicauda</i> , an endemic Peruvian primate species. <i>Molecular Phylogenetics and Evolution</i> , 2014, 79, 179-198.	1.2	29
3029	Exp2 polymorphisms associated with variation for fiber quality properties in cotton (<i>Gossypium</i> spp.). <i>Crop Journal</i> , 2014, 2, 315-328.	2.3	1
3030	DNA barcoding reveals a high level of mislabeling in Egyptian fish fillets. <i>Food Control</i> , 2014, 46, 441-445.	2.8	84
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3032	Sequential adaptive introgression of the mitochondrial genome in <i><sc>D</sc>rosophila yakuba</i> and <i><sc>D</sc>rosophila santomea</i>. <i>Molecular Ecology</i> , 2014, 23, 1124-1136.	2.0	66
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3035	Genetic data, reproduction season and reproductive strategy data support the existence of biological species in <i>Ophiderma longicauda</i> . <i>Comptes Rendus - Biologies</i> , 2014, 337, 553-560.	0.1	16
3036	Identifying signatures of natural selection in cork oak (<i>Quercus suber</i> L.) genes through SNP analysis. <i>Tree Genetics and Genomes</i> , 2014, 10, 1645-1660.	0.6	29
3037	Population structure and management of invasive cats on an Australian Island. <i>Journal of Wildlife Management</i> , 2014, 78, 968-975.	0.7	6
3038	Phylogenetic and population genetic analysis of <i>Thymallus thymallus</i> (Actinopterygii, Salmonidae) from the middle Volga and upper Ural drainages. <i>Hydrobiologia</i> , 2014, 740, 167-176.	1.0	10
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3043	Multilocus phylogeography of the sea snake <i>Hydrophis curtus</i> reveals historical vicariance and cryptic lineage diversity. <i>Zoologica Scripta</i> , 2014, 43, 472-484.	0.7	9
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3046	Artemia biodiversity in Asia with the focus on the phylogeography of the introduced American species <i>Artemia franciscana</i> Kellogg, 1906. <i>Molecular Phylogenetics and Evolution</i> , 2014, 79, 392-403.	1.2	35
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3054	Integrating Evolutionary and Functional Tests of Adaptive Hypotheses: A Case Study of Altitudinal Differentiation in Hemoglobin Function in an Andean Sparrow, <i>Zonotrichia capensis</i> . <i>Molecular Biology and Evolution</i> , 2014, 31, 2948-2962.	3.5	59
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3056	Population genetics of bisexual and unisexual populations of the scaly-winged bark louse <i>Echmepteryx hageni</i> (Insecta: Psocoptera). <i>Genetica</i> , 2014, 142, 405-418.	0.5	2
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3063	The occurrence of two species of pineapple mealybugs (<i>Dysmicoccus</i> spp.) (Hemiptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10) <i>2014</i> , 67, 36-44.	0.2	5
3064	Molecular evolution of NASP and conserved histone H3/H4 transport pathway. <i>BMC Evolutionary Biology</i> , 2014, 14, 139.	3.2	30
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3068	The evolution of mitochondrial genomes in modern frogs (Neobatrachia): nonadaptive evolution of mitochondrial genome reorganization. <i>BMC Genomics</i> , 2014, 15, 691.	1.2	52
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3072	Molecular and pathological insights into <i>Chlamydia pecorum</i> -associated sporadic bovine encephalomyelitis (SBE) in Western Australia. <i>BMC Veterinary Research</i> , 2014, 10, 121.	0.7	29
3073	No association found between the detection of either xenotropic murine leukemia virus-related virus or polytropic murine leukemia virus and chronic fatigue syndrome in a blinded, multi-site, prospective study by the establishment and use of the SolveCFS BioBank. <i>BMC Research Notes</i> , 2014, 7, 461.	0.6	14
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3075	Genetic fragmentation in India's third longest river system, the Narmada. <i>SpringerPlus</i> , 2014, 3, 385.	1.2	7
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3078	The influence of life history strategy on genetic differentiation and lineage divergence in darters (<i>Percidae: Etheostomatinae</i>). <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 3199-3216.	1.1	19
3079	Evolutionary dynamics of <i>R</i> ² retroelement and insertion inheritance in the genome of bisexual and parthenogenetic <i>Bacillus rossius</i> populations (Insecta: Tj ETQq1 1 0.784314 rgBT /Overl	0.8	7
3080	Plastid DNA sequence data help to clarify phylogenetic relationships and reticulate evolution in <i>Lycoris</i> (<i>Amaryllidaceae</i>). <i>Botanical Journal of the Linnean Society</i> , 2014, , n/a-n/a.	0.8	7
3081	DNA sequence variation of wild barley <i>Hordeum spontaneum</i> (L.) across environmental gradients in Israel. <i>Heredity</i> , 2014, 112, 646-655.	1.2	18
3082	Ecological divergence combined with ancient allopatry in lizard populations from a small volcanic island. <i>Molecular Ecology</i> , 2014, 23, 4799-4812.	2.0	8
3083	Killer Whale Nuclear Genome and mtDNA Reveal Widespread Population Bottleneck during the Last Glacial Maximum. <i>Molecular Biology and Evolution</i> , 2014, 31, 1121-1131.	3.5	61
3084	Glacial history of the European marine mussels <i>Mytilus</i> , inferred from distribution of mitochondrial DNA lineages. <i>Heredity</i> , 2014, 113, 250-258.	1.2	27
3085	The genetics of monarch butterfly migration and warning colouration. <i>Nature</i> , 2014, 514, 317-321.	13.7	264
3086	Exploration of Nuclear DNA Markers for Population Structure Assessment in the Desmid <i>Micrasterias rotata</i> (<i>Zygnematophyceae</i> , <i>Streptophyta</i>). <i>Journal of Eukaryotic Microbiology</i> , 2014, 61, 509-519.	0.8	1
3087	Historical DNA reveals the demographic history of Atlantic cod (<i>Gadus morhua</i>) in medieval and early modern Iceland. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20132976.	1.2	26

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3089	New insights into the evolutionary history of <i>Plasmodium falciparum</i> from mitochondrial genome sequence analyses of Indian isolates. <i>Molecular Ecology</i> , 2014, 23, 2975-2987.	2.0	15
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3096	One or three species in <i>Megadenia</i> (Brassicaceae): insight from molecular studies. <i>Genetica</i> , 2014, 142, 337-350.	0.5	16
3097	Molecular Taxonomy of <i>Conogethes punctiferalis</i> and <i>Conogethes pinicolalis</i> (Lepidoptera): Tj ETQq1 1 0.784314 rgBT /Overlock 10 TTS 1982-1989.	1.7	10
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3103	Genetic structure of duckweed population of <i>Spirodela</i> , <i>Landoltia</i> and <i>Lemna</i> from Lake Tai, China. <i>Planta</i> , 2014, 239, 1299-1307.	1.6	28
3104	Natural variation and genetic analysis of the tiller angle gene MsTAC1 in <i>Miscanthus sinensis</i> . <i>Planta</i> , 2014, 240, 161-175.	1.6	29
3105	Characteristics and molecular phylogeny of <i>Fasciola</i> flukes from Bangladesh, determined based on spermatogenesis and nuclear and mitochondrial DNA analyses. <i>Parasitology Research</i> , 2014, 113, 2493-2501.	0.6	52

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3107	Genetic variation and population differentiation of the endochitinase gene family in <i>Pinus monticola</i> . <i>Plant Systematics and Evolution</i> , 2014, 300, 1313-1322.	0.3	5
3108	Genetic diversity of <i>Rhododendron delavayi</i> var. <i>delavayi</i> (C. B. Clarke) Ridley inferred from nuclear and chloroplast DNA: implications for the conservation of fragmented populations. <i>Plant Systematics and Evolution</i> , 2014, 300, 1853-1866.	0.3	8
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3112	Did the parasitoid <i>Pnigalio mediterraneus</i> (Hymenoptera: Eulophidae) track the invasion of the horse chestnut leafminer?. <i>Biological Invasions</i> , 2014, 16, 843-857.	1.2	16
3113	Invasion genetics of <i>Chromolaena odorata</i> (Asteraceae): extremely low diversity across Asia. <i>Biological Invasions</i> , 2014, 16, 2351-2366.	1.2	30
3114	Population genetics of goldspotted oak borer, <i>Agrilus auroguttatus</i> Schaeffer (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 427 T Invasions, 2014, 16, 2393-2402.	1.2	17
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3119	Assessing the impact of hunting pressure on population structure of Guinea baboons (<i>Papio papio</i>) in Guinea-Bissau. <i>Conservation Genetics</i> , 2014, 15, 1339-1355.	0.8	19
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3122	Geographic variation in relict populations: genetics and phenotype of bush-cricket <i>Pholidoptera frivaldskyi</i> (Orthoptera) in Carpathians. <i>Journal of Insect Conservation</i> , 2014, 18, 257-266.	0.8	9
3123	Development of single nucleotide polymorphisms in <i>Phaseolus vulgaris</i> and related <i>Phaseolus</i> spp. <i>Molecular Breeding</i> , 2014, 33, 531-544.	1.0	23

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3125	A transposable element insertion disturbed starch synthase gene SSIIb in maize. <i>Molecular Breeding</i> , 2014, 34, 1159-1171.	1.0	4
3126	Mitochondrial ATPase 6/8 genes reveal genetic divergence in the <i>Coilia dussumieri</i> (Valenciennes, 1848) populations of north east and northwest coasts of India. <i>Molecular Biology Reports</i> , 2014, 41, 3723-3731.	1.0	9
3127	Morphological similarity and molecular divergence of <i>Trochulus striolatus</i> and <i>T. montanus</i> , and their relationship to sympatric congeners (Gastropoda: Pulmonata: Hygromiidae). <i>Systematics and Biodiversity</i> , 2014, 12, 366-384.	0.5	11
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3129	Genetic diversity, haplotypes and allele groups of Duffy binding protein (PkDBP1±II) of <i>Plasmodium knowlesi</i> clinical isolates from Peninsular Malaysia. <i>Parasites and Vectors</i> , 2014, 7, 161.	1.0	26
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3134	Genetic Diversity and Evolution of <i>Salmonella enterica</i> Serovar Enteritidis Strains with Different Phage Types. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1490-1500.	1.8	26
3135	The first European stand of <i>Paramecium sonneborni</i> (<i>P. aurelia</i> complex), a species known only from North America (Texas, USA). <i>European Journal of Protistology</i> , 2014, 50, 236-247.	0.5	12
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3137	Italian neo-endemism in a widespread group of leafhoppers insects: A revision of the <i>Eupteryx aurata</i> group (Auchenorrhyncha: Cicadellidae: Typhlocybinae) using morphology, ecology and genetics. <i>Zoologischer Anzeiger</i> , 2014, 253, 283-308.	0.4	2
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3139	Phylogeography of the genus <i>Dasiphora</i> (Rosaceae) in the Qinghai-Tibetan Plateau: divergence blurred by expansion. <i>Biological Journal of the Linnean Society</i> , 2014, 111, 777-788.	0.7	13
3140	Influence of drainage divides versus arid corridors on genetic structure and demography of a widespread freshwater turtle, <i>Emydura macquarii krefftii</i> , from Australia. <i>Ecology and Evolution</i> , 2014, 4, 606-622.	0.8	5
3141	Genotypes of <i>Klebsiella oxytoca</i> Isolates from Patients with Nosocomial Pneumonia Are Distinct from Those of Isolates from Patients with Antibiotic-Associated Hemorrhagic Colitis. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1607-1616.	1.8	69

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3155	The β -gliadin-like β -prolamin genes in the tribe Triticeae. <i>Journal of Genetics</i> , 2014, 93, 35-41.	0.4	3
3156	Comparative study of the marR genes within the family Enterobacteriaceae. <i>Journal of Microbiology</i> , 2014, 52, 452-459.	1.3	6
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3158	DNA barcoding reveals the occurrence of cryptic species in host-associated population of <i>Conogethes punctiferalis</i> (Lepidoptera: Crambidae). <i>Applied Entomology and Zoology</i> , 2014, 49, 283-295.	0.6	35
3159	Mitochondrial DNA variation in Olga Bay larch (<i>Larix olgensis</i> A. Henry) from Primorsky Krai of Russia. <i>Russian Journal of Genetics</i> , 2014, 50, 253-260.	0.2	3

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3161	Molecular data and ecological niche modeling reveal population dynamics of widespread shrub <i>Forsythia suspensa</i> (Oleaceae) in China's warm-temperate zone in response to climate change during the Pleistocene. <i>BMC Evolutionary Biology</i> , 2014, 14, 114.	3.2	27
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3172	Genetic diversity and antifungal susceptibility profiles in causative agents of sporotrichosis. <i>BMC Infectious Diseases</i> , 2014, 14, 219.	1.3	112
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3174	Genetic divergence of the Mesoamerican azure-crowned hummingbird (<i>Amazilia cyanocephala</i>) and Evolutionary Research, 2014, 52, 142-153.	0.6	18
3175	Anchovies go north and west without losing diversity: post-glacial range expansions in a small pelagic fish. <i>Journal of Biogeography</i> , 2014, 41, 1171-1182.	1.4	36
3176	Phylogeographical structure within <i>Boa constrictor imperator</i> across the lowlands and mountains of Central America and Mexico. <i>Journal of Biogeography</i> , 2014, 41, 2371-2384.	1.4	34
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3180	Genetic Variability and Geographical Diversity of the Main Chagas' Disease Vector <i>Panstrongylus megistus</i> (Hemiptera: Triatominae) in Brazil Based on Ribosomal DNA Intergenic Sequences. <i>Journal of Medical Entomology</i> , 2014, 51, 616-628.	0.9	10
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3192	Molecular epidemiology and genetic diversity of <i>Entamoeba</i> species in a chelonian collection. <i>Journal of Medical Microbiology</i> , 2014, 63, 271-283.	0.7	20
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3197	Genetic Divergence of Bradyrhizobium Strains Nodulating Soybeans as Revealed by Multilocus Sequence Analysis of Genes Inside and Outside the Symbiosis Island. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3181-3190.	1.4	41
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3200	Molecular evolution and nucleotide diversity of nuclear plastid phosphoglycerate kinase (PGK) gene in Triticeae (Poaceae). <i>Gene</i> , 2014, 533, 142-148.	1.0	11
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3202	Multilocus approach to clarify species status and the divergence history of the <i>Bemisia tabaci</i> (Hemiptera: Aleyrodidae) species complex. <i>Molecular Phylogenetics and Evolution</i> , 2014, 76, 172-180.	1.2	23
3203	One species or two? Multilocus analysis of nucleotide variation of <i>Melastoma penicillatum</i> and <i>Melastoma sanguineum</i> (Melastomataceae) in Hainan, China. <i>Biochemical Systematics and Ecology</i> , 2014, 55, 275-282.	0.6	7
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3339	Phylogeographic structure of cotton pest <i>Adelphocoris suturalis</i> (Hemiptera: Miridae): strong subdivision in China inferred from mtDNA and rDNA ITS markers. <i>Scientific Reports</i> , 2015, 5, 14009.	1.6	13
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3343	Connectivity in grey reef sharks (<i>Carcharhinus amblyrhynchos</i>) determined using empirical and simulated genetic data. <i>Scientific Reports</i> , 2015, 5, 13229.	1.6	24
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3385	A chemosynthetic weed: the tubeworm <i>Sclerolinum contortum</i> is a bipolar, cosmopolitan species. <i>BMC Evolutionary Biology</i> , 2015, 15, 280.	3.2	54
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3389	A multilocus sequence analysis scheme for characterization of <i>Flavobacterium columnare</i> isolates. <i>BMC Microbiology</i> , 2015, 15, 243.	1.3	24
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3397	DNA reveals long-distance partial migratory behavior in a cryptic owl lineage. <i>Avian Research</i> , 2015, 6, .	0.5	4
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3408	Contrasting patterns of selection and drift between two categories of immune genes in prairie chickens. <i>Molecular Ecology</i> , 2015, 24, 6095-6106.	2.0	18
3409	Inferring speciation history in the Andes with reduced representation sequence data: an example in the bay-backed antpittas (Aves; Grallariidae; <i>Grallaria hypoleuca</i> s. l.). <i>Molecular Ecology</i> , 2015, 24, 6256-6277.	2.0	28
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3438	Phylogeography of the Chinese endemic freshwater crab <i><i>Sinopotamon acutum</i></i> (Brachyura). <i>Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50</i>	0.7	20
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3628	Phylogeography of the subgenus <i>Transphlebotomus</i> Artemiev with description of two new species, <i>Phlebotomus anatolicus</i> n. sp. and <i>Phlebotomus kilicki</i> n. sp.. <i>Infection, Genetics and Evolution</i> , 2015, 34, 467-479.	1.0	39
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3830	COLD1 Confers Chilling Tolerance in Rice. <i>Cell</i> , 2015, 160, 1209-1221.	13.5	724
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3832	Mitochondrial DNA Sequence Analyses and Phylogenetic Relationships Among Two Nigerian Goat Breeds and the South African Kalahari Red. <i>Animal Biotechnology</i> , 2015, 26, 180-187.	0.7	11
3833	Population genetics of the fiddler crab <i>Uca sindensis</i> (Alcock, 1900) (Crustacea: Brachyura): Tj ETQq1 1 0.784314 rgBT /Overlock 10 T F	0.3	18
3834	Genetic structure and parasitization-related ability divergence of a nematode fungal pathogen <i>Hirsutella minnesotensis</i> following founder effect in China. <i>Fungal Genetics and Biology</i> , 2015, 81, 212-220.	0.9	5
3835	A genetic approach to the origin of <i>Millepora</i> sp. in the eastern Atlantic. <i>Coral Reefs</i> , 2015, 34, 631-638.	0.9	37
3836	Genetic variation among Corsican and continental populations of the Eurasian treecreeper (<i>Aves: Certhia familiaris</i>) reveals the existence of a palaeoendemic mitochondrial lineage. <i>Biological Journal of the Linnean Society</i> , 2015, 115, 134-153.	0.7	17
3837	<i>Trypanosoma rangeli</i> displays a clonal population structure, revealing a subdivision of KP1(âˆ”) strains and the ancestry of the Amazonian group. <i>International Journal for Parasitology</i> , 2015, 45, 225-235.	1.3	11
3838	ITS rDNA sequence comparisons resolve phylogenetic relationships in <i>Orostachys</i> subsection <i>Appendiculatae</i> (Crassulaceae). <i>Plant Systematics and Evolution</i> , 2015, 301, 1441-1453.	0.3	5
3839	Prioritizing genes for X-linked diseases using population exome data. <i>Human Molecular Genetics</i> , 2015, 24, 599-608.	1.4	18
3840	Genetic structure and diversity of <i>Triticum monococcum</i> ssp. <i>aegilopoides</i> and <i>T. urartu</i> in Iran. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2015, 13, 1-8.	0.4	5
3841	Detecting natural hybridization between two vulnerable Andean pupfishes (<i>Orestias agassizii</i> and <i>O.</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T F	0.8	8
3842	Characterisation of Toll-like receptors 4, 5 and 7 and their genetic variation in the grey partridge. <i>Genetica</i> , 2015, 143, 101-112.	0.5	15
3843	Complex biogeography and historic translocations lead to complicated phylogeographic structure of freshwater eel-tailed catfish (<i>Tandanus</i> spp.) in south-eastern Australia. <i>Conservation Genetics</i> , 2015, 16, 777-790.	0.8	7
3844	Toll-like receptor diversity in 10 threatened bird species: relationship with microsatellite heterozygosity. <i>Conservation Genetics</i> , 2015, 16, 595-611.	0.8	42
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3847	Ghosts of glaciers and the disjunct distribution of a threatened California moth (<i>Euproserpinus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1.9	1.9	10
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3849	Genetic diversity and population structure of the threatened freshwater catfish, <i>Tandanus tandanus</i> , in Victoria, Australia. <i>Conservation Genetics</i> , 2015, 16, 317-329.	0.8	2
3850	Wide-ranging phylogeographic structure of invasive red lionfish in the Western Atlantic and Greater Caribbean. <i>Marine Biology</i> , 2015, 162, 773-781.	0.7	22
3851	Multilocus Sequence Typing of <i>Leuconostoc gelidum</i> subsp. <i>gasicomitatum</i> , a Psychrotrophic Lactic Acid Bacterium Causing Spoilage of Packaged Perishable Foods. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2474-2480.	1.4	13
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3853	Extensive genetic divergence among <i>Diptychus maculatus</i> populations in northwest China. <i>Chinese Journal of Oceanology and Limnology</i> , 2015, 33, 577-584.	0.7	5
3854	Inference of domestication history and differentiation between early- and late-flowering varieties in pearl millet. <i>Molecular Ecology</i> , 2015, 24, 1387-1402.	2.0	24
3855	Parallels between two geographically and ecologically disparate cave invasions by the same species, <i>Acellularia aquatica</i> (Ciliophora: Alveolates, Ciliophora) and <i>Acellularia</i> (Ciliophora: Alveolates, Ciliophora). <i>Journal of Evolutionary Biology</i> , 2015, 28, 864-875.	0.8	57
3856	Historical demography of southern African patellid limpets: congruence of population expansions, but not phylogeography. <i>African Journal of Marine Science</i> , 2015, 37, 11-20.	0.4	22
3857	Disentangling the complex evolutionary history of the Western Palearctic blue tits (<i>Cyanistes</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 2.0 isolation. <i>Molecular Ecology</i> , 2015, 24, 2477-2494.	2.0	39
3858	The life cycle of <i>Proisorhynchoides carvajali</i> (Trematoda: Bucephalidae) involving species of bivalve and fish hosts in the intertidal zone of central Chile. <i>Journal of Helminthology</i> , 2015, 89, 584-592.	0.4	13
3859	Molecular systematics of the small-toothed palm civet (<i>Arctogalidia trivirgata</i>) reveals a strong divergence of Bornean populations. <i>Mammalian Biology</i> , 2015, 80, 347-354.	0.8	7
3860	Multilocus sequence typing of a dairy-associated <i>Leuconostoc mesenteroides</i> population reveals clonal structure with intragenic homologous recombination. <i>Journal of Dairy Science</i> , 2015, 98, 2284-2293.	1.4	11
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3862	Molecular characterisation of three regions of the nuclear ribosomal DNA unit and the mitochondrial <i>cox1</i> gene of <i>Sarcocystis fusiformis</i> from water buffaloes (<i>Bubalus bubalis</i>) in Egypt. <i>Parasitology Research</i> , 2015, 114, 3401-3413.	0.6	24
3863	Genetic divergence in wild population of endangered yellowtail catfish <i>Pangasius pangasius</i> (Hamilton-Buchanan, 1822) revealed by mtDNA. <i>Mitochondrial DNA</i> , 2015, 26, 182-186.	0.6	6

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3865	Molecular Evolution of the CYP2D Subfamily in Primates: Purifying Selection on Substrate Recognition Sites without the Frequent or Long-Tract Gene Conversion. <i>Genome Biology and Evolution</i> , 2015, 7, 1053-1067.	1.1	14
3866	Evolutionary history of the Azteca-like mariner transposons and their host ants. <i>Die Naturwissenschaften</i> , 2015, 102, 44.	0.6	7
3867	Endogenization of mouse mammary tumor virus (MMTV)-like elements in genomes of pikas (<i>Ochotona</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 10	1.1	8
3868	Diversifying selection by Desmodiinae legume species on <i>Bradyrhizobium</i> symbionts. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv075.	1.3	6
3869	Genetic differentiation of populations of Baikal endemic <i>Sergentia baicalensis</i> Tshern. (Diptera,) Tj ETQq1 1 0.784314 rgBT / Overlock 10	0.2	3
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3876	Geographical and Temporal Structures of <i>Legionella pneumophila</i> Sequence Types in Comunitat Valenciana (Spain), 1998 to 2013. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7106-7113.	1.4	10
3877	Molecular identification and allopatric divergence of the white pine species in China based on the cytoplasmic DNA variation. <i>Biochemical Systematics and Ecology</i> , 2015, 61, 161-168.	0.6	21
3878	Genetic structure of locally threatened cyprinid, <i>Osteochilus melanopleurus</i> , in Peninsular Malaysia River systems inferred from mitochondrial DNA control region. <i>Biochemical Systematics and Ecology</i> , 2015, 61, 336-343.	0.6	1
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3880	Population Structure of mtDNA Variation due to Pleistocene Fluctuations in the South American Maned Wolf (<i>Chrysocyon brachyurus</i> , Illiger, 1815): Management Units for Conservation. <i>Journal of Heredity</i> , 2015, 106, 459-468.	1.0	14
3881	Mitochondrial DNA Intraspecific Variability in <i>Sergentomyia minuta</i> (Diptera: Psychodidae). <i>Journal of Medical Entomology</i> , 2015, 52, 819-828.	0.9	11

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3884	Mitochondrial phylogeography of a surf clam <i>Mactra veneriformis</i> in the East China Sea: Genetic homogeneity across two biogeographic boundaries. <i>Biochemical Systematics and Ecology</i> , 2015, 61, 493-500.	0.6	8
3885	Temporal Genetic Dynamics of an Invasive Species, <i>Frankliniella occidentalis</i> (Pergande), in an Early Phase of Establishment. <i>Scientific Reports</i> , 2015, 5, 11877.	1.6	14
3886	Assessment of the genetic and phenotypic diversity among rhizogenic <i>Agrobacterium</i> biovar 1 strains infecting solanaceous and cucurbit crops. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv081.	1.3	19
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3889	Molecular variability in the cysteine rich protein of potato virus M. <i>VirusDisease</i> , 2015, 26, 117-122.	1.0	3
3890	Seasonal changes in gene expression and polymorphism of hsp70 in cultivated oysters (<i>Crassostrea</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.1	14
3891	The ant <i>Anochetus ghiliani</i> (Hymenoptera, Formicidae), not a Tertiary relict, but an Iberian introduction from North Africa: Evidence from mtDNA analyses. <i>Systematics and Biodiversity</i> , 2015, 13, 545-554.	0.5	3
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3893	Genotyping of Cucumber mosaic virus isolates in western New York State during epidemic years. <i>Virus Research</i> , 2015, 210, 169-177.	1.1	21
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3895	Recurrent Evolution of Melanism in South American Felids. <i>PLoS Genetics</i> , 2015, 11, e1004892.	1.5	36
3896	Environmental DNA evidence of transfer of North Sea molluscs across tropical waters through ballast water. <i>Journal of Molluscan Studies</i> , 2015, 81, 495-501.	0.4	44
3897	Low Genetic Diversity and Moderate Inbreeding Risk of an Insular Endemic Pit Viper (<i>Gloydus</i>) Tj ETQq1 1 0.784314 rgBT /5Overlock 10 Tf 5	0.2	5
3898	Genetic Assessment of Taxonomic Uncertainty in Painted Turtles. <i>Journal of Herpetology</i> , 2015, 49, 314-324.	0.2	10
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3903	Genetic diversity and recombination analysis of grapevine leafroll-associated virus 1 from China. <i>Archives of Virology</i> , 2015, 160, 1669-1678.	0.9	23
3904	Genetic variability of <i>Echinococcus granulosus</i> based on the mitochondrial 16S ribosomal RNA gene. <i>Mitochondrial DNA</i> , 2015, 26, 396-401.	0.6	18
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3906	Genetic diversity, historic population size, and population structure in 2 North American tree bats. <i>Journal of Mammalogy</i> , 2015, 96, 972-980.	0.6	18
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3911	Chloroplast heterogeneity and historical admixture within the genus <i>Malus</i> . <i>American Journal of Botany</i> , 2015, 102, 1198-1208.	0.8	36
3912	Identification and functional characterization of viperin of amphioxus <i>Branchiostoma japonicum</i> : Implications for ancient origin of viperin-mediated antiviral response. <i>Developmental and Comparative Immunology</i> , 2015, 53, 293-302.	1.0	24
3913	The <i>Ordospora colligata</i> Genome: Evolution of Extreme Reduction in Microsporidia and Host-To-Parasite Horizontal Gene Transfer. <i>MBio</i> , 2015, 6, .	1.8	36
3914	Opposing demographic histories reveal rapid evolution in grebes (Aves: Podicipedidae). <i>Auk</i> , 2015, 132, 771-786.	0.7	4
3915	Defining the RNA-binding glycine-rich (RBC) gene superfamily: new insights into nomenclature, phylogeny, and evolutionary trends obtained by genome-wide comparative analysis of Arabidopsis, Chinese cabbage, rice and maize genomes. <i>Molecular Genetics and Genomics</i> , 2015, 290, 2279-2295.	1.0	16
3916	Mitochondrial genome of the intertidal acorn barnacle <i>Tetraclita serrata</i> Darwin, 1854 (Crustacea: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2015, 22, 63-69.	0.4	17
3917	Characterization of WRKY transcription factors in <i>Solanum lycopersicum</i> reveals collinearity and their expression patterns under cold treatment. <i>Biochemical and Biophysical Research Communications</i> , 2015, 464, 962-968.	1.0	39

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3919	High nucleotide diversity and limited linkage disequilibrium in <i>Helicoverpa armigera</i> facilitates the detection of a selective sweep. Heredity, 2015, 115, 460-470.	1.2	15
3920	The complete chloroplast genome sequence of <i>Aster spathulifolius</i> (Asteraceae); genomic features and relationship with Asteraceae. Gene, 2015, 572, 214-221.	1.0	55
3921	A single sym plasmid type predominates across diverse chromosomal lineages of <i>Cupriavidus nodule</i> symbionts. Systematic and Applied Microbiology, 2015, 38, 417-423.	1.2	11
3922	Mitochondrial population genomic analyses reveal population structure and demography of Indian <i>Plasmodium falciparum</i> . Mitochondrion, 2015, 24, 9-21.	1.6	7
3923	Balancing immunity and tolerance: genetic footprint of natural selection in the transcriptional regulatory region of HLA-G. Genes and Immunity, 2015, 16, 57-70.	2.2	24
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3927	Comparative analysis of plant lycopene cyclases. Computational Biology and Chemistry, 2015, 58, 81-92.	1.1	11
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3931	Plastid DNA Homogeneity in <i>Celtis australis</i> L. (Cannabaceae) and <i>Nerium oleander</i> L. (Apocynaceae) throughout the Mediterranean Basin. International Journal of Plant Sciences, 2015, 176, 421-432.	0.6	7
3932	Motif mismatches in microsatellites: insights from genome-wide investigation among 20 insect species. DNA Research, 2015, 22, 29-38.	1.5	19
3933	Global Survey of Variation in a Human Olfactory Receptor Gene Reveals Signatures of Non-Neutral Evolution. Chemical Senses, 2015, 40, 481-488.	1.1	31
3934	Phylogeography of <i>Haplocarpha rueppelii</i> (Asteraceae) suggests a potential geographic barrier for plant dispersal and gene flow in East Africa. Science Bulletin, 2015, 60, 1184-1192.	4.3	8
3935	The evolution of soybean mosaic virus: An updated analysis by obtaining 18 new genomic sequences of Chinese strains/isolates. Virus Research, 2015, 208, 189-198.	1.1	29

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3937	The Emergence of Resistance to the Benzimidazole Anthelmintics in Parasitic Nematodes of Livestock Is Characterised by Multiple Independent Hard and Soft Selective Sweeps. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003494.	1.3	120
3938	Characterization of sequence diversity in <i>Plasmodium falciparum</i> SERA5 from Indian isolates. <i>Asian Pacific Journal of Tropical Disease</i> , 2015, 5, S80-S84.	0.5	0
3939	Planning tiger recovery: Understanding intraspecific variation for effective conservation. <i>Science Advances</i> , 2015, 1, e1400175.	4.7	63
3940	Evolutionary Relationships, Gynodioecy, and Polyploidy in the Galápagos Endemic <i>Lycium minimum</i> (Solanaceae). <i>International Journal of Plant Sciences</i> , 2015, 176, 197-210.	0.6	9
3941	Hyperdiverse Gene Cluster in Snail Host Conveys Resistance to Human Schistosome Parasites. <i>PLoS Genetics</i> , 2015, 11, e1005067.	1.5	72
3942	Spatio-Temporal Distribution of <i>Aedes aegypti</i> (Diptera: Culicidae) Mitochondrial Lineages in Cities with Distinct Dengue Incidence Rates Suggests Complex Population Dynamics of the Dengue Vector in Colombia. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003553.	1.3	30
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3944	The complete chloroplast genome provides insight into the evolution and polymorphism of <i>Panax ginseng</i> . <i>Frontiers in Plant Science</i> , 2014, 5, 696.	1.7	112
3945	Contrasting signals of genetic diversity and historical demography between two recently diverged marine and estuarine fish species. <i>Marine Ecology - Progress Series</i> , 2015, 526, 157-167.	0.9	8
3946	Nucleotide variation and identification of novel blast resistance alleles of <i>Pib</i> by allele mining strategy. <i>Physiology and Molecular Biology of Plants</i> , 2015, 21, 301-304.	1.4	2
3947	Contrasting responses to Pleistocene climate changes: a case study of two sister species <i>Allium cyathophorum</i> and <i>A. spicatum</i> (Amaryllidaceae) distributed in the eastern and western Qinghai-Tibet Plateau. <i>Ecology and Evolution</i> , 2015, 5, 1513-1524.	0.8	11
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3949	Continental-scale analysis reveals deep diversification within the polytypic Red-crowned Ant Tanager (<i>Habia rubica</i> , Cardinalidae). <i>Molecular Phylogenetics and Evolution</i> , 2015, 89, 182-193.	1.2	19
3950	Phylogenetic Relationships of <i>Apodemus</i> Kaup, 1829 (Rodentia: Muridae) Species in the Eastern Mediterranean Inferred from Mitochondrial DNA, with Emphasis on Iranian Species. <i>Journal of Mammalian Evolution</i> , 2015, 22, 583-595.	1.0	25
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3952	Genome-wide patterns of differentiation and spatially varying selection between postglacial recolonization lineages of <i>Populus alba</i> (Salicaceae), a widespread forest tree. <i>New Phytologist</i> , 2015, 207, 723-734.	3.5	40
3953	Phylogeography of the copepod <i>Calanoides carinatus</i> s.l. (Kr�yer) reveals cryptic species and delimits <i>C. carinatus</i> s.s. distribution in SW Atlantic Ocean. <i>Journal of Experimental Marine Biology and Ecology</i> , 2015, 468, 97-104.	0.7	14

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3955	Genetic diversity in <i>Monoporeia affinis</i> at polluted and reference sites of the Baltic Bothnian Bay. <i>Marine Pollution Bulletin</i> , 2015, 93, 245-249.	2.3	8
3956	Multilocus sequence analysis reveals taxonomic differences among <i>Bradyrhizobium</i> sp. symbionts of <i>Lupinus albus</i> plants growing in arenized and non-arenized areas. <i>Systematic and Applied Microbiology</i> , 2015, 38, 323-329.	1.2	29
3957	Molecular genetic analysis of <i>Plasmodium vivax</i> isolates from Eastern and Central Sudan using <i>pvcsp</i> and <i>pvmsp-3</i> genes as molecular markers. <i>Infection, Genetics and Evolution</i> , 2015, 32, 12-22.	1.0	16
3958	Molecular Characterization of Sec2 Loci in Wheat "Secale africanum" Derivatives Demonstrates Genomic Divergence of Secale Species. <i>International Journal of Molecular Sciences</i> , 2015, 16, 8324-8336.	1.8	4
3959	The effect of past climatic oscillations on spatial genetic structure of <i>Atraphaxis manshurica</i> (Polygonaceae) in the Horqin sandlands, northern China. <i>Biochemical Systematics and Ecology</i> , 2015, 60, 88-94.	0.6	5
3960	Multilocus Sequence Analysis of the redefined clade Scophthalmi in the genus <i>Vibrio</i> . <i>Systematic and Applied Microbiology</i> , 2015, 38, 169-175.	1.2	9
3961	<i>Pomphorhynchus laevis</i> (Acanthocephala) from the Sava River basin: New insights into strain formation, mtDNA-like sequences and dynamics of infection. <i>Parasitology International</i> , 2015, 64, 243-250.	0.6	17
3962	Mitogenome revealed multiple postdomestication genetic mixtures of West African sheep. <i>Journal of Animal Breeding and Genetics</i> , 2015, 132, 399-405.	0.8	10
3963	Demographic history and the South Pacific dispersal barrier for school shark (<i>Galeorhinus galeus</i>) inferred by mitochondrial DNA and microsatellite DNA mark. <i>Fisheries Research</i> , 2015, 167, 132-142.	0.9	15
3964	Contrasting patterns of population structure and demographic history in cryptic species of <i>Bostrychia intricata</i> (Rhodomelaceae, Rhodophyta) from New Zealand. <i>Journal of Phycology</i> , 2015, 51, 574-585.	1.0	22
3965	A polymorphic pseudoautosomal boundary in the <i>Carica papaya</i> sex chromosomes. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1511-1522.	1.0	11
3966	Positive and purifying selection in mitochondrial genomes of a bird with mitonuclear discordance. <i>Molecular Ecology</i> , 2015, 24, 2820-2837.	2.0	112
3967	Deep comparative genomics among <i>Chlamydia trachomatis</i> lymphogranuloma venereum isolates highlights genes potentially involved in pathoadaptation. <i>Infection, Genetics and Evolution</i> , 2015, 32, 74-88.	1.0	17
3968	Does fragmentation of wetlands affect gene flow in sympatric <i>Acrocephalus</i> warblers with different migration strategies?. <i>Journal of Avian Biology</i> , 2015, 46, 577-588.	0.6	11
3969	Molecular analysis of <i>Phytophthora</i> diversity in nursery-grown ornamental and fruit plants. <i>Plant Pathology</i> , 2015, 64, 1308-1319.	1.2	56
3970	Diversity and evolution of Rp1 rust resistance genes in four maize lines. <i>Theoretical and Applied Genetics</i> , 2015, 128, 985-998.	1.8	21
3971	Global mitochondrial DNA phylogeography and population structure of the silky shark, <i>Carcharhinus falciformis</i> . <i>Marine Biology</i> , 2015, 162, 945-955.	0.7	58

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3973	Low level of genetic divergence between Harpagifer fish species (Perciformes: Notothenioidae) suggests a Quaternary colonization of Patagonia from the Antarctic Peninsula. <i>Polar Biology</i> , 2015, 38, 607-617.	0.5	38
3974	Genomic origin, expression differentiation and regulation of multiple genes encoding CYP83A1, a key enzyme for core glucosinolate biosynthesis, from the allotetraploid <i>Brassica juncea</i> . <i>Planta</i> , 2015, 241, 651-665.	1.6	20
3976	Quaternary radiation of bifid toadflaxes (<i>Linaria</i> sect. <i>Versicolores</i>) in the Iberian Peninsula: low taxonomic signal but high geographic structure of plastid DNA lineages. <i>Plant Systematics and Evolution</i> , 2015, 301, 1411-1423.	0.3	9
3977	Phylogenetic placement of the critically endangered Townsend's Shearwater (<i>Puffinus auricularis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T mismatch between genetic and phenotypic differentiation. <i>Journal of Ornithology</i> , 2015, 156, 1025-1034.	0.5	10
3978	Effects of barred owl (<i>Strix varia</i>) range expansion on <i>Haemoproteus</i> parasite assemblage dynamics and transmission in barred and northern spotted owls (<i>Strix occidentalis caurina</i>). <i>Biological Invasions</i> , 2015, 17, 1713-1727.	1.2	11
3979	Invasion of <i>Brassica nigra</i> in North America: distributions and origins of chloroplast DNA haplotypes suggest multiple introductions. <i>Biological Invasions</i> , 2015, 17, 2447-2459.	1.2	20
3980	Population genetics of invasive <i>Citrullus lanatus</i> , <i>Citrullus colocynthis</i> and <i>Cucumis myriocarpus</i> (Cucurbitaceae) in Australia: inferences based on chloroplast and nuclear gene sequencing. <i>Biological Invasions</i> , 2015, 17, 2475-2490.	1.2	7
3981	Conservation of <i>Brosimum alicastrum</i> , an underutilized crop and keystone forest tree species; a potential win-win for conservation and development in Latin America. <i>Biodiversity and Conservation</i> , 2015, 24, 1917-1930.	1.2	14
3982	Polyphyletic ancestry of historic gray wolves inhabiting U.S. Pacific states. <i>Conservation Genetics</i> , 2015, 16, 759-764.	0.8	5
3983	Spatial genetic structure among bat hibernacula along the leading edge of a rapidly spreading pathogen. <i>Conservation Genetics</i> , 2015, 16, 1013-1024.	0.8	17
3984	Genetic diversity and demographic history of the endangered and endemic fish (<i>Platypharodon</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T Fishes, 2015, 98, 763-774.	0.4	6
3985	Life at the leading edge: genetic impoverishment of the spotted bass, <i>Micropterus punctulatus</i> , at its Western edge. <i>Environmental Biology of Fishes</i> , 2015, 98, 1823-1832.	0.4	6
3986	The endangered species <i>Brycon orbignyanus</i> : genetic analysis and definition of priority areas for conservation. <i>Environmental Biology of Fishes</i> , 2015, 98, 1845-1855.	0.4	29
3987	Disparate past demographic histories of three small Scombridae (Actinopterygii) species in Tunisian waters. <i>Hydrobiologia</i> , 2015, 758, 19-30.	1.0	4
3988	Sequence variation, differential expression, and divergent evolution in starch-related genes among accessions of <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology</i> , 2015, 87, 489-519.	2.0	11
3989	Association Analysis of the Maize Gene <i>ZmYS1</i> with Kernel Mineral Concentrations. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1327-1335.	1.0	3
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3992	Origin, evolution, and population genetics of the selfish Segregation Distorter gene duplication in European and African populations of <i>Drosophila melanogaster</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1271-1283.	1.1	36
3993	Adaptive divergence in the monkey flower <i>Mimulus guttatus</i> is maintained by a chromosomal inversion. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1476-1486.	1.1	163
3994	<i>Burkholderia stagnalis</i> sp. nov. and <i>Burkholderia territorii</i> sp. nov., two novel <i>Burkholderia cepacia</i> complex species from environmental and human sources. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 2265-2271.	0.8	149
3995	Comparison of mitochondrial genomes provides insights into intron dynamics and evolution in the caterpillar fungus <i>Cordyceps militaris</i> . <i>Fungal Genetics and Biology</i> , 2015, 77, 95-107.	0.9	86
3996	Phylogeny, phylogeography and geographical variation in the <i>Crocidura monax</i> (Soricidae) species complex from the montane islands of Tanzania, with descriptions of three new species. <i>Zoological Journal of the Linnean Society</i> , 2015, 174, 185-215.	1.0	27
3997	Phylogeny of <i>Salix</i> subgenus <i>Salix</i> s.l. (Salicaceae): delimitation, biogeography, and reticulate evolution. <i>BMC Evolutionary Biology</i> , 2015, 15, 31.	3.2	77
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4000	Comprehensive analysis of CCCH-type zinc finger family genes facilitates functional gene discovery and reflects recent allopolyploidization event in tetraploid switchgrass. <i>BMC Genomics</i> , 2015, 16, 129.	1.2	38
4001	Virus genome dynamics under different propagation pressures: reconstruction of whole genome haplotypes of west Nile viruses from NGS data. <i>BMC Genomics</i> , 2015, 16, 118.	1.2	16
4002	Analysis of the complete mitochondrial genome of <i>Pochonia chlamydosporia</i> suggests a close relationship to the invertebrate-pathogenic fungi in <i>Hypocreales</i> . <i>BMC Microbiology</i> , 2015, 15, 5.	1.3	72
4003	Genetic diversity of medically important and emerging <i>Candida</i> species causing invasive infection. <i>BMC Infectious Diseases</i> , 2015, 15, 57.	1.3	75
4004	Molecular epidemiology of human sporotrichosis in Venezuela reveals high frequency of <i>Sporothrix globosa</i> . <i>BMC Infectious Diseases</i> , 2015, 15, 94.	1.3	59
4005	Remarkable diversity of intron-1 of the para voltage-gated sodium channel gene in an <i>Anopheles gambiae</i> / <i>Anopheles coluzzii</i> hybrid zone. <i>Malaria Journal</i> , 2015, 14, 9.	0.8	7
4006	Distinct genetic difference between the Duffy binding protein (PkDBP \pm II) of <i>Plasmodium knowlesi</i> clinical isolates from North Borneo and Peninsular Malaysia. <i>Malaria Journal</i> , 2015, 14, 91.	0.8	18
4007	Field pathogenomics reveals the emergence of a diverse wheat yellow rust population. <i>Genome Biology</i> , 2015, 16, 23.	3.8	185
4008	Mitochondrial genome of <i>Hypoderaeum conoideum</i> – comparison with selected trematodes. <i>Parasites and Vectors</i> , 2015, 8, 97.	1.0	30

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4009	Geographical genetic structure of <i>Schistosoma japonicum</i> revealed by analysis of mitochondrial DNA and microsatellite markers. <i>Parasites and Vectors</i> , 2015, 8, 150.	1.0	13
4010	Contrasting patterns of insecticide resistance and knockdown resistance (kdr) in the dengue vectors <i>Aedes aegypti</i> and <i>Aedes albopictus</i> from Malaysia. <i>Parasites and Vectors</i> , 2015, 8, 181.	1.0	166
4011	Evolutionary history of <i>Leishmania killicki</i> (synonymous <i>Leishmania tropica</i>) and taxonomic implications. <i>Parasites and Vectors</i> , 2015, 8, 198.	1.0	20
4012	Mitochondrial and nuclear ribosomal DNA dataset supports that <i>Paramphistomum leydeni</i> (Trematoda: Digenea) is a distinct rumen fluke species. <i>Parasites and Vectors</i> , 2015, 8, 201.	1.0	24
4013	Genetic characterization of the scyphozoan jellyfish <i>Aurelia</i> spp. in Chinese coastal waters using mitochondrial markers. <i>Biochemical Systematics and Ecology</i> , 2015, 60, 15-23.	0.6	20
4014	The European race of <i>Gremmeniella abietina</i> hosts a single species of Gammahpartivirus showing a global distribution and possible recombinant events in its history. <i>Fungal Biology</i> , 2015, 119, 125-135.	1.1	20
4015	Admixture Between Historically Isolated Mitochondrial Lineages in Captive Western Gorillas: Recommendations for Future Management. <i>Journal of Heredity</i> , 2015, 106, 310-314.	1.0	5
4016	Concordant genetic structure in two species of woodpecker distributed across the primary West African biogeographic barriers. <i>Molecular Phylogenetics and Evolution</i> , 2015, 88, 64-74.	1.2	30
4017	Genetic population structure and demographic history of an endangered frog, <i>Babina holsti</i> . <i>Conservation Genetics</i> , 2015, 16, 987-1000.	0.8	1
4018	Positive selection drives neofunctionalization of the UbiA prenyltransferase gene family. <i>Plant Molecular Biology</i> , 2015, 87, 383-394.	2.0	12
4019	Population Demography and Genetic Diversity in the Pleistocene Cave Lion. <i>Open Quaternary</i> , 2015, 1, 4.	0.5	44
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4022	New and Common Haplotypes Shape Genetic Diversity in Asian Tiger Mosquito Populations from Costa Rica and Panama. <i>Journal of Economic Entomology</i> , 2015, 108, 761-768.	0.8	26
4023	Commensalism facilitates gene flow in mountains: a comparison between two <i>Rattus</i> species. <i>Heredity</i> , 2015, 115, 253-261.	1.2	17
4024	Impact of glaciations on genetic diversity of pelagic mollusks: Antarctic <i>Limacina antarctica</i> and Arctic <i>Limacina helicina</i> . <i>Marine Ecology - Progress Series</i> , 2015, 525, 143-152.	0.9	19
4025	Population genetic structure and its implication for conservation of <i>Coreius guichenoti</i> in the upper Yangtze River. <i>Environmental Biology of Fishes</i> , 2015, 98, 1999-2007.	0.4	6
4026	Wetland Conservation in the Gulf of Mexico: The Example of the Salt Marsh Morning Glory, <i>Ipomoea sagittata</i> . <i>Wetlands</i> , 2015, 35, 709-721.	0.7	8

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4028	Phylogeography of the Critically Endangered Brown Spider Monkey (<i>Ateles hybridus</i>): Testing the Riverine Barrier Hypothesis. <i>International Journal of Primatology</i> , 2015, 36, 530-547.	0.9	19
4029	Controversial patterns of <i>Wolbachia</i> infestation in the social parasitic <i>Maculinea</i> butterflies (Lepidoptera: Lycaenidae). <i>Organisms Diversity and Evolution</i> , 2015, 15, 591-607.	0.7	12
4030	Y-chromosomal variation of local goat breeds of Turkey close to the domestication centre. <i>Journal of Animal Breeding and Genetics</i> , 2015, 132, 449-453.	0.8	16
4031	Past climate change drives current genetic structure of an endangered freshwater mussel species. <i>Molecular Ecology</i> , 2015, 24, 1910-1926.	2.0	32
4032	Diversity and evolution of potato mop-top virus. <i>Archives of Virology</i> , 2015, 160, 1345-1351.	0.9	17
4033	At the passing gate: past introgression in the process of species formation between <i>Amazilia violiceps</i> and <i>A. viridifrons</i> hummingbirds along the Mexican Transition Zone. <i>Journal of Biogeography</i> , 2015, 42, 1305-1318.	1.4	30
4034	A phylogeographical perspective on the extirpation of <i>Aylacostoma</i> (Thiaridae, Gastropoda) from the High Paraná River (Argentina-Paraguay). <i>Zoological Journal of the Linnean Society</i> , 2015, 174, 487-499.	1.0	3
4035	Pseudogenization of CCL14 in the Ochotonidae (pika) family. <i>Innate Immunity</i> , 2015, 21, 647-654.	1.1	6
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4037	Geographical distribution and evolutionary divergence times of Asian populations of the brine shrimp <i>Artemia</i> (Crustacea, Anostraca). <i>Zoological Journal of the Linnean Society</i> , 2015, 174, 447-458.	1.0	17
4038	A new classification of the Pied Woodpeckers assemblage (Dendropicini, Picidae) based on a comprehensive multi-locus phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2015, 88, 28-37.	1.2	22
4039	16S rRNA and As-Related Functional Diversity: Contrasting Fingerprints in Arsenic-Rich Sediments from an Acid Mine Drainage. <i>Microbial Ecology</i> , 2015, 70, 154-167.	1.4	18
4040	Fine-scale matrilineal population structure in the Galapagos fur seal and its implications for conservation management. <i>Conservation Genetics</i> , 2015, 16, 1099-1113.	0.8	25
4041	Aggressive Emerging Pathovars of <i>Xanthomonas arboricola</i> Represent Widespread Epidemic Clones Distinct from Poorly Pathogenic Strains, as Revealed by Multilocus Sequence Typing. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4651-4668.	1.4	59
4042	Haplotypic diversity of porcine LEP and LEPR genes involved in growth and fatness regulation. <i>Journal of Applied Genetics</i> , 2015, 56, 525-533.	1.0	8
4043	Revisiting the Iberian honey bee (<i>Apis mellifera iberiensis</i>) contact zone: maternal and genome-wide nuclear variations provide support for secondary contact from historical refugia. <i>Molecular Ecology</i> , 2015, 24, 2973-2992.	2.0	31
4044	Combined epigenetic and intraspecific variation of the <i>DRD4</i> and <i>SERT</i> genes influence novelty seeking behavior in great tit <i>Parus major</i> . <i>Epigenetics</i> , 2015, 10, 516-525.	1.3	65

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4046	Genetic divergence and gene flow among Mesorhizobium strains nodulating the shrub legume Caragana. Systematic and Applied Microbiology, 2015, 38, 176-183.	1.2	22
4047	Haplotype Profile Comparisons Between Spodoptera frugiperda (Lepidoptera: Noctuidae) Populations From Mexico With Those From Puerto Rico, South America, and the United States and Their Implications to Migratory Behavior. Journal of Economic Entomology, 2015, 108, 135-144.	0.8	66
4048	Genetic characterization of Vibrio vulnificus strains isolated from oyster samples in Mexico. International Journal of Environmental Health Research, 2015, 25, 614-627.	1.3	7
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4052	Comparative phylogeography of the wild rice genus <i>Zizania</i> (Poaceae) in eastern Asia and North America. American Journal of Botany, 2015, 102, 239-247.	0.8	29
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4055	Tracing the genetic origin of Europe's first farmers reveals insights into their social organization. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20150339.	1.2	127
4056	Analysis of sailfish (<i>Istiophorus platyterus</i>) population structure in the North Pacific Ocean. Fisheries Research, 2015, 166, 33-38.	0.9	12
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4058	Signature of positive selection of PTK6 gene in East Asian populations: a cross talk for Helicobacter pylori invasion and gastric cancer endemicity. Molecular Genetics and Genomics, 2015, 290, 1741-1752.	1.0	9
4059	Genetic diversity and phylogeographic structure of sixteen Mediterranean chicken breeds assessed with microsatellites and mitochondrial DNA. Livestock Science, 2015, 175, 27-36.	0.6	36
4060	Genetic consequences of population expansions and contractions in the common hippopotamus (<i>Hippopotamus amphibius</i>) since the Late Pleistocene. Molecular Ecology, 2015, 24, 2507-2520.	2.0	18
4061	Genetic divergence and diversity in the Mona and Virgin Islands Boas, <i>Chilabothrus monensis</i> (<i>Epicrates monensis</i>) (Serpentes: Boidae), West Indian snakes of special conservation concern. Molecular Phylogenetics and Evolution, 2015, 88, 144-153.	1.2	9
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4064	High population connectivity and Pleistocene range expansion in the direct-developing plough shell <i>Bullia rhodostoma</i> along the South African coast. <i>African Journal of Marine Science</i> , 2015, 37, 21-31.	0.4	5
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4066	Characterization and sequence diversity of the Gsp-1 gene in diploid species of the <i>Aegilops</i> genus. <i>Journal of Cereal Science</i> , 2015, 63, 1-7.	1.8	2
4067	Host-plant dependent population genetics of the invading weevil <i>Hypera postica</i> . <i>Bulletin of Entomological Research</i> , 2015, 105, 92-100.	0.5	12
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4071	Ecological host fitting of <i>Trypanosoma cruzi</i> in Bolivia: mosaic population structure, hybridization and a role for humans in Andean parasite dispersal. <i>Molecular Ecology</i> , 2015, 24, 2406-2422.	2.0	41
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4079	Polymorphism and evolution of ribosomal DNA in tea (<i>Camellia sinensis</i> , Theaceae). <i>Molecular Phylogenetics and Evolution</i> , 2015, 89, 63-72.	1.2	15
4080	Mitochondrial diversification of the <i>Peromyscus mexicanus</i> species group in Nuclear Central America: biogeographic and taxonomic implications. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2015, 53, 300-311.	0.6	16

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4082	Intrinsic and extrinsic factors act at different spatial and temporal scales to shape population structure, distribution and speciation in Italian <i>Barbus</i> (Osteichthyes: Cyprinidae). <i>Molecular Phylogenetics and Evolution</i> , 2015, 89, 115-129.	1.2	26
4083	Post-glacial colonization of eastern Europe from the Carpathian refugium: evidence from mitochondrial DNA of the common vole <i>Microtus arvalis</i> . <i>Biological Journal of the Linnean Society</i> , 2015, 115, 927-939.	0.7	36
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4087	Recent mtDNA haplotype diversification in <i>Adesmia cancellata</i> (Coleoptera, Tenebrionidae) across the peninsular desert of Qatar. <i>Zoologischer Anzeiger</i> , 2015, 259, 1-12.	0.4	4
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4100	Comparative transcriptomics of a complex of four European pine species. <i>BMC Genomics</i> , 2015, 16, 234.	1.2	40
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4104	Morphological and genetic discrepancies in populations of <i>Oreocarya paradoxa</i> and <i>O. revealii</i> : The impact of edaphic selection on recent diversification in the Colorado Plateau. <i>American Journal of Botany</i> , 2015, 102, 1647-1658.	0.8	3
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4113	Clonal Clustering Using 10-Gene Multilocus Sequence Typing Reveals an Association Between Genotype and <i>Listeria monocytogenes</i> Maximum Growth Rate in Defined Medium. <i>Foodborne Pathogens and Disease</i> , 2015, 12, 972-982.	0.8	9
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4115	Transcriptionally active LTR retrotransposons in <i>Eucalyptus</i> genus are differentially expressed and insertionally polymorphic. <i>BMC Plant Biology</i> , 2015, 15, 198.	1.6	28
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4151	PanCoreGen Profiling, detecting, annotating protein-coding genes in microbial genomes. <i>Genomics</i> , 2015, 106, 367-372.	1.3	13
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4158	DNA-Based Identification of Lepidoptera Associated with Citrus in South Africa. <i>African Entomology</i> , 2015, 23, 165-171.	0.6	5
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4172	Diversity of <i>Listeria monocytogenes</i> Within a U.S. Dairy Herd, 2004-2010. <i>Foodborne Pathogens and Disease</i> , 2015, 12, 844-850.	0.8	27

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4174	Differences in <i>Hipposideros pomona</i> from three geographical regions in China based on morphology and molecular sequences data. <i>Journal of Mammalogy</i> , 2015, 96, 1305-1316.	0.6	7
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4185	Morphological Variation, Niche Divergence, and Phylogeography of Lizards of the <i>Liolaemus lineomaculatus</i> Section (Liolaemini) from Southern Patagonia. <i>Herpetological Monographs</i> , 2015, 29, 65.	1.1	18
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4193	Large divergence and low diversity suggest genetically informed conservation strategies for the endangered Virgin Islands Boa (<i>Chilabothrus monensis</i>). <i>Global Ecology and Conservation</i> , 2015, 3, 487-502.	1.0	11
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4204	Mitochondrial phylogeny shows multiple independent ecological transitions and northern dispersion despite of Pleistocene glaciations in meadow and steppe vipers (<i>Vipera ursinii</i> and <i>Vipera</i>) <i>Tj ETQq1 1 0.784314 rgt / Overlock 10 Tf 5</i>	1.2	9
4205	Complete mitochondrial DNA sequence of the endangered giant sable antelope (<i>Hippotragus niger</i>) <i>Tj ETQq0 0 0 rgt / Overlock 10 Tf 5</i>	1.2	9
4206	Population genetic structure and demographic history of Pacific blue sharks (<i>Prionace glauca</i>) inferred from mitochondrial DNA analysis. <i>Marine and Freshwater Research</i> , 2015, 66, 267.	0.7	31
4207	Phylogeography of the narrow-headed vole <i>Lasiopodomys</i> (<i>Stenocranius</i>) (<i>gregalis</i>) (Cricetidae, Rodentia) inferred from mitochondrial cytochrome <i>b</i> sequences: an echo of Pleistocene prosperity. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2015, 53, 97-108.	0.6	36
4208	Divergence and population traits in evolution of the genus <i>Pisum</i> L. as reconstructed using genes of two histone H1 subtypes showing different phylogenetic resolution. <i>Gene</i> , 2015, 556, 235-244.	1.0	26

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4210	Murine Cytomegalovirus Is Not Restricted to the House Mouse <i>Mus musculus domesticus</i> : Prevalence and Genetic Diversity in the European House Mouse Hybrid Zone. <i>Journal of Virology</i> , 2015, 89, 406-414.	1.5	16
4211	Genetic diversity and no evidences of recent hybridization in the endemic Italian hare (<i>Lepus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662	0.8	18
4212	Phyldynamic evidence of the migration of turnip mosaic potyvirus from Europe to Australia and New Zealand. <i>Journal of General Virology</i> , 2015, 96, 701-713.	1.3	33
4213	Complex Population Structure of <i>Borrelia burgdorferi</i> in Southeastern and South Central Canada as Revealed by Phylogeographic Analysis. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1309-1318.	1.4	26
4214	Cryptic Speciation Within the Neotropical Cichlid <i>Geophagus brasiliensis</i> (Quoy & Gaimard, 1824) (Teleostei Cichlidae): A New Paradigm in Karyotypical and Molecular Evolution. <i>Zebrafish</i> , 2015, 12, 91-101.	0.5	9
4215	Genetic diversity and evolution of two capsid protein genes of citrus tristeza virus isolates from China. <i>Archives of Virology</i> , 2015, 160, 787-794.	0.9	15
4216	Phylogeny, genetic diversity and phylogeography of the genus <i>C</i> (<i>C</i> <i>odoma</i>) (<i>T</i> <i>eleostei</i> , <i>C</i> <i>yprinidae</i>). <i>Zoologica Scripta</i> , 2015, 44, 11-28.	0.7	16
4217	New primers for DNA barcoding of digeneans and cestodes (Platyhelminthes). <i>Molecular Ecology Resources</i> , 2015, 15, 945-952.	2.2	108
4218	Identification and characterization of regions of difference between the <i>Salmonella Gallinarum</i> biovar <i>Gallinarum</i> and the <i>Salmonella Gallinarum</i> biovar <i>Pullorum</i> genomes. <i>Infection, Genetics and Evolution</i> , 2015, 30, 74-81.	1.0	19
4219	Asexual Propagation of a Virulent Clone Complex in a Human and Feline Outbreak of Sporotrichosis. <i>Eukaryotic Cell</i> , 2015, 14, 158-169.	3.4	47
4220	Emergence and early evolution of fungicide resistance in North American populations of <i>Zyoseptoria tritici</i> . <i>Plant Pathology</i> , 2015, 64, 961-971.	1.2	79
4221	Successful reintroduction of an endangered veteran tree specialist: conservation and genetics of the Great Capricorn beetle (<i>Cerambyx cerdo</i>). <i>Conservation Genetics</i> , 2015, 16, 267-276.	0.8	26
4222	Limited gene flow and high genetic diversity in the threatened Betic midwife toad (<i>Alytes dickhilleni</i>): evolutionary and conservation implications. <i>Conservation Genetics</i> , 2015, 16, 459-476.	0.8	11
4223	Divergence in morphology, calls, song, mechanical sounds, and genetics supports species status for the Inaguan hummingbird (Trochilidae: <i>Calliphlox œelynaeœlyrura</i>). <i>Auk</i> , 2015, 132, 248-264.	0.7	19
4224	The dissection of a Pleistocene refugium: phylogeography of the smooth newt, <i>Lissotriton vulgaris</i> , in the Balkans. <i>Journal of Biogeography</i> , 2015, 42, 671-683.	1.4	47
4225	Evolutionary history of a dispersal-associated locus across sympatric and allopatric divergent populations of a wing polymorphic beetle across Atlantic Europe. <i>Molecular Ecology</i> , 2015, 24, 890-908.	2.0	16
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4228	The first record of a cupped oyster species <i>Crassostrea dianbaiensis</i> in the waters of Japan. <i>Fisheries Science</i> , 2015, 81, 267-281.	0.7	7
4229	Evolution of High Mobility Group Nucleosome-Binding Proteins and Its Implications for Vertebrate Chromatin Specialization. <i>Molecular Biology and Evolution</i> , 2015, 32, 121-131.	3.5	33
4230	Molecular evidence for cryptic candidate species in Iberian Pelodytes (<i>Anura</i> , Pelodytidae). <i>Molecular Phylogenetics and Evolution</i> , 2015, 83, 224-241.	1.2	22
4231	What triggers the rising of an intraspecific biodiversity hotspot? Hints from the agile frog. <i>Scientific Reports</i> , 2014, 4, 5042.	1.6	34
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4234	Reprint of â€“Tracking the blue: A MLST approach to characterise the <i>Pseudomonas fluorescens</i> groupâ€™. <i>Food Microbiology</i> , 2015, 45, 148-158.	2.1	17
4235	Chloroplast DNA variation and genetic structure of <i>Miscanthus sinensis</i> in southwest China. <i>Biochemical Systematics and Ecology</i> , 2015, 58, 132-138.	0.6	6
4236	Evidence for two predominant viral lineages, recombination and subpopulation structure in begomoviruses associated with yellow vein mosaic disease of okra in India. <i>Plant Pathology</i> , 2015, 64, 508-518.	1.2	18
4237	How many species of <i>Paradoxurus</i> civets are there? New insights from India and Sri Lanka. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2015, 53, 161-174.	0.6	23
4238	Fineâ€“scale phylogeography reveals cryptic biodiversity in Pederson's cleaner shrimp, <i>Ancylomenes pedersoni</i> (Crustacea: Caridea: Palaemonidae), along the Florida Reef Tract. <i>Marine Ecology</i> , 2015, 36, 1379-1390.	0.4	10
4239	Extensive introgression in a malaria vector species complex revealed by phylogenomics. <i>Science</i> , 2015, 347, 1258524.	6.0	527
4240	Surveillance of <i>Echinococcus</i> isolates from Qinghai, China. <i>Veterinary Parasitology</i> , 2015, 207, 44-48.	0.7	31
4241	Mitochondrial DNA of <i>Euglossa iopoeila</i> (Apidae, Euglossini) reveals two distinct lineages for this orchid bee species endemic to the Atlantic Forest. <i>Apidologie</i> , 2015, 46, 346-358.	0.9	17
4242	Phylogeography of a Holarctic rodent (<i>Myodes rutilus</i>): testing highâ€“latitude biogeographical hypotheses and the dynamics of range shifts. <i>Journal of Biogeography</i> , 2015, 42, 377-389.	1.4	35
4243	Systematics of the Southeast Asian mongooses (Herpestidae, Carnivora): solving the mystery of the elusive collared mongoose and Palawan mongoose. <i>Zoological Journal of the Linnean Society</i> , 2015, 173, 236-248.	1.0	13
4244	Morphology and molecules reveal two new species of the poorly studied gecko genus <i>Paragehyra</i> (Squamata: Gekkonidae) from Madagascar. <i>Organisms Diversity and Evolution</i> , 2015, 15, 175-198.	0.7	8

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4246	Phylogeography of <i>Quercus glauca</i> (Fagaceae), a dominant tree of East Asian subtropical evergreen forests, based on three chloroplast DNA interspace sequences. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	67
4247	Trapped by climate: interglacial refuge and recent population expansion in the endemic Iberian adder <i>Vipera seoanei</i> . <i>Diversity and Distributions</i> , 2015, 21, 331-344.	1.9	48
4248	A comparative study of COI and 16S rRNA genes for DNA barcoding of cultivable carps in India. <i>Mitochondrial DNA</i> , 2015, 26, 79-87.	0.6	13
4249	Genetic variation and habitat conditions in <i>Betula humilis</i> Schrk. populations in Poland, Belarus and Latvia. <i>Plant Biosystems</i> , 2015, 149, 433-441.	0.8	4
4250	Population genetic structure of <i>Siniperca chuatsi</i> in the middle reach of the Yangtze River inferred from mitochondrial DNA and microsatellite loci. <i>Mitochondrial DNA</i> , 2015, 26, 61-67.	0.6	10
4251	Mitochondrial evolution across lineages of the vampire barnacle <i>Notochthamalus scabrosus</i> . <i>Mitochondrial DNA</i> , 2015, 26, 7-10.	0.6	14
4252	Update on the distribution and phylogenetics of <i>Biomphalaria</i> (Gastropoda: Planorbidae) populations in Guangdong Province, China. <i>Acta Tropica</i> , 2015, 141, 258-270.	0.9	23
4253	Phylogenetic relationship of <i>Pucrasia</i> (Aves: Galliformes) based on complete mitochondrial genome sequences. <i>Mitochondrial DNA</i> , 2015, 26, 949-950.	0.6	1
4254	Diversity of wing patterns and abdomen-generated substrate sounds in 3 European scorpionfly species. <i>Insect Science</i> , 2015, 22, 521-531.	1.5	6
4255	<i>Muscodora tigerii</i> sp. nov.-Volatile antibiotic producing endophytic fungus from the Northeastern Himalayas. <i>Annals of Microbiology</i> , 2015, 65, 47-57.	1.1	78
4256	Phylogeny and taxonomic revision of <i>Thelonectria discophora</i> (Ascomycota, Hypocreales, Nectriaceae) species complex. <i>Fungal Diversity</i> , 2015, 70, 1-29.	4.7	15
4257	Polymorphism at the ITS and NTS Loci of <i>Perkinsus marinus</i> isolated from Cultivated Oyster <i>Crassostrea corteziensis</i> in Nayarit, Mexico and Phylogenetic Relationship to <i>P. Ámarinus</i> along the Atlantic Coast. <i>Transboundary and Emerging Diseases</i> , 2015, 62, 137-147.	1.3	14
4258	<i>Plasmodium falciparum</i> : Genetic diversity and complexity of infections in an isolated village in western Thailand. <i>Parasitology International</i> , 2015, 64, 260-266.	0.6	10
4259	Phylogeographic analysis of genus <i>Herichthys</i> (Perciformes: Cichlidae), with descriptions of <i>Nosferatu</i> new genus and <i>H. tepehua</i> n. sp.. <i>Hydrobiologia</i> , 2015, 748, 201-231.	1.0	10
4260	First report on the whole genome sequence of <i>Pseudomonas cichorii</i> strain JBC1 and comparison with other <i>Pseudomonas</i> species. <i>Plant Pathology</i> , 2015, 64, 63-70.	1.2	20
4261	Portuguese mitochondrial DNA genetic diversity—An update and a phylogenetic revision. <i>Forensic Science International: Genetics</i> , 2015, 15, 27-32.	1.6	10
4262	Species distribution, genetic diversity and barcoding in the duckweed family (Lemnaceae). <i>Hydrobiologia</i> , 2015, 743, 75-87.	1.0	46

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4265	Worldwide phylogeography of the invasive ctenophore <i>Mnemiopsis leidyi</i> (Ctenophora) based on nuclear and mitochondrial DNA data. <i>Biological Invasions</i> , 2015, 17, 827-850.	1.2	39
4266	Molecular phylogenetics and phylogeography of all the Saimiri taxa (Cebidae, Primates) inferred from mt COI and COII gene sequences. <i>Primates</i> , 2015, 56, 145-161.	0.7	13
4267	Decoding cyanobacterial phylogeny and molecular evolution using an evonumeric approach. <i>Protoplasma</i> , 2015, 252, 519-535.	1.0	19
4268	Phylogeography and demographic history of <i>Zamia paucijuga</i> Wieland (Zamiaceae), a cycad species from the Mexican Pacific slope. <i>Plant Systematics and Evolution</i> , 2015, 301, 623-637.	0.3	6
4269	Acquisition of new protein domains by coronaviruses: analysis of overlapping genes coding for proteins N and 9b in SARS coronavirus. <i>Virus Genes</i> , 2015, 50, 29-38.	0.7	20
4270	Genetic diversity, population genetic structure, and demographic history of <i>Auxis thazard</i> (Perciformes), <i>Selar crumenophthalmus</i> (Perciformes), <i>Rastrelliger kanagurta</i> (Perciformes) and <i>Sardinella lemuru</i> (Clupeiformes) in Sulu-Celebes Sea inferred by mitochondrial DNA sequences. <i>Fisheries Research</i> , 2015, 162, 64-74.	0.9	21
4271	Remarkable genetic divergence of <i>Gymnodiptychus dybowskii</i> between south and north of Tianshan Mountain in northwest China. <i>Biochemical Systematics and Ecology</i> , 2015, 58, 43-50.	0.6	4
4272	Local scale connectivity in the cave-dwelling brooding fish <i>Apogon imberbis</i> . <i>Journal of Sea Research</i> , 2015, 95, 70-74.	0.6	6
4273	Untangling taxonomic confusion and diversification patterns of the Streak-breasted Scimitar Babblers (Timaliidae: <i>Pomatorhinus ruficollis</i> complex) in southern Asia. <i>Molecular Phylogenetics and Evolution</i> , 2015, 82, 183-192.	1.2	5
4274	Dispersal and speciation in purple swamphens (Rallidae: <i>Porphyrio</i>). <i>Auk</i> , 2015, 132, 140-155.	0.7	42
4275	Introgressive hybridization between the Atlantic and Pacific herrings (<i>Clupea harengus</i> and <i>C. pallasii</i>) in the north of Europe. <i>Marine Biology</i> , 2015, 162, 39-54.	0.7	21
4276	Genetic diversity analysis of mitochondrial DNA control region in artificially propagated Chinese sucker <i>Myxocyprinus asiaticus</i> . <i>Mitochondrial DNA</i> , 2015, 26, 514-519.	0.6	3
4277	Emergence of rice yellow mottle virus in eastern Uganda: Recent and singular interplay between strains in East Africa and in Madagascar. <i>Virus Research</i> , 2015, 195, 64-72.	1.1	22
4278	Genetic evidence of hybridization between the critically endangered Cuban crocodile and the American crocodile: implications for population history and in situ/ex situ conservation. <i>Heredity</i> , 2015, 114, 272-280.	1.2	53
4279	Highly Diverse Endophytic and Soil <i>Fusarium oxysporum</i> Populations Associated with Field-Grown Tomato Plants. <i>Applied and Environmental Microbiology</i> , 2015, 81, 81-90.	1.4	64
4280	Phylogenetic and diversity patterns of <i>Blanus</i> worm lizards (Squamata: Amphisbaenia): insights from mitochondrial and nuclear gene genealogies and species tree. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2015, 53, 45-54.	0.6	21

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4282	Analysis of the genetic variability of <i>Artemia franciscana</i> Kellogg, 1906 from the Great Salt Lake (USA) based on mtDNA sequences, ISSR genomic fingerprinting and biometry. Marine Biodiversity, 2015, 45, 311-319.	0.3	13
4283	Intra-individual ITS polymorphism and hybridization in <i>Pulmonaria obscura</i> Dumort. and <i>Pulmonaria angustifolia</i> L. (Boraginaceae). Plant Systematics and Evolution, 2015, 301, 893-910.	0.3	2
4284	Mitochondrial sequences yield new insight into the Quaternary history of the edible dormouse on the landbridge Adriatic islands. Mammalian Biology, 2015, 80, 128-134.	0.8	2
4285	What barcode sequencing reveals about the shark fishery in Peru. Fisheries Research, 2015, 161, 34-41.	0.9	23
4286	Population genetic structure of the Atlantic Forest endemic <i>Conopophaga lineata</i> (Passeriformes: Tj ETQq1 1 0.784314 rgBT /Overlook 85-99.	0.5	37
4287	Comparative phylogeography and population genetic structure of three widespread mollusc species in the Mediterranean and near Atlantic. Marine Ecology, 2015, 36, 701-715.	0.4	25
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4289	Sun skink diversification across the Indian–Southeast Asian biogeographical interface. Journal of Biogeography, 2015, 42, 292-304.	1.4	31
4290	Species identification and evolutionary inference of the genera <i>Megalobrama</i> and <i>Parabramis</i> (Cyprinidae: Cultrinae) in China. Mitochondrial DNA, 2015, 26, 357-366.	0.6	6
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4293	Global haplotype analysis of the whitefly <i>Bemisia tabaci</i> cryptic species Asia I in Asia. Mitochondrial DNA, 2015, 26, 232-241.	0.6	19
4294	Influence of the domestic alien fish <i>Rhynchocypris oxycephalus</i> invasion on the distribution of the closely related native fish <i>R. lagowskii</i> in the Tama River Basin, Japan. Landscape and Ecological Engineering, 2015, 11, 169-176.	0.7	4
4295	Polymorphisms in stress response genes in <i>Lactobacillus plantarum</i> : implications for classification and heat stress response. Annals of Microbiology, 2015, 65, 297-305.	1.1	5
4296	Molecular phylogeny and evogenomics of heterocystous cyanobacteria using <i>rbcl</i> gene sequence data. Annals of Microbiology, 2015, 65, 799-807.	1.1	29
4297	Characterization of proopiomelanocortin in the snakeskin gourami (<i>Trichopodus pectoralis</i>) and its expression in relation to food intake. Domestic Animal Endocrinology, 2015, 50, 1-13.	0.8	5
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4300	The Effects of Inference Method, Population Sampling, and Gene Sampling on Species Tree Inferences: An Empirical Study in Slender Salamanders (Plethodontidae: Batrachoseps). <i>Systematic Biology</i> , 2015, 64, 66-83.	2.7	18
4301	Major histocompatibility complex alleles associated with parasite susceptibility in wild giant pandas. <i>Heredity</i> , 2015, 114, 85-93.	1.2	42
4302	High diversity, expanding populations and purifying selection in phytoplasmas causing coconut lethal yellowing in Mozambique. <i>Plant Pathology</i> , 2015, 64, 597-604.	1.2	20
4303	Closely related and sympatric but not all the same: genetic variation of Indo-West Pacific <i>Rhizophora</i> mangroves across the Malay Peninsula. <i>Conservation Genetics</i> , 2015, 16, 137-150.	0.8	36
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4305	Molecular phylogeny of <i>Shortia sensu lato</i> (Diapensiaceae) based on multiple nuclear sequences. <i>Plant Systematics and Evolution</i> , 2015, 301, 523-529.	0.3	7
4306	Genetic analysis of invasive Asian Black Carp (<i>Mylopharyngodon piceus</i>) in the Mississippi River Basin: evidence for multiple introductions. <i>Biological Invasions</i> , 2015, 17, 99-114.	1.2	12
4307	Gene flow across the N-Atlantic and sex-biased dispersal inferred from mtDNA sequence variation in saithe, <i>Pollachius virens</i> . <i>Environmental Biology of Fishes</i> , 2015, 98, 67-79.	0.4	4
4308	Big fish, little divergence: phylogeography of Lake Tanganyika's giant cichlid, <i>Boulengerochromis microlepis</i> . <i>Hydrobiologia</i> , 2015, 748, 29-38.	1.0	19
4309	Genetic structure of <i>Scomber japonicus</i> (Perciformes: Scombridae) along the coast of China revealed by complete mitochondrial cytochrome <i>b</i> sequences. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3828-3836.	0.7	9
4310	Structure and evolution of the Phasianidae mitochondrial DNA control region. <i>Mitochondrial DNA</i> , 2016, 27, 350-354.	0.6	6
4311	Phylogeographical structure in mitochondrial DNA of eggplant fruit and shoot borer, <i>Leucinodes orbonalis</i> Guenée (Lepidoptera: Crambidae) in South and Southeast Asia. <i>Mitochondrial DNA</i> , 2016, 27, 198-204.	0.6	9
4312	Detecting mitochondrial signatures of selection in wild Tibetan pigs and domesticated pigs. <i>Mitochondrial DNA</i> , 2016, 27, 747-752.	0.6	20
4313	DNA barcoding and phylogenetic relationships in Anatidae. <i>Mitochondrial DNA</i> , 2016, 27, 1042-1044.	0.6	7
4314	The complete mitochondrial genome of the Asian tapirs (<i>Tapirus indicus</i>): the only extant Tapiridae species in the old world. <i>Mitochondrial DNA</i> , 2016, 27, 413-415.	0.6	6
4315	When forms meet genes: revision of the scleractinian genera <i>Micromussa</i> and <i>Homophyllia</i> (Lobophylliidae) with a description of two new species and one new genus. <i>Contributions To Zoology</i> , 2016, 85, 387-422.	0.2	27
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4318	Systematic review of the Cinnamon-throated Woodcreeper <i>Dendrexetastes rufigula</i> (Aves): Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 358-369.	0.2	4
4319	Biological control of invasive <i>Dryocosmus kuriphilus</i> with introduced parasitoid <i>Torymus sinensis</i> in Croatia, Slovenia and Hungary. <i>Periodicum Biologorum</i> , 2016, 117, 471-477.	0.1	19
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4321	Characterization and evolution of the mitochondrial DNA control region in Ranidae and their phylogenetic relationship. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	4
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4323	<i>Daphnia</i> diversity in water bodies of the Po River Basin. <i>Journal of Limnology</i> , 2016, , .	0.3	2
4324	Heterogeneous evolution of Ty3-gypsy retroelements among bamboo species. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	2
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4326	Far East Scarlet-Like Fever Caused by a Few Related Genotypes of <i>Yersinia pseudotuberculosis</i> , Russia. <i>Emerging Infectious Diseases</i> , 2016, 22, 503-506.	2.0	21
4327	Population genetic structure of the goby <i>Stiphodon rutilaureus</i> (Gobiidae) in the New Georgia Group, Solomon Islands. <i>Pacific Conservation Biology</i> , 2016, 22, 281.	0.5	3
4328	Genome-wide analysis of the TPX2 family proteins in <i>Eucalyptus grandis</i> . <i>BMC Genomics</i> , 2016, 17, 967.	1.2	8
4329	Complete Mitochondrial Genome of the Citrus Spiny Whitefly <i>Aleurocanthus spiniferus</i> (Quaintance) (Hemiptera: Aleyrodidae): Implications for the Phylogeny of Whiteflies. <i>PLoS ONE</i> , 2016, 11, e0161385.	1.1	12
4330	Ancestry analysis of locally adapted <i>Crespa</i> goats from southernmost Brazil. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	4
4331	Soybean Stem Fly, <i>Melanagromyza sojae</i> (Diptera: Agromyzidae), in the New World: detection of high genetic diversity from soybean fields in Brazil. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	15
4332	Phylogeographic Evidence for 2 Genetically Distinct Zoonotic <i>Plasmodium knowlesi</i> Parasites, Malaysia. <i>Emerging Infectious Diseases</i> , 2016, 22, 1371-1380.	2.0	45
4333	<i>Wolbachia</i> in guilds of <i>Anastrepha</i> fruit flies (Tephritidae) and parasitoid wasps (Braconidae). <i>Genetics and Molecular Biology</i> , 2016, 39, 600-610.	0.6	22
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4336	Comparación y utilidad de las regiones mitocondriales de los genes 16S y COX1 para los análisis genéticos en garrapatas (Acari: Ixodidae). <i>Biomedica</i> , 2016, 36, 295.	0.3	8
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4338	ITS2 para la identificación de Califóridos (Diptera: Calliphoridae) de importancia forense en Colombia. <i>Acta Biológica Colombiana</i> , 2016, 21, 543.	0.1	1
4339	Characterization of a Novel Polerovirus Infecting Maize in China. <i>Viruses</i> , 2016, 8, 120.	1.5	64
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4342	Presencia de <i>Aedes (Stegomyia) aegypti</i> (Linnaeus, 1762) y su infección natural con el virus del dengue en alturas no registradas para Colombia. <i>Biomedica</i> , 2016, 36, 303.	0.3	55
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4344	Molecular phylogeny of Toxoplasmatinae: comparison between inferences based on mitochondrial and apicoplast genetic sequences. <i>Brazilian Journal of Veterinary Parasitology</i> , 2016, 25, 82-89.	0.2	4
4345	Chloroplast analysis of <i>Zelkova schneideriana</i> (Ulmaceae): genetic diversity, population structure, and conservation implications. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	7
4346	Molecular characterization of different <i>Triticum monococcum</i> ssp. <i>monococcum</i> Glu-A1^mx alleles. <i>Cereal Research Communications</i> , 2016, 44, 444-452.	0.8	7
4347	Biological, serological and molecular typing of potato virus Y (PVY) isolates from Tunisia. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	4
4348	Multiple introductions and gene flow in subtropical South American populations of the fireweed, <i>Senecio madagascariensis</i> (Asteraceae). <i>Genetics and Molecular Biology</i> , 2016, 39, 135-144.	0.6	14
4349	Evolution of mustard (<i>Brassica juncea</i> Coss) subspecies in China: evidence from the chalcone synthase gene. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	6
4350	Molecular cloning, functional verification, and evolution of TmPm3, the powdery mildew resistance gene of <i>Triticum monococcum</i> L.. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	1
4351	DNA barcoding and phylogenetic relationships of Ardeidae (Aves: Ciconiiformes). <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	5
4352	Divergence and polymorphism analysis of IGF1Ra and IGF1Rb from orange-spotted grouper, <i>Epinephelus coioides</i> (Hamilton). <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	5

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4354	Tandem Duplication Events in the Expansion of the Small Heat Shock Protein Gene Family in <i>Solanum lycopersicum</i> (cv. Heinz 1706). <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3027-3034.	0.8	13
4355	Genetic Diversity and Phylogenetic Analysis of South-East Asian Duck Populations Based on the mtDNA D-loop Sequences. <i>Asian-Australasian Journal of Animal Sciences</i> , 2016, 29, 1688-1695.	2.4	6
4356	Maternal Origin of Turkish and Iranian Native Chickens Inferred from Mitochondrial DNA D-loop Sequences. <i>Asian-Australasian Journal of Animal Sciences</i> , 2016, 29, 1547-1554.	2.4	12
4357	PRESENCIA DE <i>Wolbachia</i> y <i>Leishmania</i> EN UNA POBLACION DE <i>Lutzomyia evansi</i> PRESENTE EN LA COSTA CARIBE DE COLOMBIA. <i>Revista De La Facultad De Ciencias</i> , 2016, 5, 38-54.	0.0	0
4358	Genetic analysis reveals candidate species in the <i>Scinax catharinae</i> clade (Amphibia: Anura) from Central Brazil. <i>Genetics and Molecular Biology</i> , 2016, 39, 49-53.	0.6	7
4359	Cultivar-level phylogeny using chloroplast DNA barcode <i>psbK-psbI</i> spacers for identification of Emirati date palm (<i>Phoenix dactylifera</i> L.) varieties. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	15
4360	Genetic variability of <i>Myzus persicae nicotianae</i> densovirus based on partial NS and VP gene sequences. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	1
4361	Isolation and characterization of eight microsatellite loci from <i>Galeocerdo cuvier</i> (tiger shark) and cross-amplification in <i>Carcharhinus leucas</i> , <i>Carcharhinus brevipinna</i> and <i>Carcharhinus plumbeus</i> and <i>Sphyrna lewini</i> . <i>PeerJ</i> , 2016, 4, e2041.	0.9	11
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4365	Genetic diversity of the <i>IRGSP</i> flanking region in rice landraces in northern Laos. <i>Breeding Science</i> , 2016, 66, 580-590.	0.9	14
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4367	The Mitochondrial Genomes of the Zoonotic Canine Filarial Parasites <i>Dirofilaria (Nochtiella) repens</i> and <i>Candidatus Dirofilaria (Nochtiella) honkongensis</i> Provide Evidence for Presence of Cryptic Species. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005028.	1.3	47
4368	<i>Babesia microti</i> from humans and ticks hold a genomic signature of strong population structure in the United States. <i>BMC Genomics</i> , 2016, 17, 888.	1.2	15
4369	Phylogenetic and Molecular Variability Studies Reveal a New Genetic Clade of Citrus leprosis virus C. Viruses, 2016, 8, 153.	1.5	76
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4384	Expansion of the phosphatidylethanolamine binding protein family in legumes: a case study of <i>Lupinus angustifolius</i> L. FLOWERING LOCUS T homologs, <i>LanFTc1</i> and <i>LanFTc2</i> . <i>BMC Genomics</i> , 2016, 17, 820.	1.2	28
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4392	Genetic dynamics in the sand fly (Diptera: Phlebotomidae) nuclear and mitochondrial genotypes: evidence for vector adaptation at the border of Iran with Iraq. <i>Parasites and Vectors</i> , 2016, 9, 319.	1.0	11
4393	The mitochondrial genomes of <i>Culex tritaeniorhynchus</i> and <i>Culex pipiens pallens</i> (Diptera: Culicidae) and comparison analysis with two other <i>Culex</i> species. <i>Parasites and Vectors</i> , 2016, 9, 406.	1.0	22
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4395	Colonizing the High Arctic: Mitochondrial DNA Reveals Common Origin of Eurasian Archipelagic Reindeer (<i>Rangifer tarandus</i>). <i>PLoS ONE</i> , 2016, 11, e0165237.	1.1	22
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4397	Genetic Evidence of Expansion by Passive Transport of <i>Aedes</i> (<i>Stegomyia</i>) <i>aegypti</i> in Eastern Argentina. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004839.	1.3	14
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4399	Limitations of Species Delimitation Based on Phylogenetic Analyses: A Case Study in the <i>Hypogymnia</i> <i>hypotrypa</i> Group (Parmeliaceae, Ascomycota). <i>PLoS ONE</i> , 2016, 11, e0163664.	1.1	13
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4402	Multilocus Phylogeography of the Treefrog <i>Scinax eurydice</i> (Anura, Hylidae) Reveals a Plio-Pleistocene Diversification in the Atlantic Forest. <i>PLoS ONE</i> , 2016, 11, e0154626.	1.1	41
4403	An Indel Polymorphism in the MtnA 3' Untranslated Region Is Associated with Gene Expression Variation and Local Adaptation in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2016, 12, e1005987.	1.5	40
4404	Mutation-Driven Divergence and Convergence Indicate Adaptive Evolution of the Intracellular Human-Restricted Pathogen, <i>Bartonella bacilliformis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004712.	1.3	19
4405	Molecular Diversity between Salivary Proteins from New World and Old World Sand Flies with Emphasis on <i>Bichromomyia olmeca</i> , the Sand Fly Vector of <i>Leishmania mexicana</i> in Mesoamerica. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004771.	1.3	47
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4408	Genomic Characterization of Phenylalanine Ammonia Lyase Gene in Buckwheat. PLoS ONE, 2016, 11, e0151187.	1.1	18
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4412	A Phylogeographic Assessment of the Malagasy Giant Chameleons (<i>Furcifer verrucosus</i> and <i>Furcifer</i>) Tj ETQq1 1 0.784314 rgBT /Over	1.1	8
4413	Genetic Diversity, Natural Selection and Haplotype Grouping of <i>Plasmodium knowlesi</i> Gamma Protein Region II (Pk Γ 3RII): Comparison with the Duffy Binding Protein (PkDBP Γ ±RII). PLoS ONE, 2016, 11, e0155627.	1.1	13
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4428	<i>Pyricularia graminis-tritici</i> , a new <i>Pyricularia</i> species causing wheat blast. Persoonia: Molecular Phylogeny and Evolution of Fungi, 2016, 37, 199-216.	1.6	66
4429	Chloroplast DNA analysis of Tunisian cork oak populations (<i>Quercus suber</i> L.): sequence variations and molecular evolution of the trnL (UAA)-trnF (GAA) region. Genetics and Molecular Research, 2016, 15, .	0.3	0
4430	Species Delimitation of the <i>Cycas segmentifida</i> Complex (Cycadaceae) Resolved by Phylogenetic and Distance Analyses of Molecular Data. Frontiers in Plant Science, 2016, 7, 134.	1.7	21
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4453	Morphometric and preliminary genetic characteristics of <i>Branchinecta orientalis</i> populations from Iran (Crustacea: Anostraca). <i>Zootaxa</i> , 2016, 4109, 31-45.	0.2	8
4454	Population genetic structure of critically endangered salamander (<i>Hynobius amjiensis</i>) in China: recommendations for conservation. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	2
4455	Latitude delineates patterns of biogeography in terrestrial <i>Streptomyces</i> . <i>Environmental Microbiology</i> , 2016, 18, 4931-4945.	1.8	35
4456	Phylogenetic diversity and biogeography of the Mamiellophyceae lineage of eukaryotic phytoplankton across the oceans. <i>Environmental Microbiology Reports</i> , 2016, 8, 461-469.	1.0	56
4457	Long-distance dispersal and inter-island colonization across the western Malagasy Region explain diversification in brush-warblers (Passeriformes: Nesillas). <i>Biological Journal of the Linnean Society</i> , 2016, 119, 873-889.	0.7	8
4458	Effects of past climate on <i>Passiflora actinia</i> (Passifloraceae) populations and insights into future species management in the Brazilian Atlantic forest. <i>Botanical Journal of the Linnean Society</i> , 2016, 180, 348-364.	0.8	11
4459	Hybridization and divergence in multi-species oak (<i>Quercus</i>) communities. <i>Botanical Journal of the Linnean Society</i> , 2016, 181, 99-114.	0.8	24
4460	Shared phylogeographical breaks in a Caribbean coral reef sponge and its invertebrate commensals. <i>Journal of Biogeography</i> , 2016, 43, 2136-2146.	1.4	28

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4461	Ecological divergence of two closely related <i>Roscoea</i> species associated with late Quaternary climate change. <i>Journal of Biogeography</i> , 2016, 43, 1990-2001.	1.4	48
4462	Divergent homoeolog evolution of the anthocyanin regulatory gene <i>R</i> in <i>Oryza</i> allopolyploids. <i>Journal of Systematics and Evolution</i> , 2016, 54, 511-518.	1.6	0
4463	Genetic analysis of <i>Grapevine leafroll-associated virus 3</i> population from Galicia, Spain. <i>Plant Pathology</i> , 2016, 65, 310-321.	1.2	9
4464	The evolutionary history of <i>Biston suppressaria</i> (<i>Geometridae</i>) related to complex topography and geological history. <i>Systematic Entomology</i> , 2016, 41, 732-743.	1.7	10
4465	A reinvestigation of phylogeny and divergence times of the <i>Ablepharus kitaibelii</i> species complex (Sauria, Scincidae) based on mtDNA and nuDNA genes. <i>Molecular Phylogenetics and Evolution</i> , 2016, 103, 199-214.	1.2	34
4466	Insights into the molecular phylogeny and historical biogeography of the white-clawed crayfish (Decapoda, Astacidae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 103, 26-40.	1.2	36
4467	Merging and comparing three mitochondrial markers for phylogenetic studies of Eurasian reindeer (<i>Rangifer tarandus</i>). <i>Ecology and Evolution</i> , 2016, 6, 4347-4358.	0.8	14
4468	Late Pleistocene climate change promoted divergence between <i>Picea asperata</i> and <i>P. crassifolia</i> on the Qinghai-Tibet Plateau through recent bottlenecks. <i>Ecology and Evolution</i> , 2016, 6, 4435-4444.	0.8	7
4469	<i>HMOX2</i> Functions as a Modifier Gene for High-Altitude Adaptation in Tibetans. <i>Human Mutation</i> , 2016, 37, 216-223.	1.1	40
4470	Chloroplast phylogeographic patterns of <i>Calligonum</i> sect. <i>Pterococcus</i> (Polygonaceae) in arid Northwest China. <i>Nordic Journal of Botany</i> , 2016, 34, 335-342.	0.2	5
4471	Identification of Multiple Forms of RNA Transcripts Associated with Human-Specific Retrotransposed Gene Copies. <i>Genome Biology and Evolution</i> , 2016, 8, 2288-2296.	1.1	3
4472	CWAS-identified schizophrenia risk SNPs at <i>TSPAN18</i> are highly diverged between Europeans and East Asians. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2016, 171, 1032-1040.	1.1	9
4473	Population divergence of aggregation pheromone responses in <i>Ips subelongatus</i> in northeastern China. <i>Insect Science</i> , 2016, 23, 728-738.	1.5	11
4474	A high-throughput detection method for invasive fruit fly (<i>Diptera</i>) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 227 Td</i> . <i>Journal of Applied Entomology</i> , 2016, 16, 1378-1388.	2.2	16
4475	Recurrent connections between Amazon and Atlantic forests shaped diversity in Caatinga four-eyed frogs. <i>Journal of Biogeography</i> , 2016, 43, 1045-1056.	1.4	64
4476	A phylogeographical survey of a highly dispersive spider reveals eastern Asia as a major glacial refugium for Palearctic fauna. <i>Journal of Biogeography</i> , 2016, 43, 1583-1594.	1.4	34
4477	Evolutionary history of <i>Apocheima cinerarius</i> (Lepidoptera: Geometridae), a female flightless moth in northern China. <i>Zoologica Scripta</i> , 2016, 45, 160-174.	0.7	12
4478	Spatiotemporal Analysis of Microbiological Contamination in New York State Produce Fields following Extensive Flooding from Hurricane Irene, August 2011. <i>Journal of Food Protection</i> , 2016, 79, 384-391.	0.8	11

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4480	Molecular diversity and genetic relationships in Secale. Journal of Genetics, 2016, 95, 273-281.	0.4	11
4481	Genetic population structure and relatedness in the narrow-striped mongoose (Mungotictis turgida). Journal of Biogeography, 2016, 43, 3734-3749.	0.8	5
4482	The genetic impact of chamois management in the dinarides. Journal of Wildlife Management, 2016, 80, 783-793.	0.7	15
4483	Conflicting genomic signals affect phylogenetic inference in four species of North American pines. AoB PLANTS, 2016, 8, .	1.2	2
4484	Conservation genetics assessment and phylogenetic relationships of critically endangered Hucho bleekeri in China. Journal of Applied Ichthyology, 2016, 32, 343-349.	0.3	10
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4486	Genetic and paleomodelling evidence of the population expansion of the cattle egret (Bubulcus ibis) in Africa during the climatic oscillations of the Late Pleistocene. Journal of Avian Biology, 2016, 47, 846-857.	0.6	6
4487	Mitochondrial DNA variation of indigenous goats in Nankai and Xikou counties of Kenya. Journal of Animal Breeding and Genetics, 2016, 133, 238-247.	0.8	20
4488	A bridge too far: dispersal barriers and cryptic speciation in an Arabian Peninsula grouper (Cephalopholis hemistiktos). Journal of Biogeography, 2016, 43, 820-832.	1.4	24
4489	The legacy of a vanished sea: a high level of diversification within a European freshwater amphipod species complex driven by 15 My of Paratethys regression. Molecular Ecology, 2016, 25, 795-810.	2.0	95
4490	Imprints of multiple glacial refugia in the Pyrenees revealed by phylogeography and palaeodistribution modelling of an endemic spider. Molecular Ecology, 2016, 25, 2046-2064.	2.0	31
4491	Molecular evolution and functional characterisation of haplotypes of an important rubber biosynthesis gene in Hevea brasiliensis. Plant Biology, 2016, 18, 720-728.	1.8	5
4492	Genetic variation and evolutionary forces shaping Cucurbit vein yellowing virus populations: risk of emergence of virulent isolates in Europe. Plant Pathology, 2016, 65, 847-856.	1.2	10
4493	East Asian allopatry and north Eurasian sympatry in Long-tailed Tit lineages despite similar population dynamics during the late Pleistocene. Zoologica Scripta, 2016, 45, 115-126.	0.7	14
4494	Pinpointing the level of isolation between two cryptic species sharing the same microhabitat: a case study with a scarabaeid species complex. Zoologica Scripta, 2016, 45, 407-420.	0.7	14
4495	Sequence characterization and in silico structure prediction of fatty acid desaturases in linseed varieties with differential fatty acid composition. Journal of the Science of Food and Agriculture, 2016, 96, 4896-4906.	1.7	6
4496	Sequence of the Gonium pectorale Mating Locus Reveals a Complex and Dynamic History of Changes in Volvocine Algal Mating Haplotypes. G3: Genes, Genomes, Genetics, 2016, 6, 1179-1189.	0.8	24

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4497	High occurrence of <i>Pacearchaeota</i> and <i>Woesearchaeota</i> (<i>A</i> rchaea) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 Environmental Microbiology Reports, 2016, 8, 210-217.	1.0	112
4498	Phylogeography of a Patagonian lizard and frog: Congruent signature of southern glacial refuges. Austral Ecology, 2016, 41, 399-408.	0.7	5
4499	Mitochondrial <i>DNA</i> variation of domestic sheep (<i>Ovis aries</i>) in Kenya. Animal Genetics, 2016, 47, 377-381.	0.6	19
4500	Mitochondrial <i>DNA</i> variation of <i>Protosalanx hyalocranius</i> in the Huaihe River. Animal Genetics, 2016, 47, 388-389.	0.6	2
4501	Biogeography of <i>Cyprinella lutrensis</i> : intensive genetic sampling from the Pecos River "melting pot" reveals a dynamic history and phylogenetic complexity. Biological Journal of the Linnean Society, 2016, 117, 264-284.	0.7	10
4502	Species-specific phylogeographical patterns and Pleistocene east-west divergence in <i>Annona</i> (Annonaceae) in the Brazilian Cerrado. Botanical Journal of the Linnean Society, 2016, 181, 21-36.	0.8	33
4503	Evaluating the efficacy of restoration plantings through DNA barcoding of frugivorous bird diets. Conservation Biology, 2016, 30, 763-773.	2.4	29
4504	Hybridization following recent secondary contact results in asymmetric genotypic and phenotypic introgression between island species of <i>Myzomela</i> honeyeaters. Evolution; International Journal of Organic Evolution, 2016, 70, 257-269.	1.1	25
4505	Geographic variation in advertisement calls of a Microhylid frog " testing the role of drift and ecology. Ecology and Evolution, 2016, 6, 3289-3298.	0.8	35
4506	Comparative population structure of two dominant species, <i>Shinkaia crosnieri</i> (Munidopsidae) Tj ETQq1 1 0.784314 rgBT /Overl both deep-sea vent and cold seep inferred from mitochondrial multi-genes. Ecology and Evolution, 2016, 6, 3571-3582.	0.8	27
4507	Diversity patterns of <i>Rhizobium</i> communities inhabiting soils, root surfaces and nodules reveal a strong selection of rhizobial partners by legumes. Environmental Microbiology, 2016, 18, 2375-2391.	1.8	50
4508	Preventing species invasion: A role for integrative taxonomy?. Integrative Zoology, 2016, 11, 214-228.	1.3	27
4509	High-resolution genetic analysis reveals extensive gene flow within the jellyfish <i>Pelagia noctiluca</i> (Scyphozoa) in the North Atlantic and Mediterranean Sea. Biological Journal of the Linnean Society, 2016, 117, 252-263.	0.7	7
4510	Disentangling the <i>Tillandsia capillaris</i> complex: phylogenetic relationships and taxon boundaries in Andean populations. Botanical Journal of the Linnean Society, 2016, 181, 391-414.	0.8	21
4511	Narrow water barriers prevent multiple colonizations and limit gene flow among California Channel Island wild buckwheats (<i>Eriogonum</i> : Polygonaceae). Botanical Journal of the Linnean Society, 2016, 181, 246-268.	0.8	7
4512	Social selection parapatry in Afrotropical sunbirds. Evolution; International Journal of Organic Evolution, 2016, 70, 1307-1321.	1.1	18
4513	Migratory behaviour shapes spatial genetic structure of cyprinid fishes within the Lake Malawi catchment. Freshwater Biology, 2016, 61, 1062-1074.	1.2	5
4514	Chloroplast phylogeography of <i>Dirca palustris</i> L. indicates populations near the glacial boundary at the Last Glacial Maximum in eastern North America. Journal of Biogeography, 2016, 43, 314-327.	1.4	24

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4516	Ancient river systems and phylogeographical structure in the spring salamander, <i>Gyrinophilus porphyriticus</i> . <i>Journal of Biogeography</i> , 2016, 43, 639-652.	1.4	18
4517	Partial Sequence Analysis of Geographically Close <i>Grapevine virus A</i> Isolates Reveals their High Regional Variability and an Intra-isolate Heterogeneity. <i>Journal of Phytopathology</i> , 2016, 164, 427-431.	0.5	9
4518	<i>Pseudo-nitzschia arctica</i> sp. nov., a new cold-water cryptic <i>Pseudo-nitzschia</i> species within the <i>P. pseudodelicatissima</i> complex. <i>Journal of Phycology</i> , 2016, 52, 184-199.	1.0	39
4519	Evolutionary history and conservation significance of the Javan leopard <i>Panthera pardus melas</i> . <i>Journal of Zoology</i> , 2016, 299, 239-250.	0.8	20
4520	Limited dispersal in an ectoparasitic mite, <i>Laelaps giganteus</i> , contributes to significant phylogeographic congruence with the rodent host, <i>Rhabdomys</i> . <i>Molecular Ecology</i> , 2016, 25, 1006-1021.	2.0	22
4521	Contemporary genetic structure and postglacial demographic history of the black scorpionfish, <i>Scorpaena porcus</i> , in the Mediterranean and the Black Seas. <i>Molecular Ecology</i> , 2016, 25, 2195-2209.	2.0	29
4522	Sequence variation in nuclear ribosomal small subunit, internal transcribed spacer and large subunit regions of <i>Rhizophagus irregularis</i> and <i>Gigaspora margarita</i> is high and isolate-dependent. <i>Molecular Ecology</i> , 2016, 25, 2816-2832.	2.0	64
4523	Complex longitudinal diversification across South China and Vietnam in Stejneger's pit viper, <i>Viridovipera stejnegeri</i> (Schmidt, 1925) (Reptilia: Serpentes: Viperidae). <i>Molecular Ecology</i> , 2016, 25, 2920-2936.	2.0	18
4524	Evolutionary melting pots: a biodiversity hotspot shaped by ring diversifications around the Black Sea in the Eastern tree frog (<i>Hyla orientalis</i>). <i>Molecular Ecology</i> , 2016, 25, 4285-4300.	2.0	53
4525	Genetic variation and evolutionary origins of parthenogenetic <i>Artemia</i> (Crustacea: Anostraca) with different ploidies. <i>Zoologica Scripta</i> , 2016, 45, 421-436.	0.7	23
4526	DNA barcodes, cryptic diversity and phylogeography of a W Mediterranean assemblage of thermosbaenacean crustaceans. <i>Zoologica Scripta</i> , 2016, 45, 659-670.	0.7	12
4527	Family-assisted inference of the genetic architecture of major histocompatibility complex variation. <i>Molecular Ecology Resources</i> , 2016, 16, 1353-1364.	2.2	21
4528	Using intron sequence comparisons in the <i>triose-phosphate isomerase</i> gene to study the divergence of the fall armyworm host strains. <i>Insect Molecular Biology</i> , 2016, 25, 324-337.	1.0	31
4529	Evolutionary history and species diversity of African pouched mice (<i>Peromyscus</i>) Tj ETQq0 0.0,rgBT /Overlock 10	0.7	20
4530	Phylogeographic study revealed microrefugia for an endemic species on the Qinghai-Tibetan Plateau: <i>Rhodiola chrysanthemifolia</i> (Crassulaceae). <i>Plant Systematics and Evolution</i> , 2016, 302, 1179-1193.	0.3	31
4531	Evolutionary Diversity of Suid Herpesvirus 1 Based on UI44 Partial Sequences. <i>Intervirology</i> , 2016, 59, 20-29.	1.2	4
4532	The first complete mitochondrial genome of a Belostomatidae species, <i>Lethocerus indicus</i> , the giant water bug: An important edible insect. <i>Gene</i> , 2016, 591, 108-118.	1.0	2

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4533	Multilocus analysis reveals large genetic diversity in <i>Kluyveromyces marxianus</i> strains isolated from Parmigiano Reggiano and Pecorino di Farindola cheeses. <i>International Journal of Food Microbiology</i> , 2016, 233, 1-10.	2.1	27
4534	Local genetic structure and worldwide phylogenetic position of symbiotic <i>Rhizobium leguminosarum</i> strains associated with a traditional cultivated crop, <i>Vicia ervilia</i> , from Northern Morocco. <i>Systematic and Applied Microbiology</i> , 2016, 39, 409-417.	1.2	10
4535	Molecular identification of <i>Echinococcus granulosus</i> isolates from ruminants in Greece. <i>Veterinary Parasitology</i> , 2016, 226, 138-144.	0.7	15
4536	Contrasting exome constancy and regulatory region variation in the gene encoding CYP3A4. <i>Pharmacogenetics and Genomics</i> , 2016, 26, 255-270.	0.7	5
4537	A homolog of Blade-On-Petiole 1 and 2 (BOP1/2) controls internode length and homeotic changes of the barley inflorescence. <i>Plant Physiology</i> , 2016, 171, pp.00124.2016.	2.3	41
4538	Y chromosome diversity in a linguistic isolate (Mirandese, NE Portugal). <i>American Journal of Human Biology</i> , 2016, 28, 671-680.	0.8	2
4539	Shaken not stirred: A molecular contribution to the systematics of genus <i>Mugil</i> (Teleostei). <i>Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50</i>	1.3	10
4540	Association between MHC II beta chain gene polymorphisms and resistance to infectious haematopoietic necrosis virus in rainbow trout (<i>Oncorhynchus mykiss</i> , Walbaum, 1792). <i>Aquaculture Research</i> , 2016, 47, 570-578.	0.9	12
4541	Phylogeography of the micro-endemic <i>Pedicia staryi</i> group (Insecta: Diptera): evidence of relict biodiversity in the Carpathians. <i>Biological Journal of the Linnean Society</i> , 2016, 119, 719-731.	0.7	12
4542	Phylogeography and demographic history of Shaw's Jird (<i>Meriones shawii</i> complex) in North Africa. <i>Biological Journal of the Linnean Society</i> , 2016, 118, 262-279.	0.7	13
4543	Contrasting diversity and demographic signals in sympatric narrow-range endemic shrubs of the south-west Western Australian semi-arid zone. <i>Biological Journal of the Linnean Society</i> , 2016, 118, 315-329.	0.7	13
4544	Evolutionary history of <i>Trachylepis</i> skinks in the Seychelles islands: introgressive hybridization, morphological evolution and geographic structure. <i>Biological Journal of the Linnean Society</i> , 2016, 119, 15-36.	0.7	9
4545	Speciation in mountain refugia: phylogeography and demographic history of the pine siskin and black-capped siskin complex. <i>Journal of Avian Biology</i> , 2016, 47, 335-345.	0.6	13
4546	The antiquity of <i>Cyclocarya paliurus</i> (Juglandaceae) provides new insights into the evolution of relict plants in subtropical China since the late Early Miocene. <i>Journal of Biogeography</i> , 2016, 43, 351-360.	1.4	56
4547	Phylogeography of Indo-Pacific reef fishes: sister wrasses <i>Coris gaimard</i> and <i>C. cuvieri</i> in the Red Sea, Indian Ocean and Pacific Ocean. <i>Journal of Biogeography</i> , 2016, 43, 1103-1115.	1.4	27
4548	Host plant associations and geographical factors in the diversification of the Macaronesian <i>Rhopalomesites</i> beetles (Coleoptera: Curculionidae). <i>Journal of Biogeography</i> , 2016, 43, 1608-1619.	1.4	7
4549	Phylogeny and molecular evolution of the <i>DMC1</i> gene in the polyploid genus <i>Leymus</i> (Triticeae: Poaceae) and its diploid relatives. <i>Journal of Systematics and Evolution</i> , 2016, 54, 250-263.	1.6	4
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4552	Comparing RAD-seq and microsatellites to infer complex phylogeographic patterns, an empirical perspective in the Crucian carp, <i>Carassius carassius</i> L.. <i>Molecular Ecology</i> , 2016, 25, 2997-3018.	2.0	153
4553	Adaptation to low temperatures in the wild tomato species <i>Solanum chilense</i> . <i>Molecular Ecology</i> , 2016, 25, 2853-2869.	2.0	31
4555	The evolutionary dynamics of ancient and recent polyploidy in the African semiaquatic species of the legume genus <i>Aeschynomene</i> . <i>New Phytologist</i> , 2016, 211, 1077-1091.	3.5	9
4556	Genetic structure and phylogeny of Italian and Czech populations of the cucurbit powdery mildew fungus <i>Golovinomyces orontii</i> inferred by multilocus sequence typing. <i>Plant Pathology</i> , 2016, 65, 959-967.	1.2	12
4557	Phylogeography and demographic history of the Andean degu, <i>Octodontomys gliroides</i> (Rodentia: Octodontidae). <i>Zoological Journal of the Linnean Society</i> , 2016, 178, 410-430.	1.0	10
4558	DNA barcoding and surveillance sampling strategies for <i>Culicoides</i> biting midges (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502 Td	1.0	36
4559	Flowering time adaption in Swedish landrace pea (<i>Pisum sativum</i> L.). <i>BMC Genetics</i> , 2016, 17, 117.	2.7	12
4560	Identification and characterisation of Dof transcription factors in the cucumber genome. <i>Scientific Reports</i> , 2016, 6, 23072.	1.6	73
4561	Comprehensive analysis of TCP transcription factors and their expression during cotton (<i>Gossypium</i>) Tj ETQq1 1 0.784314 rgBT /Over	1.6	35
4562	EcoTILLING revealed SNPs in GhSus genes that are associated with fiber- and seed-related traits in upland cotton. <i>Scientific Reports</i> , 2016, 6, 29250.	1.6	18
4563	Range expansion of the Bluetongue vector, <i>Culicoides imicola</i> , in continental France likely due to rare wind-transport events. <i>Scientific Reports</i> , 2016, 6, 27247.	1.6	46
4564	Targeted Sequencing of Myogenic Regulatory Factors and Myostatins Reveals an Association between MSTN and Interorbital Distance in Orange-spotted Grouper, <i>Epinephelus coioides</i> (Hamilton, 1822). <i>Journal of the World Aquaculture Society</i> , 2016, 47, 741-753.	1.2	1
4565	Origin and genetic diversity of Romanian Racka sheep using mitochondrial markers. <i>Small Ruminant Research</i> , 2016, 144, 276-282.	0.6	8
4566	Revealing hidden species diversity in closely related species using nuclear SNPs, SSRs and DNA sequences – a case study in the tree genus <i>Milicia</i> . <i>BMC Evolutionary Biology</i> , 2016, 16, 259.	3.2	36
4567	Complete chloroplast genome of a valuable medicinal plant, <i>Huperzia serrata</i> (Lycopodiaceae), and comparison with its congener. <i>Applications in Plant Sciences</i> , 2016, 4, 1600071.	0.8	22
4568	Phylogeography of <i>Sesamia cretica</i> Lederer (Lepidoptera: Noctuidae). <i>Phytoparasitica</i> , 2016, 44, 641-650.	0.6	9
4569	Phylogeography and population genetics of <i>Schizothorax oacconnori</i> : strong subdivision in the Yarlung Tsangpo River inferred from mtDNA and microsatellite markers. <i>Scientific Reports</i> , 2016, 6, 29821.	1.6	22

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4571	Strains of the Group I Lineage of <i>Acidovorax citrulli</i> , the Causal Agent of Bacterial Fruit Blotch of Cucurbitaceous Crops, are Predominant in Brazil. <i>Phytopathology</i> , 2016, 106, 1486-1494.	1.1	22
4572	The Evolution of the FT/TFL1 Genes in Amaranthaceae and Their Expression Patterns in the Course of Vegetative Growth and Flowering in <i>Chenopodium rubrum</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3065-3076.	0.8	15
4573	Evidence of male-biased dispersal in eastern grey kangaroos (<i>Macropus giganteus</i>). <i>Australian Journal of Zoology</i> , 2016, 64, 360.	0.6	4
4574	Demographic history of <i>Trinorchestia longiramus</i> (Amphipoda, Talitridae) in South Korea inferred from mitochondrial DNA sequence variation. <i>Crustaceana</i> , 2016, 89, 1559-1573.	0.1	3
4575	Genetic diversity and biogeography of the south polar water bear <i>Acutuncus antarcticus</i> (Eutardigrada : Hypsibiidae) – evidence that it is a truly pan-Antarctic species. <i>Invertebrate Systematics</i> , 2016, 30, 635.	0.5	47
4576	Effector Diversification Contributes to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Phenotypic Adaptation in a Semi-Isolated Environment. <i>Scientific Reports</i> , 2016, 6, 34137.	1.6	76
4577	Diversifying selection of the anthocyanin biosynthetic downstream gene UFGT accelerates floral diversity of island <i>Scutellaria</i> species. <i>BMC Evolutionary Biology</i> , 2016, 16, 191.	3.2	3
4578	Genetic Diversity of the Azores Blackbirds <i>Turdus merula</i> Reveals Multiple Founder Events. <i>Acta Ornithologica</i> , 2016, 51, 221-234.	0.1	9
4579	Mitochondrial DNA sequence variation in <i>Hippopotamus amphibius</i> from Kruger National Park, Republic of South Africa. <i>African Zoology</i> , 2016, 51, 77-82.	0.2	1
4580	Mitogenomes from type specimens, a genotyping tool for morphologically simple species: ten genomes of agar-producing red algae. <i>Scientific Reports</i> , 2016, 6, 35337.	1.6	41
4581	MtDNA analysis reveals enriched pathogenic mutations in Tibetan highlanders. <i>Scientific Reports</i> , 2016, 6, 31083.	1.6	22
4582	Large-scale mitogenomics enables insights into <i>Schizophora</i> (Diptera) radiation and population diversity. <i>Scientific Reports</i> , 2016, 6, 21762.	1.6	66
4583	Analyses of mitochondrial genes reveal two sympatric but genetically divergent lineages of <i>Rhipicephalus appendiculatus</i> in Kenya. <i>Parasites and Vectors</i> , 2016, 9, 353.	1.0	14
4584	Pronounced genetic differentiation and recent secondary contact in the mangrove tree <i>Lumnitzera racemosa</i> revealed by population genomic analyses. <i>Scientific Reports</i> , 2016, 6, 29486.	1.6	21
4585	Molecular evidence of RNA polymerase II gene reveals the origin of worldwide cultivated barley. <i>Scientific Reports</i> , 2016, 6, 36122.	1.6	9
4586	Genetic structure and diversity of the black-throated finch (<i>Poephila cincta</i>) across its current range. <i>Australian Journal of Zoology</i> , 2016, 64, 375.	0.6	1
4587	DNA polymorphism and selection at the <i>bindin</i> locus in three <i>Strongylocentrotus</i> sp. (Echinoidea). <i>BMC Genetics</i> , 2016, 17, 66.	2.7	4

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4589	Duplication and Whorl-Specific Down-Regulation of the Obligate AP3-PI Heterodimer Genes Explain the Origin of <i>Paeonia lactiflora</i> Plants with Spontaneous Corolla Mutation. <i>Plant and Cell Physiology</i> , 2016, 58, pcw204.	1.5	12
4590	Intraspecific rearrangement of mitochondrial genome suggests the prevalence of the tandem duplication-random loss (TDLR) mechanism in <i>Quasipaa boulengeri</i> . <i>BMC Genomics</i> , 2016, 17, 965.	1.2	61
4591	Epigenetic Regulation of the Sex Determination Gene <i>MeGI</i> in Polyploid Persimmon. <i>Plant Cell</i> , 2016, 28, 2905-2915.	3.1	97
4592	A Gene for Genetic Background in <i>Zea mays</i> : Fine-Mapping enhancer of teosinte branched1.2 to a YABBY Class Transcription Factor. <i>Genetics</i> , 2016, 204, 1573-1585.	1.2	15
4593	First record of <i>Esox cisalpinus</i> (Teleostea: Esocidae) in Sardinia with insight on its mitochondrial DNA genetic variability. <i>Italian Journal of Zoology</i> , 2016, 83, 514-523.	0.6	2
4594	<i>Cercospora</i> cf. <i>flagellaris</i> and <i>Cercospora</i> cf. <i>sigesbeckiae</i> Are Associated with <i>Cercospora</i> Leaf Blight and Purple Seed Stain on Soybean in North America. <i>Phytopathology</i> , 2016, 106, 1376-1385.	1.1	38
4595	Phylogeography of <i>Diptychus maculatus</i> (Cyprinidae) endemic to the northern margin of the QTP and Tien Shan region. <i>BMC Evolutionary Biology</i> , 2016, 16, 186.	3.2	5
4596	Maternal Genetic Ancestry and Legacy of 10th Century AD Hungarians. <i>Scientific Reports</i> , 2016, 6, 33446.	1.6	30
4597	Introgression and Habitat Segregation in a Pair of Ladybird Beetle Species in the Genus <i>Propylea</i> (Coccinellidae, Coccinellinae) in Northern Japan. <i>Zoological Science</i> , 2016, 33, 603.	0.3	3
4598	Multilocus Sequence Typing of Strains of Bacterial Spot of Lettuce Collected in the United States. <i>Phytopathology</i> , 2016, 106, 1262-1269.	1.1	11
4599	Assessing genetic variation in juvenile white sharks using teeth collected from landfills in Baja California, Mexico. <i>Conservation Genetics Resources</i> , 2016, 8, 431-434.	0.4	2
4600	Genetic diversity and population structure in <i>Bactrocera correcta</i> (Diptera: Tephritidae) inferred from mtDNA <i>cox1</i> and microsatellite markers. <i>Scientific Reports</i> , 2016, 6, 38476.	1.6	15
4601	Genomic evidence of demographic fluctuations and lack of genetic structure across flyways in a long distance migrant, the European turtle dove. <i>BMC Evolutionary Biology</i> , 2016, 16, 237.	3.2	26
4602	Identification of aphid (Hemiptera: Aphididae) species of economic importance in Kenya using DNA barcodes and PCR-RFLP-based approach. <i>Bulletin of Entomological Research</i> , 2016, 106, 63-72.	0.5	18
4603	Species delimitation in trematodes using DNA sequences: Middle-American <i>Clinostomum</i> as a case study. <i>Parasitology</i> , 2016, 143, 1773-1789.	0.7	44
4604	A new species of shrew (Soricomorpha: Crocidura) from Java, Indonesia: possible character displacement despite interspecific gene flow. <i>Journal of Mammalogy</i> , 2016, , gyw183.	0.6	6
4605	A Global Analysis of <i>CYP51</i> Diversity and Azole Sensitivity in <i>Rhynchosporium commune</i> . <i>Phytopathology</i> , 2016, 106, 355-361.	1.1	35

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4607	Population genetic isolation and limited connectivity in the purple finch (<i>Haemorhous</i>) Tj ETQq1 1 0.784314 rgBT /Overlogk 10 Tf 50	0.8	10
4608	Little White Lies: Pericarp Color Provides Insights into the Origins and Evolution of Southeast Asian Weedy Rice. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 4105-4114.	0.8	36
4609	High endemism at cave entrances: a case study of spiders of the genus <i>Uthina</i> . <i>Scientific Reports</i> , 2016, 6, 35757.	1.6	23
4610	Reduced host-specificity in a parasite infecting non-littoral Lake Tanganyika cichlids evidenced by intraspecific morphological and genetic diversity. <i>Scientific Reports</i> , 2016, 6, 39605.	1.6	33
4611	Recent origin and semi-permeable species boundaries in the scleractinian coral genus <i>Stylophora</i> from the Red Sea. <i>Scientific Reports</i> , 2016, 6, 34612.	1.6	28
4612	Pentatricopeptide repeat proteins in maize. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	21
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4614	Large-scale connectivity of <i>Grapsus grapsus</i> (Decapoda) in the Southwestern Atlantic oceanic islands: integrating genetic and morphometric data. <i>Marine Ecology</i> , 2016, 37, 1360-1372.	0.4	9
4616	A comprehensive phylogeography of the <i>Hyles euphorbiae</i> complex (Lepidoptera: Sphingidae) indicates a glacial refuge. <i>Scientific Reports</i> , 2016, 6, 29527.	1.6	11
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4618	Phylogeography of the Spanish Moon Moth <i>Graellsia isabellae</i> (Lepidoptera, Saturniidae). <i>BMC Evolutionary Biology</i> , 2016, 16, 139.	3.2	11
4619	Microdiversity of <i>Echinococcus granulosus sensu stricto</i> in Australia. <i>Parasitology</i> , 2016, 143, 1026-1033.	0.7	24
4620	High-resolution phylogeography of zoonotic tapeworm <i>Echinococcus granulosus sensu stricto</i> genotype G1 with an emphasis on its distribution in Turkey, Italy and Spain. <i>Parasitology</i> , 2016, 143, 1790-1801.	0.7	51
4621	Phylogeography of the small Indian civet and origin of introductions to western Indian Ocean islands. <i>Journal of Heredity</i> , 2016, 108, esw085.	1.0	9
4622	Genetic structure and diversity of the black and rufous sengi in Tanzanian coastal forests. <i>Journal of Zoology</i> , 2016, 300, 305-313.	0.8	2
4623	Comparative phylogeography in the Atlantic forest and Brazilian savannas: pleistocene fluctuations and dispersal shape spatial patterns in two bumblebees. <i>BMC Evolutionary Biology</i> , 2016, 16, 267.	3.2	32
4624	Assessing the diversity, host-specificity and infection patterns of apicomplexan parasites in reptiles from Oman, Arabia. <i>Parasitology</i> , 2016, 143, 1730-1747.	0.7	22

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4626	Temporal and spatial genetic differentiation in the crab <i>Liocarcinus depurator</i> across the Atlantic-Mediterranean transition. <i>Scientific Reports</i> , 2016, 6, 29892.	1.6	26
4627	Deep divergence and evidence for translocations between Iranian and European populations of the alfalfa weevil (Coleoptera: Curculionidae) based on mitochondrial DNA. <i>Canadian Entomologist</i> , 2016, 148, 703-715.	0.4	2
4628	Genome-wide characterization of the β -1,3-glucanase gene family in <i>Gossypium</i> by comparative analysis. <i>Scientific Reports</i> , 2016, 6, 29044.	1.6	16
4629	Diversity of major urinary proteins (MUPs) in wild house mice. <i>Scientific Reports</i> , 2016, 6, 38378.	1.6	25
4630	Box Jellyfish <i>Alatina alata</i> Has a Circumtropical Distribution. <i>Biological Bulletin</i> , 2016, 231, 152-169.	0.7	30
4631	Discrete phenotypes are not underpinned by genome-wide genetic differentiation in the squat lobster <i>Munida gregaria</i> (Crustacea: Decapoda: Munididae): a multi-marker study covering the Patagonian shelf. <i>BMC Evolutionary Biology</i> , 2016, 16, 258.	3.2	8
4632	Middle-Upper Pleistocene climate changes shaped the divergence and demography of <i>Cycas guizhouensis</i> (Cycadaceae): Evidence from DNA sequences and microsatellite markers. <i>Scientific Reports</i> , 2016, 6, 27368.	1.6	15
4633	Distribution of <i>Hoplolaimus</i> Species in Soybean Fields in South Carolina and North Carolina. <i>Plant Disease</i> , 2016, 100, 149-153.	0.7	10
4634	Aquatic Snails <i>Ecrobia maritima</i> (Milaschewitsch, 1916) and <i>E. Ventrosa</i> (Montagu, 1803) (Caenogastropoda: Hydrobiidae) in the East Mediterranean and Black Sea. <i>Annales Zoologici</i> , 2016, 66, 477-486.	0.1	19
4635	Mitochondrial DNA hypervariable region 1 diversity in Nigerian goats. <i>Animal Genetic Resources = Ressources Genetiques Animales = Recursos Geneticos Animales</i> , 2016, 59, 47-54.	0.2	5
4636	Genetic relationships of indigenous goats reared by pastoralists in Kenya based on mitochondria D-loop sequence. <i>Animal Genetic Resources = Ressources Genetiques Animales = Recursos Geneticos Animales</i> , 2016, 59, 73-80.	0.2	3
4637	Fine-tuning of a COI PCR-RFLP assay for fast genetic characterization of Spanish white-clawed crayfish. <i>Knowledge and Management of Aquatic Ecosystems</i> , 2016, , 32.	0.5	0
4638	Comparative Phylogenomic Assessment of Mitochondrial Introgression among Several Species of Chipmunks (<i>TAMIAS</i>). <i>Genome Biology and Evolution</i> , 2016, 9, eww254.	1.1	12
4639	Population differentiation of the Chagas disease vector <i>Triatoma maculata</i> (Erichson, 1848) from Colombia and Venezuela. <i>Journal of Vector Ecology</i> , 2016, 41, 72-79.	0.5	14
4640	Transmission bottlenecks and RNAi collectively influence tick-borne flavivirus evolution. <i>Virus Evolution</i> , 2016, 2, vew033.	2.2	35
4641	Mitochondrial DNA Variation Among Populations of <i>Rhynchophorus ferrugineus</i> (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102 T	0.6	3
4642	Species-specific diagnostics using a β -1,4-endoglucanase gene for <i>Pratylenchus</i> spp. occurring in the Pacific Northwest of North America. <i>Nematology</i> , 2016, 18, 1219-1229.	0.2	13

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4644	Gender-Associated Mitochondrial DNA Heteroplasmy in Somatic Tissues of the Endangered Freshwater Mussel <i>Unio crassus</i> (Bivalvia: Unionidae): Implications for Sex Identification and Phylogeographical Studies. <i>Journal of Experimental Zoology</i> , 2016, 325, 610-625.	1.2	20
4645	Biofortification of oilseed Brassica juncea with the anti-cancer compound glucoraphanin by suppressing GSL-ALK gene family. <i>Scientific Reports</i> , 2016, 5, 18005.	1.6	72
4646	Utility of internally transcribed spacer region of rDNA (ITS) and β -tubulin gene sequences to infer genetic diversity and migration patterns of <i>Colletotrichum truncatum</i> infecting <i>Capsicum</i> spp.. <i>Ecology and Evolution</i> , 2016, 6, 593-606.	0.8	4
4647	Are the dinaric mountains a boundary between continental and mediterranean wild boar populations in Croatia?. <i>European Journal of Wildlife Research</i> , 2016, 62, 167-177.	0.7	9
4648	High phylogeographical complexity within Mediterranean islands: insights from the Corsican fire salamander. <i>Journal of Biogeography</i> , 2016, 43, 192-203.	1.4	16
4649	Phylogenetic analysis suggests that sociality is associated with reduced effectiveness of selection. <i>Ecology and Evolution</i> , 2016, 6, 469-477.	0.8	36
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4651	The Quaternary evolutionary history, potential distribution dynamics, and conservation implications for a Qinghai-Tibet Plateau endemic herbaceous perennial, <i>Anisodus tanguticus</i> (Solanaceae). <i>Ecology and Evolution</i> , 2016, 6, 1977-1995.	0.8	37
4652	Incongruence between mtDNA and nuclear data in the freshwater mussel genus <i>Cyprogenia</i> (Bivalvia: Unionidae) and its impact on species delineation. <i>Ecology and Evolution</i> , 2016, 6, 2439-2452.	0.8	26
4653	Two seas, two lineages: How genetic diversity is structured in Atlantic and Mediterranean greater amberjack <i>Seriola dumerili</i> Risso, 1810 (Perciformes, Carangidae). <i>Fisheries Research</i> , 2016, 179, 271-279.	0.9	22
4654	Distribution and molecular phylogeny of biliary trematodes (Opisthorchiidae) infecting native <i>Lutra lutra</i> and alien <i>Neovison vison</i> across Europe. <i>Parasitology International</i> , 2016, 65, 163-170.	0.6	10
4655	Evolutionary history of the river frog genus <i>Amietia</i> (Anura: Pyxicephalidae) reveals extensive diversification in Central African highlands. <i>Molecular Phylogenetics and Evolution</i> , 2016, 99, 168-181.	1.2	18
4656	Shaping species with ephemeral boundaries: the distribution and genetic structure of desert tortoise (<i>Gopherus morafkai</i>) in the Sonoran Desert region. <i>Journal of Biogeography</i> , 2016, 43, 484-497.	1.4	11
4657	Little Polymorphism at the K13 Propeller Locus in Worldwide <i>Plasmodium falciparum</i> Populations Prior to the Introduction of Artemisinin Combination Therapies. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3340-3347.	1.4	18
4658	Polymorphic sites in complete genome sequences of Asian badger, <i>Meles leucurus amurensis</i> (Mustelidae, Melinae) mitochondria. <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 264-265.	0.2	1
4659	Assessing models of speciation under different biogeographic scenarios; an empirical study using multi-locus and RNA-seq analyses. <i>Ecology and Evolution</i> , 2016, 6, 379-396.	0.8	6
4660	Determining the extent and direction of introgression between three spruce species based on molecular markers from three genomes with different rates of gene flow. <i>Plant Systematics and Evolution</i> , 2016, 302, 691-701.	0.3	6

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4662	Population genetics of the olive-winged bulbul (<i>Pycnonotus plumosus</i>) in a tropical urban-fragmented landscape. <i>Ecology and Evolution</i> , 2016, 6, 78-90.	0.8	15
4663	Incongruent range dynamics between co-occurring Asian temperate tree species facilitated by life history traits. <i>Ecology and Evolution</i> , 2016, 6, 2346-2358.	0.8	10
4664	DNA barcoding and evaluation of genetic diversity in Cyprinidae fish in the midstream of the Yangtze River. <i>Ecology and Evolution</i> , 2016, 6, 2702-2713.	0.8	60
4665	Impacts of forest fragmentation and post-glacial colonization on the distribution of genetic diversity in the Polish population of the hazel grouse <i>Terastes bonasia</i> . <i>European Journal of Wildlife Research</i> , 2016, 62, 293-306.	0.7	7
4666	Social structure and landscape genetics of the endemic New Caledonian ant <i>Leptomyrmex pallens</i> Emery, 1883 (Hymenoptera: Formicidae: Dolichoderinae), in the context of fire-induced rainforest fragmentation. <i>Conservation Genetics</i> , 2016, 17, 931-947.	0.8	3
4667	Genetic and morphological heterogeneity among populations of <i>Eurytemora affinis</i> (Crustacea: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50	0.1	19
4668	Morphology and genetic variability within <i>Taenia multiceps</i> in ruminants from Italy. <i>Veterinary Parasitology</i> , 2016, 223, 181-185.	0.7	19
4669	Diversity of <i>Sarcocystis</i> spp shed by opossums in Brazil inferred with phylogenetic analysis of DNA coding ITS1, cytochrome B, and surface antigens. <i>Experimental Parasitology</i> , 2016, 164, 71-78.	0.5	22
4670	Sequence analysis of <i>pfprt</i> and <i>pfmdr1</i> genes and its association with chloroquine resistance in Southeast Indian <i>Plasmodium falciparum</i> isolates. <i>Genomics Data</i> , 2016, 8, 85-90.	1.3	17
4671	Lack of specific alleles for the bovine chemokine (C-X-C) receptor type 4 (CXCR4) gene in West African cattle questions its role as a candidate for trypanotolerance. <i>Infection, Genetics and Evolution</i> , 2016, 42, 30-33.	1.0	7
4672	Phylogeography of endemic <i>Xantusia</i> ™ hummingbird (<i>Hylocharis xantusii</i>) shows a different history of vicariance in the Baja California Peninsula. <i>Molecular Phylogenetics and Evolution</i> , 2016, 102, 265-277.	1.2	10
4673	Three Taxa in One: Cryptic Diversity in the Black Fly <i>Simulium nobile</i> (Diptera: Simuliidae) in Southeast Asia. <i>Journal of Medical Entomology</i> , 2016, 53, 972-976.	0.9	17
4674	Morphological and molecular investigations of <i>Gagea</i> (Liliaceae) in southeastern Kazakhstan with special reference to putative altitudinal hybrid zones. <i>Plant Systematics and Evolution</i> , 2016, 302, 985-1007.	0.3	11
4675	<i>Cladosporium lebrasiae</i> , a new fungal species isolated from milk bread rolls in France. <i>Fungal Biology</i> , 2016, 120, 1017-1029.	1.1	11
4676	Phylogeography of the marbled crab <i>Pachygrapsus marmoratus</i> (Decapoda, Grapsidae) along part of the African Mediterranean coast reveals genetic homogeneity across the Siculo-Tunisian Strait versus heterogeneity across the Gibraltar Strait. <i>Marine Biology Research</i> , 2016, 12, 471-487.	0.3	15
4677	Abundance and genetic variation of the coral-killing cyanobacteriosponge <i>Terpios hoshinota</i> in the Spermonde Archipelago, SW Sulawesi, Indonesia. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2016, 96, 453-463.	0.4	25
4678	MtDNA diversity of the Indonesian giant barrel sponge <i>Xestospongia testudinaria</i> (Porifera: Tj ETQq1 1 0.784314 rgBT /Overlock 15 Biological Association of the United Kingdom, 2016, 96, 323-332.	0.4	15

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4680	Species limits, interspecific hybridization and phylogeny in the cryptic land snail complex <i>Pyramidula</i> : The power of RADseq data. <i>Molecular Phylogenetics and Evolution</i> , 2016, 101, 267-278.	1.2	53
4681	The phenotypic plasticity in Chinese populations of <i>Daphnia similoides sinensis</i> : recurvate helmeted forms are associated with the presence of predators. <i>Journal of Plankton Research</i> , 2016, 38, 855-864.	0.8	14
4682	Lineage-specific evolutionary rate in plants: Contributions of a screening for <i>Cereus</i> (Cactaceae). <i>Applications in Plant Sciences</i> , 2016, 4, 1500074.	0.8	11
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4684	Evolution of circoviruses in lorikeets lags behind its hosts. <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 281-291.	1.2	22
4685	The lysidyl aminoacyl transfer RNA synthetase intron, a new marker for demosponge phylogeographics – case study on <i>Neopetrosia</i> . <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2016, 96, 333-339.	0.4	0
4686	Nondegenerative Evolution in Ancient Heritable Bacterial Endosymbionts of Fungi. <i>Molecular Biology and Evolution</i> , 2016, 33, 2216-2231.	3.5	14
4687	Large-scale genetic census of an elusive carnivore, the European wildcat (<i>Felis s. silvestris</i>). <i>Conservation Genetics</i> , 2016, 17, 1183-1199.	0.8	46
4688	Molecular epidemiology and genetic diversity of <i>Blastocystis</i> infection in humans in Italy. <i>Epidemiology and Infection</i> , 2016, 144, 635-646.	1.0	51
4689	Phylogenetics of DENV-1 reveals the spatiotemporal co-circulation of two distinct lineages in 2013 and multiple introductions of dengue virus in Goiás, Brazil. <i>Infection, Genetics and Evolution</i> , 2016, 43, 130-134.	1.0	17
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4691	Incipient speciation with gene flow on a continental island: Species delimitation of the Hainan Hwamei (<i>Leucodioptron canorum owstoni</i> , Passeriformes, Aves). <i>Molecular Phylogenetics and Evolution</i> , 2016, 102, 62-73.	1.2	13
4692	Mitochondrial phylogeny of the Eurasian/African reed warbler complex (<i>Acrocephalus</i> , Aves). Disagreement between morphological and molecular evidence and cryptic divergence: A case for resurrecting <i>Calamoherpe ambigua</i> Brehm 1857. <i>Molecular Phylogenetics and Evolution</i> , 2016, 102, 30-44.	1.2	16
4693	Phylogeography and genealogy of the tsetse fly <i>Glossina pallidipes</i> (Diptera: Glossinidae). <i>International Journal of Tropical Insect Science</i> , 2016, 36, 32-47.	0.4	3
4694	The influence of positive selection and trans-species evolution on DPB diversity in the golden snub-nosed monkeys (<i>Rhinopithecus roxellana</i>). <i>Primates</i> , 2016, 57, 489-499.	0.7	6
4695	DNA barcoding of Sri Lankan phlebotomine sand flies using cytochrome c oxidase subunit I reveals the presence of cryptic species. <i>Acta Tropica</i> , 2016, 161, 1-7.	0.9	15
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4698	Detection and characterisation of the biopollutant <i>Xenostrobus securis</i> (Lamarck 1819) Asturian population from DNA Barcoding and eBarcoding. Marine Pollution Bulletin, 2016, 105, 23-29.	2.3	31
4699	Origin and genetic diversity of Egyptian native chickens based on complete sequence of mitochondrial DNA D-loop region. Poultry Science, 2016, 95, 1248-1256.	1.5	41
4700	Nucleotide polymorphisms in the bovine lymphotoxin A gene and their distribution among Bos indicus zebu cattle breeds. Gene, 2016, 579, 82-94.	1.0	2
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4702	Biogeography and evolution of seeder and resprouter forms of <i>Erica coccinea</i> (Ericaceae) in the fire-prone Cape fynbos. Plant Ecology, 2016, 217, 751-761.	0.7	7
4703	Regal phylogeography: Range-wide survey of the marine angelfish <i>Pygoplites diacanthus</i> reveals evolutionary partitions between the Red Sea, Indian Ocean, and Pacific Ocean. Molecular Phylogenetics and Evolution, 2016, 100, 243-253.	1.2	22
4704	Determinants of Range Limits in Montane Woodland Salamanders (Genus <i>Plethodon</i>). Copeia, 2016, 104, 101-110.	1.4	16
4705	Genetic variation at the MHC DRB1 locus is similar across Gunnison's prairie dog (<i>Cynomys gunnisoni</i>) colonies regardless of plague history. Ecology and Evolution, 2016, 6, 2624-2651.	0.8	6
4706	How does the post-fire facultative seeding strategy impact genetic variation and phylogeographical history? The case of <i>Bossiaea ornata</i> (Fabaceae) in a fire-prone, mediterranean-climate ecosystem. Journal of Biogeography, 2016, 43, 96-110.	1.4	10
4707	Testing parasite "intimacy": the whipworm <i>T. richuris muris</i> in the European house mouse hybrid zone. Ecology and Evolution, 2016, 6, 2688-2701.	0.8	14
4708	Sequence variation in Brassica AP2 and analysis of interaction of AP2-miR172 regulatory module. Plant Cell, Tissue and Organ Culture, 2016, 125, 191-206.	1.2	10
4709	Molecular differentiation of <i>Sarcocystis buffalonis</i> and <i>Sarcocystis levinei</i> in water buffaloes (<i>Bubalus bubalis</i>) from <i>Sarcocystis hirsuta</i> and <i>Sarcocystis cruzi</i> in cattle (<i>Bos taurus</i>). Parasitology Research, 2016, 115, 2459-2471.	0.6	28
4710	Population genetic structure of <i>Cheyletus malaccensis</i> (Acari: Cheyletidae) in China based on mitochondrial COI and 12S rRNA genes. Experimental and Applied Acarology, 2016, 69, 117-128.	0.7	12
4711	First insights into the genetic diversity of <i>Echinococcus granulosus sensu stricto</i> (s.s.) in Serbia. Veterinary Parasitology, 2016, 223, 57-62.	0.7	16
4712	Candidate Gene Analysis Suggests Untapped Genetic Complexity in Melanin-Based Pigmentation in Birds. Journal of Heredity, 2016, 107, 327-335.	1.0	32
4713	Population genetic structure of the shovel-nosed lobster <i>Thenus unimaculatus</i> (Decapoda, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 T 766, 225-236.	1.0	9
4714	The cane or marine toad, <i>Rhinella marina</i> (Anura, Bufonidae): two genetically and morphologically distinct species. Zootaxa, 2016, 4103, 574-86.	0.2	53

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4715	Insights into the <i>Prunus</i> -Specific S-RNase-Based Self-Incompatibility System from a Genome-Wide Analysis of the Evolutionary Radiation of <i>S</i> -Locus-Related F-box Genes. <i>Plant and Cell Physiology</i> , 2016, 57, 1281-1294.	1.5	32
4716	Genome-wide characterization of Nuclear Factor Y (NF-Y) gene family of sorghum [<i>Sorghum bicolor</i> (L.) Moench]: a bioinformatics approach. <i>Physiology and Molecular Biology of Plants</i> , 2016, 22, 33-49.	1.4	22
4717	Colonization of the Scottish islands via long-distance Neolithic transport of red deer (<i>Cervus</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 6	1.2	23
4718	Cryptic species of Ponto-Caspian bighead goby of the genus <i>Ponticola</i> (Gobiidae). <i>Journal of Ichthyology</i> , 2016, 56, 1-18.	0.2	9
4719	Unravelling the invasion pathways of the quagga mussel (<i>Dreissena rostriformis</i>) into Western Europe. <i>Biological Invasions</i> , 2016, 18, 245-264.	1.2	13
4720	Genetic diversity in the mitochondrial DNA D-loop region of global swine (<i>Sus scrofa</i>) populations. <i>Biochemical and Biophysical Research Communications</i> , 2016, 473, 814-820.	1.0	24
4721	Revision of widespread red squirrels (genus: <i>Tamiasciurus</i>) highlights the complexity of speciation within North American forests. <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 170-182.	1.2	59
4722	A new resource of single nucleotide polymorphisms in the Japanese eel <i>Anguilla japonica</i> derived from restriction site-associated DNA. <i>Ichthyological Research</i> , 2016, 63, 496-504.	0.5	3
4723	Comparison of genetic diversity in four <i>Typha</i> species (Poales, Typhaceae) from China. <i>Hydrobiologia</i> , 2016, 770, 117-128.	1.0	13
4724	Phylogeography and connectivity of the <i>Pseudocalanus</i> (Copepoda: Calanoida) species complex in the eastern North Pacific and the Pacific Arctic Region. <i>Journal of Plankton Research</i> , 2016, 38, 610-623.	0.8	25
4725	The 5S rDNA in two <i>Abracris</i> grasshoppers (Ommatolampidinae: Acrididae): molecular and chromosomal organization. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1607-1613.	1.0	7
4726	Out of the Sichuan Basin: Rapid species diversification of the freshwater crabs in Sinopotamon (Decapoda: Brachyura: Potamidae) endemic to China. <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 80-94.	1.2	22
4727	High genetic diversity at the inter-/intra-host level of <i>Cherry leaf roll virus</i> population associated with the birch leaf-roll disease in Fennoscandia. <i>Scandinavian Journal of Forest Research</i> , 2016, 31, 546-560.	0.5	15
4728	A new species of arboreal rat, genus <i>Oecomys</i> (Rodentia, Cricetidae) from Chaco. <i>Journal of Mammalogy</i> , 2016, 97, 1177-1196.	0.6	19
4729	Combining genetic and distributional approaches to sourcing introduced species: a case study on the Nile monitor (<i>Varanus niloticus</i>) in Florida. <i>Royal Society Open Science</i> , 2016, 3, 150619.	1.1	4
4730	Mitochondrial Genomes of <i>Anopheles</i> (<i>Kerteszia</i>) (Diptera: Culicidae) From the Atlantic Forest, Brazil. <i>Journal of Medical Entomology</i> , 2016, 53, 790-797.	0.9	17
4731	Limited erosion of genetic and species diversity from small forest patches: Sacred forest groves in an Afrotropical biodiversity hotspot have high conservation value for butterflies. <i>Biological Conservation</i> , 2016, 198, 122-134.	1.9	21
4732	Chromosomal Diversification Higher Than Molecular Variation in <i>Astyanax</i> aff. <i>fasciatus</i> (Teleostei, Characidae). <i>Zebrafish</i> , 2016, 13, 345-353.	0.5	11

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4734	Comparative genomic analysis of upstream miRNA regulatory motifs in <i>Caenorhabditis</i> . <i>Rna</i> , 2016, 22, 968-978.	1.6	2
4735	Insights into the genetic structure of the cowpea pest <i>Callosobruchus maculatus</i> in Africa. <i>Journal of Pest Science</i> , 2016, 89, 449-458.	1.9	10
4736	Patterns of molecular evolution of RNAi genes in social and socially parasitic bumblebees. <i>Infection, Genetics and Evolution</i> , 2016, 42, 53-59.	1.0	5
4737	Hybridization among distantly related species: Examples from the polyploid genus <i>Curcuma</i> (Zingiberaceae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 303-321.	1.2	17
4738	The taxonomic position and the unexpected divergence of the Habu viper, <i>Protobothrops</i> among Japanese subtropical islands. <i>Molecular Phylogenetics and Evolution</i> , 2016, 101, 91-100.	1.2	10
4739	Deep sequencing of banana bract mosaic virus from flowering ginger (<i>Alpinia purpurata</i>) and development of an immunocapture RT-LAMP detection assay. <i>Archives of Virology</i> , 2016, 161, 1783-1795.	0.9	10
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4741	Phylogeographic analyses and genetic structure illustrate the complex evolutionary history of <i>Phragmites australis</i> in Mexico. <i>American Journal of Botany</i> , 2016, 103, 876-887.	0.8	25
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4744	The dual role of Andean topography in primary divergence: functional and neutral variation among populations of the hummingbird, <i>Metallura tyrianthina</i> . <i>BMC Evolutionary Biology</i> , 2016, 16, 22.	3.2	31
4745	Genetic origin and composition of a natural hybrid poplar <i>Populus trichocarpa</i> × <i>Populus deltoides</i> from two distantly related species. <i>BMC Plant Biology</i> , 2016, 16, 89.	1.6	18
4746	Species delimitation, phylogeny and evolutionary demography of co-distributed, montane frogs in the southern Brazilian Atlantic Forest. <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 345-360.	1.2	40
4747	Population genomics of dengue virus serotype 4: insights into genetic structure and evolution. <i>Archives of Virology</i> , 2016, 161, 2133-2148.	0.9	20
4748	High genetic diversity and distribution of Bubu-DQA alleles in swamp buffaloes (<i>Bubalus bubalis</i>) Tj ETQq1 1 0.784314 rgBT /Qoverlock	1.2	9
4749	Genetic diversity and population structure of the franciscana dolphin, <i>Pontoporia blainvillei</i> , in Southern Buenos Aires, Argentina. <i>New Zealand Journal of Marine and Freshwater Research</i> , 2016, 50, 326-338.	0.8	9
4750	Population genetic structure among feeding aggregations of humpback whales in the Southern Ocean. <i>Marine Biology</i> , 2016, 163, 1.	0.7	20

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4751	Pleistocene diversification and speciation of White-throated Thrush (<i>Turdus assimilis</i> ; Aves:). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 742 T</i>	0.5	9
4752	Do <i>Staphylococcus epidermidis</i> Genetic Clusters Predict Isolation Sources?. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1711-1719.	1.8	45
4753	Characterization of the complete mitochondrial genome sequence of <i>Homalogaster paloniae</i> (Gastrodiscidae, Trematoda) and comparative analyses with selected digeneans. <i>Parasitology Research</i> , 2016, 115, 3941-3949.	0.6	7
4754	Pollen-mediated gene flow promotes low nuclear genetic differentiation among populations of <i>Cycas debaoensis</i> (Cycadaceae). <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	12
4755	Variation in <i>Hipposideros pratti</i> in China based on morphology and mitochondrial genes. <i>Mammalian Biology</i> , 2016, 81, 604-611.	0.8	3
4756	Multi-locus phylogenetic inference among New World Vultures (Aves: Cathartidae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 105, 193-199.	1.2	33
4757	DNA Barcoding in Marine Perspectives. , 2016, , .		4
4758	Mitochondrial DNA Diversity of Wild and Hatchery Reared Strains of Indian Lates calcarifer (Bloch). , 2016, , 203-212.		0
4759	Low genetic diversity of Banana bunchy top virus, with a sub-regional pattern of variation, in Democratic Republic of Congo. <i>Virus Genes</i> , 2016, 52, 900-905.	0.7	13
4760	Koalas (<i>Phascolarctos cinereus</i>) From Queensland Are Genetically Distinct From 2 Populations in Victoria. <i>Journal of Heredity</i> , 2016, 107, 573-580.	1.0	4
4761	Population Genetics of <i>Hirsutella rhossiliensis</i> , a Dominant Parasite of Cyst Nematode Juveniles on a Continental Scale. <i>Applied and Environmental Microbiology</i> , 2016, 82, 6317-6325.	1.4	9
4762	Complete chloroplast genome sequence of the avocado: gene organization, comparative analysis, and phylogenetic relationships with other Lauraceae. <i>Canadian Journal of Forest Research</i> , 2016, 46, 1293-1301.	0.8	48
4763	Phylogeography and species delimitation in convict cichlids (Cichlidae: <i>Amatitlania</i>): implications for taxonomy and Plio-Pleistocene evolutionary history in Central America. <i>Biological Journal of the Linnean Society</i> , 2016, , .	0.7	7
4764	Diversifying selection is the dominant factor affecting the geographical variation of <i>MHC</i> class <i>II</i> genes in the Omei tree frog. <i>Journal of Zoology</i> , 2016, 300, 197-204.	0.8	7
4765	Multi-locus Analyses Reveal Four Giraffe Species Instead of One. <i>Current Biology</i> , 2016, 26, 2543-2549.	1.8	175
4766	Reproductive biology and feeding habits of the prickly dogfish <i>Oxynotus bruniensis</i> . <i>Journal of Fish Biology</i> , 2016, 89, 2326-2344.	0.7	15
4767	<i>QTL</i> analysis of the photoperiodic response and clinal distribution of <i>period</i> alleles in <i>Nasonia vitripennis</i> . <i>Molecular Ecology</i> , 2016, 25, 4805-4817.	2.0	52
4768	Genetic variability in anadromous fishes, chum salmon <i>Oncorhynchus keta</i> (Walbaum, 1792), and Sakhalin taimen <i>Parahucho perryi</i> (Brevoort, 1856) from the Northwestern Pacific as a reflection of paleoclimate oscillations. <i>Russian Journal of Marine Biology</i> , 2016, 42, 330-340.	0.2	1

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4770	Post-extinction discovery of a population of the highly endemic colonial tuco-tuco (<i>Ctenomys</i>) in Argentina. <i>Journal of Biogeography</i> , 2016, 43, 1073-1081.	0.6	12
4771	Multilocus coalescent species delimitation reveals widespread cryptic differentiation among Drakensberg mountain-living freshwater crabs (Decapoda : Potamonautes). <i>Invertebrate Systematics</i> , 2016, 30, 60.	0.5	22
4772	Beyond the Coral Triangle: high genetic diversity and near panmixia in Singapore's populations of the broadcast spawning sea star <i>Protoreaster nodosus</i> . <i>Royal Society Open Science</i> , 2016, 3, 160253.	1.1	16
4773	Novel Concordance Between Geographic, Environmental, and Genetic Structure in the Ecological Generalist Prickly Sculpin (<i>Cottus asper</i>) in California. <i>Journal of Heredity</i> , 2016, 107, 504-517.	1.0	7
4774	Genetic diversity and origin of <i>Dendrothrips minowai</i> (Thysanoptera: Thripidae) in Guizhou, China. <i>Journal of Asia-Pacific Entomology</i> , 2016, 19, 1035-1042.	0.4	8
4775	Mitochondrial genome of <i>Cricetulus migratorius</i> (Rodentia: Cricetidae): Insights into the characteristics of the mitochondrial genome and the phylogenetic relationships of <i>Cricetulus</i> species. <i>Gene</i> , 2016, 595, 121-129.	1.0	13
4776	Genetic variation and population structure of the mushroom <i>Pleurotus ferulae</i> in China inferred from nuclear DNA analysis. <i>Journal of Integrative Agriculture</i> , 2016, 15, 2237-2246.	1.7	8
4777	MICB gene diversity and balancing selection on its promoter region in Yao population in southern China. <i>Human Immunology</i> , 2016, 77, 1187-1193.	1.2	3
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4779	Deeper insight into maternal genetic assessments and demographic history for Egyptian indigenous chicken populations using mtDNA analysis. <i>Journal of Advanced Research</i> , 2016, 7, 615-623.	4.4	9
4780	Linking morphometric and genetic divergence with host use in the tick complex, <i>Ornithodoros capensis sensu lato</i> . <i>Infection, Genetics and Evolution</i> , 2016, 46, 12-22.	1.0	28
4781	North African hybrid sparrows (<i>Passer domesticus</i> , <i>P. hispaniolensis</i>) back from oblivion – ecological segregation and asymmetric mitochondrial introgression between parental species. <i>Ecology and Evolution</i> , 2016, 6, 5190-5206.	0.8	18
4782	Genetic diversity of bitter taste receptor gene family in Sichuan domestic and Tibetan chicken populations. <i>Journal of Genetics</i> , 2016, 95, 675-681.	0.4	9
4783	Genomewide analysis of MATE-type gene family in maize reveals microsynteny and their expression patterns under aluminum treatment. <i>Journal of Genetics</i> , 2016, 95, 691-704.	0.4	37
4784	Effective population size as a driver for divergence of an antimicrobial peptide (Hymenoptaecin) in two common European bumblebee species. <i>Biological Journal of the Linnean Society</i> , 2016, 119, 299-310.	0.7	4
4785	Different roads lead to Rome: Integrative taxonomic approaches lead to the discovery of two new lizard lineages in the <i>Liolaemus montanus</i> group (Squamata: Liolaemidae). <i>Biological Journal of the Linnean Society</i> , 2016, . .	0.7	8
4786	Repeated Duplication of Argonaute2 Is Associated with Strong Selection and Testis Specialization in <i>Drosophila</i> . <i>Genetics</i> , 2016, 204, 757-769.	1.2	20

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4788	Genetic diversity and phylogeography of Siberian roe deer, <i>Capreolus pygargus</i> , in central and peripheral populations. <i>Ecology and Evolution</i> , 2016, 6, 7286-7297.	0.8	11
4789	Genome-wide bioinformatics analysis of Dof transcription factor gene family of chickpea and its comparative phylogenetic assessment with <i>Arabidopsis</i> and rice. <i>Plant Systematics and Evolution</i> , 2016, 302, 1009-1026.	0.3	16
4790	Phylogeographic past and invasive presence of <i>Arion</i> pest slugs in Europe. <i>Molecular Ecology</i> , 2016, 25, 5747-5764.	2.0	34
4791	High genetic diversity and population differentiation in <i>Clarias gariepinus</i> of Yala Swamp: evidence from mitochondrial DNA sequences. <i>Journal of Fish Biology</i> , 2016, 89, 2557-2570.	0.7	8
4792	Mitochondrial and nuclear DNA analyses of <i>Saccostrea</i> oysters in Japan highlight the confused taxonomy of the genus. <i>Journal of Molluscan Studies</i> , 2016, 82, 492-506.	0.4	20
4793	Genetic divergence among invasive and native populations of the yellow peacock cichlid <i>Cichla kelberi</i> . <i>Journal of Fish Biology</i> , 2016, 89, 2595-2606.	0.7	17
4794	Shallow mitochondrial phylogeographical pattern and high levels of genetic connectivity of <i>Thamnaconus hypargyreus</i> in the South China Sea and the East China Sea. <i>Biochemical Systematics and Ecology</i> , 2016, 67, 110-118.	0.6	11
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4796	Taxonomic observations on stingrays of the genus <i>Dasyatis</i> (Chondrichthyes: Dasyatidae) in the Gulf of Gabès (Southeastern Mediterranean Sea). <i>Zootaxa</i> , 2016, 4173, 101-113.	0.2	6
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4798	A new species of <i>Microphysogobio</i> (Cypriniformes: Cyprinidae) from Fujian Province, China, and a molecular phylogenetic analysis of <i>Microphysogobio</i> species from southeastern China and Taiwan. <i>Proceedings of the Biological Society of Washington</i> , 2016, 129, 195-211.	0.3	6
4799	Application of a new PCR-RFLP panel suggests a restricted population structure for <i>Eimeria tenella</i> in UK and Irish chickens. <i>Veterinary Parasitology</i> , 2016, 229, 60-67.	0.7	8
4800	The taxonomic position of <i>Corydalis parviflora</i> Su & Lidón (Papaveraceae), a genetically distinct species: Evidence from cpDNA and nDNA sequences. <i>Biochemical Systematics and Ecology</i> , 2016, 67, 134-141.	0.6	6
4801	Otolith shape analysis and mitochondrial DNA markers distinguish three sand smelt species in the <i>Atherina boyeri</i> species complex in western Mediterranean. <i>Estuarine, Coastal and Shelf Science</i> , 2016, 182, 202-210.	0.9	7
4802	Distribution pattern and genetic structure of <i>Aedes zammitii</i> (Diptera: Culicidae) along the Mediterranean and Aegean coasts of Turkey. <i>Journal of Vector Ecology</i> , 2016, 41, 151-159.	0.5	5
4803	Genetic diversity and population structure of <i>Corollospora maritima sensu lato</i> : new insights from population genetics. <i>Botanica Marina</i> , 2016, 59, 307-320.	0.6	8
4804	Speciation history and species-delimitation within the Seychelles Bronze geckos, <i>Ailuronyx</i> spp.: molecular and morphological evidence. <i>Biological Journal of the Linnean Society</i> , 2016, , .	0.7	2

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4806	Deciphering the evolutionary affiliations among bacterial strains (<i>Pseudomonas</i> and <i>Frankia</i> sp.) inhabiting same ecological niche using virtual RFLP and simulation-based approaches. <i>3 Biotech</i> , 2016, 6, 178.	1.1	5
4807	Multiple cis-acting elements involved in up-regulation of a cytochrome P450 gene conferring resistance to deltamethrin in small brown planthopper, <i>Laodelphax striatellus</i> (Fallén). <i>Insect Biochemistry and Molecular Biology</i> , 2016, 78, 20-28.	1.2	20
4808	Association of <i>Bartonella</i> Species with Wild and Synanthropic Rodents in Different Brazilian Biomes. <i>Applied and Environmental Microbiology</i> , 2016, 82, 7154-7164.	1.4	43
4809	Cytochrome <i>c</i> Oxidase I and Cytochrome <i>b</i> Gene Sequences Indicate Low Genetic Diversity in South African <i>Busseola fusca</i> (Lepidoptera: Noctuidae) from maize. <i>African Entomology</i> , 2016, 24, 518-523.	0.6	6
4810	A new species of seahorse (Teleostei: Syngnathidae) from the South China Sea. <i>Zootaxa</i> , 2016, 4170, 384-392.	0.2	12
4811	Genetic diversity and phylogeography of highly zoonotic <i>Echinococcus granulosus</i> genotype G1 in the Americas (Argentina, Brazil, Chile and Mexico) based on 8279 bp of mtDNA. <i>Infection, Genetics and Evolution</i> , 2016, 45, 290-296.	1.0	37
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4813	SPECIES DIVERSITY AND PLASTID DNA HAPLOTYPE DISTRIBUTIONS OF <i>PINUS</i> SUBSECTION AUSTRALES (PINACEAE) IN GUERRERO AND OAXACA. <i>TIP Revista Especializada En Ciencias Químico-Biológicas</i> , 2016, 19, 92-101.	0.3	2
4814	Global population genetic dynamics of a highly migratory, apex predator shark. <i>Molecular Ecology</i> , 2016, 25, 5312-5329.	2.0	51
4815	Differential DNA methylation of the meiosis-specific gene <i>FKBP6</i> in testes of yak and cattle-yak hybrids. <i>Reproduction in Domestic Animals</i> , 2016, 51, 1030-1038.	0.6	10
4816	Variation in <i>Aselliscus stoliczkanus</i> based on morphology and molecular sequence data, with a new record of the genus <i>Aselliscus</i> in China. <i>Journal of Mammalogy</i> , 2016, 97, 1718-1727.	0.6	3
4817	Genetic divergence of the endangered seagrass <i>Zostera japonica</i> Ascherson & Graebner between temperate and subtropical coasts of China based on partial sequences of <i>matK</i> and ITS. <i>Biochemical Systematics and Ecology</i> , 2016, 68, 51-57.	0.6	9
4818	Timing the evolutionary history of tent-making bats, genus <i>Uroderma</i> (Phyllostomidae): A biogeographic context. <i>Mammalian Biology</i> , 2016, 81, 579-586.	0.8	7
4819	Variation of partial transferrin sequences and phylogenetic relationships among hares (<i>Lepus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182	0.5	7
4820	Panmixia in a Critically Endangered Fish: The Totoaba (<i>Totoaba macdonaldi</i>) in the Gulf of California. <i>Journal of Heredity</i> , 2016, 107, 496-503.	1.0	9
4821	PREVALENCE, GENETIC ANALYSES, AND RISK FACTORS ASSOCIATED WITH HEARTWORM (<i>DIROFILARIA</i>) Tj ETQq0 0 0 rgBT /Overlock 2016, 52, 785-792.	0.3	12
4822	High-level phylogeny of the Coleoptera inferred with mitochondrial genome sequences. <i>Molecular Phylogenetics and Evolution</i> , 2016, 104, 99-111.	1.2	85

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4823	Sequence diversity and positive selection at the Duffy-binding protein genes of <i>Plasmodium knowlesi</i> and <i>P. cynomolgi</i> : Analysis of the complete coding sequences of Thai isolates. <i>Infection, Genetics and Evolution</i> , 2016, 44, 367-375.	1.0	8
4824	Molecular systematics and taxonomic status of three latitudinally widespread nototheniid (Perciformes: Notothenioidei) fishes from the Southern Ocean. <i>Zootaxa</i> , 2016, 4061, 381.	0.2	10
4825	Hypothesis testing clarifies the systematics of the main Central American Chagas disease vector, <i>Triatoma dimidiata</i> (Latreille, 1811), across its geographic range. <i>Infection, Genetics and Evolution</i> , 2016, 44, 431-443.	1.0	21
4826	Hybridisation among groupers (genus <i>Cephalopholis</i>) at the eastern Indian Ocean suture zone: taxonomic and evolutionary implications. <i>Coral Reefs</i> , 2016, 35, 1157-1169.	0.9	12
4827	Mitochondrial DNA reveals evolutionary status and population genetics of two closely related fish (<i>Misgurnus bipartitus</i> and <i>Misgurnus mohoity</i>) in northeast China. <i>Biochemical Systematics and Ecology</i> , 2016, 68, 192-199.	0.6	8
4828	Polymorphism of the phosphoserine phosphatase gene in <i>Streptococcus thermophilus</i> and its potential use for typing and monitoring of population diversity. <i>International Journal of Food Microbiology</i> , 2016, 236, 138-147.	2.1	10
4829	Predictors of intraspecific morphological variability in a tropical hotspot: comparing the influence of random and non-random factors. <i>Journal of Biogeography</i> , 2016, 43, 2160-2172.	1.4	22
4830	High regional genetic diversity and lack of host-specificity in <i>Ostrinia nubilalis</i> (Lepidoptera: Tj ETQq1 1 0.784314 rgBJ /Overlock	0.5	10
4831	Spatial size dimorphism in New Zealand's last endemic raptor, the KÅrearea <i>Falco novaeseelandiae</i> , coincides with a narrow sea strait. <i>Ibis</i> , 2016, 158, 747-761.	1.0	6
4832	Population genetic diversity and geographical differentiation of MHC class II DAB genes in the vulnerable Chinese egret (<i>Egretta eulophotes</i>). <i>Conservation Genetics</i> , 2016, 17, 1459-1468.	0.8	5
4833	A new and highly divergent mitochondrial lineage in the Small Five-toed Jerboa, <i>Allactaga elater</i> , from Iran (Mammalia: Rodentia). <i>Zoology in the Middle East</i> , 2016, 62, 206-211.	0.2	4
4834	Specific alleles at immune genes, rather than genome-wide heterozygosity, are related to immunity and survival in the critically endangered Attwater's prairie chicken. <i>Molecular Ecology</i> , 2016, 25, 4730-4744.	2.0	61
4835	Genetic variation and phylogenetic relationship analysis of <i>Jatropha curcas</i> L. inferred from nrDNA ITS sequences. <i>Comptes Rendus - Biologies</i> , 2016, 339, 337-346.	0.1	6
4836	Phylogeography of the genus <i>Podococcus</i> (Palmae/Arecaceae) in Central African rain forests: Climate stability predicts unique genetic diversity. <i>Molecular Phylogenetics and Evolution</i> , 2016, 105, 126-138.	1.2	45
4837	Cyto-nuclear discordance suggests complex evolutionary history in the cave-dwelling salamander, <i>Urycea lucifuga</i> . <i>Ecology and Evolution</i> , 2016, 6, 6121-6138.	0.8	5
4838	Effects of dam structures on genetic diversity of freshwater fish <i>Sinibrama macrops</i> in Min River, China. <i>Biochemical Systematics and Ecology</i> , 2016, 68, 216-222.	0.6	12
4839	Secondary contact and asymmetrical gene flow in a cosmopolitan marine fish across the Benguela upwelling zone. <i>Heredity</i> , 2016, 117, 307-315.	1.2	27
4840	Nucleotide diversity, natural variation, and evolution of Flexible culm-1 and Strong culm-2 lodging resistance genes in rice. <i>Genome</i> , 2016, 59, 473-483.	0.9	11

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4841	Bottomless barrel-sponge species in the Indo-Pacific?. <i>Zootaxa</i> , 2016, 4136, 393-6.	0.2	6
4842	Assessment of genetic diversity and population structure of swamp eel <i>Monopterus albus</i> in China. <i>Biochemical Systematics and Ecology</i> , 2016, 68, 81-87.	0.6	15
4843	New data reinforcing the taxonomic status of <i>Lepidion eques</i> as synonym of <i>Lepidion lepidion</i> (Teleostei, Gadiformes). <i>Biochemical Systematics and Ecology</i> , 2016, 68, 6-10.	0.6	4
4844	New molecular data favour an anthropogenic introduction of the wood mouse (<i>Apodemus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 1-12.	0.6	15
4845	Phylogeographical patterns of the gastropod <i>Siphonaria pectinata</i> (Linnaeus, 1758). <i>Marine Ecology</i> , 2016, 37, 227-233.	0.4	4
4846	Morphological and genetic differentiation of <i>Eremina desertorum</i> (Gastropoda, Pulmonata, Helicidae) in Egypt. <i>Zoologica Scripta</i> , 2016, 45, 48-61.	0.7	13
4847	Phylogeography of the bobwhite (<i>Colinus</i>) quails. <i>Wildlife Monographs</i> , 2016, 193, 1-49.	2.0	15
4848	Impact of enrichment conditions on cross-species capture of fresh and degraded DNA. <i>Molecular Ecology Resources</i> , 2016, 16, 42-55.	2.2	70
4849	Comparative Phylogeography of Two Bird Species, <i>Tachyphonus phoenicius</i> (Thraupidae) and <i>Polytmus theresiae</i> (Trochilidae), Specialized in Amazonian White-sand Vegetation. <i>Biotropica</i> , 2016, 48, 110-120.	0.8	32
4850	The genetic basis of color-related local adaptation in a ring-like colonization around the Mediterranean. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 140-153.	1.1	31
4851	Three ways to distinguish species: using behavioural, ecological, and molecular data to tell apart two closely related ants, <i>Crematogaster amponotus renggeri</i> and <i>Crematogaster amponotus rufipes</i> (Hymenoptera: Formicidae). <i>Zoological Journal of the Linnean Society</i> , 2016, 176, 170-181.	1.0	25
4852	Morphological and genetic divergence of a small stream fish species along a watershed. <i>Biochemical Systematics and Ecology</i> , 2016, 68, 66-73.	0.6	5
4853	Colonization and demographic expansion of freshwater fauna across the Hawaiian archipelago. <i>Journal of Evolutionary Biology</i> , 2016, 29, 2054-2069.	0.8	11
4854	Pleistocene radiation of coastal species of <i>Pilosocereus</i> (Cactaceae) in eastern Brazil. <i>Journal of Arid Environments</i> , 2016, 135, 22-32.	1.2	17
4855	Demographic History of the Genus <i>Pan</i> Inferred from Whole Mitochondrial Genome Reconstructions. <i>Genome Biology and Evolution</i> , 2016, 8, 2020-2030.	1.1	19
4856	Climatic and geographic effects on the spatial genetic pattern of a landbird species (<i>Alectoris</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 0,7 3	0,7	3
4857	Evidence for ecological speciation via a host shift in the holly leaf miner, <i>Phytomyza glabricola</i> (Diptera: Agromyzidae). <i>Ecology and Evolution</i> , 2016, 6, 6565-6577.	0.8	8
4858	Conservation genetics of rare trees restricted to subtropical montane cloud forests in southern China: a case study from <i>Quercus arbutifolia</i> (Fagaceae). <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	14

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4860	New insights on the origin of the woody flora of the Chihuahuan Desert: The case of <i>Lindleya</i> . <i>American Journal of Botany</i> , 2016, 103, 1694-1707.	0.8	15
4861	Essentiality Is a Strong Determinant of Protein Rates of Evolution during Mutation Accumulation Experiments in <i>Escherichia coli</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 2914-2927.	1.1	25
4862	Conserved but Attenuated Parental Gene Expression in Allopolyploids: Constitutive Zinc Hyperaccumulation in the Allotetraploid <i>Arabidopsis kamchatica</i> . <i>Molecular Biology and Evolution</i> , 2016, 33, 2781-2800.	3.5	40
4863	Phylogeography and ecological niche modelling in <i>Eugenia uniflora</i> (Myrtaceae) suggest distinct vegetational responses to climate change between the southern and the northern Atlantic Forest. <i>Botanical Journal of the Linnean Society</i> , 2016, 182, 670-688.	0.8	41
4864	Molecular analyses and species distribution models indicate cryptic northern mountain refugia for a forest-dwelling ground beetle. <i>Journal of Biogeography</i> , 2016, 43, 2223-2236.	1.4	14
4865	Species delimitation and phylogeography of the studfish <i>Fundulus catenatus</i> species group (Ovalentaria: Cyprinodontiformes). <i>Zoological Journal of the Linnean Society</i> , 2016, , .	1.0	1
4866	Development of chloroplast genomic resources for <i>Akebia quinata</i> (Lardizabalaceae). <i>Conservation Genetics Resources</i> , 2016, 8, 447-449.	0.4	21
4867	Population dynamics of <i>Anopheles nuneztovari</i> in Colombia. <i>Infection, Genetics and Evolution</i> , 2016, 45, 56-65.	1.0	15
4868	Mitochondrial DNA sequence variation in <i>Drosophila</i> species (Diptera: Drosophilidae) along altitudinal gradient from Central Himalayan region of India. <i>Journal of Genetics</i> , 2016, 95, 357-367.	0.4	7
4869	The biogeography of kin discrimination across microbial neighbourhoods. <i>Molecular Ecology</i> , 2016, 25, 4875-4888.	2.0	39
4870	Feral Cat Globetrotters: genetic traces of historical human-mediated dispersal. <i>Ecology and Evolution</i> , 2016, 6, 5321-5332.	0.8	7
4871	Phylogeography and population structure of two <i>Brachistosternus</i> species (Scorpiones: Bothriuridae) from the Chilean coastal desert - the perils of coastal living. <i>Biological Journal of the Linnean Society</i> , 2016, , .	0.7	5
4872	Out of the forest: past and present range expansion of a parthenogenetic weevil pest, or how to colonize the world successfully. <i>Ecology and Evolution</i> , 2016, 6, 5431-5445.	0.8	14
4873	Molecular identification and genetic structure of <i>Aedes phoeniciae</i> (Diptera: Culicidae) in Northern Cyprus and Turkey. <i>Biochemical Systematics and Ecology</i> , 2016, 69, 6-14.	0.6	4
4874	High degree of clonal reproduction and lack of large-scale geographic patterning mark the introduced range of the invasive vine, kudzu (<i>Pueraria montana</i> var. <i>lobata</i>), in North America. <i>American Journal of Botany</i> , 2016, 103, 1499-1507.	0.8	19
4875	Phylogenetic relationships and genetic diversity of badgers from the Korean Peninsula: Implications for the taxonomic status of the Korean badger. <i>Biochemical Systematics and Ecology</i> , 2016, 69, 18-26.	0.6	5
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4878	Contrasting pattern of photobiont diversity in the Atlantic and Pacific populations of <i>Erioderma pedicellatum</i> (Pannariaceae). <i>Lichenologist</i> , 2016, 48, 275-291.	0.5	18
4879	Range, genetic diversity and future of the threatened butterfly, <i>Pieris virginiensis</i> . <i>Insect Conservation and Diversity</i> , 2016, 9, 506-516.	1.4	5
4880	The Evolution of Innate Immune Genes: Purifying and Balancing Selection on β -Defensins in Waterfowl. <i>Molecular Biology and Evolution</i> , 2016, 33, 3075-3087.	3.5	38
4881	What are the evolutionary mechanisms explaining the similar species richness patterns in tropical mosses? Insights from the phylogeny of the pantropical genus <i>Pelekium</i> . <i>Molecular Phylogenetics and Evolution</i> , 2016, 105, 139-145.	1.2	11
4882	Origin of year-long bean (<i>Phaseolus dumosus</i> Macfady, Fabaceae) from reticulated hybridization events between multiple <i>Phaseolus</i> species. <i>Annals of Botany</i> , 2016, 118, 957-969.	1.4	23
4883	Fleas and Ticks in Carnivores From a Domesticâ€“Wildlife Interface: Implications for Public Health and Wildlife. <i>Journal of Medical Entomology</i> , 2016, 53, 1433-1443.	0.9	23
4884	Use of next-generation molecular tools in archaeological neotropical deer sample analysis. <i>Journal of Archaeological Science: Reports</i> , 2016, 10, 403-410.	0.2	3
4885	Global diversity in the TAS2R38 bitter taste receptor: revisiting a classic evolutionary PROPosal. <i>Scientific Reports</i> , 2016, 6, 25506.	1.6	69
4886	Genetic diversity of <i>Ixodes ricinus</i> (Ixodida: Ixodidae) ticks in sympatric and allopatric zones in Baltic countries. <i>Journal of Vector Ecology</i> , 2016, 41, 244-253.	0.5	8
4887	Naturally occurring triploid hybrids between <i>Miscanthus sacchariflorus</i> and <i>M. sinensis</i> in Southern Japan, show phenotypic variation in agronomic and morphological traits. <i>Euphytica</i> , 2016, 212, 355-370.	0.6	7
4888	Structure and Migration in U.S. <i>Blumeria graminis</i> f. sp. <i>tritici</i> Populations. <i>Phytopathology</i> , 2016, 106, 295-304.	1.1	17
4889	Population Structure of <i>Phytophthora nicotianae</i> Reveals Host-Specific Lineages on Brinjal, Ridge Gourd, and Tomato in South India. <i>Phytopathology</i> , 2016, 106, 1553-1562.	1.1	16
4890	Genetic Analyses Suggest Separate Introductions of the Pine Pathogen <i>Lecanosticta acicola</i> Into Europe. <i>Phytopathology</i> , 2016, 106, 1413-1425.	1.1	30
4891	Papillomavirus in yaks: the isolates of bovine papillomavirus type 1 have a high possibility of belonging to a novel type. <i>Journal of Veterinary Medical Science</i> , 2016, 78, 1059-1061.	0.3	2
4892	Identification and characterization of the GhHsp20 gene family in <i>Gossypium hirsutum</i> . <i>Scientific Reports</i> , 2016, 6, 32517.	1.6	29
4893	Genetic diversity of two <i>Daphnia</i> -infecting microsporidian parasites, based on sequence variation in the internal transcribed spacer region. <i>Parasites and Vectors</i> , 2016, 9, 293.	1.0	8
4894	Identification and expression analysis of group III WRKY transcription factors in cotton. <i>Journal of Integrative Agriculture</i> , 2016, 15, 2469-2480.	1.7	9

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4895	Pathogenicity, vegetative compatibility and genetic diversity of <i>Verticillium dahliae</i> isolates from sugar beet. Canadian Journal of Plant Pathology, 2016, 38, 492-505.	0.8	10
4896	Comparative Phylogeography of <i>Pteropus samoensis</i> and <i>P. tonganus</i> (Pteropodidae: Chiroptera) in the South Pacific. Acta Chiropterologica, 2016, 18, 325.	0.2	8
4897	The eastern migratory caribou: the role of genetic introgression in ecotype evolution. Royal Society Open Science, 2016, 3, 150469.	1.1	27
4898	Chloroplast Sequence of <i>Treegourd</i> (<i>Crescentia cujete</i> , Bignoniaceae) to Study Phylogeography and Domestication. Applications in Plant Sciences, 2016, 4, 1600048.	0.8	13
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4900	Molecular characterization of <i>Fasciola gigantica</i> in Delhi, India and its phylogenetic relation to the species from South Asian countries. Journal of Veterinary Medical Science, 2016, 78, 1529-1532.	0.3	17
4901	Phylogeny and genetic variation within the widely distributed Bluntnose Minnow, <i>Pimephales notatus</i> (Cyprinidae), in North America. Zootaxa, 2016, 4168, 38.	0.2	5
4902	Pine marten vs. stone marten in agricultural lowlands: a landscape-scale, genetic survey. Mammal Research, 2016, 61, 327-335.	0.6	9
4903	Polymorphism in Mitochondrial Coding Regions of Mediterranean Loggerhead Turtles: Evolutionary Relevance and Structural Effects. Physiological and Biochemical Zoology, 2016, 89, 473-486.	0.6	10
4904	New insights on the history of canids in Oceania based on mitochondrial and nuclear data. Genetica, 2016, 144, 553-565.	0.5	49
4905	Dynamic changes of <i>Plasmodium vivax</i> population structure in South Korea. Infection, Genetics and Evolution, 2016, 45, 90-94.	1.0	9
4906	Integrative approach revises the frequently misidentified species of <i>Sardinella</i> (Clupeidae) of the Indo-West Pacific Ocean. Journal of Fish Biology, 2016, 89, 2282-2305.	0.7	17
4907	Comparative phylogeography of the endemic Japanese weasel (<i>Mustela itatsi</i>) and the continental Siberian weasel (<i>Mustela sibirica</i>) revealed by complete mitochondrial genome sequences. Biological Journal of the Linnean Society, 2016, , .	0.7	4
4908	Evolutionary rates and genetic diversities of mixed potyviruses in <i>Narcissus</i> . Infection, Genetics and Evolution, 2016, 45, 213-223.	1.0	23
4909	Dispersal and genetic structure of <i>Boccardia polybranchia</i> and <i>Polydora hoplura</i> (Annelida: Tj ETQq0 0 0 rgBT /Overclock 10 Tf,50 182 To	1.7	21
4910	Characteristics of <i>Vibrio parahaemolyticus</i> isolates obtained from crayfish (<i>Procambarus clarkii</i>) in freshwater. International Journal of Food Microbiology, 2016, 238, 132-138.	2.1	37
4911	Phylogenetic relationships of Eurasian Nuthatches (<i>Sitta europaea</i> Linnaeus, 1758) from the Alborz and Zagros Mountains, Iran. Zoology in the Middle East, 2016, 62, 217-226.	0.2	9
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4913	Post-glacial colonization of Europe by the wood mouse, <i>Apodemus sylvaticus</i> : evidence of a northern refugium and dispersal with humans. <i>Biological Journal of the Linnean Society</i> , 2016, , .	0.7	16
4914	DNA barcoding and evolutionary lineage of 15 insect pests of horticultural crops in South India. <i>Karbala International Journal of Modern Science</i> , 2016, 2, 156-168.	0.5	15
4915	Occasional recombination of a selfish X-chromosome may permit its persistence at high frequencies in the wild. <i>Journal of Evolutionary Biology</i> , 2016, 29, 2229-2241.	0.8	18
4916	Strong neutral genetic differentiation in a host, but not in its parasite. <i>Infection, Genetics and Evolution</i> , 2016, 44, 261-271.	1.0	7
4917	Comprehensive investigation of nucleotide diversity in yaks. <i>Animal Genetics</i> , 2016, 47, 752-755.	0.6	9
4918	Drift-driven evolution of electric signals in a Neotropical knifefish. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 2134-2144.	1.1	18
4919	Selective sweep of <i>Wolbachia</i> and parthenogenetic host genomes – the example of the weevil <i>Eusomus ovulum</i> . <i>Insect Molecular Biology</i> , 2016, 25, 701-711.	1.0	19
4920	Divergence maintained by climatic selection despite recurrent gene flow: a case study of <i>Castanopsis carlesii</i> (Fagaceae). <i>Molecular Ecology</i> , 2016, 25, 4580-4592.	2.0	28
4921	Genetic diversity and evolutionary history of the <i>Schizothorax</i> species complex in the Lancang River (upper Mekong). <i>Ecology and Evolution</i> , 2016, 6, 6023-6036.	0.8	16
4922	Population structure and selection pressure analysis among Sugarcane yellow leaf virus isolates based on PO and P1 sequences. <i>Tropical Plant Pathology</i> , 2016, 41, 237-245.	0.8	2
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4925	The Argonaute-binding platform of <i>NRPE1</i> evolves through modulation of intrinsically disordered repeats. <i>New Phytologist</i> , 2016, 212, 1094-1105.	3.5	16
4926	Genetic variability and recombination analysis of the coat protein gene of Strawberry mild yellow edge virus. <i>Australasian Plant Pathology</i> , 2016, 45, 401-409.	0.5	5
4927	Pleistocene diversification in Morocco and recent demographic expansion in the Mediterranean pond turtle <i>Mauremys leprosa</i> . <i>Biological Journal of the Linnean Society</i> , 2016, 119, 943-959.	0.7	32
4928	Ecological specialization and morphological diversification in Greater Antillean boas. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1882-1895.	1.1	24
4929	Barcoding lichen-forming fungi using 454 pyrosequencing is challenged by artifactual and biological sequence variation. <i>Genome</i> , 2016, 59, 685-704.	0.9	32
4930	Gene loss/retention and evolutionary pattern of ascorbic acid biosynthesis and recycling genes in <i>Brassica rapa</i> following whole genome triplication. <i>Genes and Genomics</i> , 2016, 38, 1129-1143.	0.5	2

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4931	Low genetic diversity and lack of genetic structure in the giant jellyfish <i>Nemopilema nomurai</i> in Chinese coastal waters. <i>Marine Biology Research</i> , 2016, 12, 769-775.	0.3	5
4932	Historical environmental change in Africa drives divergence and admixture of <i>Aedes aegypti</i> mosquitoes: a precursor to successful worldwide colonization?. <i>Molecular Ecology</i> , 2016, 25, 4337-4354.	2.0	52
4933	Some limitations in the use of the mitochondrial DNA <i>cytb</i> gene as a molecular marker for phylogenetic and population-genetic studies by the example of the <i>Apodemus</i> genus. <i>Russian Journal of Genetics: Applied Research</i> , 2016, 6, 84-90.	0.4	2
4934	Revisiting the phosphatidylethanolamine-binding protein (PEBP) gene family reveals cryptic <i>FLOWERING LOCUS T</i> gene homologs in gymnosperms and sheds new light on functional evolution. <i>New Phytologist</i> , 2016, 212, 730-744.	3.5	77
4935	Genomic location and expression analysis of expansin gene family reveals the evolutionary and functional significance in <i>Triticum aestivum</i> . <i>Genes and Genomics</i> , 2016, 38, 1021-1030.	0.5	12
4936	Revision of the water-holding frogs, <i>Cyclorana platycephala</i> (Anura: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 467) 451.	0.2	8
4937	Cryptic <i>Eimeria</i> genotypes are common across the southern but not northern hemisphere. <i>International Journal for Parasitology</i> , 2016, 46, 537-544.	1.3	66
4938	Comparative phylogeography of two symbiotic dorvilleid polychaetes (<i>Iphitime</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 467 Zoological Journal of the Linnean Society, 2016, , .	1.0	4
4939	Receptors are affected by selection with each <i>Bacillus thuringiensis israelensis</i> Cry toxin but not with the full Bti mixture in <i>Aedes aegypti</i> . <i>Infection, Genetics and Evolution</i> , 2016, 44, 218-227.	1.0	17
4940	Vivid molecular divergence over volcanic remnants: the phylogeography of <i>Megadromus guerinii</i> on Banks Peninsula, New Zealand. <i>New Zealand Journal of Zoology</i> , 2016, 43, 246-257.	0.6	1
4941	Genetic diversity and population structure of <i>Sorghum mosaic virus</i> infecting <i>Sorghum accharum</i> spp. hybrids. <i>Annals of Applied Biology</i> , 2016, 169, 398-407.	1.3	24
4942	Genetic polymorphism, haplotype distribution, and phylogeny of <i>Daphnia</i> (Cladocera: Anomopoda) species from the water bodies of russia as inferred from the 16S mtDNA gene sequencing. <i>Russian Journal of Genetics</i> , 2016, 52, 585-596.	0.2	13
4943	Evolutionary Dynamics of the Gametologous CTNNB1 Gene on the Z and W Chromosomes of Snakes. <i>Journal of Heredity</i> , 2016, 108, esw074.	1.0	18
4944	Exploiting Bacterial Whole-Genome Sequencing Data for Evaluation of Diagnostic Assays: <i>Campylobacter</i> Species Identification as a Case Study. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2882-2890.	1.8	14
4945	DNA barcoding, species-specific PCR and real-time PCR techniques for the identification of six <i>Tribolium</i> pests of stored products. <i>Scientific Reports</i> , 2016, 6, 28494.	1.6	16
4946	High expression of new genes in trochophore enlightening the ontogeny and evolution of trochozoans. <i>Scientific Reports</i> , 2016, 6, 34664.	1.6	32
4947	Genetic diversity and population structure of <i>Lactobacillus delbrueckii</i> subspecies <i>bulgaricus</i> isolated from naturally fermented dairy foods. <i>Scientific Reports</i> , 2016, 6, 22704.	1.6	16
4948	Past climate changes facilitated homoploid speciation in three mountain spiny fescues (<i>Festuca</i> ,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 467 1.6 31	1.6	31

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4949	Directional Selection from Host Plants Is a Major Force Driving Host Specificity in Magnaporthe Species. <i>Scientific Reports</i> , 2016, 6, 25591.	1.6	62
4950	Genome-wide identification and expression analysis of the IQD gene family in moso bamboo (<i>Phyllostachys edulis</i>). <i>Scientific Reports</i> , 2016, 6, 24520.	1.6	64
4951	Taxonomic position of Chinese voles of the tribe Arvicolini and the description of 2 new species from Xizang, China. <i>Journal of Mammalogy</i> , 2017, 98, gyw170.	0.6	15
4952	Inferences of population structure and demographic history for <i>Taxodium distichum</i> , a coniferous tree in North America, based on amplicon sequencing analysis. <i>American Journal of Botany</i> , 2016, 103, 1937-1949.	0.8	2
4953	Single nucleotide polymorphisms in two GID1 orthologs associate with growth and wood property traits in <i>Populus tomentosa</i> . <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	1
4954	Population genetic structure and post-LGM expansion of the plant bug <i>Nesidiocoris tenuis</i> (Hemiptera: Tj ETQq1 1.0,784314 rgBT /Over	1.6	16
4955	Lack of diversity at innate immunity Toll-like receptor genes in the Critically Endangered White-winged Flufftail (<i>Sarothrura ayresi</i>). <i>Scientific Reports</i> , 2016, 6, 36757.	1.6	19
4956	<i>Marphysa</i> (Eunicidae, polychaete, Annelida) species of the Sanguinea group from Australia, with comments on pseudo-cryptic species. <i>Invertebrate Biology</i> , 2016, 135, 328-344.	0.3	22
4957	Two species of Southeast Asian cats in the genus <i>Catopuma</i> with diverging histories: an island endemic forest specialist and a widespread habitat generalist. <i>Royal Society Open Science</i> , 2016, 3, 160350.	1.1	17
4958	Pleistocene refugia and their effects on the phylogeography and genetic structure of the wolf spider <i>Pardosa sierra</i> (Araneae: Lycosidae) on the Baja California Peninsula. <i>Journal of Arachnology</i> , 2016, 44, 367-379.	0.3	9
4959	Evidence of birth-and-death evolution of 5S rRNA gene in <i>Channa</i> species (Teleostei, Perciformes). <i>Genetica</i> , 2016, 144, 723-732.	0.5	8
4960	Rapid postglacial diversification and long-term stasis within the songbird genus <i>Junco</i> : phylogeographic and phylogenomic evidence. <i>Molecular Ecology</i> , 2016, 25, 6175-6195.	2.0	47
4961	Spatial pattern of genetic diversity and selection in the MHC class II DRB of three Neotropical bat species. <i>BMC Evolutionary Biology</i> , 2016, 16, 229.	3.2	12
4962	Phylogeography of the heavily poached African common pangolin (<i>Pholidota</i> , <i>Manis</i>) Tj ETQq1 1.0,784314 rgBT /Over	2.0	39
4963	Unravelling population genetic structure with mitochondrial DNA in a notional panmictic coastal crab species: sample size makes the difference. <i>BMC Evolutionary Biology</i> , 2016, 16, 150.	3.2	35
4964	Genotype diversity in the honey bee parasite <i>Nosema ceranae</i> : multi-strain isolates, cryptic sex or both?. <i>BMC Evolutionary Biology</i> , 2016, 16, 216.	3.2	11
4965	Spatial Patterns of bphA Gene Diversity Reveal Local Adaptation of Microbial Communities to PCB and PAH Contaminants. <i>Microbial Ecology</i> , 2016, 72, 559-570.	1.4	12
4966	Contrasting patterns of genetic diversity and spatial structure in an invasive symbiont-host association. <i>Biological Invasions</i> , 2016, 18, 3175-3191.	1.2	7

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4968	Characterization of the complete mitochondrial genome of <i>Phodopus roborovskii</i> (Rodentia: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Ecology, 2016, 69, 226-235.	0.6	6
4969	High genetic connectivity among estuarine populations of the riverbream <i>Acanthopagrus vagus</i> along the southern African coast. <i>Estuarine, Coastal and Shelf Science</i> , 2016, 183, 82-94.	0.9	5
4970	<i>Hungarosoma bokori</i> Verhoeff, 1928 (Diplopoda: Chordeumatida): new insights into its taxonomy, systematics, molecular genetics, biogeography and ecology. <i>Zootaxa</i> , 2016, 4178, 234-256.	0.2	5
4971	High genetic diversity in the offshore island populations of the tephritid fruit fly <i>Bactrocera dorsalis</i> . <i>BMC Ecology</i> , 2016, 16, 46.	3.0	7
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4973	Phylogenetic relationships among species of <i>Tamarix</i> (Tamaricaceae) in China. <i>Biochemical Systematics and Ecology</i> , 2016, 69, 213-221.	0.6	7
4974	Assessment of nuclear and mitochondrial genes in precise identification and analysis of genetic polymorphisms for the evaluation of <i>Leishmania</i> parasites. <i>Infection, Genetics and Evolution</i> , 2016, 46, 33-41.	1.0	28
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4976	Genetic Diversity in the mtDNA control region and population structure of <i>Chrysichthys nigrodigitatus</i> from selected Nigerian rivers: Implications for conservation and aquaculture. <i>Archives of Polish Fisheries</i> , 2016, 24, 85-97.	0.6	8
4977	Genomics reveals historic and contemporary transmission dynamics of a bacterial disease among wildlife and livestock. <i>Nature Communications</i> , 2016, 7, 11448.	5.8	85
4978	Tectonic and climatic impacts on the biota within the Red River Fault, evidence from phylogeography of <i>Cycas dolichophylla</i> (Cycadaceae). <i>Scientific Reports</i> , 2016, 6, 33540.	1.6	25
4979	Low genetic diversity and recent demographic expansion in the red starfish <i>Echinaster sepositus</i> (Retzius 1816). <i>Scientific Reports</i> , 2016, 6, 33269.	1.6	22
4980	Use of molecular and environmental analyses for integrated in situ and ex situ conservation: The case of the Mexican prairie dog. <i>Biological Conservation</i> , 2016, 204, 284-295.	1.9	9
4981	Comparative phylogeography of African fruit bats (Chiroptera, Pteropodidae) provide new insights into the outbreak of Ebola virus disease in West Africa, 2014–2016. <i>Comptes Rendus - Biologies</i> , 2016, 339, 517-528.	0.1	22
4982	Speciation with Gene Flow in North American <i>Myotis</i> Bats. <i>Systematic Biology</i> , 2017, 66, syw100.	2.7	50
4983	Phylogeny of <i>Fomitopsis pinicola</i> : a species complex. <i>Mycologia</i> , 2016, 108, 925-938.	0.8	20
4984	Molecular variation and expansion of a rice black-streaked dwarf virus population based on analysis of segment 1 in Jining, China. <i>Archives of Virology</i> , 2016, 161, 3435-3443.	0.9	2

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4986	The complex evolutionary history of big-eared horseshoe bats (<i>Rhinolophus macrotis</i> complex): insights from genetic, morphological and acoustic data. <i>Scientific Reports</i> , 2016, 6, 35417.	1.6	17
4987	Use of DNA barcoding to distinguish the malaria vector <i>Anopheles neivai</i> in Colombia. <i>Zootaxa</i> , 2016, 4175, 377-389.	0.2	10
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4989	Contrasting patterns of selection between <i>MHC</i> I and <i>MHC</i> II across populations of Humboldt and Magellanic penguins. <i>Ecology and Evolution</i> , 2016, 6, 7498-7510.	0.8	13
4990	Evolutionary history of subtropical evergreen broad-leaved forest in Yunnan Plateau and adjacent areas: an insight from <i>Quercus schottkyana</i> (Fagaceae). <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	25
4991	Phylogenetic and morphometric relationships between two species of genus <i>Auxis</i> from the South China Sea and Java Sea. <i>Acta Oceanologica Sinica</i> , 2016, 35, 76-82.	0.4	1
4992	Characterization and phylogenetic analysis of the complete mitogenome of <i>Allactaga sibirica</i> (Rodentia: Dipodidae). <i>Biochemical Systematics and Ecology</i> , 2016, 69, 195-203.	0.6	3
4993	Drainage isolation and climate change-driven population expansion shape the genetic structures of <i>Tuber indicum</i> complex in the Hengduan Mountains region. <i>Scientific Reports</i> , 2016, 6, 21811.	1.6	29
4994	Colonization and diversification of the <i>Euphorbia</i> species (sect. <i>Aphyllis</i> subsect. <i>Macaronesicae</i>) on the Canary Islands. <i>Scientific Reports</i> , 2016, 6, 34454.	1.6	13
4995	Mixed-Up Sex Chromosomes: Identification of Sex Chromosomes in the X1X1X2X2/X1X2Y System of the Legless Lizards of the Genus <i>Lialis</i> (Squamata: Gekkotata: Pygopodidae). <i>Cytogenetic and Genome Research</i> , 2016, 149, 282-289.	0.6	25
4996	Genetic analysis of oriental fruit fly, <i>Bactrocera dorsalis</i> (Diptera: Tephritidae) populations based on mitochondrial <i>cox1</i> and <i>nad1</i> gene sequences from India and other Asian countries. <i>Genetica</i> , 2016, 144, 611-623.	0.5	16
4997	Population genetic structure and demographic history of <i>Medicago ruthenica</i> (Fabaceae) on the Qinghai-Tibetan Plateau based on nuclear ITS and chloroplast markers. <i>Biochemical Systematics and Ecology</i> , 2016, 69, 204-212.	0.6	6
4998	DNA barcoding reveals that the common cupped oyster in Taiwan is the Portuguese oyster <i>Crassostrea angulata</i> (Ostreoida; Ostreidae), not <i>C. gigas</i> . <i>Scientific Reports</i> , 2016, 6, 34057.	1.6	32
4999	Population Genetics of Overwintering Monarch Butterflies, <i>Danaus plexippus</i> (Linnaeus), from Central Mexico Inferred from Mitochondrial DNA and Microsatellite Markers. <i>Journal of Heredity</i> , 2017, 108, esw071.	1.0	24
5000	Mutations in two pollen self-incompatibility factors in geographically marginal populations of <i>Solanum habrochaites</i> impact mating system transitions and reproductive isolation. <i>American Journal of Botany</i> , 2016, 103, 1847-1861.	0.8	26
5001	Emergence and evolution of inter-specific segregating retrocopies in cynomolgus monkey (<i>Macaca</i>). <i>PLoS ONE</i> , 2017, 12, e0170000.	1.6	2
5002	Genomic analysis reveals hidden biodiversity within colugos, the sister group to primates. <i>Science Advances</i> , 2016, 2, e1600633.	4.7	64

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5004	Colonial ascidian <i>Didemnum vexillum</i> Kott, 2002 is an alien species in Peter the Great Bay (Sea of Japan). <i>Russian Journal of Biological Invasions</i> , 2016, 7, 237-246.	0.2	11
5005	Occurrence of the Portuguese oyster <i>Crassostrea angulata</i> (Lamarck, 1819) along the coast of Shikoku Island, Japan. <i>Plankton and Benthos Research</i> , 2016, 11, 71-74.	0.2	4
5006	Limited Genetic Variability Among American Isolates of <i>Grapevine virus E</i> from <i>Vitis</i> spp.. <i>Plant Disease</i> , 2016, 100, 159-163.	0.7	6
5007	Molecular Evolution of the <i>Yersinia</i> Major Outer Membrane Protein C (OmpC). <i>Evolutionary Bioinformatics</i> , 2016, 12, EBO.S40346.	0.6	4
5008	Three chromosomal rearrangements promote genomic divergence between migratory and stationary ecotypes of Atlantic cod. <i>Scientific Reports</i> , 2016, 6, 23246.	1.6	128
5009	Inversions and adaptation to the plant toxin ouabain shape DNA sequence variation within and between chromosomal inversions of <i>Drosophila subobscura</i> . <i>Scientific Reports</i> , 2016, 6, 23754.	1.6	16
5010	Romanian wild boars and Mangalitza pigs have a European ancestry and harbour genetic signatures compatible with past population bottlenecks. <i>Scientific Reports</i> , 2016, 6, 29913.	1.6	16
5011	Contrasted phylogeographic patterns on mitochondrial DNA of shallow and deep brittle stars across the Atlantic-Mediterranean area. <i>Scientific Reports</i> , 2016, 6, 32425.	1.6	35
5012	Differentiation in putative male sex pheromone components across and within populations of the African butterfly <i>Bicyclus anynana</i> as a potential driver of reproductive isolation. <i>Ecology and Evolution</i> , 2016, 6, 6064-6084.	0.8	10
5013	Phylogeographic structure in long-tailed voles (Rodentia: Arvicolinae) belies the complex Pleistocene history of isolation, divergence, and recolonization of Northwest North America's fauna. <i>Ecology and Evolution</i> , 2016, 6, 6633-6647.	0.8	9
5014	Population demographic history of a temperate shrub, <i>Rhododendron weyrichii</i> (Ericaceae), on continental islands of Japan and South Korea. <i>Ecology and Evolution</i> , 2016, 6, 8800-8810.	0.8	15
5015	Phylogeography reveals an ancient cryptic radiation in East-Asian tree frogs (<i>Hyla japonica</i> group) and complex relationships between continental and island lineages. <i>BMC Evolutionary Biology</i> , 2016, 16, 253.	3.2	42
5016	Genome-wide characterization and expression analysis of MYB transcription factors in <i>Gossypium hirsutum</i> . <i>BMC Genetics</i> , 2016, 17, 129.	2.7	104
5017	Genetic diversity of the Tibetan antelope (<i>Pantholops hodgsonii</i>) population of Ladakh, India, its relationship with other populations and conservation implications. <i>BMC Research Notes</i> , 2016, 9, 477.	0.6	9
5018	Insights on the origin of invasive copepods colonizing Basque estuaries; a DNA barcoding approach. <i>Marine Biodiversity Records</i> , 2016, 9, .	1.2	14
5019	Several steps of lateral gene transfer followed by events of "birth-and-death" evolution shaped a fungal sorbicillinoid biosynthetic gene cluster. <i>BMC Evolutionary Biology</i> , 2016, 16, 269.	3.2	33
5020	Genomic epidemiology of Lineage 4 <i>Mycobacterium tuberculosis</i> subpopulations in New York City and New Jersey, 1999-2009. <i>BMC Genomics</i> , 2016, 17, 947.	1.2	13

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5023	Complete plastid genome of Eriobotrya japonica (Thunb.) Lindl and comparative analysis in Rosaceae. SpringerPlus, 2016, 5, 2036.	1.2	13
5024	Genomewide association analysis for awn length linked to the seed shattering gene qSH1 in rice. Journal of Genetics, 2016, 95, 639-646.	0.4	10
5025	Evidence of functional divergence in MSP7 paralogous proteins: a molecular-evolutionary and phylogenetic analysis. BMC Evolutionary Biology, 2016, 16, 256.	3.2	17
5026	Mitochondrial genome of the <i>Melophus lathami</i> . Mitochondrial DNA Part B: Resources, 2016, 1, 929-930.	0.2	1
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5028	Maternal and paternal genetic diversity of ancient sheep in Estonia from the Late Bronze Age to the post-medieval period and comparison with other regions in Eurasia. Animal Genetics, 2016, 47, 208-218.	0.6	22
5029	Barcoding, population structure, and demographic history of <i>Protoplasma longifila</i> associated with the Andes. Entomologia Experimentalis Et Applicata, 2016, 158, 217-227.	0.7	7
5030	Evolutionary distinctiveness and historical decline in genetic diversity in the Seychelles Black Parrot <i>Coracopsis nigra barklyi</i> . Ibis, 2016, 158, 380-394.	1.0	4
5031	Trans-equatorial range of a land bird lineage (Aves: Rallidae) from tropical forests to subantarctic grasslands. Journal of Avian Biology, 2016, 47, 219-226.	0.6	9
5032	Lack of haplotype structuring for two candidate genes for trypanotolerance in cattle. Journal of Animal Breeding and Genetics, 2016, 133, 105-114.	0.8	11
5033	The influence of geological movements on the population differentiation of <i>Biston panterinaria</i> (Lepidoptera: Geometridae). Journal of Biogeography, 2016, 43, 691-702.	1.4	16
5034	Pre-Pleistocene geological events shaping diversification and distribution of primitively segmented spiders on East Asian margins. Journal of Biogeography, 2016, 43, 1004-1019.	1.4	27
5035	A zoogeographical boundary between the Palaearctic and Sino-Japanese realms documented by consistent north/south phylogeographical divergences in three woodland birds in eastern China. Journal of Biogeography, 2016, 43, 2099-2112.	1.4	12
5036	The complete chloroplast genome of <i>Gracilariopsis lemaneiformis</i> (Rhodophyta) gives new insight into the evolution of family Gracilariaceae. Journal of Phycology, 2016, 52, 441-450.	1.0	43
5037	Species from the <i>Colletotrichum acutatum</i> , <i>Colletotrichum boninense</i> and <i>Colletotrichum gloeosporioides</i> species complexes associated with tree tomato and mango crops in Colombia. Plant Pathology, 2016, 65, 227-237.	1.2	42
5038	Cytoplasmic diversity, phylogenetic relationships and molecular evolution of Tunisian Citrus species as inferred from mutational events and pseudogene of chloroplast trnL-trnF spacer. Biochemical Systematics and Ecology, 2016, 67, 65-73.	0.6	1

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5040	Lineage isolation in the face of active gene flow in the coastal plant wild radish is reinforced by differentiated vernalisation responses. <i>BMC Evolutionary Biology</i> , 2016, 16, 84.	3.2	11
5041	Evidence for adaptation of porcine Toll-like receptors. <i>Immunogenetics</i> , 2016, 68, 179-189.	1.2	7
5042	The complete mitochondrial genome of <i>Gastrothylax crumenifer</i> (Gastrothylacidae, Trematoda) and comparative analyses with selected trematodes. <i>Parasitology Research</i> , 2016, 115, 2489-2497.	0.6	13
5043	Genetic population structure of <i>Crystallichthys matsushimae</i> (Cottoidei: Liparidae) with comments on color variation. <i>Ichthyological Research</i> , 2016, 63, 370-381.	0.5	7
5044	Identification and genetic diversity of two invasive <i>Pissodes</i> spp. Germar (Coleoptera: Curculionidae) in their introduced range in the southern hemisphere. <i>Biological Invasions</i> , 2016, 18, 2283-2297.	1.2	8
5045	Molecular characterization and phylogenetic analysis of Wx genes from three <i>Taeniatherum</i> diploid species. <i>Biologia Plantarum</i> , 2016, 60, 505-512.	1.9	5
5046	Genetic diversity of Guangxi chicken breeds assessed with microsatellites and the mitochondrial DNA D-loop region. <i>Molecular Biology Reports</i> , 2016, 43, 415-425.	1.0	19
5047	Update of genetic information for the white-clawed crayfish in Spain, with new insights into its population genetics and origin. <i>Organisms Diversity and Evolution</i> , 2016, 16, 533-547.	0.7	9
5049	The population history of <i>Garra orientalis</i> (Teleostei: Cyprinidae) using mitochondrial DNA and microsatellite data with approximate Bayesian computation. <i>BMC Evolutionary Biology</i> , 2016, 16, 73.	3.2	48
5050	R-gene variation across <i>Arabidopsis lyrata</i> subspecies: effects of population structure, selection and mating system. <i>BMC Evolutionary Biology</i> , 2016, 16, 93.	3.2	23
5051	Contrasting evolutionary histories of the legless lizards slow worms (<i>Anguis</i>) shaped by the topography of the Balkan Peninsula. <i>BMC Evolutionary Biology</i> , 2016, 16, 99.	3.2	46
5052	Genetic diversity and natural selection in the rhoptry-associated protein 1 (RAP-1) of recent <i>Plasmodium knowlesi</i> clinical isolates from Malaysia. <i>Malaria Journal</i> , 2016, 15, 62.	0.8	11
5053	The nuclear elongation factor-1 β gene: a promising marker for phylogenetic studies of Triatominae (Hemiptera: Reduviidae). <i>Infection, Genetics and Evolution</i> , 2016, 43, 274-280.	1.0	6
5054	Parallel Mitogenome Sequencing Alleviates Random Rooting Effect in Phylogeography. <i>Genome Biology and Evolution</i> , 2016, 8, 1267-1278.	1.1	33
5055	Capturing the Phylogeny of Holometabola with Mitochondrial Genome Data and Bayesian Site-Heterogeneous Mixture Models. <i>Genome Biology and Evolution</i> , 2016, 8, 1411-1426.	1.1	154
5056	Evolution and phylogeographic dissemination of endemic porcine picornaviruses in Vietnam. <i>Virus Evolution</i> , 2016, 2, vew001.	2.2	7
5057	Widespread green algae <i>Chlorella</i> and <i>Stichococcus</i> exhibit polar-temperate and tropical-temperate biogeography. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw122.	1.3	68

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5059	Testing the Effects of Barriers on the Genetic Connectivity in <i>Podocnemis erythrocephala</i> (Red-Headed Amazon River Turtle): Implications for Management and Conservation. <i>Chelonian Conservation and Biology</i> , 2016, 15, 12-22.	0.1	8
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5061	Species divergence in <i>Iris</i> series <i>Lactea</i> (Iridaceae) in Russia and adjacent countries based on chloroplast DNA sequence data. <i>Russian Journal of Genetics</i> , 2016, 52, 507-516.	0.2	5
5062	Genetic characterization of human bocavirus among children with severe acute respiratory infection in China. <i>Journal of Infection</i> , 2016, 73, 155-163.	1.7	8
5063	Molecular polymorphism of MHC-DRB gene and genetic diversity analysis of captive forest musk deer (<i>Moschus berezovskii</i>). <i>Biochemical Systematics and Ecology</i> , 2016, 67, 37-43.	0.6	3
5064	Postmating Reproductive isolation between strains of <i>Drosophila willistoni</i> . <i>Fly</i> , 2016, 10, 162-171.	0.9	9
5065	Widespread interspecies homologous recombination reveals reticulate evolution within the genus <i>Streptomyces</i> . <i>Molecular Phylogenetics and Evolution</i> , 2016, 102, 246-254.	1.2	29
5066	A Worldwide Map of <i>Plasmodium falciparum</i> K13-Propeller Polymorphisms. <i>New England Journal of Medicine</i> , 2016, 374, 2453-2464.	13.9	449
5067	A new species of <i>Hemiphyllodactylus</i> Bleeker, 1860 (Squamata: Gekkonidae) from Guizhou, China. <i>Zootaxa</i> , 2016, 4117, 543.	0.2	12
5068	Cryptic diversity in a chirally variable land snail. <i>Italian Journal of Zoology</i> , 2016, 83, 351-363.	0.6	7
5069	Duplication of <i>OsHAP</i> family genes and their association with heading date in rice. <i>Journal of Experimental Botany</i> , 2016, 67, 1759-1768.	2.4	34
5070	Landscape genetic structure and evolutionary genetics of insecticide resistance gene mutations in <i>Anopheles sinensis</i> . <i>Parasites and Vectors</i> , 2016, 9, 228.	1.0	40
5071	<i>Triticum mosaic virus</i> exhibits limited population variation yet shows evidence of parallel evolution after replicated serial passage in wheat. <i>Virology</i> , 2016, 492, 92-100.	1.1	2
5072	Genetic structure of Patagonian toothfish populations from otolith DNA. <i>Antarctic Science</i> , 2016, 28, 347-360.	0.5	13
5073	Low genetic differentiation between Greenlandic and Siberian Sanderling populations implies a different phylogeographic history than found in Red Knots. <i>Journal of Ornithology</i> , 2016, 157, 325-332.	0.5	16
5074	Molecular analyses of H3N2 canine influenza viruses isolated from Korea during 2013-2014. <i>Virus Genes</i> , 2016, 52, 204-217.	0.7	10
5075	Genetic variation and phylogenetic relationships among <i>Rehmannia</i> (Scrophulariaceae) species as revealed by a novel set of single-copy nuclear gene markers. <i>Biochemical Systematics and Ecology</i> , 2016, 66, 43-49.	0.6	4

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5077	Understanding the evolutionary history of a high Andean endemic: the Ecuadorian hillstar (<i>Oreotrochilus chimborazo</i>). <i>Neotropical Biodiversity</i> , 2016, 2, 37-50.	0.2	4
5078	Connectivity of the squat lobsters <i>Shinkaia crosnieri</i> (Crustacea: Decapoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667 17-31.	0.4	24
5079	Evolutionary study of leporid CD4 reveals a hotspot of genetic variability within the D2 domain. <i>Immunogenetics</i> , 2016, 68, 477-482.	1.2	4
5080	Population genetics structure of <i>Plasmodium vivax</i> circumsporozoite protein during the elimination process in low and unstable malaria transmission areas, southeast of Iran. <i>Acta Tropica</i> , 2016, 160, 23-34.	0.9	11
5081	MHC class III polymorphisms and their association with resistance/susceptibility to Singapore grouper iridovirus (SGIV) in orange-spotted grouper, <i>Epinephelus coioides</i> . <i>Aquaculture</i> , 2016, 462, 10-16.	1.7	14
5082	Anonymous nuclear markers data supporting species tree phylogeny and divergence time estimates in a cactus species complex in South America. <i>Data in Brief</i> , 2016, 6, 456-460.	0.5	3
5083	Evolutionary Scenarios Associated with the <i>Pteronotus parnellii</i> Cryptic Species-Complex (Chiroptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 667	0.2	11
5084	Variation in the number of nucleoli and incomplete homogenization of 18S ribosomal DNA sequences in leaf cells of the cultivated Oriental ginseng (<i>Panax ginseng</i> Meyer). <i>Journal of Ginseng Research</i> , 2016, 40, 176-184.	3.0	9
5085	Genetic characterisation of the endangered Gochu Asturcelta pig breed using microsatellite and mitochondrial markers: Insights for the composition of the Iberian native pig stock. <i>Livestock Science</i> , 2016, 187, 162-167.	0.6	9
5086	<i>Theileria lestoquardi</i> displays reduced genetic diversity relative to sympatric <i>Theileria annulata</i> in Oman. <i>Infection, Genetics and Evolution</i> , 2016, 43, 297-306.	1.0	16
5087	Allelic variation on DcAOX1 gene in carrot (<i>Daucus carota</i> L.): An interesting simple sequence repeat in a highly variable intron. <i>Plant Gene</i> , 2016, 5, 49-55.	1.4	25
5088	Molecular characterization of <i>Aedes aegypti</i> (L.) (Diptera: Culicidae) of Easter Island based on analysis of the mitochondrial ND4 gene. <i>Revista Brasileira De Entomologia</i> , 2016, 60, 186-187.	0.1	1
5089	High-level phylogeographic structuring of <i>Neoleucinodes elegantalis</i> GuenÃ©e (Lepidoptera,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 667	0.1	1
5090	The Evolutionary Relationships between Endosymbiotic Green Algae of <i>Paramecium bursaria</i>; Syngens Originating from Different Geographical Locations. <i>Folia Biologica</i> , 2016, 64, 47-54.	0.1	12
5091	Cytoplasmic DNA disclose high nucleotide diversity and different phylogenetic pattern in <i>Taihangia rupestris</i> Yu et Li. <i>Biochemical Systematics and Ecology</i> , 2016, 66, 201-208.	0.6	3
5092	Four-locus phylogeny of <i>Fusarium avenaceum</i> and related species and their species-specific identification based on partial phosphate permease gene sequences. <i>International Journal of Food Microbiology</i> , 2016, 225, 27-37.	2.1	24
5093	The complete chloroplast genome sequence of <i>Abies nephrolepis</i> (Pinaceae: Abietoideae). <i>Journal of Asia-Pacific Biodiversity</i> , 2016, 9, 245-249.	0.2	16

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5095	The worm has turned: Behavioural drivers of reproductive isolation between cryptic lineages. <i>Soil Biology and Biochemistry</i> , 2016, 98, 11-17.	4.2	16
5096	Molecular phylogeny and species delimitation within the ciliate genus <i>Spirostomum</i> (Ciliophora). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6</i> <i>Phylogenetics and Evolution</i> , 2016, 102, 128-144.	1.2	43
5097	Potential Impact of Mediterranean Aquaculture on the Wild Predatory Bluefish. <i>Marine and Coastal Fisheries</i> , 2016, 8, 92-99.	0.6	5
5098	Untangling a species complex of arid zone grasses (<i>Triodia</i>) reveals patterns congruent with co-occurring animals. <i>Molecular Phylogenetics and Evolution</i> , 2016, 101, 142-162.	1.2	20
5099	Evolution of CCL11: genetic characterization in lagomorphs and evidence of positive and purifying selection in mammals. <i>Innate Immunity</i> , 2016, 22, 336-343.	1.1	6
5100	Ancient pathogen-driven adaptation triggers increased susceptibility to non-celiac wheat sensitivity in present-day European populations. <i>Genes and Nutrition</i> , 2016, 11, 15.	1.2	5
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5105	Evidence of new species for malaria vector <i>Anopheles nuneztovari</i> sensu lato in the Brazilian Amazon region. <i>Malaria Journal</i> , 2016, 15, 205.	0.8	24
5106	Global genetic diversity of the <i>Plasmodium vivax</i> transmission-blocking vaccine candidate Pvs48/45. <i>Malaria Journal</i> , 2016, 15, 202.	0.8	16
5107	Clustering and genetic differentiation of the normocyte binding protein (nbp _{xa}) of <i>Plasmodium knowlesi</i> clinical isolates from Peninsular Malaysia and Malaysia Borneo. <i>Malaria Journal</i> , 2016, 15, 241.	0.8	29
5108	Genetic diversity and population genetics of the warble flies <i>Hypoderma bovis</i> and <i>H. sinense</i> in Qinghai Province, China. <i>Parasites and Vectors</i> , 2016, 9, 145.	1.0	5
5109	Large genomic differences between <i>Moraxella bovoculi</i> isolates acquired from the eyes of cattle with infectious bovine keratoconjunctivitis versus the deep nasopharynx of asymptomatic cattle. <i>Veterinary Research</i> , 2016, 47, 31.	1.1	38
5110	Analysis of virus structure variants in before- and after-thermotherapy-treated apple plants. <i>Journal of Horticultural Science and Biotechnology</i> , 2016, 91, 536-541.	0.9	0
5111	Genetic variability in captive populations of the stingless bee <i>Tetragonisca angustula</i> . <i>Genetica</i> , 2016, 144, 397-405.	0.5	7

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5113	Molecular characterization and phylogenetic analysis of <i>Fasciola gigantica</i> from western Java, Indonesia. <i>Parasitology International</i> , 2016, 65, 424-427.	0.6	23
5114	Differential introgression suggests candidate beneficial and barrier loci between two parapatric subspecies of Pearson's horseshoe bat <i>Rhinolophus pearsoni</i> . <i>Environmental Epigenetics</i> , 2016, 62, 405-412.	0.9	5
5115	Genome-wide view of genetic diversity reveals paths of selection and cultivar differentiation in peach domestication. <i>DNA Research</i> , 2016, 23, 271-282.	1.5	64
5116	The Pangenome of the <i>Anticarsia gemmatalis</i> Multiple Nucleopolyhedrovirus (AgMNPV). <i>Genome Biology and Evolution</i> , 2016, 8, 94-108.	1.1	25
5117	Diverse Ecological Strategies Are Encoded by <i>Streptococcus pneumoniae</i> Bacteriocin-Like Peptides. <i>Genome Biology and Evolution</i> , 2016, 8, 1072-1090.	1.1	43
5118	“Islands of Divergence” in the Atlantic Cod Genome Represent Polymorphic Chromosomal Rearrangements. <i>Genome Biology and Evolution</i> , 2016, 8, 1012-1022.	1.1	107
5119	Functional characterization and hormonal regulation of the <i>PHEOPHYTINASE</i> gene <i>LpPPH</i> controlling leaf senescence in perennial ryegrass. <i>Journal of Experimental Botany</i> , 2016, 67, 935-945.	2.4	58
5120	Pangenome Evolution in the Marine Bacterium <i>Alteromonas</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 1556-1570.	1.1	73
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5123	Investigating associations between biting time in the malaria vector <i>Anopheles arabiensis</i> Patton and single nucleotide polymorphisms in circadian clock genes: support for sub-structure among <i>An. arabiensis</i> in the Kilombero valley of Tanzania. <i>Parasites and Vectors</i> , 2016, 9, 109.	1.0	31
5124	Morphological and molecular characterization of <i>Sarcocystis taeniata</i> and <i>Sarcocystis pilosa</i> n. sp. from the sika deer (<i>Cervus nippon</i>) in Lithuania. <i>Parasitology Research</i> , 2016, 115, 3021-3032.	0.6	41
5125	Genetic diversity and population genetics of large lungworms (<i>Dictyocaulus</i> , Nematoda) in wild deer in Hungary. <i>Parasitology Research</i> , 2016, 115, 3295-3312.	0.6	14
5126	Avian β -defensin variation in bottlenecked populations: the Seychelles warbler and other congeners. <i>Conservation Genetics</i> , 2016, 17, 661-674.	0.8	9
5127	Geographic independence and phylogenetic diversity of red shiner introductions. <i>Conservation Genetics</i> , 2016, 17, 795-809.	0.8	7
5128	Phylogenetic relationships among cultivated <i>Zanthoxylum</i> species in China based on cpDNA markers. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	30
5129	Hybridization in contact zone between temperate European pine species. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	31

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5131	Worldwide population genetic analysis and natural selection in the <i>Plasmodium vivax</i> Generative Cell Specific 1 (PvGCS1) as a transmission-blocking vaccine candidate. <i>Infection, Genetics and Evolution</i> , 2016, 43, 50-57.	1.0	3
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5133	Genetic Variability of the Invasive Species <i>Metcalfa pruinosa</i> (Hemiptera: Flatidae) in the Republic of Korea. <i>Journal of Economic Entomology</i> , 2016, 109, 1897-1906.	0.8	6
5134	CpSAT-1, a transcribed satellite sequence from the codling moth, <i>Cydia pomonella</i> . <i>Genetica</i> , 2016, 144, 385-395.	0.5	10
5135	Geography has a greater effect than <i>Wolbachia</i> infection on population genetic structure in the spider mite, <i>Tetranychus pueraricola</i> . <i>Bulletin of Entomological Research</i> , 2016, 106, 685-694.	0.5	13
5136	How connectivity shapes genetic structure during range expansion: Insights from the Virginia's Warbler. <i>Auk</i> , 2016, 133, 213-230.	0.7	9
5137	Are sympatrically speciating Midas cichlid fish special? Patterns of morphological and genetic variation in the closely related species <i>Archocentrus centrarchus</i> . <i>Ecology and Evolution</i> , 2016, 6, 4102-4114.	0.8	21
5138	Population Relationship of <i>Vibrio parahaemolyticus</i> Isolates Derived from Aquaculture Ponds, a Seafood Market, Restaurants, and Clinical Samples. <i>Foodborne Pathogens and Disease</i> , 2016, 13, 333-342.	0.8	4
5139	Longtail tuna <i>Thunnus tonggol</i> (Bleeker, 1851) shows genetic partitioning across, but not within, basins of the Indo-Pacific based on mitochondrial DNA. <i>Journal of Applied Ichthyology</i> , 2016, 32, 318-323.	0.3	7
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5142	New insights into the evolutionary history of white sharks, <i>Carcharodon carcharias</i> . <i>Journal of Biogeography</i> , 2016, 43, 328-339.	1.4	17
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5144	Evolutionary history of the little fire ant <i>Wasmannia auropunctata</i> before global invasion: inferring dispersal patterns, niche requirements and past and present distribution within its native range. <i>Journal of Evolutionary Biology</i> , 2016, 29, 790-809.	0.8	17
5145	Prevalence and RT/RNase H Genealogy of Sugarcane Bacilliform Virus Isolates from China. <i>Journal of Phytopathology</i> , 2016, 164, 595-607.	0.5	14
5146	Genetic structure and post-glacial expansion of <i>Cornus florida</i> L. (Cornaceae): integrative evidence from phylogeography, population demographic history, and species distribution modeling. <i>Journal of Systematics and Evolution</i> , 2016, 54, 136-151.	1.6	20
5147	Evolution of the PEBP gene family and selective signature on FT-like clade. <i>Journal of Systematics and Evolution</i> , 2016, 54, 502-510.	1.6	23

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5149	The genetic structure of the exotic ascidian <i>Styela plicata</i> (Tunicata) from Italian ports, with a reappraisal of its worldwide genetic pattern. <i>Marine Ecology</i> , 2016, 37, 492-502.	0.4	14
5150	Strong and stable geographic differentiation of swamp buffalo maternal and paternal lineages indicates domestication in the China/Indochina border region. <i>Molecular Ecology</i> , 2016, 25, 1530-1550.	2.0	49
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5152	The genetic diversity of <i>SMLS</i> (<i>Sitobion miscanthi</i> L type symbiont) and its effect on the fitness, mitochondrial DNA diversity and <i>Buchnera aphidicola</i> dynamic of wheat aphid, <i>Sitobion miscanthi</i> (Hemiptera: Aphididae). <i>Molecular Ecology</i> , 2016, 25, 3142-3151.	2.0	15
5153	Evolutionary dynamics of the plastid inverted repeat: the effects of expansion, contraction, and loss on substitution rates. <i>New Phytologist</i> , 2016, 209, 1747-1756.	3.5	352
5154	Molecular phylogeography of white-bellied tree viper (<i>Trimeresurus</i> ; Viperidae). <i>Zoologica Scripta</i> , 2016, 45, 252-262.	0.7	17
5155	Contrasting phylogeographic signatures in two Australo-Papuan bowerbird species complexes (Aves: Tj ETQq1 10,784314,rgBT/Ove	0.7	21
5156	Phylogeny and taxonomic reassessment of pikas <i>Ochotona pallasii</i> and <i>O. argentata</i> (Mammalia, Lagomorpha). <i>Zoologica Scripta</i> , 2016, 45, 583-594.	0.7	4
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5160	Genetic structuring among populations of the great egret, <i>Ardea alba egretta</i> , in major Brazilian wetlands. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2016, 26, 333-349.	0.9	7
5161	A new integrative framework for large-scale assessments of biodiversity and community dynamics, using littoral gastropods and crabs of British Columbia, Canada. <i>Molecular Ecology Resources</i> , 2016, 16, 1322-1339.	2.2	11
5162	Comparative phylogeographies of six species of hinged terrapins (<i>Pelusios</i> spp.) reveal discordant patterns and unexpected differentiation in the <i>P. castaneus</i> / <i>P. chapini</i> complex and <i>P. rhodesianus</i> . <i>Biological Journal of the Linnean Society</i> , 2016, 117, 305-321.	0.7	11
5163	Mito-nuclear phylogeography of the cyprinid fish <i>Gymnodiptychus dybowskii</i> in the arid Tien Shan region of Central Asia. <i>Biological Journal of the Linnean Society</i> , 2016, 118, 304-314.	0.7	13
5164	East-to-west genetic structure in populations of <i>Aechmea calyculata</i> (Bromeliaceae) from the southern Atlantic rainforest of Brazil. <i>Botanical Journal of the Linnean Society</i> , 2016, 181, 477-490.	0.8	14
5165	Hybridization between two sister species of Bromeliaceae: <i>Vriesea carinata</i> and <i>V. incurvata</i> . <i>Botanical Journal of the Linnean Society</i> , 2016, 181, 491-504.	0.8	30

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5166	Species identification and genetic differentiation of European cavity-nesting wasps (Hymenoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 476-482.	0.6	8
5167	Molecular evidence revealed <i>Lepus hainanus</i> and <i>L. peguensis</i> have a conspecific relationship. Mitochondrial DNA, 2016, 27, 265-269.	0.6	1
5168	Evolutionary history and population genetic structure of the endemic tree frog <i>Hyla tsinlingensis</i> (Amphibia: Anura: Hylidae) inferred from mitochondrial gene analysis. Mitochondrial DNA, 2016, 27, 1348-1357.	0.6	6
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5170	DNA barcoding and molecular phylogeny in Ranidae. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4003-4007.	0.7	3
5171	Tracking the Evolution in Phylogeny, Structure and Function of H5N1 Influenza Virus PA Gene. Transboundary and Emerging Diseases, 2016, 63, 548-563.	1.3	2
5172	Mitochondrial genetic variations of an introduced freshwater fish, goldfish <i>Carassius auratus</i> at the frontier between Europe and Asia (western Anatolia, Turkey): proximity to Europe rather than East Asia?. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4008-4014.	0.7	4
5173	Molecular systematics of <i>Abelmoschus</i> (Malvaceae) and genetic diversity within the cultivated species of this genus based on nuclear ITS and chloroplast rpl16 sequence data. Genetic Resources and Crop Evolution, 2016, 63, 429-445.	0.8	8
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5175	Phylogeography and spatial structure of the lowland tapir (<i>Tapirus terrestris</i> , Perissodactyla): Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 27, 2334-2342.	0.7	13
5176	Adaptive and neutral genetic differentiation among Scottish and endangered Irish red grouse (<i>Lagopus lagopus scotica</i>). Conservation Genetics, 2016, 17, 615-630.	0.8	18
5177	Intron sequence of the taurocyamine kinase gene as a marker to investigate genetic variation of <i>Paragonimus</i> species in Japan and the origins of triploidy in <i>P. westermani</i> . Transactions of the Royal Society of Tropical Medicine and Hygiene, 2016, 110, 67-73.	0.7	7
5178	Discordance between mitochondrial and nuclear genetic structure in the bat <i>Chaerephon pumilus</i> (Chiroptera: Molossidae) from southern Africa. Mammalian Biology, 2016, 81, 115-122.	0.8	8
5179	How many native <i>Cerithium</i> species in the Mediterranean Sea? An integrative taxonomic approach. Journal of Molluscan Studies, 2016, 82, 292-304.	0.4	8
5180	Is the sword moss (<i>Bryoxiphium</i>) a preglacial Tertiary relict?. Molecular Phylogenetics and Evolution, 2016, 96, 200-206.	1.2	24
5181	Cenozoic tectonic and climatic events in southern Iberian Peninsula: Implications for the evolutionary history of freshwater fish of the genus <i>Squalius</i> (Actinopterygii, Cyprinidae). Molecular Phylogenetics and Evolution, 2016, 97, 155-169.	1.2	20
5182	Ancient balancing selection at tan underlies female colour dimorphism in <i>Drosophila erecta</i> . Nature Communications, 2016, 7, 10400.	5.8	37
5183	Using molecular markers to assess the establishment and spread of a mycovirus applied as a biological control agent against chestnut blight. BioControl, 2016, 61, 313-323.	0.9	17

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5185	Nucleotide polymorphism and phylogeographic history of an endangered conifer species <i>Pinus bungeana</i> . <i>Biochemical Systematics and Ecology</i> , 2016, 64, 89-96.	0.6	12
5186	Molecular and morphological insights into the origin of the invasive greater white-toothed shrew (<i>Crocidura russula</i>) in Ireland. <i>Biological Invasions</i> , 2016, 18, 857-871.	1.2	13
5187	Association studies reveal the effect of genetic variation in lncRNA UGTRL and its putative target PtoUGT88A1 on wood formation in <i>Populus tomentosa</i> . <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	8
5188	Partial support for the classical ring species hypothesis in the <i>Chaerephon pumilus</i> species complex (Chiroptera: Molossidae) from southeastern Africa and western Indian Ocean islands. <i>Mammalia</i> , 2016, 80, .	0.3	1
5189	Evaluation of the 5' end of the 16S rRNA gene as a DNA barcode marker for the Cephalopoda. <i>Fisheries Science</i> , 2016, 82, 279-288.	0.7	11
5190	Origin and introduction history of self-sustaining rainbow trout populations in Europe as inferred from mitochondrial DNA and a Y-linked marker. <i>Hydrobiologia</i> , 2016, 770, 129-144.	1.0	7
5191	Behavior and population structure of <i>Anopheles darlingi</i> in Colombia. <i>Infection, Genetics and Evolution</i> , 2016, 39, 64-73.	1.0	20
5192	Cryptic species of cardinalfish with evidence for old and new divergence. <i>Coral Reefs</i> , 2016, 35, 437-450.	0.9	8
5193	Genetic landscape with sharp discontinuities shaped by complex demographic history in moose (<i>Alces</i>) Tj ETQq1 1 0,784314,9rgBT /Ome	0.6	0
5194	Phylogenetic and molecular analyses of human parainfluenza type 3 virus in Buenos Aires, Argentina, between 2009 and 2013: The emergence of new genetic lineages. <i>Infection, Genetics and Evolution</i> , 2016, 39, 85-91.	1.0	15
5195	Population genetic structure of the European conger (<i>Conger conger</i>) in North East Atlantic and West Mediterranean Sea. <i>Fisheries Research</i> , 2016, 174, 245-249.	0.9	5
5196	Rarity and Incomplete Sampling in DNA-Based Species Delimitation. <i>Systematic Biology</i> , 2016, 65, 478-494.	2.7	138
5197	Do diversity patterns of the spring-inhabiting snail <i>Bythinella</i> (Gastropoda, Bythinellidae) on the Aegean Islands reflect geological history?. <i>Hydrobiologia</i> , 2016, 765, 225-243.	1.0	21
5198	Genetic diversity and molecular evolution of arabis mosaic virus based on the CP gene sequence. <i>Archives of Virology</i> , 2016, 161, 1047-1051.	0.9	19
5199	The widespread occurrences of Beet soil borne virus and RNA-5 containing Beet necrotic yellow vein virus isolates in sugar beet production areas in Turkey. <i>European Journal of Plant Pathology</i> , 2016, 144, 443-455.	0.8	15
5200	The intronic minisatellite OsMin1 within a serine protease gene in the Chinese caterpillar fungus <i>Ophiocordyceps sinensis</i> . <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 3599-3610.	1.7	0
5201	High level of microsynteny and purifying selection affect the evolution of WRKY family in Gramineae. <i>Development Genes and Evolution</i> , 2016, 226, 15-25.	0.4	9

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5202	Molecular characterisation of <i>Sarcocystis bovifelis</i> , <i>Sarcocystis bovini</i> n. sp., <i>Sarcocystis hirsuta</i> and <i>Sarcocystis cruzi</i> from cattle (<i>Bos taurus</i>) and <i>Sarcocystis sinensis</i> from water buffaloes (<i>Bubalus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	4
5203	Cloning and In Silico Analysis of a High-Temperature Inducible Lipase from <i>Brevibacillus</i> . <i>Arabian Journal for Science and Engineering</i> , 2016, 41, 2159-2170.	1.1	4
5204	Mitochondrial DNA and morphological analysis of hedgehogs (Eulipotyphla: Erinaceidae) in Algeria. <i>Biochemical Systematics and Ecology</i> , 2016, 64, 57-64.	0.6	8
5205	A multilocus assessment of nuclear and mitochondrial sequence data elucidates phylogenetic relationships among European spirilins (<i>Alburnoides</i> , <i>Cyprinidae</i>). <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 479-491.	1.2	34
5206	Genetic variations in the PSMA3, PSMA6 and PSMC6 genes are associated with type 1 diabetes in Latvians and with expression level of number of UPS-related and T1DM-susceptible genes in HapMap individuals. <i>Molecular Genetics and Genomics</i> , 2016, 291, 891-903.	1.0	22
5207	Molecular characterization and phylogenetic analysis of <i>Fasciola hepatica</i> from Peru. <i>Parasitology International</i> , 2016, 65, 171-174.	0.6	21
5208	Sri Lankan National Melioidosis Surveillance Program Uncover a Nationwide Distribution of Invasive Melioidosis. <i>American Journal of Tropical Medicine and Hygiene</i> , 2016, 94, 292-298.	0.6	26
5209	Fin whales and microplastics: The Mediterranean Sea and the Sea of Cortez scenarios. <i>Environmental Pollution</i> , 2016, 209, 68-78.	3.7	299
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5211	Analytical and Decision Support Tools for Genomics-Assisted Breeding. <i>Trends in Plant Science</i> , 2016, 21, 354-363.	4.3	70
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5213	Ancient Duplications Have Led to Functional Divergence of Vitellogenin-Like Genes Potentially Involved in Inflammation and Oxidative Stress in Honey Bees. <i>Genome Biology and Evolution</i> , 2016, 8, 495-506.	1.1	60
5214	Using a phylogeographic approach to investigate the diversity and determine the distributional range of an isopod (Crustacea: Peracarida), <i>Stenosoma nadejda</i> (Rezig, 1989) in the Atlantic-Mediterranean region. <i>Hydrobiologia</i> , 2016, 768, 315-328.	1.0	4
5215	Olfactory receptors and behavioural isolation: a study on <i>Microtus voles</i> . <i>Mammal Research</i> , 2016, 61, 399-407.	0.6	1
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5217	Update of phylogenetic and genetic diversity of <i>Sporothrix schenckii</i> sensu lato. <i>Medical Mycology</i> , 2016, 54, 248-255.	0.3	29
5218	Origin of B chromosomes in the genus <i>Astyanax</i> (Characiformes, Characidae) and the limits of chromosome painting. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1407-1418.	1.0	28
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5221	Phylogeny and population genetic structure of the ant genus <i>Acropyga</i> (Hymenoptera : Formicidae) in Papua New Guinea. <i>Invertebrate Systematics</i> , 2016, 30, 28.	0.5	13
5222	Population genetic structure and long-distance dispersal of a recently expanding migratory bird. <i>Molecular Phylogenetics and Evolution</i> , 2016, 99, 194-203.	1.2	16
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5231	Phylogeographic analysis of the brown alga <i>Codium</i> <i>utleria multifida</i> (Codiumbryales, Rhodophyta) suggests a complicated introduction history. <i>Phycological Research</i> , 2016, 64, 3-10.	0.8	6
5232	Variation in the whole mitogenome of reef-building <i>Porites</i> corals. <i>Conservation Genetics Resources</i> , 2016, 8, 123-127.	0.4	4
5233	Extreme genetic diversity in asexual grass thrips populations. <i>Journal of Evolutionary Biology</i> , 2016, 29, 887-899.	0.8	18
5234	Loss of genetic integrity and biological invasions result from stocking and introductions of <i>Barbus barbus</i> : insights from rivers in England. <i>Ecology and Evolution</i> , 2016, 6, 1280-1292.	0.8	23
5235	High levels of genetic structure and striking phenotypic variability in a sexually dimorphic suckermouth catfish from the African Highveld. <i>Biological Journal of the Linnean Society</i> , 2016, 117, 528-546.	0.7	14
5236	Morphology, molecules and taxonomy: extreme incongruence in pleurocerids (Gastropoda, Cerithioidea, Pleuroceridae). <i>Zoologica Scripta</i> , 2016, 45, 62-87.	0.7	23
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5252	<i>Paramecium jenningsi</i> complex: existence of three cryptic species confirmed by multi-locus analysis and strain crosses. <i>Systematics and Biodiversity</i> , 2016, 14, 140-154.	0.5	19
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5259	Intra and interspecific sequence variation in closely related species of <i>Cereus</i> (CACTACEAE). <i>Biochemical Systematics and Ecology</i> , 2016, 65, 137-142.	0.6	13
5260	Distribution and haplotype diversity of WKS resistance genes in wild emmer wheat natural populations. <i>Theoretical and Applied Genetics</i> , 2016, 129, 921-934.	1.8	24
5261	Genetic variation in NIN1 and C/MIF1 genes is significantly associated with <i>Populus angustifolia</i> resistance to a galling herbivore, <i>Pemphigus betae</i> . <i>Journal of Insect Physiology</i> , 2016, 84, 50-59.	0.9	12
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5263	Phylogeny and adaptation shape the teeth of insular mice. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20152820.	1.2	35
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5267	Quaternary History of an Endemic Passerine Bird on Corsica Island: Glacial Refugium and Impact of Recent Forest Regression. <i>Quaternary Research</i> , 2016, 85, 271-278.	1.0	5
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5270	Population genetics and ecological niche of invasive <i>Aedes albopictus</i> in Mexico. <i>Acta Tropica</i> , 2016, 157, 30-41.	0.9	29
5271	Genome-wide analysis of CrRLK1L gene family in <i>Gossypium</i> and identification of candidate CrRLK1L genes related to fiber development. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1137-1154.	1.0	27
5272	Contributions of ancestral inter-species recombination to the genetic diversity of extant <i>Streptomyces</i> lineages. <i>ISME Journal</i> , 2016, 10, 1731-1741.	4.4	36
5273	Genetic variation of major histocompatibility complex (MHC) in wild Red Junglefowl (<i>Gallus gallus</i>). <i>Poultry Science</i> , 2016, 95, 400-411.	1.5	23

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5284	Phylogeographic and population genetic structure of bighorn sheep (<i>Ovis canadensis</i>) in North American deserts. Journal of Mammalogy, 2016, 97, 823-838.	0.6	39
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5286	Range expansion of the invasive rusty crayfish <i>Orconectes rusticus</i> (Girard, 1852) (Decapoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262	0.3	2
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5288	Mitochondrial DNA assessment of <i>Phytophthora infestans</i> isolates from potato and tomato in Ethiopia reveals unexpected diversity. Current Genetics, 2016, 62, 657-667.	0.8	8
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5290	Phylogeography and genetic structure of the endemic cyprinid fish <i>Microphysogobio brevis</i> in northern Taiwan. Biochemical Systematics and Ecology, 2016, 65, 176-184.	0.6	9
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5293	Coexistence of cryptic <i>Brachionus calyciflorus</i> (Rotifera) species: roles of environmental variables. <i>Journal of Plankton Research</i> , 2016, 38, 478-489.	0.8	26
5294	Molecular Evolutionary Dynamics of Respiratory Syncytial Virus Group A in Recurrent Epidemics in Coastal Kenya. <i>Journal of Virology</i> , 2016, 90, 4990-5002.	1.5	32
5295	Genetic diversity, acaricide resistance status and evolutionary potential of a <i>Rhipicephalus microplus</i> population from a disease-controlled cattle farming area in South Africa. <i>Ticks and Tick-borne Diseases</i> , 2016, 7, 595-603.	1.1	32
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5298	Identification and validation of novel alleles of rice blast resistant gene Pi54, and analysis of their nucleotide diversity in landraces and wild <i>Oryza</i> species. <i>Euphytica</i> , 2016, 209, 725-737.	0.6	7
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5303	Habitat specificity enhances genetic differentiation in two species of aquatic Podostemaceae in Japan. <i>American Journal of Botany</i> , 2016, 103, 317-324.	0.8	11
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5305	Genetic diversity and evolution of Apple stem pitting virus isolates from pear in China. <i>Canadian Journal of Plant Pathology</i> , 2016, 38, 218-230.	0.8	16
5306	Genetic and physiological differences of European beech provenances (<i>F. sylvatica</i> L.) exposed to drought stress. <i>Forest Ecology and Management</i> , 2016, 361, 226-236.	1.4	39
5307	Phylogeography of the inshore fish, <i>Bostrychus sinensis</i> , along the Pacific coastline of China. <i>Molecular Phylogenetics and Evolution</i> , 2016, 96, 112-117.	1.2	41
5308	Genetic deviation in geographically close populations of the dengue vector <i>Aedes aegypti</i> (Diptera). <i>Journal of Zoology</i> , 2016, 1149-1160.	0.6	18
5309	Paradigm Shifts in the Phylogeographic Analysis of Seaweeds. , 2016, , 23-62.		7

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5311	Molecular Phylogeography of Harvest Mice (<i>Reithrodontomys megalotis</i>) Based on Cytochrome b DNA Sequences. <i>Journal of Mammalian Evolution</i> , 2016, 23, 297-307.	1.0	8
5312	Presumable incipient hybrid speciation of door snails in previously glaciated areas in the Caucasus. <i>Molecular Phylogenetics and Evolution</i> , 2016, 97, 120-128.	1.2	13
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5315	Neotropical forest expansion during the last glacial period challenges refuge hypothesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 1008-1013.	3.3	181
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5317	Radiation of <i>Grossuana</i> Radoman, 1973 (Caenogastropoda: Truncatelloidea) in the Balkans. <i>Journal of Molluscan Studies</i> , 2016, 82, 305-313.	0.4	13
5318	Comparison of beak and feather disease virus prevalence and immunity-associated genetic diversity over time in an island population of red-crowned parakeets. <i>Archives of Virology</i> , 2016, 161, 811-820.	0.9	8
5319	First time DNA barcoding of the common shipworm <i>Teredo navalis</i> Linnaeus 1758 (Mollusca: Bivalvia: Tj ETQq1 1 0.784314 rgBT /Ov... <i>Journal of Experimental Marine Biology and Ecology</i> , 2016, 475, 154-162.	0.7	17
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5321	Comparative analysis of complete mitochondrial genomes suggests that relaxed purifying selection is driving high nonsynonymous evolutionary rate of the NADH2 gene in whitefish (<i>Coregonus</i> spp.). <i>Molecular Phylogenetics and Evolution</i> , 2016, 95, 161-170.	1.2	53
5322	Complete genome sequence of a Chinese isolate of pepper vein yellows virus and evolutionary analysis based on the CP, MP and RdRp coding regions. <i>Archives of Virology</i> , 2016, 161, 677-683.	0.9	14
5323	A Genetic Mechanism for Convergent Skin Lightening during Recent Human Evolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 1177-1187.	3.5	43
5324	Molecular characterization of sympatrically distributed <i>Neotricula aperta</i> -like snails in the Mekong River, Kratie, Cambodia. <i>Mitochondrial DNA</i> , 2016, 27, 1038-1041.	0.6	2
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5326	Absence of population genetic structure in <i>Heterakis gallinarum</i> of chicken from Sichuan, inferred from mitochondrial cytochrome c oxidase subunit I gene. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3612-3617.	0.7	7
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5329	Multilocus analysis indicates that <i>Trypanosoma cruzi</i> I genetic substructure associated with sylvatic and domestic cycles is not an attribute conserved throughout Colombia. <i>Infection, Genetics and Evolution</i> , 2016, 38, 35-43.	1.0	5
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5331	Mitogenomics of the mountain tapir (<i>Tapirus pinchaque</i> , Tapiridae, Perissodactyla, Mammalia) in Colombia and Ecuador: Phylogeography and insights into the origin and systematics of the South American tapirs. <i>Mammalian Biology</i> , 2016, 81, 163-175.	0.8	17
5332	Both Hd1 and Ehd1 are important for artificial selection of flowering time in cultivated rice. <i>Plant Science</i> , 2016, 242, 187-194.	1.7	54
5333	Mycobiont-photobiont interactions of the lichen <i>Cetraria aculeata</i> in high alpine regions of East Africa and South America. <i>Symbiosis</i> , 2016, 68, 25-37.	1.2	16
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5347	Phylogeographic surveys and apomictic genetic connectivity in the North Atlantic red seaweed <i>Mastocarpus stellatus</i> . <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 463-472.	1.2	8
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5361	Genetic structure of <i>Plasmodium vivax</i> in Nicaragua, a country in the control phase, based on the carboxyl terminal region of the merozoite surface protein-1. <i>Infection, Genetics and Evolution</i> , 2016, 40, 324-330.	1.0	9
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5366	Revisiting the evolutionary events in <i>Allium</i> subgenus <i>Cyathophora</i> (Amaryllidaceae): Insights into the effect of the Hengduan Mountains Region (HMR) uplift and Quaternary climatic fluctuations to the environmental changes in the Qinghai-Tibet Plateau. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 802-813.	1.2	27
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5381	A molecular approach towards the taxonomy of fresh water prawns <i>Macrobrachium striatum</i> and <i>M. equidens</i> (Decapoda, Palaemonidae) using mitochondrial markers. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2585-2593.	0.7	7

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5392	Hints for panmixia in <i>Scomberomorus commerson</i> in Indian waters revealed by mitochondrial ATPase 6 and 8 genes. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2822-2824.	0.7	8
5393	Molecular phylogeny of commercially important lobster species from Indian coast inferred from mitochondrial and nuclear DNA sequences. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2700-2709.	0.7	6
5394	Weak genetic differentiation in cobia, <i>Rachycentron canadum</i> from Indian waters as inferred from mitochondrial DNA ATPase 6 and 8 genes. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2819-2821.	0.7	9
5395	High-altitude adaptation of Tibetan chicken from MT-COI and ATP-6 perspective. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3280-3288.	0.7	19
5396	Preliminary study of genetic diversity and population structure of the Relict Gull <i>Larus relictus</i> (Charadriiformes Laridae) using mitochondrial and nuclear genes. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4246-4249.	0.7	3
5397	Mitochondrial DNA-based genetic diversity of <i>Anopheles nivipes</i> in North East India. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4236-4239.	0.7	2
5398	Phylogenetic relationships among four new complete mitogenome sequences of <i>Pelophylax</i> (Amphibia: Anura) from the Balkans and Cyprus. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3434-3437.	0.7	8
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5408	Barcoding gap, but no support for cryptic speciation in the earthworm <i>Aporrectodea longa</i> (Clitellata: Lumbricidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 147-155.	0.7	26
5409	Extremely low genetic diversity of mtDNA control region and remarkable population differentiation of <i>Ichthyophis bannanicus</i> (Amphibia: Gymnophiona). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 98-103.	0.7	1
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5411	Identifying the species of origin in commercial sausages in South Korea. <i>Journal of Applied Animal Research</i> , 2017, 45, 179-184.	0.4	9
5412	Is there a distinct harbor porpoise subpopulation in the Marmara Sea?. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 558-564.	0.7	6
5413	DNA barcoding and phylogeny of <i>Calidris</i> and <i>Tringa</i> (Aves: Scolopacidae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 616-619.	0.7	0
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5415	Molecular diversity of some species belonging to the genus <i>Daphnia</i> O. F. MÅ¼ller, 1785 (Crustacea: Cladocera) in Turkey. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 424-433.	0.7	5
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5435	Population genetic structure of <i>Macrobrachium rosenbergii</i> (Palaemonidae) from Indian waters using mitochondrial ATPase 6 gene. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2017, 28, 602-605.	0.7	5

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5437	Phylogeny and phylogeography of <i>Altolamprologus</i> : ancient introgression and recent divergence in a rock-dwelling Lake Tanganyika cichlid genus. <i>Hydrobiologia</i> , 2017, 791, 35-50.	1.0	24
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5443	Identification and characterization of suppressors of plant cell death (SPD) effectors from <i>Magnaporthe oryzae</i> . <i>Molecular Plant Pathology</i> , 2017, 18, 850-863.	2.0	44
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5445	Phylogenetic Analysis and Functional Characterization of the Influenza A H5N1 PB2 Gene. <i>Transboundary and Emerging Diseases</i> , 2017, 64, 374-388.	1.3	2
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5448	Species clarification of oyster mushrooms in China and their DNA barcoding. <i>Mycological Progress</i> , 2017, 16, 191-203.	0.5	16
5449	Phylogeny of penduline tits inferred from mitochondrial and microsatellite genotyping. <i>Journal of Avian Biology</i> , 2017, 48, 932-940.	0.6	8
5450	Genetic differentiation and distribution of <i>Pyropia acanthophora</i> (Bangiales, Rhodophyta) in the Philippines. <i>European Journal of Phycology</i> , 2017, 52, 104-115.	0.9	20
5451	Determining the subspecies composition of bean goose harvests in Finland using genetic methods. <i>European Journal of Wildlife Research</i> , 2017, 63, 1.	0.7	9
5452	Biogeographic scenarios for the diversification of a widespread Neotropical species, <i>Glossophaga soricina</i> (Chiroptera: Phyllostomidae). <i>Systematics and Biodiversity</i> , 2017, 15, 440-450.	0.5	13
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5455	Historical biogeography and mitogenomics of two endemic Mediterranean gorgonians (<i>Holaxonia</i>), Tj ETQq1 1 0.784314 rgBT/Overlo	0.7	12
5456	A new mitochondrial haplotype confirms the distinctiveness of the Italian wolf (<i>Canis lupus</i>) population. <i>Mammalian Biology</i> , 2017, 84, 30-34.	0.8	12
5457	Strong genetic structure revealed by multilocus patterns of variation in <i>Giardia duodenalis</i> isolates of patients from Galicia (NW-Iberian Peninsula). <i>Infection, Genetics and Evolution</i> , 2017, 48, 131-141.	1.0	14
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5459	Molecular diversity of <i>Wolbachia</i> in Lepidoptera: Prevalent allelic content and high recombination of MLST genes. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 164-179.	1.2	51
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5464	Bless this phylogeographic mess – Comparative study of <i>Eiseniella tetraedra</i> (Annelida, Oligochaeta) between an Atlantic area and a continental Mediterranean area in Spain. <i>European Journal of Soil Biology</i> , 2017, 78, 50-56.	1.4	10
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5466	Complex genetic architecture underlies maize tassel domestication. <i>New Phytologist</i> , 2017, 214, 852-864.	3.5	86
5467	The genetic structure of hypoderatid mites (Actinotrichida: Astigmata) parasitizing great cormorant (<i>Phalacrocorax carbo</i>) during host post-breeding dispersal in Milicz, SW Poland. <i>Acta Parasitologica</i> , 2017, 62, 76-89.	0.4	2
5468	Comparative phylogeography of two codistributed endemic cyprinids in southeastern Taiwan. <i>Biochemical Systematics and Ecology</i> , 2017, 70, 283-290.	0.6	10
5469	Phylogeographic structure of <i>Canthon cyanellus</i> (Coleoptera: Scarabaeidae), a Neotropical dung beetle in the Mexican Transition Zone: Insights on its origin and the impacts of Pleistocene climatic fluctuations on population dynamics. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 180-190.	1.2	29
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5471	Mitochondrial <i>DNA</i> phylogeography of least cisco <i>C. oregonus sardinella</i> in <i>A. laska</i> . <i>Journal of Fish Biology</i> , 2017, 90, 1001-1020.	0.7	2

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5474	DNA barcoding of bird species in Cyprus: a tool for conservation purposes. <i>Bird Conservation International</i> , 2017, 27, 483-494.	0.7	9
5475	Molecular phylogeography and population evolution analysis of <i>Citrus ichangensis</i> (Rutaceae). <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	15
5476	Evolution of Fseg/Cseg dimorphism in region III of the <i>Plasmodium falciparum</i> eba-175 gene. <i>Infection, Genetics and Evolution</i> , 2017, 49, 251-255.	1.0	1
5477	Archipelagos of the Anthropocene: rapid and extensive differentiation of native terrestrial vertebrates in a single metropolis. <i>Molecular Ecology</i> , 2017, 26, 2466-2481.	2.0	52
5478	Genetic variation in mitochondrial genes of the tick <i>Haemaphysalis flava</i> collected from wild hedgehogs in China. <i>Experimental and Applied Acarology</i> , 2017, 71, 131-137.	0.7	6
5479	Occurrence of <i>Octopus insularis</i> Leite and Haimovici, 2008 in the Tropical Northwestern Atlantic and implications of species misidentification to octopus fisheries management. <i>Marine Biodiversity</i> , 2017, 47, 723-734.	0.3	40
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5481	Genetic differences among <i>Haplorchis taichui</i> populations in Indochina revealed by mitochondrial COX1 sequences. <i>Journal of Helminthology</i> , 2017, 91, 597-604.	0.4	7
5482	Self-fertilization, long-distance flash invasion and biogeography shape the population structure of <i>Pseudosuccinea columella</i> at the worldwide scale. <i>Molecular Ecology</i> , 2017, 26, 887-903.	2.0	40
5483	Soft selective sweeps in fungicide resistance evolution: recurrent mutations without fitness costs in grapevine downy mildew. <i>Molecular Ecology</i> , 2017, 26, 1936-1951.	2.0	54
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5485	Biogeography and diversification dynamics of the African woodpeckers. <i>Molecular Phylogenetics and Evolution</i> , 2017, 108, 88-100.	1.2	14
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5489	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 2017, 541, 536-540.	13.7	332

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5491	Inferring phylogenetic patterns of land snails of the genus <i>Albinaria</i> on the island of Dia (Crete, Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 187 0.5 3	0.5	3
5492	Molecular characterization of Prune dwarf virus cherry isolates from Slovakia shows their substantial variability and reveals recombination events in PDV RNA3. <i>European Journal of Plant Pathology</i> , 2017, 147, 877-885.	0.8	11
5493	HFB7 " A novel orphan hydrophobin of the Harzianum and Virens clades of <i>Trichoderma</i> , is involved in response to biotic and abiotic stresses. <i>Fungal Genetics and Biology</i> , 2017, 102, 63-76.	0.9	30
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5497	<i>Mesorhizobium muleiense</i> and <i>Mesorhizobium</i> sp. nov. are symbionts of <i>Cicer arietinum</i> L. in alkaline soils of Gansu, Northwest China. <i>Plant and Soil</i> , 2017, 410, 103-112.	1.8	45
5498	Genetic diversity and phylogeographic structure of Bactrian camels shown by mitochondrial sequence variations. <i>Animal Genetics</i> , 2017, 48, 217-220.	0.6	33
5499	Exploring genetic variation in haplotypes of the filariasis vector <i>Culex quinquefasciatus</i> (Diptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 187 0.9 31	0.9	31
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5503	Extreme genetic structure in a social bird species despite high dispersal capacity. <i>Molecular Ecology</i> , 2017, 26, 2812-2825.	2.0	15
5504	Extreme mitochondrial variation in the Atlantic gall crab <i>Opecarcinus hypostegus</i> (Decapoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 7, 39461. 1.6 8	1.6	8
5505	Genetic diversity of three Chinese native sheep breeds. <i>Russian Journal of Genetics</i> , 2017, 53, 118-127.	0.2	1
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5509	Reevaluating species number, distribution and endemism of the coral genus <i>Pocillopora</i> Lamarck, 1816 using species delimitation methods and microsatellites. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 430-446.	1.2	69
5510	Elusive does not always equal rare: genetic assessment of a protected Gila monster (<i>Heloderma</i>)	0.1	5
5511	New genetic lineages within Moroccan day geckos <i>Quedenfeldtia</i> (<i>Sphaerodactylidae</i>) revealed by mitochondrial and nuclear DNA sequence data. <i>Amphibia - Reptilia</i> , 2017, 38, 97-101.	0.1	4
5512	Molecular systematics of the critically-endangered North American spiny mussels (<i>Unionidae: Elliptio</i>)	0.8	15
5513	Phylogeny and phylogeography of the land hermit crab <i>Coenobita purpureus</i> (Decapoda:)	0.4	28
5514	Molecular characterization of bovine leukemia virus from Moldovan dairy cattle. <i>Archives of Virology</i> , 2017, 162, 1563-1576.	0.9	23
5515	Low genetic diversity but strong population structure reflects multiple introductions of western flower thrips (<i>Thysanoptera: Thripidae</i>) into China followed by human-mediated spread. <i>Evolutionary Applications</i> , 2017, 10, 391-401.	1.5	35
5516	Reciprocal translocation of small numbers of inbred individuals rescues immunogenetic diversity. <i>Molecular Ecology</i> , 2017, 26, 2660-2673.	2.0	13
5517	The role of ecological factors in determining phylogeographic and population genetic structure of two sympatric island skinks (<i>Plestiodon kishinouyei</i> and <i>P. stimpsonii</i>). <i>Genetica</i> , 2017, 145, 223-234.	0.5	3
5518	Study on chloroplast DNA diversity of cultivated and wild pears (<i>Pyrus L.</i>) in Northern China. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	16
5519	Warm-cold colonization: response of oaks to uplift of the Himalaya-Hengduan Mountains. <i>Molecular Ecology</i> , 2017, 26, 3276-3294.	2.0	82
5520	Genetic structure of a regionally endangered orchid, the dark red helleborine (<i>Epipactis atrorubens</i>) at the edge of its distribution. <i>Genetica</i> , 2017, 145, 209-221.	0.5	5
5521	Molecular identification of wild triatomines of the genus <i>Rhodnius</i> in the Bolivian Amazon: Strategy and current difficulties. <i>Infection, Genetics and Evolution</i> , 2017, 51, 1-9.	1.0	7
5522	Phylogeography of endangered <i>Dendrobium moniliforme</i> in East Asia based on mitochondrial DNA sequence variations. <i>Biodiversity and Conservation</i> , 2017, 26, 1659-1674.	1.2	7
5523	A combination of long term fragmentation and glacial persistence drove the evolutionary history of the Italian wall lizard <i>Podarcis siculus</i> . <i>BMC Evolutionary Biology</i> , 2017, 17, 6.	3.2	36
5524	Sequence diversification in recessive alleles of two host factor genes suggests adaptive selection for bymovirus resistance in cultivated barley from East Asia. <i>Theoretical and Applied Genetics</i> , 2017, 130, 331-344.	1.8	21
5525	Two <i>Candidatus Liberibacter asiaticus</i> ™ Strains Recently Found in California Harbor Different Prophages. <i>Phytopathology</i> , 2017, 107, 662-668.	1.1	32

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5527	Allele mining in the Argentine public maize inbred line collection of two paralogous genes encoding NAC domains. <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	4
5528	Molecular detection of Hepatozoon spp. in domestic dogs and wild mammals in southern Pantanal, Brazil with implications in the transmission route. <i>Veterinary Parasitology</i> , 2017, 237, 37-46.	0.7	44
5529	Molecular identification and distribution of leatherjackets (<i>Leptochelone</i>) (Tardigrada: Thaliacea). <i>Journal of Applied Entomology</i> , 2017, 19, 400-407.	0.7	3
5530	Phylogeography of the rare velvet tree ant <i>Liometopum microcephalum</i> (Formicidae). <i>Journal of Applied Entomology</i> , 2017, 19, 400-407.	1.4	3
5531	Success of classical biocontrol agent <i>Torymus sinensis</i> within its expanding range in Europe. <i>Journal of Applied Entomology</i> , 2017, 141, 758-767.	0.8	21
5532	Integrated Analyses of Cuticular Hydrocarbons, Chromosome and mtDNA in the Neotropical Social Wasp <i>Mischocyttarus consimilis</i> (Hymenoptera, Vespidae). <i>Neotropical Entomology</i> , 2017, 46, 642-648.	0.5	7
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5534	Quaternary climate change drives allo-peripatric speciation and refugial divergence in the <i>Dysosma versipellis</i> - <i>pleiantha</i> complex from different forest types in China. <i>Scientific Reports</i> , 2017, 7, 40261.	1.6	23
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5537	The periwinkle <i>Echinolittorina punctata</i> (Mollusca: Gastropoda) tracked the warming of the Mediterranean Sea following the Last Glacial Maximum. <i>Marine Biology</i> , 2017, 164, 1.	0.7	4
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5539	Heteroplasmy due to coexistence of mtCOI haplotypes from different lineages of the <i>Thrips tabaci</i> cryptic species group. <i>Bulletin of Entomological Research</i> , 2017, 107, 534-542.	0.5	10
5540	Occurrence of <i>Knipowitschia goerneri</i> Ahnelt, 1991 (Gobiidae) in southern Albania confirmed with molecular tools. <i>Journal of Applied Ichthyology</i> , 2017, 33, 284-290.	0.3	6
5541	Population genetic analysis of a parasitic mycovirus to infer the invasion history of its fungal host. <i>Molecular Ecology</i> , 2017, 26, 2482-2497.	2.0	25
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5543	Unpacking boxes: Integration of molecular, morphological and ecological approaches reveals extensive patterns of reticulate evolution in box eucalypts. <i>Molecular Phylogenetics and Evolution</i> , 2017, 108, 70-87.	1.2	20

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5545	Taxonomic revision and phylogenetic analyses of rubber powdery mildew fungi. <i>Microbial Pathogenesis</i> , 2017, 105, 185-195.	1.3	21
5546	Mitochondrial introgression suggests extensive ancestral hybridization events among <i>Saccharomyces</i> species. <i>Molecular Phylogenetics and Evolution</i> , 2017, 108, 49-60.	1.2	40
5547	Effects of Pleistocene sea-level fluctuations on mangrove population dynamics: a lesson from <i>Sonneratia alba</i> . <i>BMC Evolutionary Biology</i> , 2017, 17, 22.	3.2	38
5548	Ancestry and demography and descendants of Iron Age nomads of the Eurasian Steppe. <i>Nature Communications</i> , 2017, 8, 14615.	5.8	96
5549	Evidence of neofunctionalization after the duplication of the highly conserved Polycomb group gene <i>Caf1-55</i> in the <i>obscura</i> group of <i>Drosophila</i> . <i>Scientific Reports</i> , 2017, 7, 40536.	1.6	4
5550	Genome sequencing of an Indian peste des petits ruminants virus isolate, Izatnagar/94, and its implications for virus diversity, divergence and phylogeography. <i>Archives of Virology</i> , 2017, 162, 1677-1693.	0.9	23
5551	The characterization of complete mitochondrial genome and phylogenetic relationship within <i>Rattus</i> genus (Rodentia: Muridae). <i>Biochemical Systematics and Ecology</i> , 2017, 71, 179-186.	0.6	9
5552	Geographical differentiation of the <i>Euchiloglanis</i> fish complex (Teleostei: Siluriformes) in the Hengduan Mountain Region, China: Phylogeographic evidence of altered drainage patterns. <i>Ecology and Evolution</i> , 2017, 7, 928-940.	0.8	14
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5555	Phylogeography of the planktonic shrimp <i>Lucifer hanseni</i> Nobili 1905 in the Indo-Malayan Archipelago. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2017, 97, 129-140.	0.4	1
5556	Tracing the origin of a cryptic invader: phylogeography of the <i>Euwallacea fornicatus</i> (Coleoptera: Curculionidae: Scolytinae) species complex. <i>Agricultural and Forest Entomology</i> , 2017, 19, 366-375.	0.7	93
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5558	Genome-Wide analysis of the AAAP gene family in moso bamboo (<i>Phyllostachys edulis</i>). <i>BMC Plant Biology</i> , 2017, 17, 29.	1.6	51
5559	Comparative studies of the population genetic structure of the <i>Brachionus calyciflorus</i> species complex from four inland lakes in Wuhu, China. <i>Biochemical Systematics and Ecology</i> , 2017, 71, 69-77.	0.6	7
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5561	Contrasting results from molecular and pedigree-based population diversity measures in captive zebra highlight challenges facing genetic management of zoo populations. <i>Zoo Biology</i> , 2017, 36, 87-94.	0.5	15

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5563	Genetic structure and population history of wintering Asian Great Bustard (<i>Otis tarda dybowskii</i>) in China: implications for conservation. <i>Journal of Ornithology</i> , 2017, 158, 761-772.	0.5	13
5564	Phylogenetic estimation of Mytilidae in the East China Sea inferred from mitochondrial genes and nuclear DNA sequence variation. <i>Biochemical Systematics and Ecology</i> , 2017, 71, 219-224.	0.6	0
5565	Morphological, acoustic and genetic divergence in the bladder grasshopper <i>Bullacris unicolor</i> . <i>Ethology Ecology and Evolution</i> , 2017, 29, 552-573.	0.6	9
5566	Human management and hybridization shape treegourd fruits in the Brazilian Amazon Basin. <i>Evolutionary Applications</i> , 2017, 10, 577-589.	1.5	9
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5568	Life on the rocks: Multilocus phylogeography of rock hyrax (<i>Procavia capensis</i>) from southern Africa. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 49-62.	1.2	27
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5571	Patterns of Diversity and Spatial Variability of β -Defensin Innate Immune Genes in a Declining Wild Population of Tree Swallows. <i>Journal of Heredity</i> , 2017, 108, 262-269.	1.0	3
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5573	Insights into the plastid diversity of <i>Daphne blagayana</i> Freyer (Thymelaeaceae). <i>Journal of Systematics and Evolution</i> , 2017, 55, 437-445.	1.6	2
5574	Genetic Stability and Evolution of the <i>sigB</i> Allele, Used for <i>Listeria</i> Sensu Stricto Subtyping and Phylogenetic Inference. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	36
5575	Effects of Isolation by Continental Islands in the Seto Inland Sea, Japan, on Genetic Diversity of the Large Japanese Field Mouse, <i>Apodemus speciosus</i> (Rodentia: Muridae), Inferred from the Mitochondrial Dloop Region. <i>Zoological Science</i> , 2017, 34, 112.	0.3	12
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5577	Phylogenetic analysis of Tibetan mastiffs based on mitochondrial hypervariable region I. <i>Journal of Genetics</i> , 2017, 96, 119-125.	0.4	5
5578	Signatures of invasion: using an integrative approach to infer the spread of melon fly, <i>Zeugodacus cucurbitae</i> (Diptera: Tephritidae), across Southeast Asia and the West Pacific. <i>Biological Invasions</i> , 2017, 19, 1597-1619.	1.2	13
5579	A case for realigning species limits in the southern Australian whipbirds long recognised as the Western Whipbird (<i>Psophodes nigrogularis</i>). <i>Emu</i> , 2017, 117, 254-263.	0.2	5

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5581	Comprehensive assessment showed no associations of variants at the SLC10A1 locus with susceptibility to persistent HBV infection among Southern Chinese. <i>Scientific Reports</i> , 2017, 7, 46490.	1.6	20
5582	An endemic rat species complex is evidence of moderate environmental changes in the terrestrial biodiversity centre of China through the late Quaternary. <i>Scientific Reports</i> , 2017, 7, 46127.	1.6	12
5583	Probing the Evolutionary History of Human Bitter Taste Receptor Pseudogenes by Restoring Their Function. <i>Molecular Biology and Evolution</i> , 2017, 34, 1587-1595.	3.5	15
5584	Mitochondrial genomes of the hoverflies <i>Episyrphus balteatus</i> and <i>Eupeodes corollae</i> (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 58	1.6	29
5585	Insights on Mitochondrial Genetic Variation in Chesapeake Bay Summer-Resident Cownose Rays. <i>Transactions of the American Fisheries Society</i> , 2017, 146, 478-484.	0.6	4
5586	Phylogeography of <i>Sophora moorcroftiana</i> Supports Wu's Hypothesis on the Origin of Tibetan Alpine Flora. <i>Journal of Heredity</i> , 2017, 108, 405-414.	1.0	12
5587	The human retinoblastoma susceptibility gene (RB1): an evolutionary story in primates. <i>Mammalian Genome</i> , 2017, 28, 198-212.	1.0	3
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5590	Northwest Africa as a source and refuge area of plant biodiversity: a case study on <i>Campanula kremeri</i> and <i>Campanula occidentalis</i> . <i>Journal of Biogeography</i> , 2017, 44, 2057-2068.	1.4	17
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5592	Genetic variability of the banded murex (<i>Hexaplex trunculus</i>) revealed by ND2 and ITS2 sequences. <i>Russian Journal of Marine Biology</i> , 2017, 43, 92-98.	0.2	3
5593	Genome-wide analysis of VQ motif-containing proteins in Moso bamboo (<i>Phyllostachys edulis</i>). <i>Planta</i> , 2017, 246, 165-181.	1.6	50
5594	Genome-wide identification and analysis of the <i>Populus trichocarpa</i> TIFY gene family. <i>Plant Physiology and Biochemistry</i> , 2017, 115, 360-371.	2.8	38
5595	Recurrent Gene Duplication Leads to Diverse Repertoires of Centromeric Histones in <i>Drosophila</i> Species. <i>Molecular Biology and Evolution</i> , 2017, 34, 1445-1462.	3.5	42
5596	Toll-like receptor variation in the bottlenecked population of the endangered Seychelles warbler. <i>Animal Conservation</i> , 2017, 20, 235-250.	1.5	19
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5599	Genetic identification of source and likely vector of a widespread marine invader. <i>Ecology and Evolution</i> , 2017, 7, 4432-4447.	0.8	61
5600	Integrative systematic analyses of the genus <i>Chodsigoa</i> (Mammalia: Eulipotyphla: Soricidae), with descriptions of new species. <i>Zoological Journal of the Linnean Society</i> , 2017, 180, 694-713.	1.0	17
5601	A TRIM insertion in the promoter of <i>Ms2</i> causes male sterility in wheat. <i>Nature Communications</i> , 2017, 8, 15407.	5.8	79
5602	Neutral Genetic Processes Influence MHC Evolution in Threatened Gopher Tortoises (<i>Gopherus</i>). <i>Trends in Ecology and Evolution</i> , 2017, 32, 50-58.	1.0	5
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5604	W-enriched satellite sequence in the Indian meal moth, <i>Plodia interpunctella</i> (Lepidoptera, Pyralidae). <i>Chromosome Research</i> , 2017, 25, 241-252.	1.0	20
5605	First molecular identification and genetic diversity of <i>Strongyloides stercoralis</i> and <i>Strongyloides fuelleborni</i> in human communities having contact with long-tailed macaques in Thailand. <i>Parasitology Research</i> , 2017, 116, 1917-1923.	0.6	38
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5607	Hybridization and Asymmetric Introgression after Secondary Contact in Two Tropical African Climber Species, <i>Haumania danckelmaniana</i> and <i>Haumania liebrechtsiana</i> (Marantaceae). <i>International Journal of Plant Sciences</i> , 2017, 178, 421-430.	0.6	12
5608	Assessing the scope for genetic rescue of an endangered butterfly: the case of the Eltham copper. <i>Insect Conservation and Diversity</i> , 2017, 10, 399-414.	1.4	10
5609	Evaluation of a Multilocus Sequence Typing (MLST) scheme for <i>Leishmania (Viannia) braziliensis</i> and <i>Leishmania (Viannia) panamensis</i> in Colombia. <i>Parasites and Vectors</i> , 2017, 10, 236.	1.0	36
5610	Identification of evolutionarily significant units in the Cuban endemic damselfly <i>Hypolestes trinitatis</i> (Odonata: Hypolestidae). <i>Conservation Genetics</i> , 2017, 18, 1229-1234.	0.8	7
5611	The role of niche divergence and geographic arrangement in the speciation of Eared Pheasants (<i>Crossoptilon</i> , Hodgson 1938). <i>Molecular Phylogenetics and Evolution</i> , 2017, 113, 1-8.	1.2	23
5612	The population genetic structure of <i>Corythucha ciliata</i> (Say) (Hemiptera: Tingidae) provides insights into its distribution and invasiveness. <i>Scientific Reports</i> , 2017, 7, 635.	1.6	10
5613	Fuzzy species limits in Mediterranean gorgonians (Cnidaria, Octocorallia): inferences on speciation processes. <i>Zoologica Scripta</i> , 2017, 46, 767-778.	0.7	12
5614	A genomic footprint of hybrid zone movement in crested newts. <i>Evolution Letters</i> , 2017, 1, 93-101.	1.6	77
5615	Gorilla MHC class I gene and sequence variation in a comparative context. <i>Immunogenetics</i> , 2017, 69, 303-323.	1.2	12

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5618	Population structure of Purple Sandpipers (<i>Calidris maritima</i>) as revealed by mitochondrial <i>scp>DNA</scp></i> and microsatellites. <i>Ecology and Evolution</i> , 2017, 7, 3225-3242.	0.8	6
5619	Genetic variation and geographic differentiation in the marine triclad <i>Bdelloura candida</i> (Platyhelminthes, Tricladida, Maricola), ectocommensal on the American horseshoe crab <i>Limulus polyphemus</i> . <i>Marine Biology</i> , 2017, 164, 111.	0.7	8
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5623	Genetic differentiation of the soft shore barnacle <i>Fistulobalanus albicostatus</i> (Cirripedia: Tj ETQq1 1 0.784314 rgBT /Overlock 0.4 22	0.4	22
5624	Phylogeography of the dry vegetation endemic species <i>Nephila sexpunctata</i> (Araneae: Araneidae) suggests recent expansion of the Neotropical Dry Diagonal. <i>Journal of Biogeography</i> , 2017, 44, 2007-2020.	1.4	19
5625	Population genetics of the Schistosoma snail host <i>Bulinus truncatus</i> in Egypt. <i>Acta Tropica</i> , 2017, 172, 36-43.	0.9	12
5626	Population structure of <i>Rhizobium etli</i> -like strains nodulated with <i>Phaseolus vulgaris</i> in two ecoregions of China. <i>Soil Biology and Biochemistry</i> , 2017, 112, 14-23.	4.2	9
5627	Mito-nuclear discordance helps to reveal the phylogeographic patterns of <i>Melitaea ornata</i> (Lepidoptera: Nymphalidae). <i>Biological Journal of the Linnean Society</i> , 2017, 121, 267-281.	0.7	17
5628	Implications of absence of seawater-type mitochondria-rich cells and results of molecular analyses for derivation of the non-parasitic Ukrainian brook lamprey <i>Eudontomyzon mariae</i> . <i>Environmental Biology of Fishes</i> , 2017, 100, 509-518.	0.4	4
5629	Molecular phylogeny of 21 tropical bamboo species reconstructed by integrating non-coding internal transcribed spacer (ITS1 and 2) sequences and their consensus secondary structure. <i>Genetica</i> , 2017, 145, 319-333.	0.5	6
5630	The presence of Balkan and Iberian red deer (<i>Cervus elaphus</i>) mitochondrial DNA lineages in the Carpathian Basin. <i>Mammalian Biology</i> , 2017, 86, 48-55.	0.8	7
5631	Epigeal gammarids survived millions of years of severe climatic fluctuations in high latitude refugia throughout the Western Carpathians. <i>Molecular Phylogenetics and Evolution</i> , 2017, 112, 218-229.	1.2	28
5632	Cutting through the Gordian knot: unravelling morphological, molecular, and biogeographical patterns in the genus <i>Zapteryx</i> (guitarfish) from the Mexican Pacific. <i>ICES Journal of Marine Science</i> , 2017, 74, 1630-1638.	1.2	6
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5635	Reconstructing the introduction history of an invasive fish predator in South Africa. <i>Biological Invasions</i> , 2017, 19, 2261-2276.	1.2	19
5636	Ecotypic differentiation under farmers' selection: Molecular insights into the domestication of <i>Pachyrhizus</i> Rich. ex DC. (Fabaceae) in the Peruvian Andes. <i>Evolutionary Applications</i> , 2017, 10, 498-513.	1.5	8
5637	The roles of ecology, behaviour and effective population size in the evolution of a community. <i>Molecular Ecology</i> , 2017, 26, 3775-3784.	2.0	21
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5639	High Genetic Diversity and Implications for Determining Population Structure in the Blue Crab <i>Callinectes sapidus</i> . <i>Journal of Shellfish Research</i> , 2017, 36, 231-242.	0.3	21
5640	Integrative inference of population history in the Ibero-Maghrebian endemic <i>Pleurodeles waltl</i> (Salamandridae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 112, 122-137.	1.2	38
5641	Two haplotype clusters of <i>Echinococcus granulosus sensu stricto</i> in northern Iraq (Kurdistan) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.9	25
5642	High adaptive variability and virus-driven selection on major histocompatibility complex (MHC) genes in invasive wild rabbits in Australia. <i>Biological Invasions</i> , 2017, 19, 1255-1271.	1.2	15
5643	Complete mitochondrial genome of parasitic nematode <i>Cylicocycclus nassatus</i> and comparative analyses with <i>Cylicocycclus insigne</i> . <i>Experimental Parasitology</i> , 2017, 172, 18-22.	0.5	13
5644	Ecological and physical barriers shape genetic structure of the Alpine porcini (<i>Boletus reticuloceps</i>). <i>Mycorrhiza</i> , 2017, 27, 261-272.	1.3	10
5645	Multilocus Sequence Analysis of Phylogroup 1 and 2 Oral Treponeme Strains. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	8
5646	Molecular characterization and phylogenetic analysis of <i>Fasciola gigantica</i> from Nigeria. <i>Parasitology International</i> , 2017, 66, 893-897.	0.6	25
5647	Origin of modern syphilis and emergence of a pandemic <i>Treponema pallidum</i> cluster. <i>Nature Microbiology</i> , 2017, 2, 16245.	5.9	138
5648	Microevolutionary analyses of <i>Pythium insidiosum</i> isolates of Brazil and Thailand based on <i>exo-1,3-β-glucanase</i> gene. <i>Infection, Genetics and Evolution</i> , 2017, 48, 58-63.	1.0	17
5649	<i>Wolbachia</i> strains in cryptic species of the <i>Anastrepha fraterculus</i> complex (Diptera, Tephritidae) along the Neotropical Region. <i>Systematic and Applied Microbiology</i> , 2017, 40, 59-67.	1.2	11
5650	An integrative study of evolutionary diversification of <i>Eutrema</i> (Eutremeae, Brassicaceae). <i>Botanical Journal of the Linnean Society</i> , 2017, 184, 204-223.	0.8	14
5651	Minimal barcode distance between two water mite species from Madeira Island: a cautionary tale. <i>Experimental and Applied Acarology</i> , 2017, 72, 133-143.	0.7	10

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5653	Mitogenomic diversity in Russians and Poles. <i>Forensic Science International: Genetics</i> , 2017, 30, 51-56.	1.6	17
5654	Phylogeography of red muntjacs reveals three distinct mitochondrial lineages. <i>BMC Evolutionary Biology</i> , 2017, 17, 34.	3.2	24
5655	Phylogeny and systematics of Anatolian mountain frogs. <i>Biochemical Systematics and Ecology</i> , 2017, 73, 26-34.	0.6	5
5656	Analysis of mtDNA control region of an isolated population of Eldâ€™s deer (<i>Rucervus eldii</i>) reveals its vulnerability to inbreeding. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 277-280.	0.2	2
5657	A century in synonymy: molecular and morphological evidence for the revalidation of <i>Glyptosternon osÑhanini</i> (Herzenstein, 1889) (Actinopterygii: Sisoridae). <i>Zootaxa</i> , 2017, 4277, 435.	0.2	3
5658	Chloroplast Genomic Resource of Paris for Species Discrimination. <i>Scientific Reports</i> , 2017, 7, 3427.	1.6	60
5659	Evolutionary and polymorphism analyses reveal the central role of <i>BTN3A2</i> in the concerted evolution of the <i>BTN3</i> gene family. <i>Immunogenetics</i> , 2017, 69, 379-390.	1.2	21
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5661	New insights into the genetic composition and phylogenetic relationship of wolves and dogs in the Iberian Peninsula. <i>Ecology and Evolution</i> , 2017, 7, 4404-4418.	0.8	10
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5663	Exploring the genetic diversity of shallow-water Agariciidae (Cnidaria: Anthozoa) from the Saudi Arabian Red Sea. <i>Marine Biodiversity</i> , 2017, 47, 1065-1078.	0.3	17
5664	Gene flow and genetic drift contribute to high genetic diversity with low phylogeographical structure in European hoopoes (<i>Upupa epops</i>). <i>Molecular Phylogenetics and Evolution</i> , 2017, 113, 113-125.	1.2	20
5665	Evaluation of onion (<i>Allium cepa</i>) germplasm entries for resistance to onion thrips, <i>Thrips tabaci</i> (Lindeman) in Tanzania. <i>International Journal of Tropical Insect Science</i> , 2017, 37, 98-113.	0.4	17
5666	Allopatric divergence and secondary contact without genetic admixture for <i>A</i>richanna perimelaina</i> (<sc>L</sc>epidoptera: <sc>G</sc>eometridae), an alpine moth endemic to the <sc>H</sc>engduan <sc>M</sc>ountains. <i>Systematic Entomology</i>, 2017, 42, 703-713.</i>	1.7	4
5667	Genetic variation within and among populations of fairy shrimp, <i>Streptocephalus texanus</i> , from southeastern Utah. <i>Southwestern Naturalist</i> , 2017, 62, 29-38.	0.1	0
5668	Shifting Quaternary migration patterns in the Bahamian archipelago: Evidence from the <i>Zamia pumila</i> complex at the northern limits of the Caribbean island biodiversity hotspot. <i>American Journal of Botany</i> , 2017, 104, 757-771.	0.8	9
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5671	Evolutionary processes in populations of <i>Cryptosporidium</i> inferred from gp60 sequence data. <i>Parasitology Research</i> , 2017, 116, 1855-1861.	0.6	10
5672	Phylogeography and allopolyploidization of <i>Magnolia</i> sect. <i>Gynopodium</i> (Magnoliaceae) in subtropical China. <i>Plant Systematics and Evolution</i> , 2017, 303, 957-967.	0.3	2
5673	Genetic diversity of giant clams (<i>Tridacna</i> spp.) and their associated <i>Symbiodinium</i> in the central Red Sea. <i>Marine Biodiversity</i> , 2017, 47, 1209-1222.	0.3	20
5674	Population structure in <i>Zeugodacus cucurbitae</i> (Diptera: Tephritidae) across Thailand and the Thai-Malay peninsula: natural barriers to a great disperser. <i>Biological Journal of the Linnean Society</i> , 2017, 121, 540-555.	0.7	10
5675	Description of four new species of Burrowing Frogs in the <i>Fejervarya rufescens</i> complex (Dicroglossidae) with notes on morphological affinities of <i>Fejervarya</i> species in the Western Ghats. <i>Zootaxa</i> , 2017, 4277, 451.	0.2	23
5676	Evidence for Adaptive Introgression of Disease Resistance Genes Among Closely Related <i>Arabidopsis</i> Species. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2677-2683.	0.8	31
5677	Where can introduced populations learn their tricks? Searching for the geographical source of a species introduction to the Galapagos archipelago. <i>Conservation Genetics</i> , 2017, 18, 1403-1422.	0.8	1
5678	Mitochondrial sequencing and geometric morphometrics suggest two clades in the <i>Tetragonilla collina</i> (Apidae: Meliponini) population of Thailand. <i>Apidologie</i> , 2017, 48, 719-731.	0.9	6
5679	Leaf elemental stoichiometry of <i>Tamarix</i> Lour. species in relation to geographic, climatic, soil, and genetic components in China. <i>Ecological Engineering</i> , 2017, 106, 448-457.	1.6	28
5680	Identification, genealogical structure and population genetics of S-alleles in <i>Malus sieversii</i> , the wild ancestor of domesticated apple. <i>Heredity</i> , 2017, 119, 185-196.	1.2	6
5681	Phylogeographical structure and demographic expansion in the endemic alpine stream salamander (Hynobiidae: <i>Batrachuperus</i>) of the Qinling Mountains. <i>Scientific Reports</i> , 2017, 7, 1871.	1.6	23
5682	Phylogeographic relationships among multi-island populations of the tree snail <i>Partula gibba</i> (Partulidae) in the Mariana Islands. <i>Biological Journal of the Linnean Society</i> , 2017, 121, 731-740.	0.7	5
5683	Reassessment of the phylogeography and intraspecific relationships of western and eastern populations of the boll weevil, <i>Anthonomus grandis</i> Boheman (Coleoptera: Curculionidae), in North America. <i>Biological Journal of the Linnean Society</i> , 2017, 122, 29-45.	0.7	13
5684	The effects of cultural drift on geographic variation in echolocation calls of the Chinese rufous horseshoe bat (<i>Rhinolophus sinicus</i>). <i>Ethology</i> , 2017, 123, 532-541.	0.5	14
5685	Signatures of soft sweeps across the <i>Dt1</i> locus underlying determinate growth habit in soya bean [<i>Glycine max</i> (L.) Merr.]. <i>Molecular Ecology</i> , 2017, 26, 4686-4699.	2.0	11
5686	Genetic variation of the mtDNA cyt b locus in topmouth gudgeon introduced into water bodies in the northern part of the Black Sea region. <i>Russian Journal of Genetics</i> , 2017, 53, 91-99.	0.2	0
5687	The mitogenome phylogeny of Adepaga (Coleoptera). <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 166-174.	1.2	70

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5689	Prevalence and evolutionary history of endosymbiont <i>Wolbachia</i> (Rickettsiales) in <i>Tephritidae</i> flies (Diptera: Tephritidae) infesting carambola. <i>Entomological Science</i> , 2017, 20, 382-395.	0.3	5
5690	Molecular genetic analysis of two native desert palm genera, <i>Washingtonia</i> and <i>Brahea</i> , from the Baja California Peninsula and Guadalupe Island. <i>Ecology and Evolution</i> , 2017, 7, 4919-4935.	0.8	22
5691	Nucleotide polymorphisms associated with climate, phenology and physiological traits in European beech (<i>Fagus sylvatica</i> L.). <i>New Forests</i> , 2017, 48, 463-477.	0.7	15
5692	Concerted evolution, a slow process for ant satellite DNA: study of the satellite DNA in the <i>Aphaenogaster</i> genus (Hymenoptera, Formicidae). <i>Organisms Diversity and Evolution</i> , 2017, 17, 595-606.	0.7	21
5693	Genetic data reveal a cryptic species of New World flying squirrel: <i>Glaucomys oregonensis</i> . <i>Journal of Mammalogy</i> , 2017, 98, 1027-1041.	0.6	29
5694	Genetic relationships of <i>Plagioscion squamosissimus</i> (Perciformes, Sciaenidae) from five Neotropical river basins evaluated using mitochondrial <i>atpase6/8</i> gene sequences. <i>Journal of Fish Biology</i> , 2017, 91, 375-384.	0.7	3
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5697	Genetic diversity of human papillomavirus types 35, 45 and 58 in cervical cancer in Brazil. <i>Archives of Virology</i> , 2017, 162, 2855-2860.	0.9	6
5698	Genetic divergence within the monotypic tree genus <i>Platycarya</i> (Juglandaceae) and its implications for species' past dynamics in subtropical China. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	11
5699	Purifying selection and concerted evolution of RNA-sensing toll-like receptors in migratory waders. <i>Infection, Genetics and Evolution</i> , 2017, 53, 135-145.	1.0	15
5700	Genotyping <i>Toxoplasma gondii</i> with the <i>B1</i> Gene in Naturally Infected Sheep from an Endemic Region in the Pacific Coast of Mexico. <i>Vector-Borne and Zoonotic Diseases</i> , 2017, 17, 495-502.	0.6	9
5701	Integrative taxonomy of the Central African forest chameleon, <i>Kinyongia adolfifrideric</i> (Sauria): the Linnean Society, 0, , .	1.0	6
5702	New insights into the systematics of Malagasy mongoose-like carnivorans (Carnivora, Eupleridae) and Evolutionary Research, 2017, 55, 250-264.	0.6	8
5703	Gene rearrangement and sequence analysis of mitogenomes suggest polyphyly of Archaeobalanid and Balanid barnacles (Cirripedia: Balanomorph). <i>Zoologica Scripta</i> , 2017, 46, 729-739.	0.7	15
5704	Phylogeography and genetic structure of endemic <i>Acmispon argophyllus</i> and <i>A. dendroideus</i> (Fabaceae) across the California Channel Islands. <i>American Journal of Botany</i> , 2017, 104, 743-756.	0.8	4
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5707	Divergence of paralogous growth-hormone-encoding genes and their promoters in salmonidae. <i>Molecular Biology</i> , 2017, 51, 274-282.	0.4	3
5708	Genomic variation associated with local adaptation of weedy rice during de-domestication. <i>Nature Communications</i> , 2017, 8, 15323.	5.8	132
5709	An appraisal of the enzyme stability-activity trade-off. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1876-1887.	1.1	46
5710	NLR locus-mediated trade-off between abiotic and biotic stress adaptation in <i>Arabidopsis</i> . <i>Nature Plants</i> , 2017, 3, 17072.	4.7	53
5711	Pioneer study of population genetics of <i>Rhodnius ecuadoriensis</i> (Hemiptera: Reduviidae) from the central coast and southern Andean regions of Ecuador. <i>Infection, Genetics and Evolution</i> , 2017, 53, 116-127.	1.0	15
5712	World without borders- genetic population structure of a highly migratory marine predator, the blue shark (<i>Prionace glauca</i>). <i>Ecology and Evolution</i> , 2017, 7, 4768-4781.	0.8	51
5713	Disentangling Timing of Admixture, Patterns of Introgression, and Phenotypic Indicators in a Hybridizing Wolf Population. <i>Molecular Biology and Evolution</i> , 2017, 34, 2324-2339.	3.5	62
5714	A worldwide phylogeography of the whiteworm lichens <i>Thamnolia</i> reveals three lineages with distinct habitats and evolutionary histories. <i>Ecology and Evolution</i> , 2017, 7, 3602-3615.	0.8	23
5715	Rice black-streaked dwarf virus Genome in China: Diversification, Phylogeny, and Selection. <i>Plant Disease</i> , 2017, 101, 1588-1596.	0.7	13
5716	Multilocus phylogeny of East African gerbils (<i>Rodentia</i> , <i>Gerbilliscus</i>) illuminates the history of the Somali-Masai savanna. <i>Journal of Biogeography</i> , 2017, 44, 2295-2307.	1.4	33
5717	Taking a detour: invasion of an octocoral into the Tropical Eastern Pacific. <i>Biological Invasions</i> , 2017, 19, 2583-2597.	1.2	7
5718	Limited genetic diversity in the global <i>Plasmodium vivax</i> Cell traversal protein of Ookinetes and Sporozoites (CelTOS) sequences; implications for PvCelTOS-based vaccine development. <i>Infection, Genetics and Evolution</i> , 2017, 53, 239-247.	1.0	22
5719	Genetic diversity of invasive populations of the florida crab (<i>Rhithropanopeus harrisi</i> (Gould, 1841): Tj ETQq1 1 0.784314 rgBT /Over 0.2		
5720	Plant Argonaute Proteins. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	1
5721	Genetic studies in the recently divergent <i>Eligmodontia puerulus</i> and <i>E. moreni</i> (<i>Rodentia</i> , <i>Cricetidae</i> ,) Tj ETQq1 1 0.784314 rgBT /Over 0.8		
5722	Systematic revision of <i>Acanthodactylus busacki</i> (<i>Squamata</i> : <i>Lacertidae</i>) with a description of a new species from Morocco. <i>Zootaxa</i> , 2017, 4276, 357.	0.2	5
5723	Phylogeny and taxonomy of the Socorro parakeet (<i>Psittacara holochlorus brevipes</i>): recent speciation with minor morphological differentiation. <i>Journal of Ornithology</i> , 2017, 158, 965-978.	0.5	2

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5724	Genetic Structure and Phylogeography of the Leopard Cat (<i>Prionailurus bengalensis</i>) Inferred from Mitochondrial Genomes. <i>Journal of Heredity</i> , 2017, 108, 349-360.	1.0	31
5725	Signatures of adaptive molecular evolution in American pikas (<i>Ochotona princeps</i>). <i>Journal of Mammalogy</i> , 2017, 98, 1156-1167.	0.6	7
5726	Identification and Evolutionary Characterization of ARGONAUTE-Binding Platforms. <i>Methods in Molecular Biology</i> , 2017, 1640, 257-266.	0.4	1
5727	The Near East as a cradle of biodiversity: A phylogeography of banded newts (genus <i>Ommatotriton</i>) reveals extensive inter- and intraspecific genetic differentiation. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 73-81.	1.2	37
5728	Species complex delimitation and patterns of population structure at different geographic scales in Neotropical silver catfish (<i>Rhamdia: Heptapteridae</i>). <i>Environmental Biology of Fishes</i> , 2017, 100, 1047-1067.	0.4	10
5729	Occurrence and molecular characterization of hemoplasmas in domestic dogs and wild mammals in a Brazilian wetland. <i>Acta Tropica</i> , 2017, 171, 172-181.	0.9	36
5730	The niche and phylogeography of a passerine reveal the history of biological diversification between the Andean and the Atlantic forests. <i>Molecular Phylogenetics and Evolution</i> , 2017, 112, 107-121.	1.2	39
5731	Comparative Molecular and Morphological Variation Analysis of <i>Siderastrea</i> (Anthozoa, Scleractinia) Reveals the Presence of <i>Siderastrea stellata</i> in the Gulf of Mexico. <i>Biological Bulletin</i> , 2017, 232, 58-70.	0.7	5
5732	Diversity and distribution of the Italian Aesculapian snake <i>Zamenis lineatus</i> : A phylogeographic assessment with implications for conservation. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2017, 55, 222-237.	0.6	7
5733	Genetic entanglement between <i>Cercospora</i> species associating soybean purple seed stain. <i>Mycological Progress</i> , 2017, 16, 593-603.	0.5	10
5734	Genomic structure, polymorphism, and expression analysis of the spotted scat <i>Scatophagus argus</i> major histocompatibility complex class I alpha gene. <i>Fisheries Science</i> , 2017, 83, 433-446.	0.7	0
5735	Phylogeography and geno-phenotypic discordance in a widespread Australian bird, the Variegated Fairy-wren, <i>Malurus lamberti</i> (Aves: Maluridae). <i>Biological Journal of the Linnean Society</i> , 2017, 121, 655-669.	0.7	13
5736	Genetic diversity of <i>Diaphorina citri</i> and its endosymbionts across east and south-east Asia. <i>Pest Management Science</i> , 2017, 73, 2090-2099.	1.7	15
5737	Weaving through a cryptic species: Comparing the Neotropical ants <i>Camponotus senex</i> and <i>Camponotus textor</i> (Hymenoptera: Formicidae). <i>Micron</i> , 2017, 99, 56-66.	1.1	5
5738	A specific genetic marker for the discrimination of native Bulgarian honey bees (<i>Apis mellifera</i>)	0.7	8
5739	Phenotypic and genotypic variation across a stable white-eye (<i>Zosterops</i> sp.) hybrid zone in central South Africa. <i>Biological Journal of the Linnean Society</i> , 2017, 121, 670-684.	0.7	12
5740	Transposable Element-Mediated Balancing Selection at <i>Hsp90</i> Underlies Embryo Developmental Variation. <i>Molecular Biology and Evolution</i> , 2017, 34, msx062.	3.5	6
5741	Genetic structure reveals management units for the yellow cardinal (<i>Gubernatrix cristata</i>), endangered by habitat loss and illegal trapping. <i>Conservation Genetics</i> , 2017, 18, 1131-1140.	0.8	23

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5742	Mitochondrial haplotype distribution and phylogenetic relationship of an endangered species Reeve's turtle (<i>Mauremys reevesii</i>) in East Asia. <i>Journal of Asia-Pacific Biodiversity</i> , 2017, 10, 27-31.	0.2	5
5743	Distinct patterns of natural selection in Na ⁺ /H ⁺ antiporter genes in <i>Populus euphratica</i> and <i>Populus pruinosa</i> . <i>Ecology and Evolution</i> , 2017, 7, 82-91.	0.8	6
5744	Natural variation in CTB4a enhances rice adaptation to cold habitats. <i>Nature Communications</i> , 2017, 8, 14788.	5.8	192
5745	Caprine and ovine Greek dairy products: The official German method generates false-positive results due to Î²-casein gene polymorphism. <i>Journal of Dairy Science</i> , 2017, 100, 3539-3547.	1.4	3
5746	Molecular evolution of glutathione peroxidase (Gpx) family genes in desert poplar (<i>Populus</i>). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 T</i>	0.6	4
5747	Subspecies boundaries and recent evolution history of the common pheasant (<i>Phasianus colchicus</i>) across China. <i>Biochemical Systematics and Ecology</i> , 2017, 71, 155-162.	0.6	3
5748	On the importance of geographic and taxonomic sampling in phylogeography: A reevaluation of diversification and species limits in a Neotropical thrush (Aves, Turdidae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 87-97.	1.2	23
5749	Cryptic species and colonization processes in <i>Ophryotrocha</i> (Annelida, Dorvilleidae) inhabiting vertebrate remains in the shallow-water Mediterranean. <i>Zoologica Scripta</i> , 2017, 46, 611-624.	0.7	8
5750	Molecular Population Genetics. <i>Genetics</i> , 2017, 205, 1003-1035.	1.2	100
5751	Mitochondrial DNA variation and population genetic structure in the small yellow croaker at the coast of Yellow Sea and East China Sea. <i>Biochemical Systematics and Ecology</i> , 2017, 71, 236-243.	0.6	5
5752	Revision of the <i>Eurycea quadridigitata</i> (Holbrook 1842) Complex of Dwarf Salamanders (Caudata). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 T</i> 2017, 31, 18.	1.1	6
5753	The genetic diversity analysis in the donkey myostatin gene. <i>Journal of Integrative Agriculture</i> , 2017, 16, 656-663.	1.7	3
5754	Genome-wide identification of membrane-bound fatty acid desaturase genes in <i>Gossypium hirsutum</i> and their expressions during abiotic stress. <i>Scientific Reports</i> , 2017, 7, 45711.	1.6	31
5755	Population Structure of Alligator Gar in a Gulf Coast River: Insights from Otolith Microchemistry and Genetic Analyses. <i>North American Journal of Fisheries Management</i> , 2017, 37, 337-348.	0.5	16
5756	High mitochondrial DNA diversity and lack of population structure in a solitary cavity-nesting bee in an urban landscape. <i>Biological Journal of the Linnean Society</i> , 2017, 121, 564-575.	0.7	8
5757	Genetic Population Structure of <i>Dastarcus helophoroides</i> (Coleoptera: Bothrideridae) From Different Long-Horned Beetle Hosts Based on Complete Sequences of Mitochondrial COI. <i>Journal of Economic Entomology</i> , 2017, 110, 1275-1283.	0.8	4
5758	Molecular analysis of invasive <i>Cichla</i> (Perciformes: Cichlidae) populations from neotropical ecosystems. <i>Biochemical Systematics and Ecology</i> , 2017, 72, 15-22.	0.6	6
5759	The systematics of the Mexican populations of <i>Macrobrachium digueti</i> (Bouvier, 1895) (Decapoda). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 582 T</i>	0.3	7

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5760	Do larval types affect genetic connectivity at sea? Testing hypothesis in two sibling marine gastropods with contrasting larval development. <i>Marine Environmental Research</i> , 2017, 127, 92-101.	1.1	25
5761	Genetic diversity and population structure of the <i>Bacillus cereus</i> group bacteria from diverse marine environments. <i>Scientific Reports</i> , 2017, 7, 689.	1.6	47
5762	Genetic diversity and Quaternary range dynamics in Iranian and Transcaucasian tortoises. <i>Biological Journal of the Linnean Society</i> , 2017, 121, 627-640.	0.7	10
5763	Expansion after expansion: dissecting the phylogeography of the widely distributed spur-thighed tortoise, <i>Testudo graeca</i> (Testudines: Testudinidae). <i>Biological Journal of the Linnean Society</i> , 2017, 121, 641-654.	0.7	24
5764	Model-based analyses reveal insular population diversification and cryptic frog species in the <i>Ischnocnema parva</i> complex in the Atlantic forest of Brazil. <i>Molecular Phylogenetics and Evolution</i> , 2017, 112, 68-78.	1.2	20
5765	Comparative population genetics of two dominant plant species of high Andean wetlands reveals complex evolutionary histories and conservation perspectives in Chile's Norte Chico. <i>Conservation Genetics</i> , 2017, 18, 1047-1060.	0.8	6
5766	Molecular diversity and phylogenetic analysis of domestic and wild Bactrian camel populations based on the mitochondrial ATP8 and ATP6 genes. <i>Livestock Science</i> , 2017, 199, 95-100.	0.6	11
5767	asymptoticMK: A Web-Based Tool for the Asymptotic McDonald's-Kreitman Test. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1569-1575.	0.8	34
5768	Convergent adaptation to dangerous prey proceeds through the same first-step mutation in the garter snake <i>Thamnophis sirtalis</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1504-1518.	1.1	22
5769	Four new genera of funnel-web spiders (Araneae: Agelenidae) from the Baja California Peninsula in Mexico. <i>Journal of Arachnology</i> , 2017, 45, 30-66.	0.3	5
5770	Integration of molecular, bioacoustical and morphological data reveals two new cryptic species of <i>Pelodytes</i> (Anura, Pelodytidae) from the Iberian Peninsula. <i>Zootaxa</i> , 2017, 4243, 1-41.	0.2	22
5771	Sequencing and quantifying plastid DNA fragments stored in sapwood and heartwood of <i>Torreya nucifera</i> . <i>Journal of Wood Science</i> , 2017, 63, 201-208.	0.9	2
5772	Nucleotide diversity and phylogenetic relationships among <i>Gladiolus</i> cultivars and related taxa of family Iridaceae. <i>Journal of Genetics</i> , 2017, 96, 135-145.	0.4	6
5773	Genetic diversity and spatial structure of the Rufous-throated Antbird (<i>Gymnopithys rufigula</i>), an Amazonian obligate army-ant follower. <i>Ecology and Evolution</i> , 2017, 7, 2671-2684.	0.8	5
5774	Selection and genetic drift in captive versus wild populations: an assessment of neutral and adaptive (MHC-linked) genetic variation in wild and hatchery brown trout (<i>Salmo trutta</i>) populations. <i>Conservation Genetics</i> , 2017, 18, 1011-1022.	0.8	14
5775	Genetic diversity and population structure of food-borne <i>Staphylococcus carnosus</i> strains. <i>Systematic and Applied Microbiology</i> , 2017, 40, 34-41.	1.2	5
5776	Polymorphisms of the Toll-Like Receptor 2 of Goats (<i>Capra hircus</i>) may be Associated with Somatic Cell Count in Milk. <i>Animal Biotechnology</i> , 2017, 28, 112-119.	0.7	7
5777	Phylogeny and Haplotype Analysis of Fungi Within the <i>Fusarium incarnatum-equiseti</i> Species Complex. <i>Phytopathology</i> , 2017, 107, 109-120.	1.1	29

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5778	Testing eight barcoding markers for Potamogeton species at intraspecific levels. Aquatic Botany, 2017, 137, 56-64.	0.8	7
5779	Nuclear and mitochondrial DNA analysis reveals that hybridization between <i>Fasciola hepatica</i> and <i>Fasciola gigantica</i> occurred in China. Parasitology, 2017, 144, 206-213.	0.7	40
5780	New Multilocus Variable-Number Tandem-Repeat Analysis (MLVA) Scheme for Fine-Scale Monitoring and Microevolution-Related Study of <i>Ralstonia pseudosolanacearum</i> Phylotype I Populations. Applied and Environmental Microbiology, 2017, 83, .	1.4	33
5781	Co-phylogeographic study of the flatworm <i>Gyrodactylus gondae</i> and its goby host <i>Pomatoschistus minutus</i> . Parasitology International, 2017, 66, 119-125.	0.6	15
5782	Phylogeography of the reef-building polychaetes of the genus <i>Phragmatopoma</i> in the western Atlantic Region. Journal of Biogeography, 2017, 44, 1612-1625.	1.4	19
5783	Endemic species may have complex histories: within-refugium phylogeography of an endangered Iberian vole. Molecular Ecology, 2017, 26, 951-967.	2.0	26
5784	Assessment of genetic diversity among four orchids based on ddRAD sequencing data for conservation purposes. Physiology and Molecular Biology of Plants, 2017, 23, 169-183.	1.4	17
5785	Following the Antarctic Circumpolar Current: patterns and processes in the biogeography of the limpet <i>Nacella</i> (Mollusca: Patellogastropoda) across the Southern Ocean. Journal of Biogeography, 2017, 44, 861-874.	1.4	41
5786	Genetic structure in the European endemic seabird, <i>Phalacrocorax aristotelis</i> , shaped by a complex interaction of historical and contemporary, physical and nonphysical drivers. Molecular Ecology, 2017, 26, 2796-2811.	2.0	10
5787	Molecular species delimitation in the genus <i>Eumerus</i> (Diptera: Syrphidae). Bulletin of Entomological Research, 2017, 107, 126-138.	0.5	30
5788	East-west divergence in central Brazilian Cerrado revealed by cpDNA sequences of a bird-dispersed tree species. Biochemical Systematics and Ecology, 2017, 70, 247-253.	0.6	15
5789	Marked phylogeographic structure of Gentoo penguin reveals an ongoing diversification process along the Southern Ocean. Molecular Phylogenetics and Evolution, 2017, 107, 486-498.	1.2	39
5790	The genetic architecture of tristylly and its breakdown to self-fertilization. Molecular Ecology, 2017, 26, 752-765.	2.0	9
5791	<i>Ascaris</i> phylogeny based on multiple whole mtDNA genomes. Infection, Genetics and Evolution, 2017, 48, 4-9.	1.0	19
5792	Molecular phylogeny, biogeography and ecological niche modelling of <i>Cardiocrinum</i> (Liliaceae): insights into the evolutionary history of endemic genera distributed across the Sino-Japanese floristic region. Annals of Botany, 2017, 119, 59-72.	1.4	25
5793	Searching for the glacial refugia of <i>Erebia euryale</i> (Lepidoptera, Nymphalidae) - insights from mtDNA- and nDNA-based phylogeography in the Western Carpathians. Journal of Zoological Systematics and Evolutionary Research, 2017, 55, 118-128.	0.6	4
5794	Prevalence, hematological findings and genetic diversity of <i>Bartonella</i> spp. in domestic cats from Valdivia, Southern Chile. Parasitology, 2017, 144, 773-782.	0.7	27
5795	Analysis of the histone cluster in Senegalese sole (<i>Solea senegalensis</i>): evidence for a divergent evolution of two canonical histone clusters. Genome, 2017, 60, 441-453.	0.9	15

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5796	Increase in density of genetically diverse invasive Asian shore crab (<i>Hemigrapsus sanguineus</i>) populations in the Gulf of Maine. <i>Biological Invasions</i> , 2017, 19, 1153-1168.	1.2	22
5797	Molecular and phylogenetic analyses of the liver amphistome <i>Explanatum explanatum</i> (Creplin, 1847) Fukui, 1929 in ruminants from Bangladesh and Nepal based on nuclear ribosomal ITS2 and mitochondrial nad1 sequences. <i>Journal of Helminthology</i> , 2017, 91, 497-503.	0.4	7
5798	Genetic variation and population structure of Cucumber green mottle mosaic virus. <i>Archives of Virology</i> , 2017, 162, 1159-1168.	0.9	13
5799	Purifying selection and genetic drift shaped Pleistocene evolution of the mitochondrial genome in an endangered Australian freshwater fish. <i>Heredity</i> , 2017, 118, 466-476.	1.2	39
5800	Contrasting genetic diversity and intra-population polymorphism of the invasive pest <i>Henosepilachna vigintioctopunctata</i> (Coleoptera, Coccinellidae): A DNA barcoding approach. <i>Journal of Asia-Pacific Entomology</i> , 2017, 20, 23-29.	0.4	12
5801	The complete mitochondrial genome of <i>Diaphorina citri</i> (Hemiptera: Psyllidae) and phylogenetic analysis. <i>Biochemical Systematics and Ecology</i> , 2017, 70, 230-238.	0.6	5
5802	Mountains too high and valleys too deep drive population structuring and demographics in a Qinghai Tibetan Plateau frog <i>Nanorana pleskei</i> (Dicroglossidae). <i>Ecology and Evolution</i> , 2017, 7, 240-252.	0.8	18
5803	Ancient origin and recent range expansion of the maize weevil <i>Sitophilus zeamais</i> , and its genealogical relationship to the rice weevil <i>S. oryzae</i> . <i>Bulletin of Entomological Research</i> , 2017, 107, 9-20.	0.5	38
5804	Phylogeographic structuring of plastome diversity in Mediterranean oaks (<i>Quercus</i> Group Ilex). <i>Trends in Ecology and Evolution</i> , 2017, 32, 1058-1066.	0.6	58
5805	Evolutionary history of a keystone pollinator parallels the biome occupancy of angiosperms in the Greater Cape Floristic Region. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 530-537.	1.2	10
5806	Diversity of tortricid moths in apple orchards: evidence for a cryptic species of <i>Grapholita</i> (Lepidoptera: Tortricidae) from China. <i>Bulletin of Entomological Research</i> , 2017, 107, 268-280.	0.5	5
5807	GRAIN INCOMPLETE FILLING 2 regulates grain filling and starch synthesis during rice caryopsis development. <i>Journal of Integrative Plant Biology</i> , 2017, 59, 134-153.	4.1	80
5808	Phylogenetic relationships in <i>Kerkia</i> and introgression between <i>Hauffenia</i> and <i>Kerkia</i> (Caenogastropoda: Hydrobiidae). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2017, 55, 106-117.	0.6	26
5809	Dynein light chain family genes in 15 plant species: Identification, evolution and expression profiles. <i>Plant Science</i> , 2017, 254, 70-81.	1.7	14
5810	Genetic polymorphism and population structure of <i>Echinococcus ortleppi</i> . <i>Parasitology</i> , 2017, 144, 450-458.	0.7	35
5811	A reappraisal of <i>Stegastes</i> species occurring in the South Atlantic using morphological and molecular data. <i>Helgolander Marine Research</i> , 2017, 70, .	1.3	5
5812	Ancient diversification in glacial refugia leads to intraspecific diversity in a Holarctic mammal. <i>Journal of Biogeography</i> , 2017, 44, 386-396.	1.4	28
5813	Fine-scale phylogeography of <i>Rana temporaria</i> (Anura: Ranidae) in a putative secondary contact zone in the southern Alps. <i>Biological Journal of the Linnean Society</i> , 2017, 122, 824-837.	0.7	10

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5814	Genetic Diversity and Identification of Palearctic Black Flies in the Subgenus <i>Wilhelmia</i> (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 7	0.9	7
5815	Comparative analysis of complete chloroplast genome sequences of two subtropical trees, <i>Phoebe sheareri</i> and <i>Phoebe omeiensis</i> (Lauraceae). <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	30
5816	Genotypes of IFIH1 and IFIT5 in seven chicken breeds indicated artificial selection for commercial traits influenced antiviral genes. <i>Infection, Genetics and Evolution</i> , 2017, 56, 54-61.	1.0	5
5817	Inter-individual and intragenomic variations in the ITS region of <i>Clonorchis sinensis</i> (Trematoda: Tj ETQq1 1 0.784314 rgBT /Overlock 18	1.0	18
5818	Duplication of an upstream silencer of FZP increases grain yield in rice. <i>Nature Plants</i> , 2017, 3, 885-893.	4.7	121
5819	Geographic patterns of genetic variation in nuclear and chloroplast genomes of two related oaks (<i>Quercus aliena</i> and <i>Q. serrata</i>) in Japan: implications for seed and seedling transfer. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	14
5820	Assessing Genetic Diversity in Four Stink Bug Species, <i>Chinavia hilaris</i> , <i>Chlorochroa uhleri</i> , <i>Chlorochroa sayi</i> , and <i>Thyanta pallidovirens</i> (Hemiptera: Pentatomidae), Using DNA Barcodes. <i>Journal of Economic Entomology</i> , 2017, 110, 2590-2598.	0.8	14
5821	Legume isoflavone synthase genes have evolved by whole-genome and local duplications yielding transcriptionally active paralogs. <i>Plant Science</i> , 2017, 264, 149-167.	1.7	13
5822	Morphological and Molecular Characterization of <i>Aggregata</i> spp. Frenzel 1885 (Apicomplexa: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 427 Protist, 2017, 168, 636-648.	0.6	12
5823	Unexpected mosaic distribution of two hybridizing sibling lineages in the teleplanically dispersing snail <i>Stramonita haemastoma</i> suggests unusual postglacial redistribution or cryptic invasion. <i>Ecology and Evolution</i> , 2017, 7, 9016-9026.	0.8	11
5824	<i>Streptococcus Mutans</i> Adhesin Biotypes that Match and Predict Individual Caries Development. <i>EBioMedicine</i> , 2017, 24, 205-215.	2.7	58
5825	Comparative mitogenomic analysis of <i>Aposthonia borneensis</i> and <i>Aposthonia japonica</i> (Embioptera: Tj ETQq1 1 0.784314 rgBT /Overlock 3	1.6	3
5826	Low mitochondrial diversity in native Italian pig breeds is consistent with the occurrence of strong population bottlenecks. <i>Animal Genetics</i> , 2017, 48, 726-727.	0.6	0
5827	Phylogeographic and genome-wide investigations of Vietnam ethnic groups reveal signatures of complex historical demographic movements. <i>Scientific Reports</i> , 2017, 7, 12630.	1.6	17
5828	Characterization of the complete mitochondrial genomes of <i>Maiestas dorsalis</i> and <i>Japananus hyalinus</i> (Hemiptera: Cicadellidae) and comparison with other Membracoidea. <i>Scientific Reports</i> , 2017, 7, 14197.	1.6	46
5829	Genetic divergence between two phenotypically distinct bottlenose dolphin ecotypes suggests separate evolutionary trajectories. <i>Ecology and Evolution</i> , 2017, 7, 9131-9143.	0.8	32
5830	Morphometric characteristics and COI haplotype diversity of <i>Arctodiaptomus spinosus</i> (Copepoda) populations in soda pans in Hungary. <i>Acta Biologica Hungarica</i> , 2017, 68, 279-289.	0.7	2
5831	Beneath the hairy look: the hidden reproductive diversity of the <i>Gibsmithia hawaiiensis</i> complex (Dumontiaceae, Rhodophyta). <i>Journal of Phycology</i> , 2017, 53, 1171-1192.	1.0	11

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5832	Phylogeographic Characterization of Genetic Variation in the Biological Control Agent Milfoil Weevil (<i>Euhrychiopsis lecontei</i>) throughout North America. <i>American Midland Naturalist</i> , 2017, 178, 260-274.	0.2	1
5833	Association analysis of the glutelin synthesis genes GluA and GluB1 in a Japonica rice collection. <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	4
5834	The roles of barriers, refugia, and chromosomal clines underlying diversification in Atlantic Forest social wasps. <i>Scientific Reports</i> , 2017, 7, 7689.	1.6	33
5835	Origins of the Greenland shark (<i>Somniosus microcephalus</i>): Impacts of ice isolation and introgression. <i>Ecology and Evolution</i> , 2017, 7, 8113-8125.	0.8	14
5836	Phylogeographic and phylogenetic analysis for <i>Tripterygium</i> species delimitation. <i>Ecology and Evolution</i> , 2017, 7, 8612-8623.	0.8	16
5837	Genetic variations of HvP5CS1 and their association with drought tolerance related traits in barley (<i>Hordeum vulgare</i> L.). <i>Scientific Reports</i> , 2017, 7, 7870.	1.6	39
5838	Mitochondrial DNA analyses of narrow-barred Spanish mackerel (<i>Scomberomorus commerson</i>) sampled from the Arabian Sea, the Bay of Bengal, and the Indo-Malay archipelago. <i>Zoology and Ecology</i> , 2017, 27, 245-250.	0.2	2
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5840	Deep-Sea Phylogeographic Structure Shaped by Paleoenvironmental Changes and Ongoing Ocean Currents Around the Sea of Japan in a Crangonid Shrimp, <i>Argis</i> lar. <i>Zoological Science</i> , 2017, 34, 406-413.	0.3	4
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5842	Genetic variation and population structure of a threatened timber tree <i>Dalbergia cochinchinensis</i> in Cambodia. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	10
5843	Conservation implications for dingoes from the maternal and paternal genome: Multiple populations, dog introgression, and demography. <i>Ecology and Evolution</i> , 2017, 7, 9787-9807.	0.8	33
5844	Radiation of the polymorphic Little Devil poison frog (<i>Oophaga sylvatica</i>) in Ecuador. <i>Ecology and Evolution</i> , 2017, 7, 9750-9762.	0.8	19
5845	Identification and characterization of phosphate transporter genes in potato. <i>Journal of Biotechnology</i> , 2017, 264, 17-28.	1.9	29
5846	DnaSP 6: DNA Sequence Polymorphism Analysis of Large Data Sets. <i>Molecular Biology and Evolution</i> , 2017, 34, 3299-3302.	3.5	4,056
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5848	Phylogeography of the snake pipefish, <i>Entelurus aequoreus</i> (Family: Syngnathidae) in the northeastern Atlantic Ocean. <i>Biological Journal of the Linnean Society</i> , 2017, 122, 787-800.	0.7	7
5849	Phylogenetics, phylogeography and vicariance of polyphyletic <i>Grammosciadium</i> (Apiaceae: Careae) in Anatolia. <i>Botanical Journal of the Linnean Society</i> , 2017, 185, 168-188.	0.8	13

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5851	Avian haemosporidian detection across source materials: prevalence and genetic diversity. <i>Parasitology Research</i> , 2017, 116, 3361-3371.	0.6	8
5852	Characterization of classical major histocompatibility complex (MHC) class II genes in northern pig-tailed macaques (<i>Macaca leonina</i>). <i>Infection, Genetics and Evolution</i> , 2017, 56, 26-35.	1.0	6
5853	Diversification and convergence of aposematic phenotypes: truncated receptors and cellular arrangements mediate rapid evolution of coloration in harlequin poison frogs. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 2677-2692.	1.1	13
5854	Evaluating hypotheses of expansion from refugia through comparative phylogeography of southeastern Coastal Plain amphibians. <i>Journal of Biogeography</i> , 2017, 44, 2692-2705.	1.4	29
5855	Cryptic diversity of marine gastropod <i>Monodonta labio</i> (Trochidae): did the early Pleistocene glacial isolation and sea surface temperature gradient jointly drive diversification of sister species and/or subspecies in the Northwestern Pacific?. <i>Marine Ecology</i> , 2017, 38, e12443.	0.4	26
5856	Allopatric divergence, demographic history, and conservation implications of an endangered conifer <i>Cupressus chengiana</i> in the eastern Qinghai-Tibet Plateau. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	9
5857	Characterization of major histocompatibility complex class I, and class II DRB loci of captive and wild Indian leopards (<i>Panthera pardus fusca</i>). <i>Genetica</i> , 2017, 145, 541-558.	0.5	5
5858	<i>Leptospira</i> species molecular epidemiology in the genomic era. <i>Infection, Genetics and Evolution</i> , 2017, 54, 478-485.	1.0	10
5859	Exploring the role of within-island ecogeographical factors: insights from the genetic diversity of Cretan trap-door spiders (<i>Cyrtocarenum cunicularium</i> , Ctenizidae : Araneae). <i>Invertebrate Systematics</i> , 2017, 31, 506.	0.5	4
5860	The role of climatic and geological events in generating diversity in Ethiopian grass frogs (genus <i>Ptychadena</i>). <i>Royal Society Open Science</i> , 2017, 4, 170021.	1.1	11
5861	<i>Torix</i> group <i>Rickettsia</i> are widespread in <i>Culicoides</i> biting midges (Diptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50). <i>Microbiology</i> , 2017, 19, 4238-4255.	1.8	41
5862	Genetic isolation in an endemic African habitat specialist. <i>Ibis</i> , 2017, 159, 792-802.	1.0	4
5863	Low levels of genetic diversity associated with evidence of negative selection on the <i>Babesia bovis</i> apical membrane antigen 1 from parasite populations in Thailand. <i>Infection, Genetics and Evolution</i> , 2017, 54, 447-454.	1.0	15
5864	Diversity and distribution of genetic variation in gammarids: Comparing patterns between invasive and non-invasive species. <i>Ecology and Evolution</i> , 2017, 7, 7687-7698.	0.8	18
5865	Molecular phylogeny and phylogeography of genus <i>Pseudois</i> (Bovidae, Cetartiodactyla): New insights into the contrasting phylogeographic structure. <i>Ecology and Evolution</i> , 2017, 7, 7047-7057.	0.8	8
5866	Genome-Wide Analysis and Expression Profiles of the MYB Genes in <i>Brachypodium distachyon</i> . <i>Plant and Cell Physiology</i> , 2017, 58, 1777-1788.	1.5	41
5867	So similar and yet so different: taxonomic status of Pallid Swift <i>Apus pallidus</i> and Common Swift <i>Apus apus</i> . <i>Bird Study</i> , 2017, 64, 344-352.	0.4	14

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5869	Mitochondrial <i>scp</i> DNA variation in Ukrainian wild boars. <i>Animal Genetics</i> , 2017, 48, 725-726.	0.6	1
5870	Crop-wild sunflower hybridization can mediate weediness throughout growth-stress tolerance trade-offs. <i>Agriculture, Ecosystems and Environment</i> , 2017, 249, 12-21.	2.5	17
5871	Maedi-visna virus persistence: Antigenic variation and latency. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2017, 55, 6-12.	0.7	5
5872	Development of chloroplast genome resources for peanut (<i>Arachis hypogaea</i> L.) and other species of <i>Arachis</i> . <i>Scientific Reports</i> , 2017, 7, 11649.	1.6	44
5873	Genetic diversity and population structure of <i>Taxus cuspidata</i> Sieb. et Zucc. ex Endl. (Taxaceae) in Russia according to data of the nucleotide polymorphism of intergenic spacers of the chloroplast genome. <i>Russian Journal of Genetics</i> , 2017, 53, 865-874.	0.2	5
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5876	Phylogeography and demographic history of Siberian rubythroat <i>Luscinia calliope</i> . <i>Russian Journal of Genetics</i> , 2017, 53, 885-902.	0.2	4
5877	Evaluating the role of Pleistocene refugia, rivers and environmental variation in the diversification of central African duikers (genera <i>Cephalophus</i> and <i>Philantomba</i>). <i>BMC Evolutionary Biology</i> , 2017, 17, 212.	3.2	7
5878	Phylogeographic studies of schizothoracine fishes on the central Qinghai-Tibet Plateau reveal the highest known glacial microrefugia. <i>Scientific Reports</i> , 2017, 7, 10983.	1.6	35
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5881	Control Region of mtDNA identifies three migration events of sheep breeds in Algeria. <i>Small Ruminant Research</i> , 2017, 155, 66-71.	0.6	20
5882	Genetic diversity within populations of an arctic alpine species declines with decreasing latitude across the Northern Hemisphere. <i>Journal of Biogeography</i> , 2017, 44, 2740-2751.	1.4	21
5883	Genetic diversity of the pulmonate mollusk <i>Arianta arbustorum</i> L. in Leningrad region. <i>Russian Journal of Genetics: Applied Research</i> , 2017, 7, 640-647.	0.4	1
5884	Mitogenome Sequencing in the Genus <i>Camelus</i> Reveals Evidence for Purifying Selection and Long-term Divergence between Wild and Domestic Bactrian Camels. <i>Scientific Reports</i> , 2017, 7, 9970.	1.6	45
5885	Evolutionarily significant units of the critically endangered leaf frog <i>Pithecopus ayeaye</i> (Anura, Phyllomedusidae) are not effectively preserved by the Brazilian protected areas network. <i>Ecology and Evolution</i> , 2017, 7, 8812-8828.	0.8	20

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5887	Vertical Transmission of Hepatitis C Virus: Variable Transmission Bottleneck and Evidence of Midgestation <i>In Utero</i> Infection. <i>Journal of Virology</i> , 2017, 91, .	1.5	18
5888	Genetic diversity of bottlenose dolphin (<i>Tursiops</i> sp.) populations in the western North Pacific and the conservation implications. <i>Marine Biology</i> , 2017, 164, 202.	0.7	18
5889	Genomic DNA variation confirmed <i>Seriola lalandi</i> comprises three different populations in the Pacific, but with recent divergence. <i>Scientific Reports</i> , 2017, 7, 9386.	1.6	24
5890	The extraordinary variation of the organellar genomes of the <i>Aneura pinguis</i> revealed advanced cryptic speciation of the early land plants. <i>Scientific Reports</i> , 2017, 7, 9804.	1.6	34
5891	The complete mtDNA sequence of the griffon vulture (<i>Gyps fulvus</i>): Phylogenetic analysis and haplotype frequency variations after restocking in the Sardinian population. <i>Biological Conservation</i> , 2017, 214, 195-205.	1.9	11
5892	Origin and invasion of the emerging infectious pathogen <i>Sphaerothecum destruens</i> . <i>Emerging Microbes and Infections</i> , 2017, 6, 1-8.	3.0	11
5893	Genomic insights into the ancient spread of Lyme disease across North America. <i>Nature Ecology and Evolution</i> , 2017, 1, 1569-1576.	3.4	39
5894	Cryptic diversity of the jewel beetles <i>Agrilus viridis</i> (Coleoptera: Buprestidae) hosted on hazelnut. , 2017, 84, 465-472.		4
5895	Pleistocene refugia in the Chihuahuan Desert: the phylogeographic and demographic history of the gymnosperm <i>Ephedra compacta</i> . <i>Journal of Biogeography</i> , 2017, 44, 2706-2716.	1.4	35
5896	The effects of Quaternary sea-level fluctuations on the evolutionary history of an endemic ground lizard (<i>Tropidurus hygomi</i>). <i>Zoologischer Anzeiger</i> , 2017, 270, 1-8.	0.4	2
5897	Crossing the Divide: Admixture Across the Antarctic Polar Front Revealed by the Brittle Star <i>Astrota agassizii</i> . <i>Biological Bulletin</i> , 2017, 232, 198-211.	0.7	24
5898	Application of the ITS2 region for barcoding plants of the genus <i>Triticum</i> L. and <i>Aegilops</i> L.. <i>Cereal Research Communications</i> , 2017, 45, 381-389.	0.8	7
5899	Complete chloroplast genome sequences of <i>Lilium</i> : insights into evolutionary dynamics and phylogenetic analyses. <i>Scientific Reports</i> , 2017, 7, 5751.	1.6	96
5900	Low intraspecific genetic divergence and weak niche differentiation despite wide ranges and extensive sympatry in two epigeal <i>Niphargus</i> species (Crustacea: Amphipoda). <i>Zoological Journal of the Linnean Society</i> , 2017, 181, 485-499.	1.0	28
5901	Incomplete lineage sorting and hybridization in the evolutionary history of closely related, endemic yellow-flowered <i>Aechmea</i> species of subgenus <i>Ortgiesia</i> (Bromeliaceae). <i>American Journal of Botany</i> , 2017, 104, 1073-1087.	0.8	31
5902	Cryptic lineages and high population genetic structure in the exploited marine snail <i>Hexaplex trunculus</i> (Gastropoda: Muricidae). <i>Biological Journal of the Linnean Society</i> , 2017, 122, 411-428.	0.7	9
5903	Population genetic structure of <i>Calanoides natalis</i> (Copepoda, Calanoida) in the eastern Atlantic Ocean and Benguela upwelling system. <i>Journal of Plankton Research</i> , 2017, 39, 618-630.	0.8	6

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5905	Genetic variability of anchovy in the Azov-Black Sea basin. <i>Russian Journal of Genetics</i> , 2017, 53, 680-687.	0.2	5
5906	Molecular systematics, species delimitation and diversification patterns of the <i>Phyllodactylus lanei</i> complex (Gekkota: Phyllodactylidae) in Mexico. <i>Molecular Phylogenetics and Evolution</i> , 2017, 115, 82-94.	1.2	12
5907	Multilocus sequence typing and clonal population genetic structure of <i>Cyclospora cayatanensis</i> in humans. <i>Parasitology</i> , 2017, 144, 1890-1897.	0.7	23
5908	Time scaled phylogeography and demography of <i>Bradypus torquatus</i> (Pilosa: Bradypodidae). <i>Global Ecology and Conservation</i> , 2017, 11, 224-235.	1.0	8
5909	Population structure and cryptic species in the cosmopolitan rotifer <i>Euchlanis dilatata</i> . <i>Zoological Journal of the Linnean Society</i> , 2017, 181, 757-777.	1.0	18
5910	Trans-biome diversity in Australian grass-specialist lizards (Diplodactylidae: Strophurus). <i>Molecular Phylogenetics and Evolution</i> , 2017, 115, 62-70.	1.2	16
5911	Pathogen richness and abundance predict patterns of adaptive major histocompatibility complex variation in insular amphibians. <i>Molecular Ecology</i> , 2017, 26, 4671-4685.	2.0	23
5912	Molecular data and distribution dynamics indicate a recent and incomplete separation of manakins species of the genus <i>Antilophia</i> (Aves: Pipridae) in response to Holocene climate change. <i>Journal of Avian Biology</i> , 2017, 48, 1177-1188.	0.6	17
5913	<i>Plasmodium vivax</i> rhomboid-like protease 1 gene diversity in Thailand. <i>Experimental Parasitology</i> , 2017, 181, 1-6.	0.5	0
5914	Single nucleotide polymorphisms minisequencing in hypervariable regions for screening of Thais. <i>Gene</i> , 2017, 627, 538-542.	1.0	1
5915	Wider geographic distribution and higher diversity of hexaploids than tetraploids in <i>Carassius</i> species complex reveal recurrent polyploidy effects on adaptive evolution. <i>Scientific Reports</i> , 2017, 7, 5395.	1.6	37
5916	Dynamics of genetic and morphological diversification in an incipient intra-island radiation of Philippine rodents (Muridae: <i>Bullimus</i>). <i>Journal of Biogeography</i> , 2017, 44, 2585-2594.	1.4	9
5917	Complete genome sequencing of cucumber mosaic virus from black pepper revealed rare deletion in the methyltransferase domain of 1a gene. <i>VirusDisease</i> , 2017, 28, 309-314.	1.0	12
5918	Genetic differentiation and historical demography of wood stork populations in Brazilian wetlands: Implications for the conservation of the species and associated ecosystems. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2017, 27, 1313-1324.	0.9	3
5919	Analysis of the molecular phylogenetics and genetic structure of an invasive alien species, <i>Ricania shantungensis</i> , in Korea. <i>Journal of Asia-Pacific Entomology</i> , 2017, 20, 901-906.	0.4	10
5920	Mitochondrial DNA genetic variations among four horse populations in Egypt. <i>Journal of Genetic Engineering and Biotechnology</i> , 2017, 15, 469-474.	1.5	9
5921	Genetic variability in captive individuals of the endangered species <i>Tapirus bairdii</i> in Mexico. <i>Revista Mexicana De Biodiversidad</i> , 2017, 88, 480-484.	0.4	1

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5922	Phylogenetic relationships between <i>Dicrocoelium chinensis</i> populations in Japan and China based on mitochondrial nad1 gene sequences. <i>Parasitology Research</i> , 2017, 116, 2605-2609.	0.6	9
5923	Diversity of MHC class II DRB alleles in the Eurasian population of the least weasel, <i>Mustela nivalis</i> (Mustelidae: Mammalia). <i>Biological Journal of the Linnean Society</i> , 2017, 121, 28-37.	0.7	11
5924	Disentangling sources of variation in SSU rDNA sequences from single cell analyses of ciliates: impact of copy number variation and experimental error. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170425.	1.2	75
5925	<i>Amblyomma sculptum</i> : genetic diversity and rickettsias in the Brazilian cerrado biome. <i>Medical and Veterinary Entomology</i> , 2017, 31, 427-437.	0.7	22
5926	Genetic stock structure of white steenbras <i>Lithognathus lithognathus</i> (Cuvier, 1829), an overexploited fishery species in South African waters. <i>African Journal of Marine Science</i> , 2017, 39, 27-41.	0.4	8
5927	The effects of historical fragmentation on major histocompatibility complex class II and microsatellite variation in the Aegean island reptile, <i>Podarcis erhardii</i> . <i>Ecology and Evolution</i> , 2017, 7, 4568-4581.	0.8	14
5928	Prediction of harmful variants on mitochondrial genes: Test of habitat-dependent and demographic effects in a euryhaline fish. <i>Ecology and Evolution</i> , 2017, 7, 3826-3835.	0.8	5
5929	Drivers of Cape Verde archipelagic endemism in keyhole limpets. <i>Scientific Reports</i> , 2017, 7, 41817.	1.6	14
5930	Geographic barriers and Pleistocene climate change shaped patterns of genetic variation in the Eastern Afrotropical biodiversity hotspot. <i>Scientific Reports</i> , 2017, 7, 45749.	1.6	58
5931	Genetic Structure of the <i>Aphis craccivora</i> (Hemiptera: Aphididae) From Thailand Inferred From Mitochondrial COI Gene Sequence. <i>Journal of Insect Science</i> , 2017, 17, .	0.6	8
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5933	Population genomics reveals a candidate gene involved in bumble bee pigmentation. <i>Ecology and Evolution</i> , 2017, 7, 3406-3413.	0.8	13
5934	Genetic diversity and population structure in the narrow endemic Chinese walnut <i>Juglans hopeiensis</i> Hu: implications for conservation. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	28
5935	Humoral and cytokine response elicited during immunisation with recombinant Immune Mapped protein-1 (EtIMP-1) and oocysts of <i>Eimeria tenella</i> . <i>Veterinary Parasitology</i> , 2017, 244, 44-53.	0.7	30
5936	Signatures of mito-nuclear discordance in <i>Schistosoma turkestanicum</i> indicate a complex evolutionary history of emergence in Europe. <i>Parasitology</i> , 2017, 144, 1752-1762.	0.7	8
5937	Phylogeography of the Tyrrhenian red deer (<i>Cervus elaphus corsicanus</i>) resolved using ancient DNA of radiocarbon-dated subfossils. <i>Scientific Reports</i> , 2017, 7, 2331.	1.6	23
5938	Origin and evolutionary history of freshwater Rhodophyta: further insights based on phylogenomic evidence. <i>Scientific Reports</i> , 2017, 7, 2934.	1.6	25
5939	Effects of Population Bottleneck and Balancing Selection on the Chinese Alligator Are Revealed by Locus-Specific Characterization of MHC Genes. <i>Scientific Reports</i> , 2017, 7, 5549.	1.6	11

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5940	Experimental evidence reveals the UCP1 genotype changes the oxygen consumption attributed to non-shivering thermogenesis in humans. <i>Scientific Reports</i> , 2017, 7, 5570.	1.6	27
5941	Contrasting evolutionary patterns between two haplogroups of <i>Haematobia exigua</i> (Diptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.6	10
5942	Genetic differentiation of the <i>Schizothorax</i> species complex (Cyprinidae) in the Nujiang River (upper) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.6	7
5943	Comparative Analysis of Four Buckwheat Species Based on Morphology and Complete Chloroplast Genome Sequences. <i>Scientific Reports</i> , 2017, 7, 6514.	1.6	34
5944	Multiple uprising invasions of <i>Pelophylax</i> water frogs, potentially inducing a new hybridogenetic complex. <i>Scientific Reports</i> , 2017, 7, 6506.	1.6	31
5945	Evolution, expression and association of the chemosensory protein genes with the outbreak phase of the two main pest locusts. <i>Scientific Reports</i> , 2017, 7, 6653.	1.6	23
5946	Methylation profile of a satellite DNA constituting the intercalary G+C-rich heterochromatin of the cut trough shell <i>Spisula subtruncata</i> (Bivalvia, Mactridae). <i>Scientific Reports</i> , 2017, 7, 6930.	1.6	8
5947	Using Genomic Location and Coalescent Simulation to Investigate Gene Tree Discordance in <i>Medicago L.</i> <i>Systematic Biology</i> , 2017, 66, 934-949.	2.7	10
5948	Novel geneâ€œsequence markers for isolate tracking within <i>Monilinia fructicola</i> lesions. <i>Pest Management Science</i> , 2017, 73, 1822-1829.	1.7	2
5949	Phylogeography of freshwater fishes of the Qilian Mountains area (<i>Triplophysa leptosoma</i> , Cobitidae: Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.4	8
5950	Haplotype diversity in MC1R locus between the Min and white-haired pig breeds. <i>Acta Agriculturae Scandinavica - Section A: Animal Science</i> , 2017, 67, 28-33.	0.2	0
5951	Messinian Salinity Crisis and Quaternary glacial events shaped genetic diversification in Siculo-Maghrebian blister beetles (Coleoptera: Meloidae). <i>Biological Journal of the Linnean Society</i> , 2017, 122, 455-468.	0.7	8
5952	The mitogenome of the brown pod-sucking bug <i>Clavigralla tomentosicollis</i> Stål (Hemiptera: Coreidae). <i>Agri Gene</i> , 2017, 5, 27-36.	1.9	4
5953	The evolution of the major histocompatibility complex in upstream versus downstream river populations of the longnose dace. <i>Ecology and Evolution</i> , 2017, 7, 3297-3311.	0.8	4
5954	Populations genetically rifted within a complex geological system: The case of strong structure and low genetic diversity in the migratory freshwater catfish, <i>Bagrus docmak</i> , in East Africa. <i>Ecology and Evolution</i> , 2017, 7, 6172-6187.	0.8	6
5955	Speciation history of a species complex of <i>Primulina eburnea</i> (Gesneriaceae) from limestone karsts of southern China, a biodiversity hot spot. <i>Evolutionary Applications</i> , 2017, 10, 919-934.	1.5	26
5956	Phylogeny and taxonomy of the genus <i>Ilyodon</i> Eigenmann, 1907 (Teleostei: Goodeidae), based on mitochondrial and nuclear DNA sequences. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2017, 55, 340-355.	0.6	13
5957	Investigating the ancestry of putative hybrids: are Arctic fox and red fox hybridizing?. <i>Polar Biology</i> , 2017, 40, 2055-2062.	0.5	3

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5958	High intraspecific genetic divergence in the versatile fairy shrimp <i>Branchinecta lindahli</i> with a comment on cryptic species in the genus <i>Branchinecta</i> (Crustacea: Anostraca). <i>Hydrobiologia</i> , 2017, 801, 59-69.	1.0	17
5959	Genetic divergence between the South Korean and Mongolian populations of the dung beetle, <i>Gymnopleurus mopsus</i> (Coleoptera: Scarabaeidae) based on mitochondrial cytochrome c oxidase subunit I (COI) gene sequences. <i>Entomological Research</i> , 2017, 47, 366-372.	0.6	4
5960	Differences in spatial communities of European perch (<i>Perca fluviatilis</i> Linnaeus, 1758) fry in a canyon-shaped reservoir are not attributable to genetics. <i>Journal of Applied Ichthyology</i> , 2017, 33, 306-313.	0.3	7
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5977	Taxonomic Evaluation of the Greater Horseshoe Bat <i>Rhinolophus ferrumequinum</i> (Chiroptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.3	17
5978	Genetic and morphological diversity of the cosmopolitan chaetognath <i>Pseudosagitta maxima</i> (Conant,) Tj ETQq0 0 0 rgBT /Overlock 10	1.2	6
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6013	Genetic footprint of population fragmentation and contemporary collapse in a freshwater cetacean. <i>Scientific Reports</i> , 2017, 7, 14449.	1.6	9
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6024	Phylogeography of the New Zealand giraffe weevil <i>Lasiorhynchus barbicornis</i> (Coleoptera: Brentidae): A comparison of biogeographic boundaries. <i>Biological Journal of the Linnean Society</i> , 2017, 122, 13-28.	0.7	6
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6033	Detection of misidentifications of species from the <i>Burkholderia cepacia</i> complex and description of a new member, the soil bacterium <i>Burkholderia catarinensis</i> sp. nov.. <i>Pathogens and Disease</i> , 2017, 75, .	0.8	70
6034	Seasonal distribution and reproductive strategy of seahorses. <i>ICES Journal of Marine Science</i> , 2017, 74, 2170-2179.	1.2	17
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6051	Differences in <i>Fusarium</i> Species in brown midrib Sorghum and in Air Populations in Production Fields. <i>Phytopathology</i> , 2017, 107, 1353-1363.	1.1	7
6052	Genetic structure of dioecious and trioecious <i>Salix myrsinifolia</i> populations at the border of geographic range. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	8
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6054	Genetic diversity and population structure of blue-crested lizard, <i>Calotes mystaceus</i> Dumail & Bibron, 1837 (Squamata: Agamidae) in Thailand. <i>Journal of Genetics</i> , 2017, 96, 377-382.	0.4	4
6055	Characterization of twenty <i>Camelina</i> spp. accessions using single nucleotide polymorphism genotyping. <i>Horticulture Environment and Biotechnology</i> , 2017, 58, 187-194.	0.7	4
6056	Javan mongoose or small Indian mongoose "who is where?". <i>Mammalian Biology</i> , 2017, 87, 62-70.	0.8	20
6057	The colonization and divergence patterns of Brandt's vole (<i>Lasiopodomys brandtii</i>) populations reveal evidence of genetic surfing. <i>BMC Evolutionary Biology</i> , 2017, 17, 145.	3.2	12
6058	Genome-wide identification and expression analysis of SBP-like transcription factor genes in Moso Bamboo (<i>Phyllostachys edulis</i>). <i>BMC Genomics</i> , 2017, 18, 486.	1.2	64
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6069	Evolutionary history of <i>Podarcis tiliguerta</i> on Corsica and Sardinia. <i>BMC Evolutionary Biology</i> , 2017, 17, 27.	3.2	6
6070	Ruminant-specific multiple duplication events of PRDM9 before speciation. <i>BMC Evolutionary Biology</i> , 2017, 17, 79.	3.2	3
6071	Selection on the mitochondrial ATP synthase 6 and the NADH dehydrogenase 2 genes in hares (<i>Lepus</i>) Tj ETQq1 1 0.784314 rgBT /Over 46.	3.2	20
6072	Digging up the roots of an insular hotspot of genetic diversity: decoupled mito-nuclear histories in the evolution of the Corsican-Sardinian endemic lizard <i>Podarcis tiliguerta</i> . <i>BMC Evolutionary Biology</i> , 2017, 17, 63.	3.2	24
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6080	Genetic diversity and selection of three nuclear genes in <i>Schistosoma japonicum</i> populations. <i>Parasites and Vectors</i> , 2017, 10, 87.	1.0	7
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6083	Molecular phylogeny of <i>Anopheles hyrcanus</i> group (Diptera: Culicidae) based on mtDNA COI. <i>Infectious Diseases of Poverty</i> , 2017, 6, 61.	1.5	22

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6086	Rediscovering a forgotten canid species. <i>BMC Zoology</i> , 2017, 2, .	0.3	38
6087	Contrasting patterns of nucleotide polymorphism suggest different selective regimes within different parts of the <i>PgiC1</i> gene in <i>Festuca ovina</i> L.. <i>Hereditas</i> , 2017, 154, 11.	0.5	1
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6089	DNA Barcoding of Chinese species of the genus <i>Eurydema</i> Laporte, 1833 (Hemiptera: Pentatomidae). <i>Zootaxa</i> , 2017, 4286, .	0.2	5
6090	A new genus and new species of freshwater crab (Decapoda: Brachyura: Potamidae Ortmann, 1896) from Yunnan Province, China. <i>Zootaxa</i> , 2017, 4286, .	0.2	16
6091	Multiple origins and a narrow genepool characterise the African tea germplasm: concordant patterns revealed by nuclear and plastid DNA markers. <i>Scientific Reports</i> , 2017, 7, 4053.	1.6	22
6092	Phylogeography of direct-developing sea stars in the genus <i>Leptasterias</i> in relation to San Francisco Bay outflow in central California. <i>Marine Biology</i> , 2017, 164, 1.	0.7	9
6093	Spatio-temporal patterns of genetic variations in populations of yellowtail kingfish <i>Seriola lalandi</i> from the south-eastern Pacific Ocean and potential implications for its fishery management. <i>Journal of Fish Biology</i> , 2017, 90, 249-264.	0.7	15
6094	Population genetics and ecological niche modeling shed light on conservation of the island endemic damselfly <i>Pseudolestes mirabilis</i> (Odonata, Pseudolestidae). <i>Hydrobiologia</i> , 2017, 790, 273-286.	1.0	3
6095	Inter- and intra-colonial genotypic diversity in hermatypic hydrozoans of the family Milleporidae. <i>Marine Ecology</i> , 2017, 38, e12388.	0.4	10
6096	Recombination changes at the boundaries of fully and partially sex-linked regions between closely related <i>Silene</i> species pairs. <i>Heredity</i> , 2017, 118, 395-403.	1.2	19
6097	Population genetics and geometric morphometrics of the <i>Bombus ephippiatus</i> species complex with implications for its use as a commercial pollinator. <i>Conservation Genetics</i> , 2017, 18, 553-572.	0.8	23
6098	Multilocus approaches reveal underestimated species diversity and inter-specific gene flow in pikas (<i>Ochotona</i>) from southwestern China. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 239-245.	1.2	32
6099	A single base change explains the independent origin of and selection for the nonshattering gene in African rice domestication. <i>New Phytologist</i> , 2017, 213, 1925-1935.	3.5	23
6100	Phylogeography of <i>Hydropuntia cornea</i> / <i>Hydropuntia usneoides</i> complex (Gracilariales, Rhodophyta) in the Yucatan Peninsula. <i>Phycologia</i> , 2017, 56, 14-20.	0.6	5
6101	Evolutionary and Functional Analysis of <i>LEAFY COTYLEDON1</i> in <i>Isoetes</i> L. from China. <i>Plant Molecular Biology Reporter</i> , 2017, 35, 154-165.	1.0	0

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6103	High genetic diversity and absence of phylogeographic structure in breeding populations of vulnerable <i>Saundersilarus saundersi</i> (Charadriiformes: Laridae) in Bohai Bay, China. <i>Conservation Genetics</i> , 2017, 18, 495-500.	0.8	7
6104	Molecular phylogeny of the genus <i>Capoeta</i> (Teleostei: Cyprinidae) in Anatolia, Turkey. <i>Biochemical Systematics and Ecology</i> , 2017, 70, 80-94.	0.6	24
6105	Complete mitochondrial genome and evolutionary analysis of <i>Turritopsis dohrnii</i> , the "immortal" jellyfish with a reversible life-cycle. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 232-238.	1.2	13
6106	Genome-scale analysis of the non-cultivable <i>Treponema pallidum</i> reveals extensive within-patient genetic variation. <i>Nature Microbiology</i> , 2017, 2, 16190.	5.9	81
6107	Phylogeography and historical demography of the orchid bee <i>Euglossa iopoeila</i> : signs of vicariant events associated to Quaternary climatic changes. <i>Conservation Genetics</i> , 2017, 18, 539-552.	0.8	33
6108	Genetic diversity and structure in apple-infesting pests of <i>Carposina sasakii</i> , <i>Grapholita dimorpha</i> and <i>Grapholita molesta</i> in Korea. <i>Journal of Asia-Pacific Entomology</i> , 2017, 20, 13-16.	0.4	4
6109	Genome-wide identification and comparative analysis of Alfin-like transcription factors in maize. <i>Genes and Genomics</i> , 2017, 39, 261-275.	0.5	12
6110	Genetic diversity of golden takin (<i>Budorcas taxicolor bedfordi</i>) population from Qinling Mountains in China revealed by sequence analysis of mitochondrial DNA control region. <i>Biochemical Systematics and Ecology</i> , 2017, 70, 1-6.	0.6	5
6111	Genotype-Phenotype Study of the Middle Gangetic Plain in India Shows Association of rs2470102 with Skin Pigmentation. <i>Journal of Investigative Dermatology</i> , 2017, 137, 670-677.	0.3	18
6112	Phylogeny and variability of <i>Colletotrichum truncatum</i> associated with soybean anthracnose in Brazil. <i>Journal of Applied Microbiology</i> , 2017, 122, 402-415.	1.4	36
6113	Genome-Wide Identification and Expression Analysis of the HD-Zip Gene Family in Moso Bamboo (<i>Phyllostachys edulis</i>). <i>Journal of Plant Growth Regulation</i> , 2017, 36, 323-337.	2.8	36
6114	Population genetic structure of the Amazonian black flannelmouth characin (<i>Characiformes</i>), <i>Tij ETQq0 0 0 rgBT /Overlock 10 Tf 50 267</i> flow of a migratory and abundant fishery species. <i>Environmental Biology of Fishes</i> , 2017, 100, 1-16.	0.4	38
6115	Occurrence of length polymorphism and heteroplasmy in brown trout. <i>Gene Reports</i> , 2017, 6, 1-7.	0.4	8
6116	Outnumbered: a new dominant ant species with genetically diverse supercolonies in Ethiopia. <i>Insectes Sociaux</i> , 2017, 64, 141-147.	0.7	5
6117	Interisland gene flow among populations of the buff-banded rail (<i>Aves: Rallidae</i>) and its implications for insular endemism in Oceania. <i>Journal of Avian Biology</i> , 2017, 48, 679-690.	0.6	12
6118	Displacement of native Patagonian freshwater silverside populations (<i>Odontesthes hatcheri</i>), <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107</i> 2017, 19, 971-988.	1.2	13
6119	Natural variations in stearoyl- <i>acp</i> desaturase genes affect the conversion of stearic to oleic acid in maize kernel. <i>Theoretical and Applied Genetics</i> , 2017, 130, 151-161.	1.8	23

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6121	Pleistocene demographic expansion and high gene flow in the Globe Skimmer dragonfly <i>Pantala flavescens</i> Fabricius (Odonata: Libellulidae) in Peninsular Malaysia. <i>Zoologischer Anzeiger</i> , 2017, 266, 23-27.	0.4	15
6122	Evolutionary history of the thicket rats (genus <i>Grammomys</i>) mirrors the evolution of African forests since late Miocene. <i>Journal of Biogeography</i> , 2017, 44, 182-194.	1.4	47
6123	Is the Antarctic <i>Ophryotrocha orensanzi</i> (Annelida: Dorvilleidae) a circumpolar non-specialized opportunist?. <i>Systematics and Biodiversity</i> , 2017, 15, 105-114.	0.5	6
6124	Molecular Epidemiology of <i>Ascaris</i> Infection Among Pigs in Iowa. <i>Journal of Infectious Diseases</i> , 2017, 215, 131-138.	1.9	24
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6126	Host range and genetic strains of leafminer flies (Diptera: Agromyzidae) in eastern Brazil reveal a new divergent clade of <i>Liriomyza sativae</i> . <i>Agricultural and Forest Entomology</i> , 2017, 19, 235-244.	0.7	15
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6128	Phylogenetics, biogeography and population genetics of the ascidian <i>Botryllus schlosseri</i> in the Mediterranean Sea and beyond. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 221-231.	1.2	22
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6131	Does population distribution matter? Influence of a patchy versus continuous distribution on genetic patterns in a wind-pollinated shrub. <i>Journal of Biogeography</i> , 2017, 44, 361-374.	1.4	16
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6134	Morphological and taxonomic demarcation of <i>Brachionus asplanchnoidis</i> Charin within the <i>Brachionus plicatilis</i> cryptic species complex (Rotifera, Monogononta). <i>Hydrobiologia</i> , 2017, 796, 19-37.	1.0	28
6135	Comparative analyses within <i>Gyrodactylus</i> (Platyhelminthes: Monogenea) mitochondrial genomes and conserved polymerase chain reaction primers for gyrodactylid mitochondrial <i>scp>DNA</scp></i> . <i>Journal of Fish Diseases</i> , 2017, 40, 541-555.	0.9	13
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6137	Rare or cryptic? The first report of an Omura's whale (<i>Balaenoptera omurai</i>) in the South Atlantic Ocean. <i>Marine Mammal Science</i> , 2017, 33, 80-95.	0.9	14

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6139	Structure and variation of the Fringillidae (Aves: Passeriformes) mitochondrial DNA control region and their phylogenetic relationship. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 867-871.	0.7	6
6140	Effects of Wolbachia on mitochondrial DNA variation in populations of <i>Athetis lepigone</i> (Lepidoptera: Tj ETQq0 0 0 rgBT /Overlock 10 T 826-834.	0.7	9
6141	Diversification across major biogeographic breaks in the African Shining/Square-tailed Drongos complex (Passeriformes: Dicruridae). <i>Zoologica Scripta</i> , 2017, 46, 27-41.	0.7	20
6142	Characterization and development of qPCR for early detection and quantification of <i>Pseudocercospora macadamiae</i> at different stages of infection process. <i>European Journal of Plant Pathology</i> , 2017, 147, 85-102.	0.8	4
6143	Spread and global population structure of the diamondback moth <i>Plutella xylostella</i> (Lepidoptera: Plutellidae) and its larval parasitoids <i>Diadegma semiclausum</i> and <i>Diadegma fenestrale</i> (Hymenoptera: Ichneumonidae) based on mtDNA. <i>Bulletin of Entomological Research</i> , 2017, 107, 155-164.	0.5	18
6144	Novel allelic variants in <i>ACD6</i> cause hybrid necrosis in local collection of <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2017, 213, 900-915.	3.5	40
6145	Evolutionary history of the Persian Jird, <i>Meriones persicus</i> , based on genetics, species distribution modelling and morphometric data. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2017, 55, 29-45.	0.6	32
6146	Phylogeography and taxonomy of the <i>Psorodonotus caucasicus</i> (Orthoptera, Tettigoniidae) group: independent double invasion of the Balkans from the Caucasus. <i>Systematic Entomology</i> , 2017, 42, 118-133.	1.7	19
6147	Effect of migration patterns on maternal genetic structure: a case of Tai-Kadai migration from China to Thailand. <i>Journal of Human Genetics</i> , 2017, 62, 223-228.	1.1	10
6148	A phylogenetic perspective on diversity of Galatheaidea (Munida, Munidopsis) from cold-water coral and cold seep communities in the western North Atlantic Ocean. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2017, 137, 258-272.	0.6	13
6149	Spatial genetic structure of the cyprinid fish <i>Onychostoma lepturum</i> on Hainan Island. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 901-908.	0.7	11
6150	DNA barcoding reflects the diversity and variety of brooding traits of fish species in the family Syngnathidae along China's coast. <i>Fisheries Research</i> , 2017, 185, 137-144.	0.9	23
6151	Population genetic and behavioural variation of the two remaining colonies of Providence petrel (<i>Pterodroma solandri</i>). <i>Conservation Genetics</i> , 2017, 18, 117-129.	0.8	5
6152	Genetic variability and historic stability of the California spiny lobster <i>Panulirus interruptus</i> in the Gulf of California. <i>Fisheries Research</i> , 2017, 185, 130-136.	0.9	3
6153	Importance of incomplete lineage sorting and introgression in the origin of shared genetic variation between two closely related pines with overlapping distributions. <i>Heredity</i> , 2017, 118, 211-220.	1.2	73
6154	Like a pig out of water: seaborne spread of domestic pigs in Southern Italy and Sardinia during the Bronze and Iron Ages. <i>Heredity</i> , 2017, 118, 154-159.	1.2	10
6155	Population expansion, current and past gene flow in Gould's petrel: implications for conservation. <i>Conservation Genetics</i> , 2017, 18, 105-115.	0.8	4

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6157	Multilocus approach reveals an incipient differentiation process in the Stone-curlew, <i>Burhinus oedicnemus</i> around the Mediterranean basin. <i>Conservation Genetics</i> , 2017, 18, 197-209.	0.8	14
6158	SNP-based PCR-RFLP, T-RFLP and FINS methodologies for the identification of commercial fish species in Egypt. <i>Fisheries Research</i> , 2017, 185, 34-42.	0.9	12
6159	Rapid Functional and Sequence Differentiation of a Tandemly Repeated Species-Specific Multigene Family in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, 51-65.	3.5	11
6160	Evolutionary history and species delimitations: a case study of the hazel dormouse, <i>Muscardinus avellanarius</i> . <i>Conservation Genetics</i> , 2017, 18, 181-196.	0.8	16
6161	MHC class II $\hat{\eta}^2$ exon 2 variation in pardalotes (<i>Pardalotidae</i>) is shaped by selection, recombination and gene conversion. <i>Immunogenetics</i> , 2017, 69, 101-111.	1.2	9
6162	Allelic variation in <i>PtoPsbW</i> associated with photosynthesis, growth, and wood properties in <i>Populus tomentosa</i> . <i>Molecular Genetics and Genomics</i> , 2017, 292, 77-91.	1.0	10
6163	The Evolutionary History and Genetic Diversity of Kinkajous, <i>Potos flavus</i> (Carnivora, Procyonidae). <i>Journal of Mammalian Evolution</i> , 2017, 24, 439-451.	1.0	16
6164	Trace element concentrations, risks and their correlation with metallothionein genes polymorphism: A case study of narrow-ridged finless porpoises (<i>Neophocaena asiaeorientalis</i>) in the East China Sea. <i>Science of the Total Environment</i> , 2017, 575, 628-638.	3.9	10
6165	Transmission between Archaic and Modern Human Ancestors during the Evolution of the Oncogenic Human Papillomavirus 16. <i>Molecular Biology and Evolution</i> , 2017, 34, 4-19.	3.5	103
6166	Phylogeographical insight into the Aleutian flora inferred from the historical range shifts of the alpine shrub <i>Therorhodion camtschaticum</i> (Pall.) Small (Ericaceae). <i>Journal of Biogeography</i> , 2017, 44, 283-293.	1.4	10
6167	Species delimitation and phylogeographic analyses in the <i>Ectocarpus</i> subgroup <i>siliculosi</i> (Ectocarpales, Phaeophyceae). <i>Journal of Phycology</i> , 2017, 53, 17-31.	1.0	54
6168	The Anatolia-Balkan phylogeographic fault: a snapshot from the genus <i>Isophya</i> (Orthoptera). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i>	0.7	28
6169	Species delimitation for cryptic species complexes: case study of <i>Pyramidula</i> (Gastropoda). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 36</i>	0.7	36
6170	Genetic variation and evolutionary analysis of <i>Pepino mosaic virus</i> in Sicily: insights into the dispersion and epidemiology. <i>Plant Pathology</i> , 2017, 66, 368-375.	1.2	26
6171	Species diversity can be overestimated by a fixed empirical threshold: insights from <i>DNA</i> barcoding of the genus <i>Cletus</i> (Hemiptera: Coreidae) and the meta-analysis of <i>COI</i> data from previous phylogeographical studies. <i>Molecular Ecology Resources</i> , 2017, 17, 314-323.	2.2	13
6172	Mitochondrial and Nuclear DNA Based Genetic Assessment Indicated Distinct Variation and Low Genetic Exchange Among the Three Subspecies of Swamp Deer (<i>Rucervus Aduvaucelii</i>). <i>Evolutionary Biology</i> , 2017, 44, 31-42.	0.5	19
6173	Population characteristics of a large whale shark aggregation inferred from seawater environmental DNA. <i>Nature Ecology and Evolution</i> , 2017, 1, 4.	3.4	223

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6175	Genetic differentiation between humpback whales (<i>Megaptera novaeangliae</i>) from Atlantic and Pacific breeding grounds of South America. <i>Marine Mammal Science</i> , 2017, 33, 457-479.	0.9	13
6176	Oceanographic drivers of population differentiation in Indo-Pacific bottlenose (<i>Tursiops aduncus</i>) and humpback (<i>Sousa spp.</i>) dolphins of the northern Bay of Bengal. <i>Conservation Genetics</i> , 2017, 18, 371-381.	0.8	27
6177	Molecular genetic analysis and evolution of begomoviruses and betasatellites causing yellow mosaic disease of bhendi. <i>Virus Genes</i> , 2017, 53, 275-285.	0.7	23
6178	Genetic Relationships and Spatial Genetic Structure Among Populations of <i>Rhodnius prolixus</i> (Hemiptera: Reduviidae) in Colombia and Venezuela Based on Mitochondrial Cytochrome-b Sequences. <i>Neotropical Entomology</i> , 2017, 46, 341-355.	0.5	3
6179	A cryptic mitochondrial DNA link between North European and West African dogs. <i>Journal of Genetics and Genomics</i> , 2017, 44, 163-170.	1.7	11
6180	Diversity of bat astroviruses in Lao PDR and Cambodia. <i>Infection, Genetics and Evolution</i> , 2017, 47, 41-50.	1.0	18
6181	Sherpas share genetic variations with Tibetans for high-altitude adaptation. <i>Molecular Genetics & Genomic Medicine</i> , 2017, 5, 76-84.	0.6	17
6182	Specific populations of the yeast <i>Geotrichum candidum</i> revealed by molecular typing. <i>Yeast</i> , 2017, 34, 165-178.	0.8	31
6183	Specialist and generalist symbionts show counterintuitive levels of genetic diversity and discordant demographic histories along the Florida Reef Tract. <i>Coral Reefs</i> , 2017, 36, 339-354.	0.9	15
6184	Parallel evolution evidenced by molecular data in the banded-tetra (<i>Astyanax fasciatus</i>). <i>Biochemical Systematics and Ecology</i> , 2017, 70, 141-146.	0.6	4
6185	Homologous Recombination and <i>Xylella fastidiosa</i> Host-Pathogen Associations in South America. <i>Phytopathology</i> , 2017, 107, 305-312.	1.1	49
6186	Chloroplast phylogenomic analyses maternal relationships among sections in the genus <i>Populus</i> . <i>Biochemical Systematics and Ecology</i> , 2017, 70, 132-140.	0.6	5
6187	Phylogeography of a freshwater crustacean species complex reflects a long-gone archipelago. <i>Journal of Biogeography</i> , 2017, 44, 421-432.	1.4	43
6188	Regional selection of the brain size regulating gene <i>CASC5</i> provides new insight into human brain evolution. <i>Human Genetics</i> , 2017, 136, 193-204.	1.8	14
6189	A novel hotspot of vertebrate endemism and an evolutionary refugium in tropical Australia. <i>Diversity and Distributions</i> , 2017, 23, 53-66.	1.9	38
6190	Genetic diversity and demographic history of the giant river catfish <i>Sperata seenghala</i> inferred from mitochondrial DNA markers. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 920-926.	0.7	5
6191	Population genetic structure of cotton pink bollworm, <i>Pectinophora gossypiella</i> (Saunders) (Lepidoptera: Gelechiidae) using mitochondrial cytochrome oxidase I (<i>COI</i>) gene sequences from India. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 941-948.	0.7	7

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6193	Multilocus species delimitation in <i>Mesoamerican</i> <i>Scaptotrigona</i> stingless bees (<i>Apididae</i> : <i>Meliponini</i>) supports the existence of cryptic species. <i>Systematic Entomology</i> , 2017, 42, 171-181.	1.7	16
6194	Cryptic speciation and limited hybridization within <i>Lumbricus</i> earthworms (Clitellata: Lumbricidae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 106, 18-27.	1.2	42
6195	Phylogeny and phylogeography of the roaches, genus <i>Rutilus</i> (Cyprinidae), at the Eastern part of its range as inferred from mtDNA analysis. <i>Hydrobiologia</i> , 2017, 788, 33-46.	1.0	38
6196	Lineage diversification of fringe-toed lizards (Phrynosomatidae: <i>Uma notata</i> complex) in the Colorado Desert: Delimiting species in the presence of gene flow. <i>Molecular Phylogenetics and Evolution</i> , 2017, 106, 103-117.	1.2	28
6197	Leapfrogging into new territory: How Mascarene ridged frogs diversified across Africa and Madagascar to maintain their ecological niche. <i>Molecular Phylogenetics and Evolution</i> , 2017, 106, 254-269.	1.2	44
6198	High genetic diversity vs. low genetic and morphological differentiation of <i>Argiope trifasciata</i> (Araneae, Araneidae) in Tunisia. <i>Systematics and Biodiversity</i> , 2017, 15, 1-15.	0.5	14
6199	Introgressive replacement of natives by invading <i>Arion</i> pest slugs. <i>Scientific Reports</i> , 2017, 7, 14908.	1.6	31
6200	Walrus (<i>Odobenus rosmarus rosmarus</i>) in the Pechora Sea in the context of contemporary population structure of Northeast Atlantic walrus. <i>Biological Journal of the Linnean Society</i> , 2017, 122, 897-915.	0.7	18
6201	Are There Two Varieties in <i>Hylomecon japonica</i> (Papaveraceae)? Morphological and Molecular Evidence. <i>Annales Botanici Fennici</i> , 2017, 54, 391-399.	0.0	4
6202	Genetic Diversity and Prevalence of <i>Leishmania mexicana</i> in <i>Bichromomyia olmeca olmeca</i> in an Endemic Area of Mexico. <i>Southwestern Entomologist</i> , 2017, 42, 983-994.	0.1	4
6203	Phylogeography and ecological niche modelling uncover the evolutionary history of <i>Tibouchina hatschbachii</i> (Melastomataceae), a taxon restricted to the subtropical grasslands of South America. <i>Botanical Journal of the Linnean Society</i> , 2017, 183, 616-632.	0.8	7
6204	The evolutionary history of the subgenus <i>Haplomylomys</i> (Cricetidae: <i>Peromyscus</i>). <i>Journal of Mammalogy</i> , 2017, 98, 1627-1640.	0.6	5
6205	Complex Coding and Regulatory Polymorphisms in a Restriction Factor Determine the Susceptibility of <i>Drosophila</i> to Viral Infection. <i>Genetics</i> , 2017, 206, 2159-2173.	1.2	26
6206	Plastid Phylogenomics Resolve Deep Relationships among Eupolypod II Ferns with Rapid Radiation and Rate Heterogeneity. <i>Genome Biology and Evolution</i> , 2017, 9, 1646-1657.	1.1	67
6207	Mitochondrial-nuclear crosstalk, haplotype and copy number variation distinct in muscle fiber type, mitochondrial respiratory and metabolic enzyme activities. <i>Scientific Reports</i> , 2017, 7, 14024.	1.6	16
6208	Multiple gene genealogy reveals high genetic diversity and evidence for multiple origins of Chinese <i>Plasmopara viticola</i> population. <i>Scientific Reports</i> , 2017, 7, 17304.	1.6	16
6209	A Worldwide Molecular Phylogeny Provides New Insight on Cryptic Diversity Within the Moonworts (<i>Botrychium</i> s. s., Ophioglossaceae). <i>Systematic Botany</i> , 2017, 42, 620-639.	0.2	23

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6211	Conserved molecular structure of the centromeric histone CENH3 in <i>Secale</i> and its phylogenetic relationships. <i>Scientific Reports</i> , 2017, 7, 17628.	1.6	22
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6224	Genetic structure and demographic history of <i>Lymantria dispar</i> (Linnaeus, 1758) (Lepidoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 13	0.8	13
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6227	The broad-snouted caiman population recovery in Argentina. A case of genetics conservation. <i>Amphibia - Reptilia</i> , 2017, 38, 411-424.	0.1	11

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6259	Comparative Analysis of Six <i>Lagerstroemia</i> Complete Chloroplast Genomes. <i>Frontiers in Plant Science</i> , 2017, 8, 15.	1.7	138
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6276	Phylogenetic Resolution in <i>Juglans</i> Based on Complete Chloroplast Genomes and Nuclear DNA Sequences. <i>Frontiers in Plant Science</i> , 2017, 8, 1148.	1.7	105
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6281	Effects of Mountain Uplift and Climatic Oscillations on Phylogeography and Species Divergence in Four Endangered <i>Notopterygium</i> Herbs. <i>Frontiers in Plant Science</i> , 2017, 8, 1929.	1.7	33

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6286	Genome-wide organization and expression profiling of the R2R3-MYB transcription factor family in pineapple (<i>Ananas comosus</i>). <i>BMC Genomics</i> , 2017, 18, 503.	1.2	90
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6310	Plasmid Replicons from <i>Pseudomonas</i> Are Natural Chimeras of Functional, Exchangeable Modules. <i>Frontiers in Microbiology</i> , 2017, 8, 190.	1.5	20
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6322	Mitochondrial DNA Phylogenetics of Black Rhinoceros in Kenya in relation to Southern Africa Population. <i>International Journal of Biodiversity</i> , 2017, 2017, 1-6.	0.7	1
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6329	Molecular cloning, sequence analysis and tissue expression of bovine imprinted <i>ASCL2</i> gene. <i>South African Journal of Animal Sciences</i> , 2017, 47, 813.	0.2	0
6330	Population genetics of Triatominae. , 2017, , 169-196.		4
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6333	Colonization in North American Arid Lands: The Journey of <i>Agarito</i> (<i>Berberis trifoliolata</i>) Revealed by Multilocus Molecular Data and Packrat Midden Fossil Remains. <i>PLoS ONE</i> , 2017, 12, e0168933.	1.1	17
6334	Genetic Analysis of <i>Vibrio parahaemolyticus</i> O3:K6 Strains That Have Been Isolated in Mexico Since 1998. <i>PLoS ONE</i> , 2017, 12, e0169722.	1.1	12
6335	The First Chloroplast Genome Sequence of <i>Boswellia sacra</i> , a Resin-Producing Plant in Oman. <i>PLoS ONE</i> , 2017, 12, e0169794.	1.1	19

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6338	Multilocus Intron Trees Reveal Extensive Male-Biased Homogenization of Ancient Populations of Chamois (<i>Rupicapra</i> spp.) across Europe during Late Pleistocene. PLoS ONE, 2017, 12, e0170392.	1.1	13
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6341	Opening the treasure chest: A DNA-barcoding primer set for most higher taxa of Central European birds and mammals from museum collections. PLoS ONE, 2017, 12, e0174449.	1.1	17
6342	The mitochondrial genome of pin-tailed snipe <i>Gallinago stenura</i> , and its implications for the phylogeny of Charadriiformes. PLoS ONE, 2017, 12, e0175244.	1.1	15
6343	Discordant population histories of host and its parasite: A role for ecological permeability of extreme environment?. PLoS ONE, 2017, 12, e0175286.	1.1	3
6344	Alternative glacial-interglacial refugia demographic hypotheses tested on <i>Cephalocereus columna-trajani</i> (Cactaceae) in the intertropical Mexican drylands. PLoS ONE, 2017, 12, e0175905.	1.1	20
6345	Combining phylogenetic and demographic inferences to assess the origin of the genetic diversity in an isolated wolf population. PLoS ONE, 2017, 12, e0176560.	1.1	31
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6348	Phylogeography of the reticulated python (<i>Malayopython reticulatus</i> ssp.): Conservation implications for the world's™ most traded snake species. PLoS ONE, 2017, 12, e0182049.	1.1	7
6349	Genetic and morphological analyses of <i>Gracilaria firma</i> and <i>G. changii</i> (Gracilariaceae, Rhodophyta), the commercially important agarophytes in western Pacific. PLoS ONE, 2017, 12, e0182176.	1.1	14
6350	New data on Weddell seal (<i>Leptonychotes weddellii</i>) colonies: A genetic analysis of a top predator from the Ross Sea, Antarctica. PLoS ONE, 2017, 12, e0182922.	1.1	8
6351	The complete chloroplast genome sequences of three <i>Adenophora</i> species and comparative analysis with Campanuloid species (Campanulaceae). PLoS ONE, 2017, 12, e0183652.	1.1	19
6352	High genetic diversity and demographic history of captive Siamese and Saltwater crocodiles suggest the first step toward the establishment of a breeding and reintroduction program in Thailand. PLoS ONE, 2017, 12, e0184526.	1.1	25
6353	Contribution of both positive selection and relaxation of selective constraints to degeneration of flyability during geese domestication. PLoS ONE, 2017, 12, e0185328.	1.1	7

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6355	Genetic diversity and connectivity in the East African giant mud crab <i>Scylla serrata</i> : Implications for fisheries management. PLoS ONE, 2017, 12, e0186817.	1.1	21
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6358	Genetic variation and factors affecting the genetic structure of the lichenicolous fungus <i>Heterocephalacia bachmannii</i> (Filobasidiales, Basidiomycota). PLoS ONE, 2017, 12, e0189603.	1.1	9
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6360	Umbilicariaceae (lichenized Ascomycota) – Trait evolution and a new generic concept. Taxon, 2017, 66, 1282-1303.	0.4	30
6361	Population structure and demographic history of Pacific herring <i>Clupea pallasii</i> around Japan inferred from mitochondrial DNA sequences. Nippon Suisan Gakkaishi, 2017, 83, 163-173.	0.0	4
6362	Signs of introgression of Baikal omul (<i>Coregonus migratorius</i>) or Arctic cisco (<i>C. autumnalis</i>) into European whitefish (<i>C. lavaretus</i>) in the eastern Baltic Sea. Fundamental and Applied Limnology, 2017, 189, 209-225.	0.4	4
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6365	Convergent evolution of SWS2 opsin facilitates adaptive radiation of threespine stickleback into different light environments. PLoS Biology, 2017, 15, e2001627.	2.6	55
6366	From east to west across the Palearctic: Phylogeography of the invasive lime leaf miner <i>Phyllonorycter issikii</i> (Lepidoptera: Gracillariidae) and discovery of a putative new cryptic species in East Asia. PLoS ONE, 2017, 12, e0171104.	1.1	25
6367	Pleistocene climate changes shaped the population structure of <i>Partamona seridoensis</i> (Apidae,) Tj ETQq1 1 0.784314 rgBT /Overlock 14	1.1	14
6368	Characterization of the complete chloroplast genome of <i>Arabis stellari</i> and comparisons with related species. PLoS ONE, 2017, 12, e0183197.	1.1	26
6369	Phylogeography of bivalve <i>Meretrix petechialis</i> in the Northwestern Pacific indicated by mitochondrial and nuclear DNA data. PLoS ONE, 2017, 12, e0183221.	1.1	23
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6371	MLST-Based Population Genetic Analysis in a Global Context Reveals Clonality amongst <i>Cryptococcus neoformans</i> var. <i>grubii</i> VNI Isolates from HIV Patients in Southeastern Brazil. PLoS Neglected Tropical Diseases, 2017, 11, e0005223.	1.3	59

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6373	Phylogeography of <i>Angiostrongylus cantonensis</i> (Nematoda: Angiostrongylidae) in southern China and some surrounding areas. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005776.	1.3	13
6374	Phylogeographic structure, cryptic speciation and demographic history of the sharpbelly (Hemiculter) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i> 17, 216.	3.2	45
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6381	The complete chloroplast genome of <i>Primulina</i> and two novel strategies for development of high polymorphic loci for population genetic and phylogenetic studies. <i>BMC Evolutionary Biology</i> , 2017, 17, 224.	3.2	18
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6386	The satellite DNA AflaSAT-1 in the A and B chromosomes of the grasshopper <i>Abracris flavolineata</i> . <i>BMC Genetics</i> , 2017, 18, 81.	2.7	8
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6389	A new method for sequencing the hypervariable <i>Plasmodium falciparum</i> gene var2csa from clinical samples. <i>Malaria Journal</i> , 2017, 16, 343.	0.8	12

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6391	A deep sequencing approach to estimate Plasmodium falciparum complexity of infection (COI) and explore apical membrane antigen 1 diversity. <i>Malaria Journal</i> , 2017, 16, 490.	0.8	48
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6403	Evolutionary history of the NAM-B1 gene in wild and domesticated tetraploid wheat. <i>BMC Genetics</i> , 2017, 18, 118.	2.7	16
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6405	The underlying process of early ecological and genetic differentiation in a facultative mutualistic Sinorhizobium meliloti population. <i>Scientific Reports</i> , 2017, 7, 675.	1.6	4
6406	Evidence for rangewide panmixia despite multiple barriers to dispersal in a marine mussel. <i>Scientific Reports</i> , 2017, 7, 10279.	1.6	20
6407	Genetic diversity of Leishmania donovani that causes cutaneous leishmaniasis in Sri Lanka: a cross sectional study with regional comparisons. <i>BMC Infectious Diseases</i> , 2017, 17, 791.	1.3	30

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6409	Unexpected differences in the population genetics of phasmavirids (Bunyavirales) from subarctic ponds. <i>Virus Evolution</i> , 2017, 3, vex015.	2.2	27
6410	Variations in coat protein sequence of Wheat streak mosaic virus among crop and non-crop hosts. <i>Crop and Pasture Science</i> , 2017, 68, 328.	0.7	12
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6412	Genetic variability of populations of <i>Nyssomyia neivai</i> in the Northern State of Paraná, Brazil. <i>Revista Do Instituto De Medicina Tropical De Sao Paulo</i> , 2017, 59, e10.	0.5	1
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6414	Comparative genetic diversity of potato virus Y populations based on coat protein gene. <i>Acta Virologica</i> , 2017, 61, 161-174.	0.3	3
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6418	Longitudinal evaluation of humoral immune response and merozoite surface antigen diversity in calves naturally infected with <i>Babesia bovis</i> , in São Paulo, Brazil. <i>Brazilian Journal of Veterinary Parasitology</i> , 2017, 26, 479-490.	0.2	9
6419	Molecular characterization of two sugarcane streak mosaic virus isolates from Iran with emphasis on its population structure. <i>Acta Virologica</i> , 2017, 61, 428-437.	0.3	3
6420	Genome-wide analysis of EgEVE_1, a transcriptionally active endogenous viral element associated to small RNAs in <i>Eucalyptus</i> genomes. <i>Genetics and Molecular Biology</i> , 2017, 40, 217-225.	0.6	8
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6425	The Complete Chloroplast Genome Sequences of <i>Aconitum pseudolaevae</i> and <i>Aconitum longecassidatum</i> , and Development of Molecular Markers for Distinguishing Species in the <i>Aconitum</i> Subgenus <i>Lycoctonum</i> . <i>Molecules</i> , 2017, 22, 1012.	1.7	40
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6428	Polymorphism of mitochondrial DNA in the Brazilian Canind� goat breed. <i>Genetics and Molecular Research</i> , 2017, 16, .	0.3	1
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6432	Polymorphism in the major histocompatibility complex (MHC class II B) genes of the Rufous-backed Bunting (<i>Emberiza jankowskii</i>). <i>PeerJ</i> , 2017, 5, e2917.	0.9	9
6433	High levels of genetic structuring in the Antarctic springtail <i>Cryptopygus terranovus</i> . <i>Antarctic Science</i> , 2017, 29, 311-323.	0.5	11
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6435	Are there autochthonous <i>Ferrissia</i> (Mollusca: Planorbidae) in the Palaeartic? Molecular evidence of a widespread North American invasion of the Old World. , 2017, 84, 411-419.		8
6436	Genome-wide Identifi-cation, Classifi-cation and Expression Analysis of the Mildew Resistance Locus O () Tj ETQq1 1 0.784314 rgBT /Ove 2017, 60, .	0.5	8
6437	The complete mitochondrial genome of <i>Engyodontium album</i> and comparative analyses with Ascomycota mitogenomes. <i>Genetics and Molecular Biology</i> , 2017, 40, 844-854.	0.6	5
6438	Molecular evidence of the presence of <i>Dictyota dichotoma</i> (Dictyotales: Phaeophyceae) in Argentina based on sequences from mtDNA and cpDNA and a discussion of its possible origin. <i>New Zealand Journal of Botany</i> , 2017, 55, 293-305.	0.8	5
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6444	Cryptic species and their utilization of indigenous and non-indigenous intermediate hosts in the acanthocephalan <i>Polymorphus minutus sensu lato</i> (Polymorphidae). <i>Parasitology</i> , 2018, 145, 1421-1429.	0.7	16

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6446	Retracing the history and planning the future of the red squirrel (<i>Sciurus vulgaris</i>) in Ireland using non-invasive genetics. <i>Mammal Research</i> , 2018, 63, 173-184.	0.6	9
6447	Phylogeography and population genetic analyses reveal the speciation of the <i>Tuber indicum</i> complex. <i>Fungal Genetics and Biology</i> , 2018, 113, 14-23.	0.9	25
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6449	Anthropogenic cause of range shifts and gene flow between two grasshopper species revealed by environmental modelling, geometric morphometrics and population genetics. <i>Insect Conservation and Diversity</i> , 2018, 11, 415-434.	1.4	16
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6459	Human cystic echinococcosis in Turkey: a preliminary study on DNA polymorphisms of hydatid cysts removed from confirmed patients. <i>Parasitology Research</i> , 2018, 117, 1257-1263.	0.6	14
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6466	Genetic diversity and population structure of penis fish (<i>Urechis unicinctus</i>) based on mitochondrial and nuclear gene markers. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 1261-1268.	0.7	9
6467	Assessment of the genetic diversity and population structure of Maire yew (<i>Taxus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 587 Td (chir 48, 589-598.	0.8	6
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6470	Molecular pilot study on peripheral populations of Kenyan greenbul in an afro-montane fragmented forest. African Journal of Ecology, 2018, 56, 610-619.	0.4	0
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6472	Systematics and phylogeography of the Australasian mangrove crabs <i>Parasesarma semperi</i> and <i>P. longicristatum</i> (Decapoda : Brachyura : Sesarmidae) based on morphological and molecular data. Invertebrate Systematics, 2018, 32, 196.	0.5	4
6473	A first assessment of genetic variability in the longhorn beetle <i>Rosalia alpina</i> (Coleoptera): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 34		
6474	High genetic diversity and demographic stability in <i>Aechmea kertesziae</i> (Bromeliaceae), a species of sandy coastal plains (restinga habitat) in southern Brazil. Botanical Journal of the Linnean Society, 2018, 186, 374-388.	0.8	13
6475	Lay mistletoes on the Yucatán Peninsula: post-glacial expansion and genetic differentiation of <i>Psittacanthus mayanus</i> (Loranthaceae). Botanical Journal of the Linnean Society, 2018, 186, 334-360.	0.8	8
6476	High Plasmodium Infection Rate and Reduced Bed Net Efficacy in Multiple Insecticide-Resistant Malaria Vectors in Kinshasa, Democratic Republic of Congo. Journal of Infectious Diseases, 2018, 217, 320-328.	1.9	59
6477	Evolutionary analysis of Porcine circovirus 3 (PCV3) indicates an ancient origin for its current strains and a worldwide dispersion. Virus Genes, 2018, 54, 376-384.	0.7	36
6478	Genetic and haplotype analyses targeting cytochrome b gene of <i>Plasmodium knowlesi</i> isolates of Malaysian Borneo and Peninsular Malaysia. Acta Tropica, 2018, 181, 35-39.	0.9	5
6479	Conventional octaplex PCR for the simultaneous identification of eight mainstream closely related <i>Dendrobium</i> species. Industrial Crops and Products, 2018, 112, 569-576.	2.5	11
6480	Molecular Characterization of the Horn Fly <i>Haematobia irritans</i> Infesting Horses in Central Anatolia Region in Turkey. Journal of Equine Veterinary Science, 2018, 64, 49-54.	0.4	2

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6482	New record of the Oriental house rat, <i>Rattus tanezumi</i> , in Nepal inferred from mitochondrial <i>Cytochrome B</i> gene sequences. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 386-390.	0.2	5
6483	The role of landscape change and paleoclimatic events in shaping the evolutionary history of the <i>Polioptila</i> gnatcatchers (Passeriformes, Polioptilidae) with emphasis on species associated with open habitats. <i>Journal of Avian Biology</i> , 2018, 49, jav-012409.	0.6	10
6484	Population Genetic Structure of Transcaucasian Mole Vole (<i>Ellobius lutescens</i>) Along Zagros Mountains, Iran. <i>Contemporary Problems of Ecology</i> , 2018, 11, 239-245.	0.3	3
6485	Roads to isolation: Similar genomic history patterns in two species of freshwater crabs with contrasting environmental tolerances and range sizes. <i>Ecology and Evolution</i> , 2018, 8, 4657-4668.	0.8	2
6486	Systematic analysis and comparison of the PHD-Finger gene family in Chinese pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 519-531.	1.4	21
6487	Phylogenetic relationship and genetic diversity of citrus psyllid populations from China and Pakistan and their associated <i>Candidatus</i> bacterium. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 173-180.	1.2	16
6488	Population genetics, phylogenomics and hybrid speciation of <i>Juglans</i> in China determined from whole chloroplast genomes, transcriptomes, and genotyping-by-sequencing (GBS). <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 250-265.	1.2	78
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6490	Genetic connectivity of the South American fur seal (<i>Arctocephalus australis</i>) across Atlantic and Pacific oceans revealed by mitochondrial genes. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2018, 28, 315-323.	0.9	12
6491	Genetic Structure and Diversity Among Historic and Modern Populations of the Sumatran Rhinoceros (<i>Dicerorhinus sumatrensis</i>). <i>Journal of Heredity</i> , 2018, 109, 553-565.	1.0	8
6492	Population diversity of <i>Diaphorina citri</i> (Hemiptera: Liviidae) in China based on whole mitochondrial genome sequences. <i>Pest Management Science</i> , 2018, 74, 2569-2577.	1.7	10
6493	The ash dieback invasion of Europe was founded by two genetically divergent individuals. <i>Nature Ecology and Evolution</i> , 2018, 2, 1000-1008.	3.4	82
6494	Genetic variation and structure of Ubame oak, <i>Quercus phillyraeoides</i> , in Japan revealed by chloroplast DNA and nuclear microsatellite markers. <i>Genes and Genetic Systems</i> , 2018, 93, 37-50.	0.2	5
6495	Resolving evolutionary changes in parasite life cycle complexity: Molecular phylogeny of the trematode genus <i>Alloglossidium</i> indicates more than one origin of precociousness. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 371-381.	1.2	17
6496	Multilocus sequence analysis of <i>Borrelia burgdorferi</i> sensu lato isolates from Western Siberia, Russia and Northern Mongolia. <i>Infection, Genetics and Evolution</i> , 2018, 62, 160-169.	1.0	16
6497	Genetic polymorphism and structure of wild and zoo populations of the fosa (<i>Eupleridae</i> , Carnivora), the largest living carnivoran of Madagascar. <i>Mammalian Biology</i> , 2018, 92, 68-77.	0.8	4
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6500	Genetic structure and environmental niche modeling confirm two evolutionary and conservation units within the western spadefoot (<i>Spea hammondi</i>). <i>Conservation Genetics</i> , 2018, 19, 937-946.	0.8	15
6501	Survival in northern microrefugia in an endemic Carpathian gammarid (Crustacea: Amphipoda). <i>Zoologica Scripta</i> , 2018, 47, 357-372.	0.7	18
6502	Genetic diversity and phylogeography of the elusive, but epidemiologically important <i>Echinococcus granulosus</i> sensu stricto genotype G3. <i>Parasitology</i> , 2018, 145, 1613-1622.	0.7	41
6503	First report of <i>Atyaephyra thymisensis</i> Christodoulou, Antoniou, Magoulas & Koukouras, 2012 (Decapoda, Caridea, Atyidae) from Albania and the Republic of Macedonia confirmed by DNA barcodes. <i>Crustaceana</i> , 2018, 91, 599-610.	0.1	1
6504	Inferring spatial patterns and drivers of population divergence of <i>Neolitsea sericea</i> (Lauraceae), based on molecular phylogeography and landscape genomics. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 162-172.	1.2	18
6505	Genetic diversity of MHC class II DRB alleles in the continental and Japanese populations of the sable <i>Martes zibellina</i> (Mustelidae, Carnivora, Mammalia). <i>Mammal Research</i> , 2018, 63, 369-378.	0.6	5
6506	Molecular Evolution at a Meiosis Gene Mediates Species Differences in the Rate and Patterning of Recombination. <i>Current Biology</i> , 2018, 28, 1289-1295.e4.	1.8	44
6507	Comparative analysis of rhizobial chromosomes and plasmids to estimate their evolutionary relationships. <i>Plasmid</i> , 2018, 96-97, 13-24.	0.4	19
6508	mtDNA analysis of <i>Mytilopsis</i> (Bivalvia, Dreissenidae) invasion in Brazil reveals the existence of two species. <i>Hydrobiologia</i> , 2018, 817, 97-110.	1.0	17
6509	Mycobiota of maize seeds revealed by rDNA ITS sequence analysis of samples with varying storage times. <i>MicrobiologyOpen</i> , 2018, 7, e00609.	1.2	26
6510	DNA barcoding of five Japanese encephalitis mosquito vectors (<i>Culex fuscocephala</i> , <i>Culex gelidus</i>), Tj ETQq1 1 0.784314 rgBT ₂₁ /Overlook	0.9	21
6511	Genetic relationships of wild boars highlight the importance of Southern Iran in forming a comprehensive picture of the species' phylogeography. <i>Mammalian Biology</i> , 2018, 92, 21-29.	0.8	6
6512	Biogeography of <i>Leptospira</i> in wild animal communities inhabiting the insular ecosystem of the western Indian Ocean islands and neighboring Africa. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-12.	3.0	30
6513	Genetic and oceanographic tools reveal high population connectivity and diversity in the endangered pen shell <i>Pinna nobilis</i> . <i>Scientific Reports</i> , 2018, 8, 4770.	1.6	31
6514	Ancient DNA tracks the mainland extinction and island survival of the Tasmanian devil. <i>Journal of Biogeography</i> , 2018, 45, 963-976.	1.4	22
6515	Genetic diversity and evolution of reduced sulfur storage during domestication of maize. <i>Plant Journal</i> , 2018, 94, 943-955.	2.8	5
6516	A Y-Encoded Suppressor of Feminization Arose via Lineage-Specific Duplication of a Cytokinin Response Regulator in Kiwifruit. <i>Plant Cell</i> , 2018, 30, 780-795.	3.1	151

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6518	Differentiation of phylogenetic lineages within the <i>Colletotrichum gloeosporioides</i> species complex™ associated with cassava anthracnose disease by PCR-RFLP. <i>Tropical Plant Pathology</i> , 2018, 43, 194-201.	0.8	5
6519	A nation-wide genetic survey revealed a complex population structure of <i>Bemisia tabaci</i> in Pakistan. <i>Acta Tropica</i> , 2018, 183, 119-125.	0.9	27
6520	The Rocky Mountains as a dispersal barrier between barn owl (<i>Tyto alba</i>) populations in North America. <i>Journal of Biogeography</i> , 2018, 45, 1288-1300.	1.4	41
6521	Mitochondrial introgression obscures phylogenetic relationships among manakins of the genus <i>Lepidothrix</i> (Aves: Pipridae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 314-320.	1.2	21
6522	Phylogeography of the widespread spider <i>Nephila clavipes</i> (Araneae: Araneidae) in South America indicates geologically and climatically driven lineage diversification. <i>Journal of Biogeography</i> , 2018, 45, 1246-1260.	1.4	11
6523	Characterization and transcriptional regulation of chlorophyll b reductase gene NON-YELLOW COLORING 1 associated with leaf senescence in perennial ryegrass (<i>Lolium perenne</i> L.). <i>Environmental and Experimental Botany</i> , 2018, 149, 43-50.	2.0	14
6524	Multiple Pleistocene refugia and repeated phylogeographic breaks in the southern Caspian Sea region: Insights from the freshwater crab <i>Potamon ibericum</i> . <i>Journal of Biogeography</i> , 2018, 45, 1234-1245.	1.4	20
6525	Some mitochondrial genes perform better for damselfly phylogenetics: species- and population-level analyses of four complete mitogenomes of <i>Euphaea</i> sibling species. <i>Systematic Entomology</i> , 2018, 43, 702-715.	1.7	11
6526	Evolutionary relationships of two balitorids (Cypriniformes, Balitoridae) revealed by comparative mitogenomics. <i>Zoologica Scripta</i> , 2018, 47, 300-310.	0.7	9
6527	Phoretic or not? Phylogeography of the pseudoscorpion <i>Chernes hahnii</i> (Pseudoscorpiones). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	0.3	18
6528	Disintegrating over space and time: Paraphyly and species delimitation in the Wehrle's Salamander complex. <i>Zoologica Scripta</i> , 2018, 47, 285-299.	0.7	18
6529	Genetic interaction and diversity of the families Libellulidae and Gomphidae through COI gene from China and Pakistan. <i>Acta Tropica</i> , 2018, 182, 92-99.	0.9	15
6530	Population genetic structure of <i>Diaphorina citri</i> Kuwayama (Hemiptera: Liviidae): host-driven genetic differentiation in China. <i>Scientific Reports</i> , 2018, 8, 1473.	1.6	15
6531	Chloroplast genomes of <i>Byrsonima</i> species (Malpighiaceae): comparative analysis and screening of high divergence sequences. <i>Scientific Reports</i> , 2018, 8, 2210.	1.6	108
6532	Phylogenetic Diversity and Host Specialization of <i>Corynespora cassiicola</i> Responsible for Emerging Target Spot Disease of Cotton and Other Crops in the Southeastern United States. <i>Phytopathology</i> , 2018, 108, 892-901.	1.1	40
6533	Spiroides shrubs on Qinghai-Tibetan Plateau: Multilocus phylogeography and palaeodistributional reconstruction of <i>Spiraea alpina</i> and <i>S. Mongolica</i> (Rosaceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 123, 137-148.	1.2	31
6534	Persistence with episodic range expansion from the early Pleistocene: the distribution of genetic variation in the forest tree <i>Corymbia calophylla</i> (Myrtaceae) in south-western Australia. <i>Biological Journal of the Linnean Society</i> , 2018, 123, 545-560.	0.7	18

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6536	Glacial refugia and postglacial spread of an iconic large European land snail, <i>Helix pomatia</i> (Pulmonata: Helicidae). <i>Biological Journal of the Linnean Society</i> , 2018, 123, 218-234.	0.7	16
6537	Genetic Differentiation and Demographic History of the Northern Rufous Mouse Lemur (<i>Microcebus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Primatology, 2018, 39, 65-89.	0.9	16
6538	Phylogenetic and environmental DNA insights into emerging aquatic parasites: implications for risk management. <i>International Journal for Parasitology</i> , 2018, 48, 473-481.	1.3	9
6539	Genetic diversity of the <i>Plasmodium vivax</i> phosphatidylinositol 3-kinase gene in two regions of the China-Myanmar border. <i>Infection, Genetics and Evolution</i> , 2018, 61, 45-52.	1.0	4
6540	Plastome-wide comparison reveals new SNV resources for the authentication of <i>Dendrobium huoshanense</i> and its corresponding medicinal slice (Huoshan Fengdou). <i>Acta Pharmaceutica Sinica B</i> , 2018, 8, 466-477.	5.7	23
6541	Genetic diversity of the invasive crayfish <i>Procambarus clarkii</i> in France. <i>Limnologica</i> , 2018, 69, 135-141.	0.7	6
6542	Molecular phylogeny of Neotropical rock frogs reveals a long history of vicariant diversification in the Atlantic forest. <i>Molecular Phylogenetics and Evolution</i> , 2018, 122, 142-156.	1.2	30
6543	A population genetics analysis in clinical isolates of <i>Sporothrix schenckii</i> based on calmodulin and calcium/calmodulin-dependent kinase partial gene sequences. <i>Mycoses</i> , 2018, 61, 383-392.	1.8	10
6544	Worldwide sampling reveals low genetic variability in populations of the freshwater ciliate <i>Paramecium biaurelia</i> (<i>P. aurelia</i> species complex, Ciliophora, Protozoa). <i>Organisms Diversity and Evolution</i> , 2018, 18, 39-50.	0.7	8
6545	Molecular characterization of <i>Rhodnius robustus</i> specimens, potential vectors for Chagas disease in French Guiana, South America. <i>Infection, Genetics and Evolution</i> , 2018, 59, 28-31.	1.0	4
6546	Analysis of genetic diversity and population structure of gene encoding cell-traversal protein for ookinetes and sporozoites (CelTOS) vaccine candidate antigen in global <i>Plasmodium falciparum</i> populations. <i>Infection, Genetics and Evolution</i> , 2018, 59, 113-125.	1.0	10
6547	The Complete Phylogeny of Pangolins: Scaling Up Resources for the Molecular Tracing of the Most Trafficked Mammals on Earth. <i>Journal of Heredity</i> , 2018, 109, 347-359.	1.0	64
6548	When is a native species invasive? Incursion of a novel predatory marsupial detected using molecular and historical data. <i>Diversity and Distributions</i> , 2018, 24, 831-840.	1.9	23
6549	Contrasting patterns of variation in weedy traits and unique crop features in divergent populations of US weedy rice (<i>Oryza sativa</i> sp.) in Arkansas and California. <i>Pest Management Science</i> , 2018, 74, 1404-1415.	1.7	20
6550	Genome-wide identification and comparative analysis of phosphate starvation-responsive transcription factors in maize and three other gramineous plants. <i>Plant Cell Reports</i> , 2018, 37, 711-726.	2.8	21
6551	Morphological diversity and phylogeography of the Georgian durmast oak (<i>Q. petraea</i> subsp. <i>iberica</i>) and related Caucasian oak species in Georgia (South Caucasus). <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	11
6552	Mitochondrial genome diversity and population structure of two western honey bee subspecies in the Republic of South Africa. <i>Scientific Reports</i> , 2018, 8, 1333.	1.6	23

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6554	DNA barcoding for identifying synanthropic flesh flies (Diptera, Sarcophagidae) of Colombia. <i>Acta Tropica</i> , 2018, 182, 291-297.	0.9	15
6555	Assessment of genetic structuring in the Lygodium fern moths <i>Austromusotima camptozonale</i> and <i>Neomusotima conspurcatalis</i> in their native range: implications for biological control. <i>Biological Control</i> , 2018, 121, 8-13.	1.4	10
6556	Population genetic structure of the intertidal kinorhynch <i>Echinoderes marthae</i> (Kinorhyncha). <i>Tj ETQq1 1 0.784314 rgBT /Overl</i> <i>Society of Washington</i> , 2018, 131, 36-46.	0.3	4
6557	On the origin and genetic variability of the two invasive biotypes of <i>Chromolaena odorata</i> . <i>Biological Invasions</i> , 2018, 20, 2033-2046.	1.2	12
6558	Cryptic diversity, pathogenicity, and evolutionary species boundaries in <i>Cercospora</i> populations associated with <i>Cercospora</i> leaf spot of <i>Beta vulgaris</i> . <i>Fungal Biology</i> , 2018, 122, 264-282.	1.1	16
6559	The reunion of two lineages of the Neotropical brown stink bug on soybean lands in the heart of Brazil. <i>Scientific Reports</i> , 2018, 8, 2496.	1.6	33
6560	Characterization and Genetic Structure of a <i>Tospovirus</i> Causing Chlorotic Ring Spots and Chlorosis Disease on Peanut; Comparison with Iranian and Polish Populations of Tomato yellow fruit ring virus. <i>Plant Disease</i> , 2018, 102, 1509-1519.	0.7	7
6561	Phylogeography of the Asian lesser white-toothed shrew, <i>Crocidura shantungensis</i> , in East Asia: role of the Korean Peninsula as refugium for small mammals. <i>Genetica</i> , 2018, 146, 211-226.	0.5	9
6562	Maize chlorotic mottle virus exhibits low divergence between differentiated regional sub-populations. <i>Scientific Reports</i> , 2018, 8, 1173.	1.6	36
6563	A heading date QTL, qHD7.2, from wild rice (<i>Oryza rufipogon</i>) delays flowering and shortens panicle length under long-day conditions. <i>Scientific Reports</i> , 2018, 8, 2928.	1.6	26
6564	From laboratory to point of entry: development and implementation of a loop-mediated isothermal amplification (LAMP)-based genetic identification system to prevent introduction of quarantine insect species. <i>Pest Management Science</i> , 2018, 74, 1504-1512.	1.7	55
6565	The <i>Câ€“Sâ€“A</i> gene system regulates hull pigmentation and reveals evolution of anthocyanin biosynthesis pathway in rice. <i>Journal of Experimental Botany</i> , 2018, 69, 1485-1498.	2.4	114
6566	Current Status and Future Prospects of Next-Generation Data Management and Analytical Decision Support Tools for Enhancing Genetic Gains in Crops. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2018, 164, 277-292.	0.6	4
6567	Origin of Pest Lineages of the Colorado Potato Beetle (Coleoptera: Chrysomelidae). <i>Journal of Economic Entomology</i> , 2018, 111, 868-878.	0.8	35
6568	Dispersal and mating strategies in two neotropical soil-feeding termites, <i>Embiratermes neotenicus</i> and <i>Silvestritermes minutus</i> (Termitidae, Syntermitinae). <i>Insectes Sociaux</i> , 2018, 65, 251-262.	0.7	8
6569	Extra-Mediterranean glacial refuges in barred and common grass snakes (<i>Natrix helvetica</i> , <i>N. natrix</i>). <i>Scientific Reports</i> , 2018, 8, 1821.	1.6	20
6570	Genetic diversity and recombination analysis based on capsid protein gene of Chilli veinal mottle virus isolates from Pakistan. <i>European Journal of Plant Pathology</i> , 2018, 151, 891-900.	0.8	13

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6571	The genetic landscape of Mediterranean North African populations through complete mtDNA sequences. <i>Annals of Human Biology</i> , 2018, 45, 98-104.	0.4	16
6572	Unexpected absence of island endemics: Long-distance dispersal in higher latitude sub-Antarctic <i>Siphonaria</i> (Gastropoda: Euthyneura) species. <i>Journal of Biogeography</i> , 2018, 45, 874-884.	1.4	34
6573	Morphological, chemical, and molecular analyses differentiate populations of the subterranean nesting stingless bee <i>Mourella caerulea</i> (Apidae: Meliponini). <i>Apidologie</i> , 2018, 49, 367-377.	0.9	12
6574	Phylogeography of <i>Orinus</i> (Poaceae), a dominant grass genus on the Qinghai-Tibet Plateau. <i>Botanical Journal of the Linnean Society</i> , 2018, 186, 202-223.	0.8	18
6575	Characterization of OglDREB2A gene from African rice (<i>Oryza glaberrima</i>), comparative analysis and its transcriptional regulation under salinity stress. <i>3 Biotech</i> , 2018, 8, 91.	1.1	10
6576	High genetic diversity and low-population differentiation in the Patagonian sprat (<i>Sprattus fuegensis</i>) based on mitochondrial DNA. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 1148-1155.	0.7	5
6577	Population genetic structure of the sword prawn <i>Parapenaeopsis hardwickii</i> (Miers, 1878) (Decapoda: Tj ETQq0 0 0 rgBT /Overlock 10 T	0.3	3
6578	<i>Afrina sporoboliae</i> sp. n. (Nematoda: Anguinidae) Associated with <i>Sporobolus cryptandrus</i> from Idaho, United States: Phylogenetic Relationships and Population Structure. <i>Phytopathology</i> , 2018, 108, 768-779.	1.1	1
6579	The complete plastome of macaw palm [<i>Acrocomia aculeata</i> (Jacq.) Lodd. ex Mart.] and extensive molecular analyses of the evolution of plastid genes in Arecaceae. <i>Planta</i> , 2018, 247, 1011-1030.	1.6	38
6580	Papain-like cysteine proteases in <i>Carica papaya</i> : lineage-specific gene duplication and expansion. <i>BMC Genomics</i> , 2018, 19, 26.	1.2	28
6581	Ancient Human Migrations to and through Jammu Kashmir- India were not of Males Exclusively. <i>Scientific Reports</i> , 2018, 8, 851.	1.6	21
6582	Integrative taxonomy of the neotropical genus <i>Omalonyx</i> (Elasmognatha: Succineidae). <i>Zoologica Scripta</i> , 2018, 47, 174-186.	0.7	7
6583	A case of biodiversity overestimation in the Balkan <i>Belgrandiella</i> A. J. Wagner, 1927 (Caenogastropoda: Hydrobiidae): molecular divergence not paralleled by high morphological variation. <i>Journal of Natural History</i> , 2018, 52, 323-344.	0.2	26
6584	Description of <i>Pseudo-nitzschia cuspidata</i> var. <i>manzanillensis</i> var. nov. (Bacillariophyceae): morphology and molecular characterization of a variety from the central Mexican pacific. <i>Diatom Research</i> , 2018, 33, 55-68.	0.5	6
6585	Reflection of paleoclimate oscillations and tectonic events in the phylogeography of moustache toads in southern China. <i>Journal of Zoology</i> , 2018, 305, 17-26.	0.8	10
6586	Characterization of a satellite DNA in the genera <i>Lacerta</i> and <i>Timon</i> (Reptilia, Lacertidae) and its role in the differentiation of the W chromosome. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2018, 330, 83-95.	0.6	20
6587	Human migration and the spread of malaria parasites to the New World. <i>Scientific Reports</i> , 2018, 8, 1993.	1.6	76
6588	Genetic diversity through time and space: diversity and demographic history from natural history specimens and serially sampled contemporary populations of the threatened Gouldian finch (<i>Erythrura gouldiae</i>). <i>Conservation Genetics</i> , 2018, 19, 737-754.	0.8	4

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6589	The complete chloroplast genome sequence of <i>Fritillaria thunbergii</i> Miq., an important medicinal plant, and identification of DNA markers to authenticate <i>Fritillariae Bulbus</i> . <i>Horticulture Environment and Biotechnology</i> , 2018, 59, 71-80.	0.7	7
6590	Identifying source populations for the reintroduction of the Eurasian beaver, <i>Castor fiber</i> L. 1758, into Britain: evidence from ancient DNA. <i>Scientific Reports</i> , 2018, 8, 2708.	1.6	12
6591	Population genetic structure and molecular diversity of <i>Leucinodes orbonalis</i> based on mitochondrial COI gene sequences. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 1231-1239.	0.7	7
6592	Flickers of speciation: Sympatric colour morphs of the arcâ€eye hawkfish, <i>Paracirrhites arcatus</i> , reveal key elements of divergence with gene flow. <i>Molecular Ecology</i> , 2018, 27, 1479-1493.	2.0	20
6593	Evolution of methicillin-resistant <i>Staphylococcus aureus</i> : Evidence of positive selection in a penicillin-binding protein (PBP) 2a coding gene <i>mecA</i> . <i>Infection, Genetics and Evolution</i> , 2018, 59, 16-22.	1.0	20
6594	Molecular detection of hemogregarines and haemosporidians in Brazilian free-living testudines. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2018, 7, 75-84.	0.6	9
6595	Potential for re-emergence of wheat stem rust in the United Kingdom. <i>Communications Biology</i> , 2018, 1, 13.	2.0	107
6596	Genetic diversity of <i>Fusarium</i> spp. in pineapple "PÃ©rola" cultivar. <i>European Journal of Plant Pathology</i> , 2018, 150, 853-868.	0.8	3
6597	Genome and secretome analysis of <i>Pochonia chlamydosporia</i> provide new insight into egg-parasitic mechanisms. <i>Scientific Reports</i> , 2018, 8, 1123.	1.6	20
6598	Mitochondrial DNA suggests cryptic speciation in <i>Prodiptosis longifila</i> (Diptera: Tj ETQq1 1 0.784314 rgBT /Overlock Entomological Research, 2018, 108, 739-749.	0.5	8
6599	Interspecies introgressive hybridization in spiny frogs <i>Quasipaa</i> (Family Dicroglossidae) revealed by analyses on multiple mitochondrial and nuclear genes. <i>Ecology and Evolution</i> , 2018, 8, 1260-1270.	0.8	10
6600	Distribution and the origin of invasive apple snails, <i>Pomacea canaliculata</i> and <i>P. maculata</i> (Gastropoda: Ampullariidae) in China. <i>Scientific Reports</i> , 2018, 8, 1185.	1.6	42
6601	Bph6 encodes an exocyst-localized protein and confers broad resistance to planthoppers in rice. <i>Nature Genetics</i> , 2018, 50, 297-306.	9.4	158
6602	Gene encoding the CTP synthetase as an appropriate molecular tool for identification and phylogenetic study of the family <i>Bifidobacteriaceae</i> . <i>MicrobiologyOpen</i> , 2018, 7, e00579.	1.2	10
6603	Chloroplast genomic resources for phylogeny and DNA barcoding: a case study on <i>Fritillaria</i> . <i>Scientific Reports</i> , 2018, 8, 1184.	1.6	120
6604	Patterns of Genome-Wide Nucleotide Diversity in the Gynodioecious Plant <i>Thymus vulgaris</i> Are Compatible with Recent Sweeps of Cytoplasmic Genes. <i>Genome Biology and Evolution</i> , 2018, 10, 239-248.	1.1	8
6605	Lack of evidence for selection favouring MHC haplotypes that combine high functional diversity. <i>Heredity</i> , 2018, 120, 396-406.	1.2	14
6606	A new species of <i>Petroleuciscus</i> (<i>T</i> - <i>eleostei</i> : <i>C</i> - <i>yprinidae</i>) from the <i>B</i> - <i>M</i> - <i>R</i> - <i>A</i> - <i>T</i> - <i>urkey</i> . <i>Journal of Fish Biology</i> , 2018, 92, 875-887.	0.7	7

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6608	Complex signatures of natural selection at GYPA. <i>Human Genetics</i> , 2018, 137, 151-160.	1.8	20
6609	Combining morphology and molecular data to improve <i>Drosophila paulistorum</i> (Diptera). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66</i>	0.9	9
6610	Evolutionary analyses of the avirulence effector <i>AvrStb6</i> in global populations of <i>Zymoseptoria tritici</i> identify candidate amino acids involved in recognition. <i>Molecular Plant Pathology</i> , 2018, 19, 1836-1846.	2.0	30
6611	Genetic divergence of isolated populations of the native micromoth <i>Bucculatrix mirnae</i> (Lepidoptera: Bucculatricidae) in the arid environments of Northern Chile. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 1139-1147.	0.7	4
6612	Entrapped by the uneven central and Middle Eastern terrains: Genetic status of populations of <i>Hirudo orientalis</i> (Annelida, Clitellata, Hirudinida) with a phylogenetic review of the genus <i>Hirudo</i> . <i>Molecular Phylogenetics and Evolution</i> , 2018, 121, 52-60.	1.2	3
6613	Complete mitogenomes of ancient Caribbean Guinea pigs (<i>Cavia porcellus</i>). <i>Journal of Archaeological Science: Reports</i> , 2018, 17, 678-688.	0.2	15
6614	High genetic variability of <i>Alexandrium catenella</i> directly detected in environmental samples from the Southern Austral Ecosystem of Chile. <i>Marine Pollution Bulletin</i> , 2018, 127, 437-444.	2.3	9
6615	Do multiple karyomorphs and population genetics of freshwater darter characines (<i>Apareiodon</i>). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 42</i>	0.4	20
6616	Comparing the genetic diversity and structure of indigenous Korean and Chinese populations of <i>Laodelphax striatellus</i> Fall�n using mitochondrial haplotypes. <i>Journal of Asia-Pacific Entomology</i> , 2018, 21, 233-238.	0.4	7
6617	Differing phylogeographic patterns within the Indo�West Pacific mangrove genus <i>Xylocarpus</i> (Meliaceae). <i>Journal of Biogeography</i> , 2018, 45, 676-689.	1.4	21
6618	The curious case of <i>Bradypus variegatus</i> sloths: populations in threatened habitats are biodiversity components needing protection. <i>Biodiversity and Conservation</i> , 2018, 27, 1291-1308.	1.2	4
6619	Phylogeny and Molecular Evolution of miR820 and miR396 microRNA Families in <i>Oryza AA</i> Genomes. <i>Tropical Plant Biology</i> , 2018, 11, 1-16.	1.0	6
6620	Determination of genetic variations in the genus <i>Dryomys</i> Thomas, 1906 (Rodentia: Gliridae) distributed in Turkey using NADH dehydrogenase 1 (<i>ND1</i>) gene. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 933-942.	0.7	6
6621	Genome-wide identification of PHD-finger genes and expression pattern analysis under various treatments in moso bamboo (<i>Phyllostachys edulis</i>). <i>Plant Physiology and Biochemistry</i> , 2018, 123, 378-391.	2.8	41
6622	Cryptic lineage differentiation among Indo-Pacific bottlenose dolphins (<i>Tursiops aduncus</i>) in the northwest Indian Ocean. <i>Molecular Phylogenetics and Evolution</i> , 2018, 122, 1-14.	1.2	21
6623	Geographical isolation and environmental heterogeneity contribute to the spatial genetic patterns of <i>Quercus kerrii</i> (Fagaceae). <i>Heredity</i> , 2018, 120, 219-233.	1.2	32
6624	Differences in Molecular Characteristics of Segment 8 in <i>Rice black-streaked dwarf virus</i> and <i>Southern rice black-streaked dwarf virus</i> . <i>Plant Disease</i> , 2018, 102, 1115-1123.	0.7	5

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6626	Genome-Wide Assessment of Polygalacturonases-Like (PGL) Genes of <i>Medicago truncatula</i> , <i>Sorghum bicolor</i> , <i>Vitis vinifera</i> and <i>Oryza sativa</i> Using Comparative Genomics Approach. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2018, 10, 704-721.	2.2	5
6627	Complex selection on a regulator of social cognition: Evidence of balancing selection, regulatory interactions and population differentiation in the prairie vole <i>Avpr1a</i> locus. <i>Molecular Ecology</i> , 2018, 27, 419-431.	2.0	3
6628	Riverscape genetics identifies speckled dace (<i>Rhinichthys osculus</i>) cryptic diversity in the Klamath-Trinity Basin. <i>Conservation Genetics</i> , 2018, 19, 111-127.	0.8	5
6629	Genetic admixture of mitten crabs in the Northeast Asia hybrid zones. <i>Hydrobiologia</i> , 2018, 806, 203-214.	1.0	7
6630	Diversity and characterization of <i>Azotobacter</i> isolates obtained from rice rhizosphere soils in Taiwan. <i>Annals of Microbiology</i> , 2018, 68, 17-26.	1.1	20
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6632	Genome-wide Analysis of Transcriptional Variability in a Large Maize-Teosinte Population. <i>Molecular Plant</i> , 2018, 11, 443-459.	3.9	87
6633	Genetic origin and dispersal of the invasive soybean aphid inferred from population genetic analysis and approximate Bayesian computation. <i>Integrative Zoology</i> , 2018, 13, 536-552.	1.3	6
6634	Mitogenomic differences between the normal and tumor cells of colorectal cancer patients. <i>Human Mutation</i> , 2018, 39, 691-701.	1.1	16
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6636	Adding injury to infection: The relationship between injury status and genetic diversity of <i>Theileria</i> infecting plains zebra, <i>Equus quagga</i> . <i>Infection, Genetics and Evolution</i> , 2018, 58, 269-278.	1.0	3
6637	Gone with the trees: Phylogeography of <i>Rhodiola</i> sect. <i>Trifida</i> (Crassulaceae) reveals multiple refugia on the Qinghai-Tibetan Plateau. <i>Molecular Phylogenetics and Evolution</i> , 2018, 121, 110-120.	1.2	33
6638	Genetic Diversity of <i>Bartonella</i> spp. in Wild Mammals and Ectoparasites in Brazilian Pantanal. <i>Microbial Ecology</i> , 2018, 76, 544-554.	1.4	26
6639	Chloroplast phylogeography of a widely distributed mangrove species, <i>Excoecaria agallocha</i> , in the Indo-West Pacific region. <i>Hydrobiologia</i> , 2018, 807, 333-347.	1.0	17
6640	Evaluation of genetic diversity and population structure of Macqueen's Bustard <i>Chlamydotis macqueenii</i> in Iran. <i>Bird Study</i> , 2018, 65, 108-113.	0.4	2
6641	Strong population bottleneck and repeated demographic expansions of <i>Populus adenopoda</i> (Salicaceae) in subtropical China. <i>Annals of Botany</i> , 2018, 121, 665-679.	1.4	25
6642	Phylogeographical study reveals high genetic diversity in a widespread desert rodent, <i>Dipus sagitta</i> (Dipodidae: Rodentia). <i>Biological Journal of the Linnean Society</i> , 2018, 123, 445-462.	0.7	18

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6644	Mitochondrial <i>scp</i> DNA variation reveals maternal origins and demographic dynamics of Ethiopian indigenous goats. <i>Ecology and Evolution</i> , 2018, 8, 1543-1553.	0.8	35
6645	Long-distance dispersal or postglacial contraction? Insights into disjunction between Himalaya-Hengduan Mountains and Taiwan in a cold-adapted herbaceous genus, <i>Triplostegia</i> . <i>Ecology and Evolution</i> , 2018, 8, 1131-1146.	0.8	23
6646	An AlgU-Regulated Antisense Transcript Encoded within the <i>Pseudomonas syringae fleQ</i> Gene Has a Positive Effect on Motility. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	11
6647	SERT gene polymorphisms are associated with risk-taking behaviour and breeding parameters in wild great tits. <i>Journal of Experimental Biology</i> , 2018, 221, .	0.8	8
6648	Colonization and diversification of the white-browed shortwing (Aves: Muscicapidae: Brachypteryx) Tj ETQq1 1 0.784314 rgBT /Overlock	1.2	14
6649	The phylogeography of the cycad genus <i>Dioon</i> (Zamiaceae) clarifies its Cenozoic expansion and diversification in the Mexican transition zone. <i>Annals of Botany</i> , 2018, 121, 535-548.	1.4	42
6650	Cryptic diversity in the <i>Oecomys roberti</i> complex: revalidation of <i>Oecomys tapajinus</i> (Rodentia,) Tj ETQq1 1 0.784314 rgBT /Overlock	0.6	8
6651	Human-mediated introduction of introgressed deer across Wallace's line: Historical biogeography of <i>Rusa unicolor</i> and <i>R. timorensis</i> . <i>Ecology and Evolution</i> , 2018, 8, 1465-1479.	0.8	21
6652	Genetic and morphological characterization of <i>Thysaniezia</i> tapeworms from cattle and sheep in Senegal. <i>Veterinary Parasitology: Regional Studies and Reports</i> , 2018, 11, 27-31.	0.3	1
6653	Phylogeography of <i>Crocidura suaveolens</i> (Mammalia: Soricidae) in Iberia has been shaped by competitive exclusion by <i>C. russula</i> . <i>Biological Journal of the Linnean Society</i> , 2018, 123, 81-95.	0.7	14
6654	Genome-wide mosaicism in divergence between zoonotic malaria parasite subpopulations with separate sympatric transmission cycles. <i>Molecular Ecology</i> , 2018, 27, 860-870.	2.0	16
6655	<i>Rhizobium laguerreae</i> is the main nitrogen-fixing symbiont of cultivated lentil (<i>Lens culinaris</i>) in Morocco. <i>Systematic and Applied Microbiology</i> , 2018, 41, 113-121.	1.2	16
6656	The origins of diversity in ancient landscapes: Deep phylogeographic structuring in a pseudoscorpion (<i>Pseudotyranochthoniidae</i> : <i>Pseudotyranochthonius</i>) reflects Plio-Pleistocene climate fluctuations. <i>Zoologischer Anzeiger</i> , 2018, 273, 112-123.	0.4	26
6657	Fingerprinting by amplified fragment length polymorphism (AFLP) and barcoding by three plastidic markers in the genus <i>Wolffiella</i> Hegelm. <i>Plant Systematics and Evolution</i> , 2018, 304, 373-386.	0.3	8
6658	Genetic connectivity from the Arctic to the Antarctic: <i>Sclerolinum contortum</i> and <i>Nicomache lokii</i> (Annelida) are both widespread in reducing environments. <i>Scientific Reports</i> , 2018, 8, 4810.	1.6	33
6659	Evolution of Darwin's Peloric <i>Gloxinia</i> (<i>Sinningia speciosa</i>) Is Caused by a Null Mutation in a Pleiotropic TCP Gene. <i>Molecular Biology and Evolution</i> , 2018, 35, 1901-1915.	3.5	24
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6662	Patterns of geographic variation of thermal adapted candidate genes in <i>Drosophila subobscura</i> sex chromosome arrangements. <i>BMC Evolutionary Biology</i> , 2018, 18, 60.	3.2	11
6663	Characterization of the late embryogenesis abundant (LEA) proteins family and their role in drought stress tolerance in upland cotton. <i>BMC Genetics</i> , 2018, 19, 6.	2.7	216
6664	Meta-population demes constitute a reservoir for large MHC allele diversity in wild house mice (<i>Mus musculus</i>). <i>Frontiers in Zoology</i> , 2018, 15, 15.	0.9	11
6665	Spatio-temporal genetic structure of <i>Anopheles gambiae</i> in the Northwestern Lake Victoria Basin, Uganda: implications for genetic control trials in malaria endemic regions. <i>Parasites and Vectors</i> , 2018, 11, 246.	1.0	11
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6667	Signatures of historical selection on MHC reveal different selection patterns in the moor frog (<i>Rana</i>). <i>Trends in Ecology and Evolution</i> , 2018, 33, 17.	9.2	17
6668	Mitogenomic analysis of the Australian lungfish (<i>Neoceratodus forsteri</i>) reveals structuring of indigenous riverine populations and late Pleistocene movement between drainage basins. <i>Conservation Genetics</i> , 2018, 19, 587-597.	0.8	13
6669	Good practices for common sole assessment in the Adriatic Sea: Genetic and morphological differentiation of <i>Solea solea</i> (Linnaeus, 1758) from <i>S. aegyptiaca</i> (Chabanaud, 1927) and stock identification. <i>Journal of Sea Research</i> , 2018, 137, 57-64.	0.6	8
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6671	Simultaneous detection of <i>Plasmodium vivax</i> dhfr, dhps, mdr1 and crt-o resistance-associated mutations in the Colombian Amazonian region. <i>Malaria Journal</i> , 2018, 17, 130.	0.8	12
6672	Molecular evidence for new sympatric cryptic species of <i>Aedes albopictus</i> (Diptera: Culicidae) in China: A new threat from <i>Aedes albopictus</i> subgroup?. <i>Parasites and Vectors</i> , 2018, 11, 228.	1.0	39
6673	What Role Has Hybridization Played in the Replacement of Native Roanoke Bass with Invasive Rock Bass?. <i>Transactions of the American Fisheries Society</i> , 2018, 147, 497-513.	0.6	4
6674	Occurrence and molecular characterization of <i>Clinostomum complanatum</i> (Trematoda). <i>Trends in Parasitology</i> , 2018, 33, 15.	0.6	15
6675	Phenotypic and Molecular-Phylogenetic Analysis Provide Novel Insights into the Diversity of <i>Curtobacterium flaccumfaciens</i> . <i>Phytopathology</i> , 2018, 108, 1154-1164.	1.1	29
6676	Mitonuclear discordance as a confounding factor in the DNA taxonomy of monogonont rotifers. <i>Zoologica Scripta</i> , 2018, 47, 122-132.	0.7	19
6677	Large-scale genetic panmixia in the blue shark (<i>Prionace glauca</i>): A single worldwide population, or a genetic lag-time effect of the grey zone of differentiation?. <i>Evolutionary Applications</i> , 2018, 11, 614-630.	1.5	40
6678	Chasing the phantom: biogeography and conservation of <i>Vipera latastei-monticola</i> in the Maghreb (North Africa). <i>Amphibia - Reptilia</i> , 2018, 39, 145-161.	0.1	9

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6680	Reconciling the biogeography of an invader through recent and historic genetic patterns: the case of topmouth gudgeon <i>Pseudorasbora parva</i> . <i>Biological Invasions</i> , 2018, 20, 2157-2171.	1.2	22
6681	Contrasting patterns of Holocene genetic variation in two parapatric species of <i>Ctenomys</i> from Northern Patagonia, Argentina. <i>Biological Journal of the Linnean Society</i> , 2018, 123, 96-112.	0.7	9
6682	Chloroplastic and nuclear diversity of wild beets at a large geographical scale: Insights into the evolutionary history of the <i>Beta</i> section. <i>Ecology and Evolution</i> , 2018, 8, 2890-2900.	0.8	9
6683	Interglacial refugia on tropical mountains: Novel insights from the summit rat (<i>Rattus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 Td (1.9	26
6684	Investigating species boundaries using DNA and morphology in the mite <i>Tyrophagus curvipenis</i> (Acari:) Tj ETQq1 1 0.784314 rgBT /Over Experimental and Applied Acarology, 2018, 75, 167-189.	0.7	10
6685	Multi-locus Analyses Indicate that <i>Melastoma dendrisetosum</i> , an Endemic and Endangered Shrub in Hainan, is a Distinct Species. <i>Systematic Botany</i> , 2018, 43, 258-265.	0.2	5
6686	Genetic diversity and gene flow among the giant mud crabs (<i>Scylla serrata</i>) in anthropogenic-polluted mangroves of mainland Tanzania: Implications for conservation. <i>Fisheries Research</i> , 2018, 205, 96-104.	0.9	11
6687	Genetic structure and phylogeographic evolution of the West African populations of <i>Sitophilus zeamais</i> (Coleoptera, Curculionidae). <i>Journal of Stored Products Research</i> , 2018, 77, 135-143.	1.2	6
6688	Genetic diversity distribution among seasonal colonies of a nectar-feeding bat (<i>Leptonycteris</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.8	11
6689	Crossing the Mid-Aegean Trench: vicariant evolution of the Eastern pine processionary moth, <i>Thaumetopoea wilkinsoni</i> (Lepidoptera: Notodontidae), in Crete. <i>Biological Journal of the Linnean Society</i> , 2018, 124, 228-236.	0.7	4
6690	Evidence for intragenic recombination and selective sweep in an effector gene of <i>Phytophthora infestans</i> . <i>Evolutionary Applications</i> , 2018, 11, 1342-1353.	1.5	34
6691	A fungal avirulence factor encoded in a highly plastic genomic region triggers partial resistance to septoria tritici blotch. <i>New Phytologist</i> , 2018, 219, 1048-1061.	3.5	103
6692	Micro- and macroevolutionary adaptation through repeated loss of a complete metabolic pathway. <i>New Phytologist</i> , 2018, 219, 757-766.	3.5	27
6693	Inducible variation in anaerobic energy metabolism reflects hypoxia tolerance across the intertidal and subtidal distribution of the Pacific oyster (<i>Crassostrea gigas</i>). <i>Marine Environmental Research</i> , 2018, 138, 135-143.	1.1	49
6694	Molecular and morphological divergence in a stygobiont gastropod lineage (Truncatelloidea,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T Journal of Zoological Systematics and Evolutionary Research, 2018, 56, 493-504.	0.6	5
6695	Global species delimitation and phylogeography of the circumtropical "sexy shrimp" <i>Thor amboinensis</i> reveals a cryptic species complex and secondary contact in the Indo-West Pacific. <i>Journal of Biogeography</i> , 2018, 45, 1275-1287.	1.4	14
6696	Multilocus sequence analysis reveals a novel phylogroup of <i>Xanthomonas euvesicatoria</i> pv <i>perforans</i> causing bacterial spot of tomato in Iran. <i>Plant Pathology</i> , 2018, 67, 1601-1611.	1.2	19

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6697	Robust <i>Frankia</i> phylogeny, species delineation and intraspecies diversity based on Multi-Locus Sequence Analysis (MLSA) and Single-Locus Strain Typing (SLST) adapted to a large sample size. <i>Systematic and Applied Microbiology</i> , 2018, 41, 311-323.	1.2	29
6698	First record and DNA barcodes of the aquarium shrimp, <i>Neocaridina davidi</i> , in Central Europe from thermally polluted River Oder canal, Poland. <i>Knowledge and Management of Aquatic Ecosystems</i> , 2018, , 14.	0.5	19
6699	Pliocene–Pleistocene ecological niche evolution shapes the phylogeography of a Mediterranean plant group. <i>Molecular Ecology</i> , 2018, 27, 1696-1713.	2.0	25
6700	Genetic Diversity of <i>Halyomorpha halys</i> (Hemiptera, Pentatomidae) in Korea and Comparison with <i>COI</i> Sequence Datasets from East Asia, Europe, and North America. <i>Florida Entomologist</i> , 2018, 101, 49-54.	0.2	15
6701	Whole Mitochondrial Genome of Blakiston's Fish Owl <i>Bubo (Ketupa) blakistoni</i> Suggests Its Redescription in the Genus <i>Ketupa</i> . <i>Russian Journal of Genetics</i> , 2018, 54, 369-373.	0.2	5
6702	Phylogenetic insights on Mediterranean and Afrotropical <i>Rhipicephalus</i> species (Acari: Ixodida) based on mitochondrial DNA. <i>Experimental and Applied Acarology</i> , 2018, 75, 107-128.	0.7	17
6703	Conservation genetics of eastern hellbenders <i>Cryptobranchus alleganiensis alleganiensis</i> in the Tennessee Valley. <i>Conservation Genetics</i> , 2018, 19, 571-585.	0.8	5
6704	Genetic diversity of the melon aphid <i>Aphis gossypii</i> (Hemiptera: Aphididae) in a diversified vegetable growing area. <i>Applied Entomology and Zoology</i> , 2018, 53, 259-266.	0.6	3
6705	Genomic, Recombinational and Phylogenetic Characterization of Global Feline Herpesvirus 1 Isolates. <i>Virology</i> , 2018, 518, 385-397.	1.1	21
6706	Comparative phylogeography of <i>Aedes</i> mosquitoes and the role of past climatic change for evolution within Africa. <i>Ecology and Evolution</i> , 2018, 8, 3019-3036.	0.8	3
6707	DNA Sequencing Data Analysis. <i>Methods in Molecular Biology</i> , 2018, 1754, 1-13.	0.4	2
6708	The genetic history of whaling in the Cantabrian Sea during the 13th–18th centuries: Were North Atlantic right whales (<i>Eubalaena glacialis</i>) the main target species?. <i>Journal of Archaeological Science: Reports</i> , 2018, 18, 393-398.	0.2	2
6709	Historical introgression among the species of <i>Rodgersia</i> (Saxifragaceae) in mountainous forests of southwest China. <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 93-99.	1.2	5
6710	Geomorphology Influencing the Diversification of Fish in Small-Order Rivers of Neighboring Basins. <i>Zebrafish</i> , 2018, 15, 389-397.	0.5	18
6711	The bud midge <i>P_{rodiplosis} floricola</i> in citrus crops in Colombia. <i>Entomologia Experimentalis Et Applicata</i> , 2018, 166, 204-214.	0.7	2
6712	Divergent in shape and convergent in function: Adaptive evolution of the mandible in Sub-Antarctic mice. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 878-892.	1.1	15
6713	Morphological and Genetic Features of Cisco (<i>Coregonidae: Coregonus</i> sp.) from Lake Sobachye (Putorana Plateau). <i>Russian Journal of Genetics: Applied Research</i> , 2018, 8, 37-43.	0.4	7
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6716	Genome-wide identification and expression analysis of the fatty acid desaturase genes in <i>Medicago truncatula</i> . Biochemical and Biophysical Research Communications, 2018, 499, 361-367.	1.0	23
6717	Spiny mice of the Zambezian bioregion – phylogeny, biogeography and ecological differentiation within the <i>Acomys spinosissimus</i> complex. Mammalian Biology, 2018, 91, 79-90.	0.8	13
6718	Mitochondrial signatures revealed panmixia in <i>Lutjanus argentimaculatus</i> (Forsskål 1775). Journal of Genetics, 2018, 97, 179-187.	0.4	2
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6727	Revisiting the Distribution of <i>Thaumetopoea pityocampa</i> (Lepidoptera: Notodontidae) and <i>T. pityocampa</i> ENA Clade in Greece. Journal of Economic Entomology, 2018, 111, 1256-1260.	0.8	3
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6729	Antiviral Effect of Ribavirin against HCV Associated with Increased Frequency of G-to-A and C-to-U Transitions in Infectious Cell Culture Model. Scientific Reports, 2018, 8, 4619.	1.6	33
6730	Epidemiology and phylogeny of spike gene of porcine epidemic diarrhea virus from Yunnan, China. Virus Research, 2018, 249, 45-51.	1.1	13
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6732	Relationships among Brazilian and worldwide isolates of <i>Fusarium oxysporum</i> f. sp. <i>lactucae</i> race 1 inferred from ribosomal intergenic spacer (IGS-rDNA) region and EF-1 α gene sequences. European Journal of Plant Pathology, 2018, 152, 81-94.	0.8	7

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6734	Ancient diversity and geographical sub-structuring in African buffalo <i>Theileria parva</i> populations revealed through metagenetic analysis of antigen-encoding loci. <i>International Journal for Parasitology</i> , 2018, 48, 287-296.	1.3	27
6735	A new natural allotriploid, <i>Lycoris</i> <i>hubeiensis</i> hybr. nov. (Amaryllidaceae), identified by morphological, karyological and molecular data. <i>Nordic Journal of Botany</i> , 2018, 36, njb-01780.	0.2	11
6736	Mitochondrial DNA analyses and ecological niche modeling reveal post-LGM expansion of the Assam macaque (<i>Macaca assamensis</i>) in the foothills of Nepal Himalaya. <i>American Journal of Primatology</i> , 2018, 80, e22748.	0.8	13
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6739	Matrilineal population structure and distribution of the Angolan giraffe in the Namib desert and beyond. <i>Ecological Genetics and Genomics</i> , 2018, 7-8, 1-5.	0.3	9
6740	Population genetic dynamics of Himalayan-Hengduan tree peonies, <i>Paeonia</i> subsect. <i>Delavayanae</i> . <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 62-77.	1.2	25
6741	Phylogeography of the Chilean red cricket <i>Cratomelus armatus</i> (Orthoptera: Anostostomatidae) reveals high cryptic diversity in central Chile. <i>Biological Journal of the Linnean Society</i> , 2018, 123, 712-727.	0.7	15
6742	Speciation of silverside <i>Chirostoma attenuatum</i> (Pisces: Atheriniformes) in Central Mexico. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2018, 56, 323-334.	0.6	7
6743	Genetic variations and population structure in three populations of beardless barb, <i>Cyclocheilichthys apogon</i> (Valenciennes, 1842) inferred from mitochondrial cytochrome b sequences. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 82-90.	0.7	3
6744	DNA barcoding of the fishes of the genus <i>Alburnoides</i> (Actinopterygii, Cyprinidae) from Caucasus. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 49-55.	0.7	18
6745	Identification of marine traditional Chinese medicine dried seahorses in the traditional Chinese medicine market using DNA barcoding. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 107-112.	0.7	25
6746	New insights on geographical/ecological populations within <i>Coilia nasus</i> (Clupeiformes): Tj ETQq1 1 0.784314 rgBT /Overlock 107 Mapping, Sequencing, and Analysis, 2018, 29, 158-164.	0.7	7
6747	Population structure and genetic diversity of Indian Major Carp, <i>Labeo rohita</i> (Hamilton, 1822) from three phylo-geographically isolated riverine ecosystems of India as revealed by mtDNA cytochrome b region sequences. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 199-205.	0.7	11
6748	Phylogeography of the littoral prawn species <i>Palaemon elegans</i> (Crustacea: Caridea: Palaemonidae) across the Mediterranean Sea unveils disparate patterns of population genetic structure and demographic history in the two sympatric genetic types II and III. <i>Marine Biodiversity</i> , 2018, 48, 1979-2001.	0.3	9
6749	DNA barcodes and insights into the phylogenetic relationships of Corvidae (Aves: Passeriformes). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 529-534.	0.7	4
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6752	Polymorphisms, differentiation, and phylogeny of 10 Tibetan goat populations inferred from mitochondrial D-loop sequences. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 439-445.	0.7	12
6753	One or two species of the rare Malagasy carnivoran <i>Eupleres</i> (Eupleridae)? New insights from molecular data. Mammalia, 2018, 82, 107-112.	0.3	7
6754	Sepiolid paralarval diversity in a regional upwelling area of the NE Atlantic. Hydrobiologia, 2018, 808, 57-70.	1.0	6
6755	Four evolutionarily significant units among narrow-barred Spanish mackerel (<i>Scomberomorus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582	0.3	6
6756	The phylogeny of Galerucinae (Coleoptera: Chrysomelidae) and the performance of mitochondrial genomes in phylogenetic inference compared to nuclear <i>rRNA</i> genes. Cladistics, 2018, 34, 113-130.	1.5	62
6757	Demographic histories of three predatory lady beetles reveal complex patterns of diversity and population size change in the United States. Insect Science, 2018, 25, 1065-1079.	1.5	9
6758	Characterization, genetic diversity, phylogenetic relationships, and expression of the aluminum tolerance MATE1 gene in <i>Secale</i> species. Biologia Plantarum, 2018, 62, 109-120.	1.9	13
6759	Proposed synonymy for <i>Micropogonias altipinnis</i> (Günther 1864), <i>Micropogonias ectenes</i> (Jordan & Gilbert 1882), and <i>Micropogonias megalops</i> (Gilbert 1890). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 136-146.	0.7	1
6760	Phylogeography of freshwater fish <i>Puntius sophore</i> in India. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 256-265.	0.7	5
6761	Biodiversity in the Amazon: Origin Hypotheses, Intrinsic Capacity of Species Colonization, and Comparative Phylogeography of River Otters (<i>Lontra longicaudis</i> and <i>Pteronura brasiliensis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342 T Evolution, 2018, 25, 213-240.	1.0	8
6762	Genetic diversity of <i>Nephtys hombergii</i> (Phyllodocida, Polychaeta) associated with environmental factors in a highly fluctuating ecosystem. Journal of the Marine Biological Association of the United Kingdom, 2018, 98, 777-789.	0.4	1
6763	Mitochondria COI-based genetic diversity of the cotton leafhopper <i>Amrasca biguttula biguttula</i> (Ishida) populations from India. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 228-235.	0.7	6
6764	Habitat fragmentation influences gene structure and gene differentiation among the <i>Loxoblemmus aomoriensis</i> populations in the Thousand Island Lake. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 222-227.	0.7	2
6765	Mitochondrial DNA genetic diversity in six Italian donkey breeds (<i>Equus asinus</i>). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 409-418.	0.7	11
6766	DNA barcoding and genetic diversity analyses of fishes of Kaladan River of Indo-Myanmar biodiversity hotspot. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 367-378.	0.7	13
6767	Genetic diversity and population demography of the endemic species <i>Acrossocheilus longipinnis</i> (Teleostei, Cyprinidae) based on mtDNA COI and <i>cyt b</i> gene sequences. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 403-408.	0.7	5
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6770	Mitochondrial DNA sequence variation in Iranian native dogs. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 394-402.	0.7	1
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6772	Comparing the utility of host and primary endosymbiont loci for predicting global invasive insect genetic structuring and migration patterns. Biological Control, 2018, 116, 10-16.	1.4	6
6773	With no gap to mind: a shallow genealogy within the world's most widespread small pelagic fish. Ecography, 2018, 41, 491-504.	2.1	16
6774	Genetic variation in mitochondrial <i>cox2</i> of <i>Heterakis gallinarum</i> from poultry in Sichuan, China. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 629-634.	0.7	5
6775	Genetic differentiation between Mediterranean and Atlantic populations of the common prawn <i>Palaemon serratus</i> (Crustacea: Palaemonidae) reveals uncommon phylogeographic break. Journal of the Marine Biological Association of the United Kingdom, 2018, 98, 1425-1434.	0.4	9
6776	Molecular analysis and genetic diversity of <i>Aedes albopictus</i> (Diptera, Culicidae) from China. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 594-599.	0.7	20
6777	First molecular evidence of <i>Mus musculus bactrianus</i> in Nepal inferred from the mitochondrial DNA cytochrome B gene sequences. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 561-566.	0.7	8
6778	Is there genetic connectivity among the critically endangered White-winged Flufftail (<i>Sarothrura</i>) Tj ETQq1 1 0,784314 rgBT /Over 0,4	0.4	1
6779	Metagenomic-based impact study of transgenic grapevine rootstock on its associated virome and soil bacteriome. Plant Biotechnology Journal, 2018, 16, 208-220.	4.1	31
6780	Genetic diversity and population structure of <i>Acrossocheilus yunnanensis</i> (Teleostei, Cyprinidae) inferred from four mitochondrial gene sequences. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 606-614.	0.7	4
6781	Phylogenetic structure and ancestry of Korean clawed salamander, <i>Onychodactylus koreanus</i> (Caudata: Hynobiidae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 650-658.	0.7	6
6782	Contrasting species boundaries between sections <i>Alternaria</i> and <i>Porri</i> of the genus <i>Alternaria</i> . Plant Pathology, 2018, 67, 303-314.	1.2	14
6783	<i>Bartonella</i> in Rodents and Ectoparasites in the Canary Islands, Spain: New Insights into Host-Vector-Pathogen Relationships. Microbial Ecology, 2018, 75, 264-273.	1.4	16
6784	Evolutionary history of <i>Bathygobius</i> (Perciformes: Gobiidae) in the Atlantic biogeographic provinces: a new endemic species and old mitochondrial lineages. Zoological Journal of the Linnean Society, 2018, 182, 360-384.	1.0	13
6785	Low genetic variation in the MHC class II DRB gene and MHC-linked microsatellites in endangered island populations of the leopard cat (<i>Prionailurus bengalensis</i>) in Japan. Immunogenetics, 2018, 70, 115-124.	1.2	11
6786	Genetic divergence between colonies of Flesh-footed Shearwater <i>Ardenna carneipes</i> exhibiting different foraging strategies. Conservation Genetics, 2018, 19, 27-41.	0.8	11

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6787	Phylogeography and population genetics of the riparian relict tree <i>Pterocarya fraxinifolia</i> (Juglandaceae) in the South Caucasus. <i>Systematics and Biodiversity</i> , 2018, 16, 14-27.	0.5	15
6788	Molecular evolution of the TMS5 gene in rice (<i>Oryza sativa</i> L.). <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 307-318.	0.8	0
6789	Phylogeographic patterns in <i>Maguimithrax spinosissimus</i> (Decapoda: Mithracidae) from Colombian Caribbean. <i>New Zealand Journal of Marine and Freshwater Research</i> , 2018, 52, 118-137.	0.8	4
6790	Significant genetic differentiation of <i>Gobiopterus lacustris</i> , a newly recorded transparent goby in China. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 785-791.	0.7	8
6791	Morphological and genetic divergence between lake and river populations of <i>Triplophysa</i> in Ngangtse Co, Tibet. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 778-784.	0.7	5
6792	Genetic diversity and invasion history of the European subterranean termite <i>Reticulitermes urbis</i> (Blattodea, Termitoidea, Rhinotermitidae). <i>Biological Invasions</i> , 2018, 20, 33-44.	1.2	4
6793	Metabarcoding and post-sampling strategies to discover non-indigenous species: A case study in the estuaries of the central south Bay of Biscay. <i>Journal for Nature Conservation</i> , 2018, 42, 67-74.	0.8	15
6794	Multi-locus phylogenetic analyses support the monophyly and the Miocene diversification of <i>Iksookimia</i> (Teleostei: Cypriniformes: Cobitidae). <i>Systematics and Biodiversity</i> , 2018, 16, 81-88.	0.5	12
6795	Genetic diversity and phylogenetic relationships of seven <i>Amorphophallus</i> species in southwestern China revealed by chloroplast DNA sequences. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 679-686.	0.7	12
6796	Elevational divergence in the great tit complex revealed by major hemoglobin genes. <i>Environmental Epigenetics</i> , 2018, 64, 455-464.	0.9	7
6797	Analysis of the genetic diversity and structure of the Eastern Marsh Harrier in Japan using mitochondrial DNA. <i>Journal of Ornithology</i> , 2018, 159, 73-78.	0.5	7
6798	Genetic variation of the land-locked freshwater shrimp <i>Caridina pseudodenticulata</i> (Decapoda: Tj ETQq1 1 0.784314 rgBT /Overlock 103). <i>Systematics and Biodiversity</i> , 2018, 29, 687-694.	0.7	3
6799	Genetic analysis of <i>Bactrocera zonata</i> (Diptera: Tephritidae) populations from India based on <i>cox1</i> and <i>nad1</i> gene sequences. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 727-736.	0.7	29
6800	Phylogeography and ecological niche modeling unravel the evolutionary history of the African green toad, <i>Bufootes boulengeri boulengeri</i> (Amphibia: Bufonidae), through the Quaternary. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2018, 56, 102-116.	0.6	19
6801	Army imposters: diversification of army ant-mimicking beetles with their Eciton hosts. <i>Insectes Sociaux</i> , 2018, 65, 59-75.	0.7	7
6802	Multilocus phylogeny and taxonomy of East Asian voles <i>Alexandromys</i> (Rodentia, Arvicolinae). <i>Zoologica Scripta</i> , 2018, 47, 9-20.	0.7	19
6803	Historical demography and colonization pathways of the widespread intertidal seaweed <i>Hormosira banksii</i> (Phaeophyceae) in southeastern Australia. <i>Journal of Phycology</i> , 2018, 54, 56-65.	1.0	7
6804	Genetic diversity of Jiangsu native chicken breeds assessed with the mitochondrial DNA D-loop region. <i>British Poultry Science</i> , 2018, 59, 34-39.	0.8	6

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6806	Molecular systematics, biogeography, and colony fusion in the European dry-wood termites <i>Kalotermes</i> spp. (Blattodea, Termitoidae, Kalotermitidae). <i>Bulletin of Entomological Research</i> , 2018, 108, 523-531.	0.5	5
6807	Pathogenicity and phylogenetic analysis of <i>Clavibacter michiganensis</i> strains associated with tomato plants in Iran. <i>Plant Pathology</i> , 2018, 67, 957-970.	1.2	37
6808	New insights into the systematics of North Atlantic <i>Gaidropsarus</i> (Gadiformes, Gadidae): flagging synonymies and hidden diversity. <i>Marine Biology Research</i> , 2018, 14, 17-29.	0.3	5
6809	Genealogical and niche modeling analyses reveal recent expansion and limited genetic divergence in the <i>Formicivora serrana</i> complex (Passeriformes: Thamnophilidae). <i>Journal of Ornithology</i> , 2018, 159, 79-92.	0.5	2
6810	Inferring the demographic history of an oligophagous grasshopper: Effects of climatic niche stability and host-plant distribution. <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 343-356.	1.2	8
6811	Phylogeography and Population Genetic Analyses in the Iberian Toothcarp (<i>Aphanius iberus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502 T	1.0	11
6812	Genetic assessment of an isolated endemic Samango monkey (<i>Cercopithecus albogularis labiatus</i>) population in the Amathole Mountains, Eastern Cape Province, South Africa. <i>Primates</i> , 2018, 59, 197-207.	0.7	5
6813	Reticulate Pleistocene evolution of Ethiopian rodent genus along remarkable altitudinal gradient. <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 75-87.	1.2	48
6814	Compositional heterogeneity in true bug mitochondrial phylogenomics. <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 135-144.	1.2	112
6815	Origin and distribution of desert ants across the Gibraltar Straits. <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 122-134.	1.2	9
6816	Phylogeography of a widespread sub-Saharan murid rodent <i>Aethomys chrysophilus</i> : the role of geographic barriers and paleoclimate in the Zambezian bioregion. <i>Mammalia</i> , 2018, 82, 373-387.	0.3	20
6817	Genetic population structure and phylogeny of the common octopus <i>Octopus vulgaris</i> Cuvier, 1797 in the western Mediterranean Sea through nuclear and mitochondrial markers. <i>Hydrobiologia</i> , 2018, 807, 277-296.	1.0	26
6818	Systematic evaluation of the genus <i>Alburnus</i> (Cyprinidae) with description of a new species. <i>Hydrobiologia</i> , 2018, 807, 297-312.	1.0	16
6819	A comparison of genetic diversity and population structure of the endangered scaleshell mussel (<i>Leptodea leptodon</i>), the fragile papershell (<i>Leptodea fragilis</i>) and their host-fish the freshwater drum (<i>Aplodinotus grunniens</i>). <i>Conservation Genetics</i> , 2018, 19, 425-437.	0.8	7
6820	Species Identification and Phylogenetic Analysis of <i>Borrelia burgdorferi</i> Sensu Lato Using Molecular Biological Methods. <i>Methods in Molecular Biology</i> , 2018, 1690, 13-33.	0.4	4
6821	Genetic differentiation in populations of lane snapper (<i>Lutjanus synagris</i> "Lutjanidae) from Western Atlantic as revealed by multilocus analysis. <i>Fisheries Research</i> , 2018, 198, 138-149.	0.9	12
6822	Cryptic speciation in the <i>Merodon luteomaculatus</i> complex (Diptera: Syrphidae) from the eastern Mediterranean. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2018, 56, 170-191.	0.6	25

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6823	Basin-scale distribution and haplotype partitioning in different genetic lineages of the Neotropical migratory fish <i>Salminus brasiliensis</i> . <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2018, 28, 444-456.	0.9	10
6824	A molecular phylogeny of East African <i>Amytta</i> (Orthoptera: Tettigoniidae, Meconematinae) with data on their cytogenetics. <i>Systematic Entomology</i> , 2018, 43, 239-249.	1.7	7
6825	Phylogenomics reveals habitat-associated body shape divergence in <i>Oryzias woworae</i> species group (Teleostei: Adrianichthyidae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 194-203.	1.2	15
6826	Introgression from non-native species unveils a hidden threat to the migratory Neotropical fish <i>Prochilodus hartii</i> . <i>Biological Invasions</i> , 2018, 20, 555-566.	1.2	30
6827	Ancient mitochondrial genomes reveal the demographic history and phylogeography of the extinct, enigmatic thylacine (<i>Thylacinus cynocephalus</i>). <i>Journal of Biogeography</i> , 2018, 45, 1-13.	1.4	29
6828	Conservation genetics of reddsides dace (<i>Clinostomus elongatus</i>): phylogeography and contemporary spatial structure. <i>Conservation Genetics</i> , 2018, 19, 409-424.	0.8	7
6829	Development of chloroplast genomic resources for <i>Pyrus hopeiensis</i> (Rosaceae). <i>Conservation Genetics Resources</i> , 2018, 10, 511-513.	0.4	8
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6831	Origin and phylogeography of African savannah elephants (<i>Loxodonta africana</i>) in Kruger and nearby parks in southern Africa. <i>Conservation Genetics</i> , 2018, 19, 155-167.	0.8	8
6832	A short-range endemic species from south-eastern Atlantic Rain Forest shows deep signature of historical events: phylogeography of harvestmen <i>Acutisoma longipes</i> (Arachnida: Opiliones). <i>Systematics and Biodiversity</i> , 2018, 16, 171-187.	0.5	35
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6837	Genetic characterization of the Turkish gray hamster (<i>Cricetulus migratorius</i>) based on mitochondrial cytochrome b and 12S rRNA sequences. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 819-830.	0.7	3
6838	<i>Maculinea rebeli</i> (<i>Hirschke</i>) a phantom or reality? Novel contribution to a long-standing debate over the taxonomic status of an enigmatic <i>Lycenidae</i> butterfly. <i>Systematic Entomology</i> , 2018, 43, 166-182.	1.7	14
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6842	Molecular diversity and phylogeny of indigenous <i>Rhizobium leguminosarum</i> strains associated with <i>Trifolium repens</i> plants in Romania. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 135-153.	0.7	8
6843	Phylogeography of the eight-barbel loach <i>Lefua nikkonis</i> (Cypriniformes: Nemacheilidae): how important were straits in northern Japan as biogeographical barriers?. <i>Ichthyological Research</i> , 2018, 65, 115-126.	0.5	9
6844	Codon adaptation to tRNAs with Inosine modification at position 34 is widespread among Eukaryotes and present in two Bacterial phyla. <i>RNA Biology</i> , 2018, 15, 500-507.	1.5	49
6845	Genetic effects of released swimming crab (<i>Portunus trituberculatus</i>) on wild populations inferred from mitochondrial control region sequences. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 856-861.	0.7	4
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6847	A new species of Proctoeces and reinstatement of <i>Proctoeces humboldti</i> George-Nascimento and Quiroga 1983 (Digenea: Fellodistomidae) based on molecular and morphological evidence. <i>Parasitology International</i> , 2018, 67, 159-169.	0.6	10
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6850	Effects of the Pleistocene on the mitochondrial population genetic structure and demographic history of the silky shark (<i>Carcharhinus falciformis</i>) in the western Atlantic Ocean. <i>Reviews in Fish Biology and Fisheries</i> , 2018, 28, 213-227.	2.4	30
6851	A new allele of the kappa-casein gene in local zebu cattle breeds. <i>Journal of Dairy Research</i> , 2018, 85, 3-6.	0.7	0
6852	Genetic diversity and genetic structure of farmed and wild Chinese mitten crab (<i>Eriocheir</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 sequences. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 1081-1089.	0.7	16
6853	Single nucleotide polymorphism markers for assessing potential maternal population structure in European eel (<i>Anguilla anguilla</i>). <i>Conservation Genetics Resources</i> , 2018, 10, 907-909.	0.4	3
6854	Population genetic structure of the mantis shrimp <i>Oratosquilla oratoria</i> (Crustacea: Squillidae) in the Yellow Sea and East China Sea. <i>Journal of Oceanology and Limnology</i> , 2018, 36, 905-912.	0.6	4
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6856	Fishes in the desert: mitochondrial variation and phylogeography of <i>Danakilia</i> (Actinopterygii): Tj ETQq1 1 0.784314 rgBT /Overlock 10 northeastern Africa. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 1025-1040.	0.7	9
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6858	Analysis of sequence divergence in redbfin (Cypriniformes, Cyprinidae, Tribolodon) based on mtDNA and nDNA markers with inferences in systematics and genetics of speciation. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 975-992.	0.7	3

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6871	Prevalence and genetic diversity of human diarrheagenic <i>Escherichia coli</i> isolates by multilocus sequence typing. <i>International Journal of Infectious Diseases</i> , 2018, 67, 7-13.	1.5	27
6872	Complete taxon sampling of the avian genus <i>Pica</i> (magpies) reveals ancient relictual populations and synchronous Late-Pleistocene demographic expansion across the Northern Hemisphere. <i>Journal of Avian Biology</i> , 2018, 49, jav-01612.	0.6	20
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6874	The polymorphisms of MHCII γ gene of <i>Trachinotus ovatus</i> and their association with resistance/susceptibility to <i>Photobacterium damsela</i> . <i>Aquaculture</i> , 2018, 485, 160-165.	1.7	10
6875	Cryptic diversity in <i>Rhampholeon boulengeri</i> (Sauria: Chamaeleonidae), a pygmy chameleon from the Albertine Rift biodiversity hotspot. <i>Molecular Phylogenetics and Evolution</i> , 2018, 122, 125-141.	1.2	17
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6878	Systematics of <i>Oligoryzomys</i> (Rodentia, Cricetidae, Sigmodontinae) from southern Chilean Patagonia, with the description of a new species. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2018, 56, 280-299.	0.6	6
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6885	Discovery of gorilla MHC-C expressing C1 ligand for KIR. <i>Immunogenetics</i> , 2018, 70, 293-304.	1.2	1
6886	Genetic diversification and population structure of <i>Barbus cyri</i> De Filippi, 1865 (Teleostei: Cyprinidae) in northern Iran inferred from the mitochondrial D-loop gene sequence. <i>Environmental Biology of Fishes</i> , 2018, 101, 181-192.	0.4	9
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6889	Morphological variation, genetic differentiation and phylogeography of the <i>E</i> <i>ast</i> <i>A</i> <i>sia</i> cicada <i>Hyalessa maculaticollis</i> (Hemiptera: Cicadidae). <i>Systematic Entomology</i> , 2018, 43, 308-329.	1.7	22
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6891	Population genetic structure and differential selection in mussel <i>Mytilus chilensis</i> . <i>Aquaculture Research</i> , 2018, 49, 919-927.	0.9	10
6892	Mitogenomic diversity and differentiation of the Buryats. <i>Journal of Human Genetics</i> , 2018, 63, 71-81.	1.1	10
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6897	Evolution of vomeronasal receptor 1 (V1R) genes in the common marmoset (<i>Callithrix jacchus</i>). <i>Gene</i> , 2018, 642, 343-353.	1.0	22
6898	A late Pleistocene marine glacial refugium in the south-west of Hainan Island, China: Phylogeographical insights from the brown alga <i>Sargassum polycystum</i> . <i>Journal of Biogeography</i> , 2018, 45, 355-366.	1.4	20
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6910	Extensive shared polymorphism at non-MHC immune genes in recently diverged North American prairie grouse. <i>Immunogenetics</i> , 2018, 70, 195-204.	1.2	4
6911	Molecular detection of <i>Wolbachia pipientis</i> in natural populations of sandfly vectors of <i>Leishmania infantum</i> in endemic areas: first detection in <i>Lutzomyia longipalpis</i> . <i>Medical and Veterinary Entomology</i> , 2018, 32, 111-114.	0.7	12
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6942	Testing Hypotheses of Diversification in Panamanian Frogs and Freshwater Fishes Using Hierarchical Approximate Bayesian Computation with Model Averaging. <i>Diversity</i> , 2018, 10, 120.	0.7	9
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6950	Complete mitochondrial genome of black-shanked douc langurs (<i>Pygathrix nigripes</i>) and its phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1085-1086.	0.2	0
6951	How strong was the bottleneck associated to the peopling of the Americas? New insights from multilocus sequence data. <i>Genetics and Molecular Biology</i> , 2018, 41, 206-214.	0.6	31
6952	Phylogeography of Jackson's Forest Lizard <i>Adolfus jacksoni</i> (Sauria: Lacertidae) Reveals Cryptic Diversity in the Highlands of East Africa. <i>Herpetological Monographs</i> , 2018, 32, 51.	1.1	5
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6955	The first set of universal nuclear protein-coding loci markers for avian phylogenetic and population genetic studies. <i>Scientific Reports</i> , 2018, 8, 15723.	1.6	16
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6957	RNA-seq analysis reveals considerable genetic diversity and provides genetic markers saturating all chromosomes in the diploid wild wheat relative <i>Aegilops umbellulata</i> . <i>BMC Plant Biology</i> , 2018, 18, 271.	1.6	27
6958	Molecular Analysis of Forensically Important Blow Flies in Thailand. <i>Insects</i> , 2018, 9, 159.	1.0	12
6959	Contrasting phylogeographic patterns and demographic history in closely related species of <i>Daphnia longispina</i> group (Crustacea: Cladocera) with focus on North-Eastern Eurasia. <i>PLoS ONE</i> , 2018, 13, e0207347.	1.1	15
6960	Deep Intraspecific Divergence in the Endemic Herb <i>Lancea tibetica</i> (Mazaceae) Distributed Over the Qinghai-Tibetan Plateau. <i>Frontiers in Genetics</i> , 2018, 9, 492.	1.1	6
6961	Genetic structure and differentiation in <i>Dendrocalamus sinicus</i> (Poaceae: Bambusoideae) populations provide insight into evolutionary history and speciation of woody bamboos. <i>Scientific Reports</i> , 2018, 8, 16933.	1.6	18
6962	Complete mitochondrial genome of Black Soft-shell Turtle (<i>Nilssonina nigricans</i>) and comparative analysis with other Trionychidae. <i>Scientific Reports</i> , 2018, 8, 17378.	1.6	14
6963	Historical biogeography reveals new independent evolutionary lineages in the <i>Pantosteus plebeius-nebuliferus</i> species-group (Actinopterygii: Catostomidae). <i>BMC Evolutionary Biology</i> , 2018, 18, 173.	3.2	7
6964	Genetic variation of <i>Aedes aegypti</i> mosquitoes across Thailand based on nuclear DNA sequences. <i>Agriculture and Natural Resources</i> , 2018, 52, 596-602.	0.4	1
6965	Long-term population persistence of flightless weevils (<i>Eurhoptus pyriformis</i>) across old- and second-growth forests patches in southern Appalachia. <i>BMC Evolutionary Biology</i> , 2018, 18, 165.	3.2	9
6966	Stonewall and Brickwall: Two Partially Redundant Determinants Required for the Maintenance of Female Germline in <i>Drosophila</i> . <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2027-2041.	0.8	6

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6969	Pseudogenization and Resurrection of a Speciation Gene. <i>Current Biology</i> , 2018, 28, 3776-3786.e7.	1.8	57
6970	Legume Cytosolic and Plastid Acetyl-Coenzyme A Carboxylase Genes Differ by Evolutionary Patterns and Selection Pressure Schemes Acting before and after Whole-Genome Duplications. <i>Genes</i> , 2018, 9, 563.	1.0	10
6971	Cryptic diversity in the southern Appalachian Mountains: genetic data reveal that the red centipede, <i>Scolopocryptops sexspinosus</i> , is a species complex. <i>Journal of Insect Conservation</i> , 2018, 22, 799-805.	0.8	14
6972	DNA barcodes of Antipode marine invertebrates in Bay of Biscay and Gulf of Lion ports suggest new biofouling challenges. <i>Scientific Reports</i> , 2018, 8, 16214.	1.6	12
6973	Exploring insecticide resistance mechanisms in three major malaria vectors from Bangui in Central African Republic. <i>Pathogens and Global Health</i> , 2018, 112, 349-359.	1.0	19
6974	Intraspecific Polymorphism of the Mitochondrial DNA Control Region and Phylogeography of Little Ground Squirrel (<i>Spermophilus pygmaeus</i> , Sciuridae, Rodentia). <i>Russian Journal of Genetics</i> , 2018, 54, 1332-1341.	0.2	3
6975	Can-SINE dynamics in the giant panda and three other Caniformia genomes. <i>Mobile DNA</i> , 2018, 9, 32.	1.3	9
6976	Genotype frequency contributions of Mx1 gene in eight chicken breeds under different selection pressures. <i>3 Biotech</i> , 2018, 8, 483.	1.1	5
6977	Phylogeography and demographic history of the Chagas disease vector <i>Rhodnius nasutus</i> (Hemiptera: Tj ETQq0 0 0 rgBT /Overlock 10 T	1.3	6
6978	Molecular analysis of clinical <i>Burkholderia pseudomallei</i> isolates from southwestern coastal region of India, using multi-locus sequence typing. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006915.	1.3	13
6979	Cyprus as an ancient hub for house mice and humans. <i>Journal of Biogeography</i> , 2018, 45, 2619-2630.	1.4	12
6980	A survey of molecular diversity and population genetic structure in North American clearwing moths (Lepidoptera: Sesiiidae) using cytochrome c oxidase I. <i>PLoS ONE</i> , 2018, 13, e0202281.	1.1	6
6981	Comparative population genetics and demographic history of two polychaete species suggest that coastal lagoon populations evolve under alternate regimes of gene flow. <i>Marine Biology</i> , 2018, 165, 1.	0.7	4
6982	Genetic Diversity of the First Baltic Population of <i>Rangia cuneata</i> (Bivalvia: Mactridae). <i>Russian Journal of Biological Invasions</i> , 2018, 9, 114-118.	0.2	4
6983	Comparative analysis of the mitochondrial genomes of oriental spittlebug tribe <i>Cosmoscartini</i> : insights into the relationships among closely related taxa. <i>BMC Genomics</i> , 2018, 19, 961.	1.2	20
6984	Genetic polymorphism and natural selection in the C-terminal 42 kDa region of merozoite surface protein-1 (MSP-1) among <i>Plasmodium knowlesi</i> samples from Malaysia. <i>Parasites and Vectors</i> , 2018, 11, 626.	1.0	7

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6985	Mitochondrial DNA Barcoding of the Pacific Oyster <i>Crassostrea gigas</i> (Thunberg, 1793) (Mollusca: Tj ETQq0 0 0 rgBTj/Overlock 10 Tf 50	0.2	3
6986	<i>Corydalis ternatifolia</i> belongs to <i>C. sect. Asterostigmata</i> , not <i>C. sect. Incisae</i> (Papaveraceae): Evidence from morphological and phylogenetic study. <i>Phytotaxa</i> , 2018, 382, 193.	0.1	4
6987	Comparative chloroplast genomes of Paris Sect. <i>Marmorata</i> : insights into repeat regions and evolutionary implications. <i>BMC Genomics</i> , 2018, 19, 878.	1.2	60
6988	Whole genome sequencing of <i>Moraxella bovoculi</i> reveals high genetic diversity and evidence for interspecies recombination at multiple loci. <i>PLoS ONE</i> , 2018, 13, e0209113.	1.1	19
6989	Historical translocations by Māori may explain the distribution and genetic structure of a threatened surf clam in Aotearoa (New Zealand). <i>Scientific Reports</i> , 2018, 8, 17241.	1.6	10
6990	Avian Toll-like receptor allelic diversity far exceeds human polymorphism: an insight from domestic chicken breeds. <i>Scientific Reports</i> , 2018, 8, 17878.	1.6	33
6991	Species delimitation of <i>Stemona</i> (Stemonaceae) based on sequences of five plastid DNA regions. <i>Phytotaxa</i> , 2018, 374, 291.	0.1	1
6992	Mutations in the melanocortin-1 receptor (MC1R) gene have no influence on the distinct patterns of melanic plumage found in the manakins of the genus <i>Antilophia</i> (Aves: Pipridae). <i>Anais Da Academia Brasileira De Ciencias</i> , 2018, 90, 2873-2879.	0.3	2
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6996	Homologous recombination changes the context of Cytochrome b transcription in the mitochondrial genome of <i>Silene vulgaris</i> KRA. <i>BMC Genomics</i> , 2018, 19, 874.	1.2	16
6997	Latitudinal Adaptation and Genetic Insights Into the Origins of <i>Cannabis sativa</i> L.. <i>Frontiers in Plant Science</i> , 2018, 9, 1876.	1.7	54
6998	Fitness Costs of the Glutathione S-Transferase Epsilon 2 (L119F-GSTe2) Mediated Metabolic Resistance to Insecticides in the Major African Malaria Vector <i>Anopheles Funestus</i> . <i>Genes</i> , 2018, 9, 645.	1.0	45
6999	Genetic diversity analysis of Thai indigenous chickens based on complete sequences of mitochondrial DNA D-loop region. <i>Asian-Australasian Journal of Animal Sciences</i> , 2018, 31, 804-811.	2.4	24
7000	Evolutionary Analysis of Plastid Genomes of Seven <i>Lonicera</i> L. Species: Implications for Sequence Divergence and Phylogenetic Relationships. <i>International Journal of Molecular Sciences</i> , 2018, 19, 4039.	1.8	23
7001	Molecular basis of permethrin and DDT resistance in an <i>Anopheles funestus</i> population from Benin. <i>Parasites and Vectors</i> , 2018, 11, 602.	1.0	25
7002	Phylogenetic analysis of <i>Spirocerca lupi</i> and <i>Spirocerca vulpis</i> reveal high genetic diversity and intra-individual variation. <i>Parasites and Vectors</i> , 2018, 11, 639.	1.0	22

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7004	Mitochondrial DNA D-Loop Diversity of the Helmeted Guinea Fowls in Kenya and Its Implications on HSP70 Gene Functional Polymorphism. <i>BioMed Research International</i> , 2018, 2018, 1-12.	0.9	7
7005	Playing Hide-and-Seek in Beta-Globin Genes: Gene Conversion Transferring a Beneficial Mutation between Differentially Expressed Gene Duplicates. <i>Genes</i> , 2018, 9, 492.	1.0	9
7006	Analysis of mitochondrial DNA sequence and copy number variation across five high-altitude species and their low-altitude relatives. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 847-851.	0.2	11
7007	DNA barcoding of the family Sparidae along the coast of China and revelation of potential cryptic diversity in the Indo- West Pacific oceans based on COI and 16S rRNA genes. <i>Journal of Oceanology and Limnology</i> , 2018, 36, 1753-1770.	0.6	12
7008	Genetic divergence of <i>Platycerus hongwonpyoi</i> (Coleoptera: Lucanidae) in South Korea. <i>Entomological Science</i> , 2018, 22, 86.	0.3	16
7009	A genome-wide association analysis reveals a potential role for recombination in the evolution of antimicrobial resistance in <i>Burkholderia multivorans</i> . <i>PLoS Pathogens</i> , 2018, 14, e1007453.	2.1	28
7010	Out of Refugia: Population Genetic Structure and Evolutionary History of the Alpine Medicinal Plant <i>Gentiana lawrencei</i> var. <i>farreri</i> (Gentianaceae). <i>Frontiers in Genetics</i> , 2018, 9, 564.	1.1	10
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7015	Phylogeography of the widespread creek chub <i>Semotilus atromaculatus</i> (Cypriniformes: Leuciscidae). <i>Journal of Fish Biology</i> , 2018, 93, 778-791.	0.7	8
7016	Molecular signatures of divergence and selection in closely related pine taxa. <i>Tree Genetics and Genomes</i> , 2018, 14, 83.	0.6	15
7017	Integrative taxonomic methods reveal an incorrect synonymisation of the South African <i>Pseudonereis podocirra</i> (Schmarda) as the widespread <i>Pseudonereis variegata</i> (Grube) from Chile. <i>Invertebrate Systematics</i> , 2018, 32, 1282.	0.5	14
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7020	Characterization of the complete mitochondrial genome of <i>Hydrotaea spinigera</i> (Diptera: Muscidae) with phylogenetic implications. <i>Journal of Asia-Pacific Entomology</i> , 2018, 21, 1416-1423.	0.4	3

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7022	How Many Species, Taxa, or Lineages of <i>Cebus albifrons</i> (Platyrrhini, Primates) Inhabit Ecuador? Insights from Mitogenomics. <i>International Journal of Primatology</i> , 2018, 39, 1068-1104.	0.9	4
7023	Comparative analysis of two mitochondrial genomes of flesh flies (<i>Sarcophaga antilope</i> and) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667 T</i> of <i>Biological Macromolecules</i> , 2018, 120, 1955-1964.	3.6	9
7024	Phylogenetics of <i>Mycoplasma hominis</i> clinical strains associated with gynecological infections or infertility as disclosed by an expanded multilocus sequence typing scheme. <i>Scientific Reports</i> , 2018, 8, 14854.	1.6	14
7025	Genomic analyses of human European diversity at the southwestern edge: isolation, African influence and disease associations in the Canary Islands. <i>Molecular Biology and Evolution</i> , 2018, 35, 3010-3026.	3.5	17
7026	Geographic variation and taxonomy of red-tailed <i>Gymnophthalmus</i> (Squamata: Gymnophthalmidae) from Amazonian Savannas. <i>Zootaxa</i> , 2018, 4497, 61.	0.2	3
7027	Measles virus genotype D4 strains with non-standard length M-F non-coding region circulated during the major outbreaks of 2011-2012 in Spain. <i>PLoS ONE</i> , 2018, 13, e0199975.	1.1	14
7028	Genetic Diversity of Mitochondrial DNA of Chinese Black-bone Chicken. <i>Brazilian Journal of Poultry Science</i> , 2018, 20, 565-572.	0.3	5
7029	Historical Refugia and Isolation by Distance of the Mud Snail, <i>Bullacta exarata</i> (Philippi, 1849) in the Northwestern Pacific Ocean. <i>Frontiers in Genetics</i> , 2018, 9, 486.	1.1	3
7030	Genetic Variation in Coat Colour Genes MC1R and ASIP Provides Insights Into Domestication and Management of South American Camelids. <i>Frontiers in Genetics</i> , 2018, 9, 487.	1.1	31
7031	TCP Transcription Factors in Moso Bamboo (<i>Phyllostachys edulis</i>): Genome-Wide Identification and Expression Analysis. <i>Frontiers in Plant Science</i> , 2018, 9, 1263.	1.7	60
7032	Is the genetic variability of Cathepsin B important in the pathogenesis of <i>Blastocystis</i> spp.?. <i>Parasitology Research</i> , 2018, 117, 3935-3943.	0.6	8
7033	Analyses of the internal transcribed rDNA spacers (ITS1 and ITS2) of Indian weevils of <i>Odoiporus longicollis</i> (Olivier) reveal gene flow between locations. <i>International Journal of Tropical Insect Science</i> , 2018, 38, 313-329.	0.4	4
7034	Deletions linked to PROG1 gene participate in plant architecture domestication in Asian and African rice. <i>Nature Communications</i> , 2018, 9, 4157.	5.8	63
7035	Genetic identification of two mudskipper species (Pisces: Gobiidae) from Bogowonto Lagoon (Yogyakarta, Indonesia) using COI mitochondrial gene as a DNA barcoding marker. <i>AIP Conference Proceedings</i> , 2018, , .	0.3	2
7036	Genetic diversity in the camellia weevil, <i>Curculio chinensis</i> (Chevrolat) (Coleoptera: Curculionidae). <i>Journal of Insect Science</i> , 2018, 21, 447-460.	0.3	10
7037	Molecular taxonomy of the genus <i>Physokermes</i> (Hemiptera: Coccidae) species in Greece, based on mtDNA sequencing data. <i>Journal of Apicultural Research</i> , 2018, 57, 479-483.	0.7	2
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7040	DREB2 (dehydration-responsive element-binding protein 2) type transcription factor in sorghum (<i>Sorghum bicolor</i>): genome-wide identification, characterization and expression profiles under cadmium and salt stresses. <i>3 Biotech</i> , 2018, 8, 426.	1.1	28
7041	Biogeography and Distribution of the Cryptic Species Rosyface Shiner <i>Notropis rubellus</i> and Carmine Shiner <i>Notropis percobromus</i> in Illinois. <i>Copeia</i> , 2018, 106, 524-531.	1.4	1
7042	Complete genome sequence of sacbrood virus isolated from Asiatic honey bee <i>Apis cerana indica</i> in India. <i>Virus Disease</i> , 2018, 29, 453-460.	1.0	5
7043	Human mitochondrial DNA haplogroup M8a influences the penetrance of m.8684C>T in Han Chinese men with non-obstructive azoospermia. <i>Reproductive BioMedicine Online</i> , 2018, 37, 480-488.	1.1	2
7044	On the Evolution and Function of Plasmodium vivax Reticulocyte Binding Surface Antigen (pvrbsa). <i>Frontiers in Genetics</i> , 2018, 9, 372.	1.1	12
7045	The Phylogeographic History of Common Walnut in China. <i>Frontiers in Plant Science</i> , 2018, 9, 1399.	1.7	39
7046	Genetic variability of <i>Panstrongylus geniculatus</i> (Reduviidae: Triatominae) in the Metropolitan District of Caracas, Venezuela. <i>Infection, Genetics and Evolution</i> , 2018, 66, 236-244.	1.0	7
7047	Positive selection at sites of chemosensory genes is associated with the recent divergence and local ecological adaptation in cactophilic <i>Drosophila</i> . <i>BMC Evolutionary Biology</i> , 2018, 18, 144.	3.2	5
7048	Genetic and population analyses of <i>Vibrio parahaemolyticus</i> isolates from three major coastal regions in China. <i>Future Microbiology</i> , 2018, 13, 1261-1269.	1.0	5
7049	Mitochondrial introgression and interspecies recombination in the <i>Fusarium fujikuroi</i> species complex. <i>IMA Fungus</i> , 2018, 9, 37-48.	1.7	28
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7051	Genome-wide identification and expression analyses of TCP transcription factor genes in <i>Gossypium barbadense</i> . <i>Scientific Reports</i> , 2018, 8, 14526.	1.6	37
7052	Interspecific chloroplast genome sequence diversity and genomic resources in <i>Diospyros</i> . <i>BMC Plant Biology</i> , 2018, 18, 210.	1.6	55
7053	A new riparian <i>Mantidactylus</i> (Brygoo) frog from the Tsaratanana and Manongarivo Massifs in northern Madagascar. <i>Zootaxa</i> , 2018, 4486, 575.	0.2	7
7054	Development of 10 single-copy nuclear <i>scnDNA</i> markers for <i>Euchresta horsfieldii</i> (Fabaceae), a rare medicinal plant. <i>Applications in Plant Sciences</i> , 2018, 6, e01178.	0.8	3
7055	Genome-Wide Characterization of DNA Demethylase Genes and Their Association with Salt Response in <i>Pyrus</i> . <i>Genes</i> , 2018, 9, 398.	1.0	14
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7059	Variabilidad genética de <i>Aedes aegypti</i> en el departamento de Sucre, Colombia, mediante el análisis de la secuencia de nucleótidos del gen mitocondrial ND4. Biomedica, 2018, 38, 267-276.	0.3	8
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7063	Genetic variability of wildlife-derived <i>Sarcoptes scabiei</i> determined by the ribosomal ITS-2 and mitochondrial 16S genes. Experimental and Applied Acarology, 2018, 76, 53-70.	0.7	5
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7065	Novel genetic variation in an isolated population of the nationally critical Haast tokoeka (<i>Apteryx</i>) Conservation Genetics, 2018, 19, 1401-1410.	0.8	6
7066	Tracking the Origins of Fly Invasions; Using Mitochondrial Haplotype Diversity to Identify Potential Source Populations in Two Genetically Intertwined Fruit Fly Species (<i>Bactrocera carambolae</i> and) Conservation Genetics, 2018, 19, 1401-1410.	0.8	6
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7068	Polymorphism in merozoite surface protein-7E of <i>Plasmodium vivax</i> in Thailand: Natural selection related to protein secondary structure. PLoS ONE, 2018, 13, e0196765.	1.1	6
7069	Clarifying the taxonomic status of the alien species <i>Branchiommia bairdi</i> and <i>Branchiommia boholense</i> (Annelida: Sabellidae) using molecular and morphological evidence. PLoS ONE, 2018, 13, e0197104.	1.1	18
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7071	Reverse taxonomy applied to the <i>Brachionus calyciflorus</i> cryptic species complex: Morphometric analysis confirms species delimitations revealed by molecular phylogenetic analysis and allows the (re)description of four species. PLoS ONE, 2018, 13, e0203168.	1.1	66
7072	Range dynamics of Palaearctic steppe species under glacial cycles: the phylogeography of <i>Proterebia afro</i> (Lepidoptera: Nymphalidae: Satyrinae). Biological Journal of the Linnean Society, 0, , .	0.7	2
7073	Phylogenetic position of the extinct blue antelope, <i>Hippotragus leucophaeus</i> (Pallas, 1766) (Bovidae:) 2018, 182, 225-235.	1.0	9
7074	Phylogeographic pattern of the plane leaf miner, <i>Phyllonorycter platani</i> (STAUDINGER, 1870) (Lepidoptera: Gracillariidae) in Europe. BMC Evolutionary Biology, 2018, 18, 135.	3.2	10

#	ARTICLE	IF	CITATIONS
7075	Large-scale mitochondrial DNA analysis reveals new light on the phylogeography of Central and Eastern-European Brown hare (<i>Lepus europaeus</i> Pallas, 1778). <i>PLoS ONE</i> , 2018, 13, e0204653.	1.1	15
7076	Description and genetic variation of a distinct species of <i>Potyvirus</i> infecting saffron (<i>Crocus sativus</i> L.) plants in major production regions in Iran. <i>Annals of Applied Biology</i> , 2018, 173, 233-242.	1.3	10
7077	Phylogeography of the endangered saproxylic beetle <i>Rosalia longicorn</i> , <i>Rosalia alpina</i> (Coleoptera, Cerambycidae), corresponds with its main host, the European beech (<i>Fagus</i>) Tj ETQq0 0 0 rgBT / Overlock 1016 50 657 7	1.1	16
7078	Genetic Diversity of MHC Class II DRB1 Exon 2 in the Red Fox (<i>Vulpes vulpes</i>) on Hokkaido, Japan. <i>Zoological Science</i> , 2018, 35, 402.	0.3	5
7079	On the genetic distinctiveness of tailorbirds (Cisticolidae: <i>Orthotomus</i>) from the South-east Asian mainland with the description of a new subspecies. <i>Avian Research</i> , 2018, 9, .	0.5	2
7080	Genetic diversity and biogeography of <i>T. officinale</i> inferred from multi locus sequence typing approach. <i>PLoS ONE</i> , 2018, 13, e0203275.	1.1	3
7081	Identification, Structural Characterization and Gene Expression Analysis of Members of the Nuclear Factor-Y Family in Chickpea (<i>Cicer arietinum</i> L.) under Dehydration and Abscisic Acid Treatments. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3290.	1.8	14
7082	Sequence characterization of the 5S ribosomal DNA and the internal transcribed spacer (ITS) region in four European <i>Donax</i> species (<i>Bivalvia</i> : Donacidae). <i>BMC Genetics</i> , 2018, 19, 97.	2.7	6
7083	Molecular characterization and phylogenetic analysis of <i>Taenia multiceps</i> from China. <i>Acta Parasitologica</i> , 2018, 63, 721-727.	0.4	4
7084	Genetic diversity and population differentiation of the freshwater copepod <i>Sinocalanus tenellus</i> (Calanoida, Centropagidae) in China. <i>Journal of Limnology</i> , 2018, 77, .	0.3	4
7085	Title is missing!. <i>Turkish Journal of Fisheries and Aquatic Sciences</i> , 2018, 18, .	0.4	4
7086	Riverine barrier effects on population genetic structure of the Hanuman langur (<i>Semnopithecus</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 1016 50 657 7	3.2	10
7087	Evidence of peripheral olfactory impairment in the domestic silkworms: insight from the comparative transcriptome and population genetics. <i>BMC Genomics</i> , 2018, 19, 788.	1.2	14
7088	Genetic analyses of brown hare (<i>Lepus europaeus</i>) support limited migration and translocation of Greek populations. <i>PLoS ONE</i> , 2018, 13, e0206327.	1.1	9
7089	Rapid Intraspecific Diversification of the Alpine Species <i>Saxifraga sinomontana</i> (Saxifragaceae) in the Qinghai-Tibetan Plateau and Himalayas. <i>Frontiers in Genetics</i> , 2018, 9, 381.	1.1	18
7090	High Order Formation and Evolution of Hornerin in Primates. <i>Genome Biology and Evolution</i> , 2018, 10, 3167-3175.	1.1	7
7091	Effects of Geological and Environmental Events on the Diversity and Genetic Divergence of Four Closely Related Pines: <i>Pinus koraiensis</i> , <i>P. armandii</i> , <i>P. griffithii</i> , and <i>P. pumila</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1264.	1.7	8
7092	Single-nucleotide polymorphisms(SNPs) in a sucrose synthase gene are associated with wood properties in <i>Catalpa fargesii</i> bur. <i>BMC Genetics</i> , 2018, 19, 99.	2.7	5

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7093	Population genetic structure of domain I of apical membrane antigen-1 in <i>Plasmodium falciparum</i> isolates from Hazara division of Pakistan. <i>Malaria Journal</i> , 2018, 17, 389.	0.8	2
7094	Glacial refugia and speciation in a group of wind-pollinated and -dispersed, endemic Alpine species of <i>Helictotrichon</i> (Poaceae). <i>PLoS ONE</i> , 2018, 13, e0205354.	1.1	1
7095	Grapevine virus T diversity as revealed by full-length genome sequences assembled from high-throughput sequence data. <i>PLoS ONE</i> , 2018, 13, e0206010.	1.1	19
7096	Genome-Wide Characterization of the sHsp Gene Family in <i>Salix suchowensis</i> Reveals Its Functions under Different Abiotic Stresses. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3246.	1.8	20
7097	Whole chloroplast genome sequences of the Japanese hemlocks, <i>Tsuga diversifolia</i> and <i>T. sieboldii</i> , and development of chloroplast microsatellite markers applicable to East Asian <i>Tsuga</i> . <i>Journal of Forest Research</i> , 2018, 23, 318-323.	0.7	27
7098	Tests of hypotheses for morphological and genetic divergence in <i>Megaloprepus</i> damselflies across Neotropical forests. <i>Biological Journal of the Linnean Society</i> , 0, , .	0.7	2
7099	MHC class IIA polymorphisms and their association with resistance to susceptibility to <i>Streptococcus agalactiae</i> in Nile tilapia, <i>Oreochromis niloticus</i> . <i>Journal of Fish Biology</i> , 2018, 93, 1207-1215.	0.7	2
7100	Genome-Wide Evolutionary Analysis of Natural History and Adaptation in the World's Tigers. <i>Current Biology</i> , 2018, 28, 3840-3849.e6.	1.8	60
7101	Nunataks or massif de refuge? A phylogeographic study of <i>Rhodiola crenulata</i> (Crassulaceae) on the world's highest sky islands. <i>BMC Evolutionary Biology</i> , 2018, 18, 154.	3.2	19
7102	Description and post-glacial demography of <i>Gammarus jazdzewskii</i> sp. nov. (Crustacea: Tj ETQq1 1 0.784314 rgBT / Overlock 107 0.3 19		
7103	Contrasting Demographic History and Population Structure of <i>Zamia</i> (Cycadales: Zamiaceae) on Six Islands of the Greater Antilles Suggests a Model for Population Diversification in the Caribbean Clade of the Genus. <i>International Journal of Plant Sciences</i> , 2018, 179, 730-757.	0.6	7
7104	Integrative approach reveals a new species of <i>Nematocharax</i> (Teleostei: Characidae). <i>Journal of Fish Biology</i> , 2018, 93, 1151-1162.	0.7	8
7105	Genetic structure of Japanese sea cucumbers (<i>Apostichopus japonicus</i>) along the Sanriku coast supports the effect of earthquakes and related tsunamis. <i>Genetica</i> , 2018, 146, 497-503.	0.5	1
7106	Impacts of the Asian interior arid zone on phylogeographic patterns in the eastern Asian flora revealed by two <i>Potamogeton</i> species (Potamogetonaceae): east-west divergence within species and barriers to north-south dispersal. <i>Botanical Journal of the Linnean Society</i> , 2018, , .	0.8	0
7107	Positive selection in coding regions and motif duplication in regulatory regions of bottlenose dolphin MHC class II genes. <i>PLoS ONE</i> , 2018, 13, e0203450.	1.1	20
7108	Recent Fragmentation May Not Alter Genetic Patterns in Endangered Long-Lived Species: Evidence From <i>Taxus cuspidata</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1571.	1.7	24
7109	Spotlight on islands: on the origin and diversification of an ancient lineage of the Italian wall lizard <i>Podarcis siculus</i> in the western Pontine Islands. <i>Scientific Reports</i> , 2018, 8, 15111.	1.6	11
7110	Siberian Whitefish (<i>Coregonus lavaretus pidschian</i> , Coregonidae) from the Anabar River: Morphogenetic Structure of the Population. <i>Russian Journal of Genetics</i> , 2018, 54, 1078-1088.	0.2	8

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7111	Multiple refugia from penultimate glaciations in East Asia demonstrated by phylogeography and ecological modelling of an insect pest. <i>BMC Evolutionary Biology</i> , 2018, 18, 152.	3.2	26
7112	Insights into the evolutionary dynamics of Neotropical biomes from the phylogeography and paleodistribution modeling of <i>Bromelia balansae</i> . <i>American Journal of Botany</i> , 2018, 105, 1725-1734.	0.8	5
7113	Molecular epidemiology and evolution of drug-resistant genes in the malaria parasite <i>Plasmodium falciparum</i> in southwestern Nigeria. <i>Infection, Genetics and Evolution</i> , 2018, 66, 222-228.	1.0	11
7114	Impact of Pleistocene geoclimatic events on the genetic structure in mid-latitude South American plants: insights from the phylogeography of <i>Turnera sidoides</i> complex (Passifloraceae, Turneroideae). <i>Botanical Journal of the Linnean Society</i> , 0, , .	0.8	4
7115	Evidence for Introgression Among Three Species of the <i>Anastrepha fraterculus</i> Group, a Radiating Species Complex of Fruit Flies. <i>Frontiers in Genetics</i> , 2018, 9, 359.	1.1	15
7116	Genetic Diversity of Aphid (Hemiptera: Aphididae) Species Attacking Amaranth and Nightshades in Different Agro-Ecological Zones of Kenya and Tanzania. <i>African Entomology</i> , 2018, 26, 407-421.	0.6	1
7117	Genetic signatures of plant resistance genes with known function within and between species. <i>Genetica</i> , 2018, 146, 517-528.	0.5	3
7118	Diversidad genética y estructura poblacional de <i>Anopheles triannulatus</i> s.l. en Córdoba, Colombia, determinadas mediante el método de región de código de barras de ADN. <i>Biomedica</i> , 2018, 38, 117-126.	0.3	2
7119	Rates of population differentiation and speciation are decoupled in sea snakes. <i>Biology Letters</i> , 2018, 14, 20180563.	1.0	12
7120	Phylogeography of the Common Vole <i>Microtus arvalis</i> , the Obscure Form (Rodentia, Arvicolinae): New Data on the Mitochondrial DNA Variability. <i>Russian Journal of Genetics</i> , 2018, 54, 1185-1198.	0.2	9
7121	Understanding the cryptic introgression and mixed ancestry of Red Junglefowl in India. <i>PLoS ONE</i> , 2018, 13, e0204351.	1.1	6
7122	Genetic polymorphism and natural selection of circumsporozoite surface protein in <i>Plasmodium falciparum</i> field isolates from Myanmar. <i>Malaria Journal</i> , 2018, 17, 361.	0.8	18
7123	An integrated morpho-molecular approach to delineate species boundaries of <i>Millepora</i> from the Red Sea. <i>Coral Reefs</i> , 2018, 37, 967-984.	0.9	26
7124	Integrative taxonomy of the Amazonian red-sided opossum <i>Monodelphis glirina</i> (J.A. Wagner, 1842) (Didelphimorphia: Didelphidae). <i>Zootaxa</i> , 2018, 4508, 28-46.	0.2	12
7125	Range, population structure and morphological characterization of the small range endemic bush-cricket <i>Lluciapomaresius panteli</i> (Orthoptera: Tettigoniidae: Bradyporinae). <i>Journal of Insect Conservation</i> , 2018, 22, 659-674.	0.8	0
7126	Title is missing!. <i>Turkish Journal of Fisheries and Aquatic Sciences</i> , 2018, 18, .	0.4	2
7127	Connections and containers: Using genetic data to understand how watershed evolution and human activities influence cutthroat trout biogeography. <i>PLoS ONE</i> , 2018, 13, e0202043.	1.1	8
7128	Genetic structure of the grey side-gilled sea slug (<i>Pleurobranchaea maculata</i>) in coastal waters of New Zealand. <i>PLoS ONE</i> , 2018, 13, e0202197.	1.1	7

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7129	Genetic Structure of the Hyrcanian Wood Frog, <i>Rana pseudodalmatina</i> (Amphibia: Ranidae) Using mtDNA Gene Sequences. <i>Russian Journal of Genetics</i> , 2018, 54, 1221-1228.	0.2	8
7130	Genetic characterization of <i>Plasmodium vivax</i> in the Kyrgyz Republic. <i>Infection, Genetics and Evolution</i> , 2018, 66, 262-268.	1.0	4
7131	Modelling the invasion history of <i>Sinanodonta woodiana</i> in Europe: Tracking the routes of a sedentary aquatic invader with mobile parasitic larvae. <i>Evolutionary Applications</i> , 2018, 11, 1975-1989.	1.5	25
7132	Plastid DNA variation of the endemic species <i>Oxytropis glandulosa</i> Turcz. (Fabaceae). <i>Turkish Journal of Botany</i> , 2018, 42, 38-50.	0.5	12
7133	Global genetic diversity of var2csa in <i>Plasmodium falciparum</i> with implications for malaria in pregnancy and vaccine development. <i>Scientific Reports</i> , 2018, 8, 15429.	1.6	35
7134	The Complete Plastome Sequences of Eleven Capsicum Genotypes: Insights into DNA Variation and Molecular Evolution. <i>Genes</i> , 2018, 9, 503.	1.0	25
7135	Testing the validity of two putative sympatric species from <i>Sinocyclocheilus</i> (Cypriniformes: Cyprinidae). <i>Journal of Fish Biology</i> , 2018, 92, 502-512.	0.2	1
7136	The Prehistoric Indian Ayurvedic Rice Shashtika Is an Extant Early Domesticated With a Distinct Selection History. <i>Frontiers in Plant Science</i> , 2018, 9, 1203.	1.7	2
7137	Adaptive Evolution of RH5 in Ape <i>Plasmodium</i> species of the <i>Laverania</i> Subgenus. <i>MBio</i> , 2018, 9, .	1.8	13
7138	Thriving populations with low genetic diversity in giant clam species, <i>Tridacna maxima</i> and <i>Tridacna noae</i> , at Dongsha Atoll, South China Sea. <i>Regional Studies in Marine Science</i> , 2018, 24, 278-287.	0.4	14
7139	Mitochondrial phylogeography and population structure of the cattle tick <i>Rhipicephalus appendiculatus</i> in the African Great Lakes region. <i>Parasites and Vectors</i> , 2018, 11, 329.	1.0	11
7140	Limited introgression supports division of giraffe into four species. <i>Ecology and Evolution</i> , 2018, 8, 10156-10165.	0.8	40
7141	Genetic Differentiation of the Daurian Ground Squirrel <i>Spermophilus dauricus</i> Brandt, 1843 according to Variability of the Mitochondrial DNA Control Region. <i>Biology Bulletin</i> , 2018, 45, 438-447.	0.1	4
7142	Morphological and genetic divergence between Mediterranean and Caribbean populations of <i>Madracis pharensis</i> (Heller 1868) (Scleractinia, Pocilloporidae): too much for one species?. <i>Zootaxa</i> , 2018, 4471, 473-492.	0.2	5
7143	Analysis of structure-function relationship in porcine rotavirus A enterotoxin gene. <i>Journal of Veterinary Science</i> , 2018, 19, 35.	0.5	6
7144	Genetic characteristics of the P1 coding region of Coxsackievirus A16 associated with hand, foot, and mouth disease in China. <i>Molecular Biology Reports</i> , 2018, 45, 1947-1955.	1.0	5
7145	Using phylogenomics to reconstruct phylogenetic relationships within tribe Polygonateae (Asparagaceae), with a special focus on <i>Polygonatum</i> . <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 202-213.	1.2	29
7146	Complex Haplotypes of <i>GSTM1</i> Gene Deletions Harbor Signatures of a Selective Sweep in East Asian Populations. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2953-2966.	0.8	8

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7147	Molecular and Biological Characterisation of Turnip mosaic virus Isolates Infecting Poppy (Papaver) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.5	9
7148	Plant Genetics and Molecular Biology. Advances in Biochemical Engineering/Biotechnology, 2018, , .	0.6	6
7149	Ancient Endogenous Pararetroviruses in Oryza Genomes Provide Insights into the Heterogeneity of Viral Gene Macroevolution. Genome Biology and Evolution, 2018, 10, 2686-2696.	1.1	9
7150	Absence of spatial genetic structure in common dentex (<i>Dentex dentex</i> Linnaeus, 1758) in the Mediterranean Sea as evidenced by nuclear and mitochondrial molecular markers. PLoS ONE, 2018, 13, e0203866.	1.1	8
7151	Colonization and divergence: phylogeography and population genetics of the Atlantic coast beach mice. Systematics and Biodiversity, 2018, 16, 757-773.	0.5	3
7152	Population structure and phylogenetic relationships of a new shallow-water Antarctic phyllodocid annelid. Zoologica Scripta, 2018, 47, 714-726.	0.7	9
7153	The evolutionary history of Mediterranean Batoidea (Chondrichthyes: Neoselachii). Zoologica Scripta, 2018, 47, 686-698.	0.7	12
7154	Mitogenomics of the jaguarundi (<i>Puma yagouaroundi</i> , Felidae, Carnivora): Disagreement between morphological subspecies and molecular data. Mammalian Biology, 2018, 93, 153-168.	0.8	8
7155	Chromosome Spreading of the Retrotransposable <i>Rex-3</i> Element and Microsatellite Repeats in Karyotypes of the <i>Ancistrus</i> Populations. Zebrafish, 2018, 15, 504-514.	0.5	7
7157	DNA Barcodes Suggest Possible New Cryptic Species in the <i>Codatractus melon</i> Species Group (Hesperiidae: Eudaminae) in North America. Journal of the Lepidopterists' Society, 2018, 72, 203-211.	0.0	3
7158	Genetic Characterization of <i>Paracentrotus lividus</i> (Lamarck, 1816) Populations from Nw Spain and the Canary Islands. Journal of Shellfish Research, 2018, 37, 651-658.	0.3	4
7159	Phylogeography of the palm <i>Syagrus coronata</i> (Martius) Beccari (Arecaceae): distribution in the Caatinga and Atlantic forest domains. Revista Brasileira De Botanica, 2018, 41, 849-857.	0.5	13
7160	Phylogeny and genetic structure of the goitered gazelle (<i>Artiodactyla</i> , Bovidae) in north-western China indicated by the hypervariable mitochondrial control region. Systematics and Biodiversity, 2018, 16, 527-537.	0.5	5
7161	Different low-competition island habitats in Central Europe harbour similar levels of genetic diversity in relict populations of <i>Galium pusillum</i> agg. (Rubiaceae). Biological Journal of the Linnean Society, 0, , .	0.7	2
7162	Phylogeography of Muller's termite frog suggests the vicariant role of the Central Brazilian Plateau. Journal of Biogeography, 2018, 45, 2508-2519.	1.4	22
7163	Genome-wide identification and expression analyses of the pectate lyase (PEL) gene family in cotton (<i>Gossypium hirsutum</i> L.). BMC Genomics, 2018, 19, 661.	1.2	32
7164	<i>Garra dengba</i> , a new species of cyprinid fish (Pisces: Teleostei) from eastern Tibet, China. Zootaxa, 2018, 4476, 94-108.	0.2	8
7165	Stepwise cis-Regulatory Changes in ZCN8 Contribute to Maize Flowering-Time Adaptation. Current Biology, 2018, 28, 3005-3015.e4.	1.8	116

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7166	Secondary Intergradation of Various Forms of Pidschian-Like Whitefishes (<i>Coregonus lavaretus sensu</i> Tj ETQqO 0 0 rgBT /Overlock 10 T Applied Research, 2018, 8, 178-189.	0.4	5
7167	Tracing the <i>De Novo</i> Origin of Protein-Coding Genes in Yeast. MBio, 2018, 9, .	1.8	19
7168	Cytonuclear diversity and shared mitochondrial haplotypes among <i>Daphnia galeata</i> populations separated by seven thousand kilometres. BMC Evolutionary Biology, 2018, 18, 130.	3.2	9
7169	Population genetic structure of banana corm weevil <i>Cosmopolites sordidus</i> (Germar) in India. Journal of Asia-Pacific Entomology, 2018, 21, 1222-1232.	0.4	2
7170	Ecological drivers of plant genetic diversity at the southern edge of geographical distributions: Forestal vines in a temperate region. Genetics and Molecular Biology, 2018, 41, 318-326.	0.6	8
7171	A New Species of <i>Proceratophrys</i> (Amphibia: Anura: Odontophrynidae) from the Araripe Plateau, CearÃ¡ State, Northeastern Brazil. Herpetologica, 2018, 74, 255.	0.2	20
7172	Comparative Analyses of Chloroplast Genomes of Cucurbitaceae Species: Lights into Selective Pressures and Phylogenetic Relationships. Molecules, 2018, 23, 2165.	1.7	21
7173	DNA barcoding of the medically important freshwater snail <i>Physa acuta</i> reveals multiple invasion events into Africa. Acta Tropica, 2018, 188, 86-92.	0.9	13
7174	Molecular authentication of Pargo filets <i>Lutjanus purpureus</i> (Perciformes: Lutjanidae) by DNA barcoding reveals commercial fraud. Neotropical Ichthyology, 2018, 16, .	0.5	20
7175	Genetic analysis of European red foxes reveals multiple distinct peripheral populations and central continental admixture. Quaternary Science Reviews, 2018, 197, 257-266.	1.4	11
7176	Cultural Transmission of Fine-Scale Fidelity to Feeding Sites May Shape Humpback Whale Genetic Diversity in Russian Pacific Waters. Journal of Heredity, 2018, 109, 724-734.	1.0	9
7177	Three new Diplozoidae mitogenomes expose unusual compositional biases within the Monogenea class: implications for phylogenetic studies. BMC Evolutionary Biology, 2018, 18, 133.	3.2	28
7178	Molecular variation across populations of a widespread North American firefly, <i>Photinus pyralis</i> , reveals that coding changes do not underlie flash color variation or associated visual sensitivity. BMC Evolutionary Biology, 2018, 18, 129.	3.2	14
7179	Geographical distribution of <i>Aedes aegypti</i> and <i>Aedes albopictus</i> (Diptera: Culicidae) and genetic diversity of invading population of <i>Ae. albopictus</i> in the Republic of the Congo. Wellcome Open Research, 2018, 3, 79.	0.9	18
7180	Two new bioluminescent <i>Henlea</i> from Siberia and lack of molecular support for <i>Hepatogaster</i> (Annelida, Clitellata, Enchytraeidae). Organisms Diversity and Evolution, 2018, 18, 291-312.	0.7	7
7181	Can we identify the Mexican hairless dog in the archaeological record? Morphological and genetic insights from Tizayuca, Basin of Mexico. Journal of Archaeological Science, 2018, 98, 128-136.	1.2	4
7182	The influence of latitude, geographic distance, and habitat discontinuities on genetic variation in a high latitude montane species. Scientific Reports, 2018, 8, 11846.	1.6	14
7183	Phylogenetic and biogeographic insights into long-lived Mediterranean <i>Cupressus</i> taxa with a schizo-endemic distribution and Tertiary origin. Botanical Journal of the Linnean Society, 2018, 188, 190-212.	0.8	21

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7184	High level of genetic connectivity in a deep-sea water reef fish, <i>Caulolatilus microps</i> . <i>Journal of Fish Biology</i> , 2018, 93, 766-777.	0.7	3
7185	Genetic diversity of common <i>Gasterophilus</i> spp. from distinct habitats in China. <i>Parasites and Vectors</i> , 2018, 11, 474.	1.0	7
7186	BA9 lineage of respiratory syncytial virus from across the globe and its evolutionary dynamics. <i>PLoS ONE</i> , 2018, 13, e0193525.	1.1	31
7187	Evolutionary history and spatio-temporal dynamics of dengue virus serotypes in an endemic region of Colombia. <i>PLoS ONE</i> , 2018, 13, e0203090.	1.1	19
7188	Variabilidad genética en poblaciones de <i>Elionurus muticus</i> (Poaceae) de Corrientes, Argentina, a partir de marcadores moleculares de ADN nuclear y cloroplástico. <i>Boletín De La Sociedad Argentina De Botánica</i> , 2018, 53, 255-266.	0.1	0
7189	Genetic diversity of the entomopathogenic fungus <i>Cordyceps tenuipes</i> in forests and butterfly gardens in Quindío, Colombia. <i>Fungal Biology</i> , 2018, 122, 891-899.	1.1	9
7190	Evolutionary divergence of mitochondrial genomes in two <i>Tetranychus</i> species distributed across different climates. <i>Insect Molecular Biology</i> , 2018, 27, 698-709.	1.0	40
7191	Function of the evolutionarily conserved plant methionine-S-sulfoxide reductase without the catalytic residue. <i>Protoplasma</i> , 2018, 255, 1741-1750.	1.0	7
7192	The <i>Crambe abyssinica</i> plastome: Brassicaceae phylogenomic analysis, evolution of RNA editing sites, hotspot and microsatellite characterization of the tribe Brassiceae. <i>Gene</i> , 2018, 671, 36-49.	1.0	15
7193	Evolutionary dynamics of avian influenza A H7N9 virus across five waves in mainland China, 2013–2017. <i>Journal of Infection</i> , 2018, 77, 205-211.	1.7	12
7194	Characterization of Papaya ringspot virus isolates infecting transgenic papaya ‘Huanong No.1’™ in South China. <i>Scientific Reports</i> , 2018, 8, 8206.	1.6	16
7195	Assessing the role of aridity-induced vicariance and ecological divergence in species diversification in North-West Africa using <i>Agama</i> lizards. <i>Biological Journal of the Linnean Society</i> , 2018, 124, 363-380.	0.7	17
7196	Phylogeography, evolutionary history and effects of glaciations in a species (<i>Zootoca vivipara</i>) inhabiting multiple biogeographic regions. <i>Journal of Biogeography</i> , 2018, 45, 1616-1627.	1.4	35
7197	How small an island? Speciation by endemic mammals (<i>Apomys</i> , Muridae) on an oceanic Philippine island. <i>Journal of Biogeography</i> , 2018, 45, 1675-1687.	1.4	13
7198	The mitochondrial genome of the Kentish Plover <i>Charadrius alexandrinus</i> (Charadriiformes: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182 T	0.5	10
7199	A hyper-diverse genus of acanthocephalans revealed by tree-based and non-tree-based species delimitation methods: Ten cryptic species of <i>Neoechinorhynchus</i> in Middle American freshwater fishes. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 30-45.	1.2	43
7200	Genetic characters of the globally spread tiger mosquito, <i>Aedes albopictus</i> (Diptera, Culicidae): implications from mitochondrial gene COI. <i>Journal of Vector Ecology</i> , 2018, 43, 89-97.	0.5	7
7201	Global phylogeography and genetic diversity of the zoonotic tapeworm <i>Echinococcus granulosus</i> sensu stricto genotype G1. <i>International Journal for Parasitology</i> , 2018, 48, 729-742.	1.3	77

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7202	Host range, host specificity, regional host preferences and genetic variability of <i>Korthalsella</i> Tiegh. (Viscaceae) mistletoes in New Zealand. <i>New Zealand Journal of Botany</i> , 2018, 56, 127-162.	0.8	5
7203	Mountain barriers and trans-Saharan connections shape the genetic structure of <i>Pimelia</i> darkling beetles (Coleoptera: Tenebrionidae). <i>Biological Journal of the Linnean Society</i> , 2018, 124, 547-556.	0.7	10
7204	Integrating a comprehensive <scp>DNA</scp> barcode reference library with a global map of yews (<i>Taxus</i> L.) for forensic identification. <i>Molecular Ecology Resources</i> , 2018, 18, 1115-1131.	2.2	38
7205	Environmental transition zone and rivers shape intraspecific population structure and genetic diversity of an Amazonian rain forest tree frog. <i>Evolutionary Ecology</i> , 2018, 32, 359-378.	0.5	28
7206	Phylogenetic analysis of the tree-kangaroos (<i>Dendrolagus</i>) reveals multiple divergent lineages within New Guinea. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 589-599.	1.2	28
7207	Cryptic diversity in the common flap-necked chameleon<i>Chamaeleo dilepis</i> in South Africa. <i>African Zoology</i> , 2018, 53, 11-16.	0.2	5
7208	Cryptic dispersal of Cyanidiophytina (Rhodophyta) in non-acidic environments from Turkey. <i>Extremophiles</i> , 2018, 22, 713-723.	0.9	20
7209	Species assignment and population genetic studies of <i>Gran Paraná</i> pejerrey (<i>Odontesthes</i> sp.), Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.0	10
7210	Phylogenetic analyses of Bradyrhizobium symbionts associated with invasive <i>Crotalaria zanzibarica</i> and its coexisting legumes in Taiwan. <i>Systematic and Applied Microbiology</i> , 2018, 41, 619-628.	1.2	5
7211	Geographic variation in a South American clade of mormoopid bats, <i>Pteronotus</i> (Phyllodia), with description of a new species. <i>Journal of Mammalogy</i> , 2018, 99, 624-645.	0.6	38
7212	Occurrence of <i>Glaucus atlanticus</i> in the Midriff Islands Region, Gulf of California, Mexico. <i>American Malacological Bulletin</i> , 2018, 36, 145-149.	0.2	2
7213	Genetic, host and environmental factors associated with a high prevalence of <i>Anaplasma marginale</i> . <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 1286-1295.	1.1	18
7214	Is genetic drift to blame for testicular dysgenesis syndrome in Semliki chimpanzees (<i>Pan</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 T	0.3	3
7215	Phylogenetics and dispersal patterns of Brassicaceae around the Qinghaiâ€Tibet Plateau. <i>Journal of Systematics and Evolution</i> , 2018, 56, 202-217.	1.6	7
7216	Concerted Pleistocene dispersal and genetic differentiation in passerine birds from the Tres MarÃas Archipelago, Mexico. <i>Auk</i> , 2018, 135, 716-732.	0.7	10
7217	The secret of Pianosa island: an Italian native population of European brown hare (<i>Lepus europaeus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.8	4
7218	Fine-scale genetic structure across a New Zealand disjunction for the direct-developing intertidal whelk <i>Cominella maculosa</i> (Gastropoda: Buccinidae). <i>Biological Journal of the Linnean Society</i> , 2018, 123, 593-602.	0.7	5
7219	<i>Wolbachia</i> strains, and lack of genetic diversity and parthenogenesis in Brazilian populations of <i>Tuta absoluta</i> (Lepidoptera: Gelechiidae). <i>Journal of Applied Entomology</i> , 2018, 142, 905-910.	0.8	6

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7220	Molecular and plumage analyses indicate the incomplete separation of two woodpeckers (Aves.) <i>Tj ETQq0 0 0 rgBT /Overlock 4 10 Tf 50 7</i>	0.7	4
7221	Analysis of genetic diversity in CYTB and control region sequences of <i>Melanochelys trijuga</i> (Schweigger, 1812) from Karnataka. <i>Journal of Asia-Pacific Biodiversity</i> , 2018, 11, 346-352.	0.2	2
7222	Geographic patterns of phenotypic diversity in incipient species of North American blister beetles (Coleoptera: Meloidae) are not determined by species niches, but driven by demography along the speciation process. <i>Invertebrate Systematics</i> , 2018, 32, 672.	0.5	4
7223	Marked intra-genomic variation and pseudogenes in the ITS1-5.8S-ITS2 rDNA of <i>Symphurus plagiusa</i> (Pleuronectiformes: Cynoglossidae). <i>Animal Biology</i> , 2018, 68, 353-365.	0.6	1
7224	Restructuring of a mutualism following introduction of Australian fig trees and pollinating wasps to Europe and the USA. <i>Biological Invasions</i> , 2018, 20, 3037-3045.	1.2	4
7225	Resolution of the <i>Daphnia umbra</i> problem (Crustacea: Cladocera) using an integrated taxonomic approach. <i>Zoological Journal of the Linnean Society</i> , 0, , .	1.0	8
7226	Molecular phylogenetic species in <i>Alternaria</i> pathogens infecting pistachio and wild relatives. <i>3 Biotech</i> , 2018, 8, 250.	1.1	6
7227	Divergent evolutionary origins and biogeographic histories of two freshwater crabs (Brachyura): <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10</i> <i>Phylogenetics and Evolution</i> , 2018, 127, 119-128.	1.2	14
7228	Seasonal dynamics, geographical range size, hosts, genetic diversity and phylogeography of <i>Amblyomma sculptum</i> in Argentina. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 1264-1274.	1.1	11
7229	Mysteries of host switching: Diversification and host specificity in rodent-coccidia associations. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 179-189.	1.2	27
7230	Morphology and molecular data reveal the presence of two new species under <i>Rhamdia quelen</i> (Quoy) <i>Tj ETQq0 0 0 rgBT /Overlock 10</i>	0.2	9
7231	Parallel evolution of site-specific changes in divergent caribou lineages. <i>Ecology and Evolution</i> , 2018, 8, 6053-6064.	0.8	9
7232	ZW, XY, and yet ZW: Sex chromosome evolution in snakes even more complicated. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 1701-1707.	1.1	39
7233	Local adaptation versus historical isolation as sources of melanin-based coloration in the white-throated thrush <i>Turdus assimilis</i> . <i>Journal of Avian Biology</i> , 2018, 49, e01790.	0.6	7
7234	Pathway position constrains the evolution of an ecologically important pathway in aspens (<i>Populus tremula</i> L.). <i>Molecular Ecology</i> , 2018, 27, 3317-3330.	2.0	5
7235	A new genus and species of primary freshwater crab and a new species of Artopotamon Dai & Chen, 1985 (Crustacea, Brachyura, Potamidae) from western Yunnan, China. <i>Zootaxa</i> , 2018, 4422, 115.	0.2	13
7237	Genetic Diversity and Distribution of <i>Blastocystis</i> Subtype 3 in Human Populations, with Special Reference to a Rural Population in Central Mexico. <i>BioMed Research International</i> , 2018, 2018, 1-7.	0.9	19
7238	Peripatric speciation associated with genome expansion and female-biased sex ratios in the moss genus <i>Ceratodon</i> . <i>American Journal of Botany</i> , 2018, 105, 1009-1020.	0.8	12

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7239	In silico analysis of putative dormancy genes in <i>Plasmodium vivax</i> . <i>Acta Tropica</i> , 2018, 186, 24-34.	0.9	2
7240	Concordance between genetic diversity and marine biogeography in a highly mobile marine mammal, the Risso's dolphin. <i>Journal of Biogeography</i> , 2018, 45, 2092-2103.	1.4	11
7241	Phylogeography, genetic structure and wing pattern variation of <i>Erebia pronoe</i> (Esper, 1780) (Lepidoptera: Nymphalidae) in Europe. <i>Zootaxa</i> , 2018, 4441, 279.	0.2	4
7242	Comparative mitogenome analysis on species of four apple snails (Ampullariidae: Pomacea). <i>International Journal of Biological Macromolecules</i> , 2018, 118, 525-533.	3.6	13
7243	The Complete Mitochondrial Genome of <i>Ugyops</i> sp. (Hemiptera: Delphacidae). <i>Journal of Insect Science</i> , 2018, 18, .	0.6	14
7244	Three new species of nocturnal geckos of the <i>Paroedura oviceps</i> clade from xeric environments of Madagascar (Squamata: Gekkonidae). <i>Zootaxa</i> , 2018, 4433, 305.	0.2	5
7245	Cascading speciation among mutualists and antagonists in a treeâ€“beetleâ€“fungi interaction. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20180694.	1.2	31
7246	An updated phylogeny and morphological study of the <i>Phymaturus vociferator</i> clade (Iguania: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.2	5
7247	DNA barcoding and a precise morphological comparison revealed a cryptic species in the <i>Nippolachnus piri</i> complex (Hemiptera: Aphididae: Lachninae). <i>Scientific Reports</i> , 2018, 8, 8998.	1.6	20
7248	High Diversity of mtDNA Haplotypes Confirms Syntopic Occurrence of Two Field Mouse Species <i>Apodemus uralensis</i> and <i>A. witherbyi</i> (Muridae: <i>Apodemus</i>) in Armenia. <i>Russian Journal of Genetics</i> , 2018, 54, 687-697.	0.2	2
7249	Genetic Variability in the Yellow-Necked Field Mouse (<i>Sylvaemus flavicollis</i> Melch., 1834, Muridae.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.2	4
7250	Assessing the genetic diversity of the critically endangered Chinese sturgeon <i>Acipenser sinensis</i> using mitochondrial markers and genome-wide single-nucleotide polymorphisms from RAD-seq. <i>Science China Life Sciences</i> , 2018, 61, 1090-1098.	2.3	5
7251	Five BoLA-DRB3 genotypes detected in Egyptian buffalo infected with Foot and Mouth disease virus serotype O. <i>Journal of Genetic Engineering and Biotechnology</i> , 2018, 16, 513-518.	1.5	10
7252	Massive lateral transfer of genes encoding plant cell wall-degrading enzymes to the mycoparasitic fungus <i>Trichoderma</i> from its plant-associated hosts. <i>PLoS Genetics</i> , 2018, 14, e1007322.	1.5	143
7253	Genome- Wide Analysis and Characterization of the TRX Gene Family in Upland Cotton. <i>Tropical Plant Biology</i> , 2018, 11, 119-130.	1.0	15
7254	Genetic diversity of the <i>Plasmodium vivax</i> multidrug resistance 1 gene in Thai parasite populations. <i>Infection, Genetics and Evolution</i> , 2018, 64, 168-177.	1.0	10
7255	Genetic and chemical differentiation characterizes top-geoherb and non-top-geoherb areas in the TCM herb rhubarb. <i>Scientific Reports</i> , 2018, 8, 9424.	1.6	18
7256	Hybridisation and species delimitation of Scandinavian <i>Eisenia</i> spp. (Clitellata: Lumbricidae). <i>European Journal of Soil Biology</i> , 2018, 88, 41-47.	1.4	10

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7257	Revealing genetic hybridization and DNA recombination of <i>Fasciola hepatica</i> and <i>Fasciola gigantica</i> in nuclear introns of the hybrid <i>Fasciola</i> flukes. <i>Molecular and Biochemical Parasitology</i> , 2018, 223, 31-36.	0.5	17
7258	DNA barcoding a taxonomically complex hemiparasitic genus reveals deep divergence between ploidy levels but lack of species-level resolution. <i>AoB PLANTS</i> , 2018, 10, ply026.	1.2	21
7259	Phylogeny of Maleae (Rosaceae) Based on Multiple Chloroplast Regions: Implications to Genera Circumscription. <i>BioMed Research International</i> , 2018, 2018, 1-10.	0.9	23
7260	<i>Onychostoma brevibarba</i> , a new cyprinine fish (Pisces: Teleostei) from the middle Chang Jiang basin in Hunan Province, South China. <i>Zootaxa</i> , 2018, 4410, 147.	0.2	3
7261	Gene flow and Andean uplift shape the diversification of <i>Gasteracantha cancriformis</i> (Araneae: Tj ETQq0 0 0 rgBT /Overlock 10 T	0.8	25
7262	Cryptic diversity, low connectivity and suspected human-mediated dispersal among 17 widespread Indo-Pacific hydroid species of the south-western Indian Ocean. <i>Journal of Biogeography</i> , 2018, 45, 2104-2117.	1.4	19
7263	Comparative <i>scRNA-seq</i> analysis of nickel hyperaccumulating and non-accumulating populations of <i>Senecio coronatus</i> (Asteraceae). <i>Plant Journal</i> , 2018, 95, 1023-1038.	2.8	32
7264	On the distinctiveness of <i>Amapasaurus</i> , its relationship with <i>Loxopholis</i> Cope 1869, and description of a new genus for <i>L. guianensis</i> and <i>L. hoogmoedi</i> (Gymnophthalmoidea/Ecpleopodini: Squamata). <i>Zootaxa</i> , 2018, 4441, 332-346.	0.2	10
7265	Molecular systematics and phylogeography of the endemic Osgood's deer mouse <i>Osgoodomys banderanus</i> (Rodentia: Cricetidae) in the lowlands of western Mexico. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 867-877.	1.2	1
7266	Phylogeographic mitogenomics of Atlantic cod <i>Gadus morhua</i> : Variation in and among trans-Atlantic, trans-Laurentian, Northern cod, and landlocked fjord populations. <i>Ecology and Evolution</i> , 2018, 8, 6420-6437.	0.8	11
7267	Resources for studies of iron walnut (<i>Juglans sigillata</i>) gene expression, genetic diversity, and evolution. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	12
7268	Species delineation and hybrid identification using diagnostic nuclear markers for <i>Plectropomus leopardus</i> and <i>Plectropomus maculatus</i> . <i>Fisheries Research</i> , 2018, 206, 287-291.	0.9	6
7269	Comparative evolutionary and phylogenomic analysis of Avian avulaviruses 1-20. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 931-951.	1.2	21
7270	Genetic structure of teak beehole borer, <i>Xyleutes ceramicus</i> (Lepidoptera: Cossidae), in northern Thailand. <i>Agriculture and Natural Resources</i> , 2018, 52, 66-74.	0.4	3
7271	Discrimination of <i>Anopheles</i> species of the <i>Arribalzagia</i> Series in Colombia using a multilocus approach. <i>Infection, Genetics and Evolution</i> , 2018, 64, 76-84.	1.0	4
7272	Distribution of the Related Weevil Species <i>Sitophilus oryzae</i> and <i>S. zeamais</i> (Coleoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.8	5
7273	Contrasting patterns of molecular diversity and <i>Wolbachia</i> infection in bisexual and parthenogenetic <i>Strophosoma</i> weevils (Coleoptera: Curculionidae). <i>Entomological Science</i> , 2018, 21, 385-395.	0.3	7
7274	Molecular and morphological data of the freshwater fish <i>Glandulocauda melanopleura</i> (Characiformes: Characidae) provide evidences of river captures and local differentiation in the Brazilian Atlantic Forest. <i>PLoS ONE</i> , 2018, 13, e0194247.	1.1	19

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7276	Complete chloroplast genome of <i>Tetragonia tetragonioides</i> : Molecular phylogenetic relationships and evolution in Caryophyllales. PLoS ONE, 2018, 13, e0199626.	1.1	10
7277	Testing the impact of oceanic barriers on population subdivision, speciation and zoogeographical community assembly in <i>Xylotrupes</i> beetles across the Indo-Australian Archipelago. Biological Journal of the Linnean Society, 2018, 125, 152-164.	0.7	4
7278	Gnp4/LAX2, a RAWUL protein, interferes with the OsIAA3-OsARF25 interaction to regulate grain length via the auxin signaling pathway in rice. Journal of Experimental Botany, 2018, 69, 4723-4737.	2.4	62
7279	Intraspecific mitogenomics of three marine species-at-risk: Atlantic, spotted, and northern wolffish (<i>Anarhichas</i> spp.). Genome, 2018, 61, 625-634.	0.9	4
7280	Barcoding and morphometry to identify and assess genetic population differentiation and size variability in loliginid squid paralarvae from NE Atlantic (Spain). Marine Biology, 2018, 165, 1.	0.7	9
7281	Genetic homogeneity in South American tomato pinworm, <i>Tuta absoluta</i> : a new invasive pest to oriental region. 3 Biotech, 2018, 8, 350.	1.1	10
7282	Purifying Selective Pressure Suggests the Functionality of a Vitamin B12 Biosynthesis Pathway in a Global Population of <i>Mycobacterium tuberculosis</i> . Genome Biology and Evolution, 2018, 10, 2326-2337.	1.1	30
7283	First Record of the Invasive Pest <i>Pseudococcus jackbeardsleyi</i> (Hemiptera: Pseudococcidae) on the Chinese Mainland and Its Rapid Identification Based on Species-Specific Polymerase Chain Reaction. Journal of Economic Entomology, 2018, 111, 2120-2128.	0.8	5
7284	Synonymize <i>Arma chinensis</i> as <i>Arma custos</i> based on morphological, molecular and geographical data. Zootaxa, 2018, 4455, 161-176.	0.2	18
7285	Common Bean Subtelomeres Are Hot Spots of Recombination and Favor Resistance Gene Evolution. Frontiers in Plant Science, 2018, 9, 1185.	1.7	54
7286	Global Molecular Diversity of the Halotolerant Fungus <i>Hortaea werneckii</i> . Life, 2018, 8, 31.	1.1	25
7287	High sequence variation in the exon 10 of TSHR gene is associated with flightless-domestic geese. 3 Biotech, 2018, 8, 353.	1.1	1
7288	Characterization of Mutations Conferring Resistance to Rifampin in <i>Mycobacterium tuberculosis</i> Clinical Strains. Antimicrobial Agents and Chemotherapy, 2018, 62, .	1.4	29
7289	Molecular characterization of banana bract mosaic virus from India reveals recombination and positive selection in the VPg gene. Journal of Plant Pathology, 2018, 100, 523-531.	0.6	3
7290	No Evidence for Recent Selection at FOXP2 among Diverse Human Populations. Cell, 2018, 174, 1424-1435.e15.	13.5	99
7291	Polymorphisms of the growth hormone gene in domesticated red sea bream populations (<i>Pagrus major</i>) Tj ETQq0 0 0 rgBT /Overlock 10 2833-2843.	0.9	3
7292	<i>Echinococcus multilocularis</i> and <i>Echinococcus shiquicus</i> in a small mammal community on the eastern Tibetan Plateau: host species composition, molecular prevalence, and epidemiological implications. Parasites and Vectors, 2018, 11, 302.	1.0	23

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7293	Comparative mitogenomics supports synonymy of the genera <i>Ligula</i> and <i>Digramma</i> (Cestoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74).	1.0	17
7294	The Complete Chloroplast Genomes of Six <i>Ipomoea</i> Species and Indel Marker Development for the Discrimination of Authentic <i>Pharbitidis</i> Semen (Seeds of <i>I. nil</i> or <i>I. purpurea</i>). <i>Frontiers in Plant Science</i> , 2018, 9, 965.	1.7	61
7295	Comparative Analysis of Complete Chloroplast Genomes of <i>Anemoclema</i> , <i>Anemone</i> , <i>Pulsatilla</i> , and <i>Hepatica</i> Revealing Structural Variations Among Genera in Tribe <i>Anemoneae</i> (Ranunculaceae). <i>Frontiers in Plant Science</i> , 2018, 9, 1097.	1.7	53
7296	Spatial versus temporal structure: Implications of interâ€haul variation and relatedness in the Northâ€east Atlantic spurdog <scp><i>Squalus acanthias</i></scp>. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2018, 28, 1167-1180.	0.9	5
7297	Forest corridors between the central Andes and the southern Atlantic Forest enabled dispersal and peripatric diversification without niche divergence in a passerine. <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 221-232.	1.2	24
7298	Genetic variation and relationships in the mitochondrial DNA D-loop region of Qinghai indigenous and commercial pig breeds. <i>Cellular and Molecular Biology Letters</i> , 2018, 23, 31.	2.7	19
7299	â€More Than Meets the Eyeâ€: Cryptic Diversity and Contrasting Patterns of Host-Specificity in Feather Mites Inhabiting Seabirds. <i>Frontiers in Ecology and Evolution</i> , 2018, 6, .	1.1	14
7300	Genetic diversity of merozoite surface protein-1 C-terminal 42 kDa of <i>Plasmodium falciparum</i> (PfMSP-142) may be greater than previously known in global isolates. <i>Parasites and Vectors</i> , 2018, 11, 455.	1.0	5
7301	On the Origin of the Non-brittle Rachis Trait of Domesticated Einkorn Wheat. <i>Frontiers in Plant Science</i> , 2017, 8, 2031.	1.7	58
7302	Domestication Origin and Breeding History of the Tea Plant (<i>Camellia sinensis</i>) in China and India Based on Nuclear Microsatellites and cpDNA Sequence Data. <i>Frontiers in Plant Science</i> , 2017, 8, 2270.	1.7	71
7303	Ecological and Genetic Divergences with Gene Flow of Two Sister Species (<i>Leucomeris decora</i> and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 31.	1.7	13
7304	Interspecific Divergence of Two <i>Sinallaria</i> (Brassicaceae) Species in Eastern China. <i>Frontiers in Plant Science</i> , 2018, 9, 77.	1.7	3
7305	Development and Application of Genomic Resources in an Endangered Palaeoendemic Tree, <i>Parrotia subaequalis</i> (Hamamelidaceae) From Eastern China. <i>Frontiers in Plant Science</i> , 2018, 9, 246.	1.7	14
7306	Climate Is Not All: Evidence From Phylogeography of <i>Rhodiola fastigiata</i> (Crassulaceae) and Comparison to Its Closest Relatives. <i>Frontiers in Plant Science</i> , 2018, 9, 462.	1.7	8
7307	Phylogenetic and CRISPR/Cas9 Studies in Deciphering the Evolutionary Trajectory and Phenotypic Impacts of Rice <i>ERECTA</i> Genes. <i>Frontiers in Plant Science</i> , 2018, 9, 473.	1.7	33
7308	The Complete Plastome Sequences of Seven Species in <i>Gentiana</i> sect. <i>Kudoa</i> (Gentianaceae): Insights Into Plastid Gene Loss and Molecular Evolution. <i>Frontiers in Plant Science</i> , 2018, 9, 493.	1.7	45
7309	Combined Analyses of Chloroplast DNA Haplotypes and Microsatellite Markers Reveal New Insights Into the Origin and Dissemination Route of Cultivated Pears Native to East Asia. <i>Frontiers in Plant Science</i> , 2018, 9, 591.	1.7	18
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7312	The variome of pneumococcal virulence factors and regulators. <i>BMC Genomics</i> , 2018, 19, 10.	1.2	32
7313	Comparative analysis of plant MKK gene family reveals novel expansion mechanism of the members and sheds new light on functional conservation. <i>BMC Genomics</i> , 2018, 19, 407.	1.2	29
7314	Over a Thousand Years of Evolutionary History of Domestic Geese from Russian Archaeological Sites, Analysed Using Ancient DNA. <i>Genes</i> , 2018, 9, 367.	1.0	16
7315	Mitochondrial DNA analyses of <i>Donax trunculus</i> (Mollusca: Bivalvia) population structure in the Iberian Peninsula, a bivalve with high commercial importance. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2018, 28, 1139-1152.	0.9	9
7316	Multilocus phylogeny and species delimitation within the <i>philippinensis</i> group (Chiroptera: Tj ETQq1 1 0.784314 rgBT _g /Overlo	0.7	8
7317	Molecular characterization of Moenkhausia (Pisces: Characiformes) populations with different lateral line developmental levels. <i>Anais Da Academia Brasileira De Ciencias</i> , 2018, 90, 2815-2825.	0.3	3
7318	Conservation genetics of the threatened catfish <i>Conorhynchos conirostris</i> (Siluriformes: incertae Tj ETQq1 1 0.784314 rgBT _g /Overlo	0.8	3
7319	Genetic diversity and geographic distribution of the <i>Bemisia tabaci</i> species complex in Bangladesh. <i>Acta Tropica</i> , 2018, 187, 28-36.	0.9	13
7320	Evidence of the genetic diversity and clonal population structure of <i>Oenococcus oeni</i> strains isolated from different wine-making regions of China. <i>Journal of Microbiology</i> , 2018, 56, 556-564.	1.3	4
7321	Genome-wide Characterization of Brassica rapa Genes Encoding Serine/arginine-rich Proteins: Expression and Alternative Splicing Events by Abiotic Stresses. <i>Journal of Plant Biology</i> , 2018, 61, 198-209.	0.9	14
7322	Remarkable sequence polymorphisms in 18S rDNA of <i>Pleuronichthys cornutus</i> (Pleuronectiformes: Tj ETQq1 1 0.784314 rgBT _g /Overlo	1.0	6
7323	A complex virome unveiled by deep sequencing analysis of RNAs from a French Pinot Noir grapevine exhibiting strong leafroll symptoms.. <i>Archives of Virology</i> , 2018, 163, 2937-2946.	0.9	38
7324	The genetic structure of <i>Squalidus multimaculatus</i> revealing the historical pattern of serial colonization on the tip of East Asian continent. <i>Scientific Reports</i> , 2018, 8, 10629.	1.6	5
7325	Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry identification of <i>Moraxella bovoculi</i> and <i>Moraxella bovis</i> isolates from cattle. <i>Journal of Veterinary Diagnostic Investigation</i> , 2018, 30, 739-742.	0.5	13
7326	Landscape genomics: natural selection drives the evolution of mitogenome in penguins. <i>BMC Genomics</i> , 2018, 19, 53.	1.2	27
7327	Phylogeographic analyses of the pampas cat (<i>Leopardus colocola</i> ; Carnivora, Felidae) reveal a complex demographic history. <i>Genetics and Molecular Biology</i> , 2018, 41, 273-287.	0.6	15
7329	Evaluation of the <i>infB</i> and <i>rpsB</i> gene fragments as genetic markers intended for identification and phylogenetic analysis of particular representatives of the order Lactobacillales. <i>Archives of Microbiology</i> , 2018, 200, 1427-1437.	1.0	7

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7330	A genome-wide diversity study of grapevine rupestris stem pitting-associated virus. Archives of Virology, 2018, 163, 3105-3111.	0.9	29
7331	Ecology can inform genetics: Disassortative mating contributes to MHC polymorphism in Leach's storm-petrels (<i>Oceanodroma leucorhoa</i>). Molecular Ecology, 2018, 27, 3371-3385.	2.0	37
7332	Multilocus sequence typing of clinical <i>Borrelia afzelii</i> strains: population structure and differential ability to disseminate in humans. Parasites and Vectors, 2018, 11, 374.	1.0	4
7333	First Molecular Identification and Phylogeny of Moroccan <i>Anopheles sergentii</i> (Diptera: Culicidae) Based on Second Internal Transcribed Spacer (ITS2) and Cytochrome c Oxidase I (COI) Sequences. Vector-Borne and Zoonotic Diseases, 2018, 18, 479-484.	0.6	3
7334	Small-scale spatial variation in infection risk shapes the evolution of a <i>Borrelia</i> resistance gene in wild rodents. Molecular Ecology, 2018, 27, 3515-3524.	2.0	17
7335	Variation in intronic microsatellites and exon 2 of the <i>Plasmodium falciparum</i> chloroquine resistance transporter gene during modification of artemisinin combination therapy in Thailand. Infection, Genetics and Evolution, 2018, 65, 35-42.	1.0	1
7336	High Level of Identity of Calreticulin Gene Sequences of <i>Ixodes persulcatus</i> and <i>Ixodes pavlovskyi</i> Ticks. Journal of Parasitology, 2018, 104, 337-341.	0.3	2
7337	Genetic diversity and population structure of Sugarcane streak mosaic virus in Yunnan province, China. Tropical Plant Pathology, 2018, 43, 514-519.	0.8	6
7338	Characterization of the APETALA2/Ethylene-responsive factor (AP2/ERF) transcription factor family in sunflower. Scientific Reports, 2018, 8, 11576.	1.6	52
7339	A preliminary assessment of genetic divergence and distribution of Malagasy cave fish in the genus <i>Typhleotris</i> (Teleostei: Milyeringidae). Zootaxa, 2018, 4378, 367-376.	0.2	5
7340	Phylogeography and genetics of the globally invasive snail <i>Physa acuta</i> Draparnaud 1805, and its potential to serve as an intermediate host to larval digenetic trematodes. BMC Evolutionary Biology, 2018, 18, 103.	3.2	54
7341	The first next-generation sequencing approach to the mitochondrial phylogeny of African monogenean parasites (Platyhelminthes: Gyrodactylidae and Dactylogyridae). BMC Genomics, 2018, 19, 520.	1.2	36
7342	Integrative analysis of chromosome banding, telomere localization and molecular genetics in the highly variable <i>Ctenomys</i> of the Corrientes group (Rodentia; Ctenomyidae). Genetica, 2018, 146, 403-414.	0.5	6
7343	Evolution and diversification of the plant gibberellin receptor GID1. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7844-E7853.	3.3	51
7344	Comparative Genomic Analysis of 130 Bacteriophages Infecting Bacteria in the Genus <i>Pseudomonas</i> . Frontiers in Microbiology, 2018, 9, 1456.	1.5	20
7345	Genetic and Historical Colonization Analyses of an Endemic Savanna Tree, <i>Qualea grandiflora</i> , Reveal Ancient Connections Between Amazonian Savannas and Cerrado Core. Frontiers in Plant Science, 2018, 9, 981.	1.7	31
7346	Genetic Pattern and Demographic History of <i>Salminus brasiliensis</i> : Population Expansion in the Pantanal Region during the Pleistocene. Frontiers in Genetics, 2018, 9, 1.	1.1	208
7347	Identifying Potential <i>Plasmodium vivax</i> Sporozoite Stage Vaccine Candidates: An Analysis of Genetic Diversity and Natural Selection. Frontiers in Genetics, 2018, 9, 10.	1.1	15

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7349	Little Divergence Among Mitochondrial Lineages of <i>Prochilodus</i> (Teleostei, Characiformes). <i>Frontiers in Genetics</i> , 2018, 9, 107.	1.1	22
7350	Phylogeography of <i>Parasyncalathium souliei</i> (Asteraceae) and Its Potential Application in Delimiting Phylogeoregions in the Qinghai-Tibet Plateau (QTP)-Hengduan Mountains (HDM) Hotspot. <i>Frontiers in Genetics</i> , 2018, 9, 171.	1.1	16
7351	Evolutionary Pattern and Large-Scale Architecture of Mutation Networks of 2009 A (H1N1) Influenza A Virus. <i>Frontiers in Genetics</i> , 2018, 9, 204.	1.1	2
7352	Whole-Genome Resequencing of Red Junglefowl and Indigenous Village Chicken Reveal New Insights on the Genome Dynamics of the Species. <i>Frontiers in Genetics</i> , 2018, 9, 264.	1.1	84
7353	Dolphins, Love and Enchantment: Tracing the Use of Cetacean Products in Brazil. <i>Frontiers in Marine Science</i> , 2018, 5, .	1.2	9
7354	Morpho-Molecular Characterization of Two <i>Ampelomyces</i> spp. (Pleosporales) Strains Mycoparasites of Powdery Mildew of <i>Hevea brasiliensis</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 12.	1.5	42
7355	A Novel Hypovirus Species From Xylariaceae Fungi Infecting Avocado. <i>Frontiers in Microbiology</i> , 2018, 9, 778.	1.5	30
7356	Virulence Gene Sequencing Highlights Similarities and Differences in Sequences in <i>Listeria monocytogenes</i> Serotype 1/2a and 4b Strains of Clinical and Food Origin From 3 Different Geographic Locations. <i>Frontiers in Microbiology</i> , 2018, 9, 1103.	1.5	37
7357	Analysis of <i>Leuconostoc citreum</i> strains using multilocus sequence typing. <i>Food Science and Biotechnology</i> , 2018, 27, 1755-1760.	1.2	7
7358	Evolutionary Dynamics of the W Chromosome in Caenophidian Snakes. <i>Genes</i> , 2018, 9, 5.	1.0	39
7359	Pyrethroid Resistance in the Major Malaria Vector <i>Anopheles funestus</i> is Exacerbated by Overexpression and Overactivity of the P450 CYP6AA1 Across Africa. <i>Genes</i> , 2018, 9, 140.	1.0	29
7360	Full Mitogenomes in the Critically Endangered <i>Kärköp</i> Reveal Major Post-Glacial and Anthropogenic Effects on Neutral Genetic Diversity. <i>Genes</i> , 2018, 9, 220.	1.0	24
7361	Genome Wide Identification, Evolutionary, and Expression Analysis of VQ Genes from Two <i>Pyrus</i> Species. <i>Genes</i> , 2018, 9, 224.	1.0	16
7362	Genome-Wide Identification and Expression Profiling Analysis of the Xyloglucan Endotransglucosylase/Hydrolase Gene Family in Tobacco (<i>Nicotiana tabacum</i> L.). <i>Genes</i> , 2018, 9, 273.	1.0	47
7363	The Complete Mitochondrial Genome of <i>Glyptothorax macromaculatus</i> Provides a Well-Resolved Molecular Phylogeny of the Chinese Sisorid Catfishes. <i>Genes</i> , 2018, 9, 282.	1.0	12
7364	Genetic Diversity in the UV Sex Chromosomes of the Brown Alga <i>Ectocarpus</i> . <i>Genes</i> , 2018, 9, 286.	1.0	18
7365	Species identification of horse flies (Diptera: Tabanidae) in Thailand using DNA barcoding. <i>Veterinary Parasitology</i> , 2018, 259, 35-43.	0.7	19

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7366	Isolation drives increased diversification rates in freshwater amphipods. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 746-757.	1.2	17
7367	Genomic evaluations of <i>Wolbachia</i> and mtDNA in the population of coconut hispine beetle, <i>Brontispa longissima</i> (Coleoptera: Chrysomelidae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 1000-1009.	1.2	18
7368	Taxonomic changes and description of two new species for the <i>Phyllodactylus lanei</i> complex (Gekkota: Phyllodactylidae) in Mexico. <i>Zootaxa</i> , 2018, 4407, 151-190.	0.2	11
7369	Genetic diversity, phylogeography and molecular clock of the <i>Lutzomyia longipalpis</i> complex (Diptera: Tj ETQq1 1 0,784314 rgBT /Over 1.3 28	1.3	28
7370	Molecular evolution of DNMT1 in vertebrates: Duplications in marsupials followed by positive selection. <i>PLoS ONE</i> , 2018, 13, e0195162.	1.1	14
7371	Comparative mitochondrial genomic analyses of three chemosynthetic vesicomylid clams from deep-sea habitats. <i>Ecology and Evolution</i> , 2018, 8, 7261-7272.	0.8	5
7372	Variation in lipid synthesis, but genetic homogeneity, among <i>Leptopilina</i> parasitic wasp populations. <i>Ecology and Evolution</i> , 2018, 8, 7355-7364.	0.8	12
7373	Genetic diversity of the toll-like receptor 2 (TLR2) in hare (<i>Lepus capensis</i>) populations from Tunisia. <i>Comptes Rendus - Biologies</i> , 2018, 341, 315-324.	0.1	3
7374	Plastome organization, genome-based phylogeny and evolution of plastid genes in Podophylloideae (Berberidaceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 978-987.	1.2	44
7375	Incidence, distribution and limited genetic variability among Turkish isolates of Grapevine Pinot gris virus from different grapevine cultivars. <i>Journal of Plant Diseases and Protection</i> , 2018, 125, 469-476.	1.6	3
7376	Invasion of the assassin bug <i>Agriosphodrus dohrni</i> (Hemiptera: Reduviidae) to Japan: Source estimation inferred from mitochondrial and nuclear gene sequences. <i>International Journal of Biological Macromolecules</i> , 2018, 118, 1565-1573.	3.6	2
7377	Enzootic frog pathogen <i>Batrachochytrium dendrobatidis</i> in Asian tropics reveals high ITS haplotype diversity and low prevalence. <i>Scientific Reports</i> , 2018, 8, 10125.	1.6	14
7378	Molecular phylogeography of East Asian <i>Boea clarkeana</i> (Gesneriaceae) in relation to habitat restriction. <i>PLoS ONE</i> , 2018, 13, e0199780.	1.1	4
7379	Remarkably conserved plastid genomes of <i>Quercus</i> group <i>Cerris</i> in China: comparative and phylogenetic analyses. <i>Nordic Journal of Botany</i> , 2018, 36, e01921.	0.2	13
7380	Phylogenetic analyses of four Chinese endemic wheat landraces based on two single copy genes. <i>Cereal Research Communications</i> , 2018, 46, 191-200.	0.8	0
7381	Different Natural Selection Pressures on the <i>atpF</i> Gene in Evergreen Sclerophyllous and Deciduous Oak Species: Evidence from Comparative Analysis of the Complete Chloroplast Genome of <i>Quercus aquifolioides</i> with Other Oak Species. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1042.	1.8	57
7382	Complete Chloroplast Genome of <i>Cercis chuniana</i> (Fabaceae) with Structural and Genetic Comparison to Six Species in Caesalpinoideae. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1286.	1.8	28
7383	Genome-Wide Screening and Characterization of the Dof Gene Family in Physic Nut (<i>Jatropha curcas</i>) Tj ETQq1 1 0,784314 rgBT /Over 1.8 34	1.8	34

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7384	Comparative Analysis of the Chloroplast Genomes of the Chinese Endemic Genus <i>Urophysa</i> and Their Contribution to Chloroplast Phylogeny and Adaptive Evolution. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1847.	1.8	92
7385	Determination of Genetic Diversity in <i>Chilo partellus</i> , <i>Busseola fusca</i> , and <i>Spodoptera frugiperda</i> Infesting Sugarcane in Southern Malawi Using DNA Barcodes. <i>Insects</i> , 2018, 9, 74.	1.0	4
7386	Complete Chloroplast Genomes of <i>Papaver rhoeas</i> and <i>Papaver orientale</i> : Molecular Structures, Comparative Analysis, and Phylogenetic Analysis. <i>Molecules</i> , 2018, 23, 437.	1.7	73
7387	Coumarin Content, Morphological Variation, and Molecular Phylogenetics of <i>Melilotus</i> . <i>Molecules</i> , 2018, 23, 810.	1.7	18
7388	A Comparative Genomic Survey Provides Novel Insights into Molecular Evolution of l-Aromatic Amino Acid Decarboxylase in Vertebrates. <i>Molecules</i> , 2018, 23, 917.	1.7	7
7389	The Sucrose Synthase Gene Family in Chinese Pear (<i>Pyrus bretschneideri</i> Rehd.): Structure, Expression, and Evolution. <i>Molecules</i> , 2018, 23, 1144.	1.7	47
7390	The Late Embryogenesis Abundant Protein Family in Cassava (<i>Manihot esculenta</i> Crantz): Genome-Wide Characterization and Expression during Abiotic Stress. <i>Molecules</i> , 2018, 23, 1196.	1.7	22
7391	Full mitochondrial genome sequences reveal new insights about post-glacial expansion and regional phylogeographic structure in the Atlantic silverside (<i>Menidia menidia</i>). <i>Marine Biology</i> , 2018, 165, 1.	0.7	16
7392	Genetic diversity of <i>Pneumocystis jirovecii</i> from a cluster of cases of pneumonia in renal transplant patients: Cross-sectional study. <i>Mycoses</i> , 2018, 61, 845-852.	1.8	9
7393	Population genetic structure and evolutionary history of Bale monkeys (<i>Chlorocebus djamdjamensis</i>) in the southern Ethiopian Highlands. <i>BMC Evolutionary Biology</i> , 2018, 18, 106.	3.2	18
7394	The Application and Limitation of Universal Chloroplast Markers in Discriminating East Asian Evergreen Oaks. <i>Frontiers in Plant Science</i> , 2018, 9, 569.	1.7	21
7395	Population Genetics and Speciation of Yellow-Bellied, Red-Naped, and Red-Breasted Sapsuckers (<i>Sphyrapicus varius</i> , <i>S. nuchalis</i> , and <i>S. ruber</i>). <i>Journal of Heredity</i> , 2018, 109, 663-674.	1.0	9
7396	In silico characterisation of the two-component system regulators of <i>Streptococcus pyogenes</i> . <i>PLoS ONE</i> , 2018, 13, e0199163.	1.1	10
7397	Comparative Analysis of the Complete Chloroplast Genomes of Four <i>Aconitum</i> Medicinal Species. <i>Molecules</i> , 2018, 23, 1015.	1.7	49
7398	Population genetic structure and expansion patterns of the cotton pest <i>Adelphocoris fasciaticollis</i> . <i>Journal of Pest Science</i> , 2018, 91, 539-550.	1.9	10
7399	Pleistocene range expansions promote divergence with gene flow between migratory and sedentary populations of <i>Calothorax</i> hummingbirds. <i>Biological Journal of the Linnean Society</i> , 2018, 124, 645-667.	0.7	14
7400	Genome-Wide Assessment of Diversity and Divergence Among Extant Galapagos Giant Tortoise Species. <i>Journal of Heredity</i> , 2018, 109, 611-619.	1.0	22
7401	Grapevine virus T is relatively widespread in Slovakia and Czech Republic and genetically diverse. <i>Virus Genes</i> , 2018, 54, 737-741.	0.7	11

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7402	Haplosporidium pinnae sp. nov., a haplosporidan parasite associated with mass mortalities of the fan mussel, <i>Pinna nobilis</i> , in the Western Mediterranean Sea. <i>Journal of Invertebrate Pathology</i> , 2018, 157, 9-24.	1.5	99
7403	Variability of Some Milk-Associated Genes and Proteins in Several Breeds of Saudi Arabian Camels. <i>Protein Journal</i> , 2018, 37, 333-352.	0.7	4
7404	Natural variation in <i>Gm<scp>GBP</scp>1</i> promoter affects photoperiod control of flowering time and maturity in soybean. <i>Plant Journal</i>, 2018, 96, 147-162.</i>	2.8	45
7405	First molecular identification of an agent of diplostomiasis, <i>Diplostomum pseudospathaceum</i> (Niewiadomska 1984) in the United Kingdom and its genetic relationship with populations in Europe. <i>Acta Parasitologica</i> , 2018, 63, 444-453.	0.4	7
7406	The systematics of the amphidromous shrimp <i>Macrobrachium hobbsi</i> Nates & Villalobos, 1990 (Decapoda: Caridea: Palaemonidae) from the Mexican Pacific slope. <i>Journal of Crustacean Biology</i> , 2018, 38, 586-599.	0.3	3
7407	Phylogeography of the critically endangered neotropical annual fish, <i>Austrolebias wolterstorffi</i> (Cyprinodontiformes: Aplocheilidae): genetic and morphometric evidence of a new species complex. <i>Environmental Biology of Fishes</i> , 2018, 101, 1503-1515.	0.4	6
7408	Efficiency of RAPD, ISSR and ITS markers in detecting genetic variability among <i>Salacia</i> species sampled from the Western Ghats of Karnataka. <i>Molecular Biology Reports</i> , 2018, 45, 931-941.	1.0	3
7409	The first plastid genome of a filamentous taxon <i>Bangia</i> ™ sp. OUCPT-01 in the Bangiales. <i>Scientific Reports</i> , 2018, 8, 10688.	1.6	6
7410	Morphological and Genetic Identification of <i>Pseudo-nitzschia</i> H. Peragallo, 1900 (Bacillariophyta) from the Sea of Japan. <i>Russian Journal of Marine Biology</i> , 2018, 44, 192-201.	0.2	5
7411	Genetic differentiation in the mountainous star coral <i>Orbicella faveolata</i> around Cuba. <i>Coral Reefs</i> , 2018, 37, 1217-1227.	0.9	6
7412	Genetic variation and phylogenetic analyses reveal transmission clues of <i>Lentinula edodes</i> partitivirus 1 (LePV1) from the Chinese <i>L. edodes</i> core collection. <i>Virus Research</i> , 2018, 255, 127-132.	1.1	8
7413	Multilocus phylogeny of the zebra mussel family Dreissenidae (Mollusca: Bivalvia) reveals a fourth Neotropical genus sister to all other genera. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 1020-1033.	1.2	13
7414	An integrative approach to discovering cryptic species within the <i>Bemisia tabaci</i> whitefly species complex. <i>Scientific Reports</i> , 2018, 8, 10886.	1.6	51
7415	Entire industrial chain botanical origin authenticity control of ginseng formula granule products using simple PCR-based identification. <i>Industrial Crops and Products</i> , 2018, 123, 556-562.	2.5	3
7416	Historical biogeography and phylogeny of Cucurbita: Insights from ancestral area reconstruction and niche evolution. <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 38-54.	1.2	29
7417	Red-headed Amazon River Turtles in Venezuela and Colombia: population separation and connection along the famous route of Alexander von Humboldt. <i>Zoology</i> , 2018, 130, 67-78.	0.6	5
7418	Genomic analysis of MHC-based mate choice in the monogamous California mouse. <i>Behavioral Ecology</i> , 2018, 29, 1167-1180.	1.0	9
7419	The Complete Chloroplast Genomes of Two <i>Lancea</i> Species with Comparative Analysis. <i>Molecules</i> , 2018, 23, 602.	1.7	17

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7420	Selective constraints in cold-temperate region wild boars may defuse the effects of small effective population size on molecular evolution of mitogenomes. <i>Ecology and Evolution</i> , 2018, 8, 8102-8114.	0.8	19
7421	Bottlenecks, remoteness and admixture shape genetic variation in island populations of Atlantic and Mediterranean common kestrels <i>Falco tinnunculus</i> . <i>Journal of Avian Biology</i> , 2018, 49, e01768.	0.6	23
7422	Genetic variability of the Lessepsian migrant mussel <i>Brachidontes pharaonis</i> (Bivalvia: Mytilidae) in Tunisia. <i>African Journal of Marine Science</i> , 2018, 40, 211-217.	0.4	3
7423	High polymorphism in MHC-DRB genes in golden snub-nosed monkeys reveals balancing selection in small, isolated populations. <i>BMC Evolutionary Biology</i> , 2018, 18, 29.	3.2	18
7424	Parapatric genetic divergence among deep evolutionary lineages in the Mediterranean green crab, <i>Carcinus aestuarii</i> (Brachyura, Portunoidea, Carcinidae), accounts for a sharp phylogeographic break in the Eastern Mediterranean. <i>BMC Evolutionary Biology</i> , 2018, 18, 53.	3.2	6
7425	Malaria parasites of long-tailed macaques in Sarawak, Malaysian Borneo: a novel species and demographic and evolutionary histories. <i>BMC Evolutionary Biology</i> , 2018, 18, 49.	3.2	24
7426	Evolving in the highlands: the case of the Neotropical Lerma live-bearing <i>Poeciliopsis infans</i> (Woolman, 1894) (Cyprinodontiformes: Poeciliidae) in Central Mexico. <i>BMC Evolutionary Biology</i> , 2018, 18, 56.	3.2	12
7427	Complex evolution of the GSTM gene family involves sharing of GSTM1 deletion polymorphism in humans and chimpanzees. <i>BMC Genomics</i> , 2018, 19, 293.	1.2	12
7428	Genetic diversity and natural selection of <i>Plasmodium knowlesi</i> merozoite surface protein 1 paralog gene in Malaysia. <i>Malaria Journal</i> , 2018, 17, 115.	0.8	18
7429	Population genetics analysis of <i>Phlebotomus papatasi</i> sand flies from Egypt and Jordan based on mitochondrial cytochrome b haplotypes. <i>Parasites and Vectors</i> , 2018, 11, 214.	1.0	13
7430	Genetic analysis of <i>Aedes albopictus</i> (Diptera, Culicidae) reveals a deep divergence in the original regions. <i>Acta Tropica</i> , 2018, 185, 27-33.	0.9	4
7431	Population genetic and evolution analysis of controversial genus <i>Edwardsiella</i> by multilocus sequence typing. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 513-521.	1.2	11
7432	Taxonomy of <i>Cladonia angustiloba</i> and related species. <i>Lichenologist</i> , 2018, 50, 267-282.	0.5	15
7433	Phylogeography of Walton's Mudskipper, <i>Periophthalmus waltoni</i> Koumans, 1941 (Perciformes: Tj ETQq1 1 0.784314 rgBT / 0.2 13	0.2	13
7434	Population structure and patterns of geographic differentiation of <i>Bactrocera oleae</i> (Diptera: Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 187 Analysis, 2018, 29, 1051-1062.	0.7	6
7435	Distribution and genetic variability of alfalfa dwarf virus, a cytorhabdovirus associated with alfalfa dwarf disease in Argentina. <i>Virus Genes</i> , 2018, 54, 612-615.	0.7	16
7436	The Taxonomic Status and Intraspecific Differentiation of the Black Sea Horse Mackerel, <i>Trachurus mediterraneus ponticus</i> (Alev, 1956) (Carangidae). <i>Russian Journal of Marine Biology</i> , 2018, 44, 112-121.	0.2	2
7437	Herpetofauna of Cay Sal Bank, Bahamas and Phylogenetic Relationships of <i>Anolis fairchildi</i> , <i>Anolis sagrei</i> , and <i>Tropidophis curtus</i> from the Region. <i>Breviora</i> , 2018, 560, 1.	0.2	1

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7438	<i>Ommatissus lybicus</i> (Hemiptera: Tropiduchidae), an economically important pest of date palm (Arecaceae) with highly divergent populations. <i>Canadian Entomologist</i> , 2018, 150, 378-392.	0.4	8
7439	The genus <i>Xanthogramma</i> Schiner, 1861 (Diptera: Syrphidae) in southeastern Europe, with descriptions of two new species. <i>Canadian Entomologist</i> , 2018, 150, 440-464.	0.4	11
7440	Molecular identification of temperate Cricetidae and Muridae rodent species using fecal samples collected in a natural habitat. <i>Mammal Research</i> , 2018, 63, 379-385.	0.6	3
7441	Diversity of <i>AvrE</i> and <i>AvrSm</i> effector genes in Polish and Norwegian populations of <i>Phytophthora infestans</i> . <i>Plant Pathology</i> , 2018, 67, 1792-1802.	1.2	9
7442	Strong genetic subdivision in <i>Leptobranchium hendricksoni</i> (Anura: Megophryidae) in Southeast Asia. <i>Amphibia - Reptilia</i> , 2018, 39, 99-111.	0.1	0
7443	Allele phasing is critical to revealing a shared allopolyploid origin of <i>Medicago arborea</i> and <i>M. strasseri</i> (Fabaceae). <i>BMC Evolutionary Biology</i> , 2018, 18, 9.	3.2	34
7444	Association between sequence variants in panicle development genes and the number of spikelets per panicle in rice. <i>BMC Genetics</i> , 2018, 19, 5.	2.7	11
7445	Molecular analysis of carnivore <i>Protoparvovirus</i> detected in white blood cells of naturally infected cats. <i>BMC Veterinary Research</i> , 2018, 14, 41.	0.7	22
7446	Global sequence diversity of the lactate dehydrogenase gene in <i>Plasmodium falciparum</i> . <i>Malaria Journal</i> , 2018, 17, 16.	0.8	13
7447	Genetic diversity of three surface protein genes in <i>Plasmodium malariae</i> from three Asian countries. <i>Malaria Journal</i> , 2018, 17, 24.	0.8	9
7448	Population genetic structure and natural selection of <i>Plasmodium falciparum</i> apical membrane antigen-1 in Myanmar isolates. <i>Malaria Journal</i> , 2018, 17, 71.	0.8	15
7449	Multiplicity and molecular epidemiology of <i>Plasmodium vivax</i> and <i>Plasmodium falciparum</i> infections in East Africa. <i>Malaria Journal</i> , 2018, 17, 185.	0.8	30
7450	Computational analysis of envelope glycoproteins from diverse geographical isolates of bovine leukemia virus identifies highly conserved peptide motifs. <i>Retrovirology</i> , 2018, 15, 2.	0.9	10
7451	Genotype and biotype of invasive <i>Anopheles stephensi</i> in Mannar Island of Sri Lanka. <i>Parasites and Vectors</i> , 2018, 11, 3.	1.0	31
7452	Size and sequence polymorphisms in the glutamate-rich protein gene of the human malaria parasite <i>Plasmodium falciparum</i> in Thailand. <i>Parasites and Vectors</i> , 2018, 11, 49.	1.0	3
7453	Chloroplast genome analyses and genomic resource development for epilithic sister genera <i>Oresitrophe</i> and <i>Mukdenia</i> (Saxifragaceae), using genome skimming data. <i>BMC Genomics</i> , 2018, 19, 235.	1.2	106
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7466	Cross-species analysis of apical asparagine-rich protein of <i>Plasmodium vivax</i> and <i>Plasmodium knowlesi</i> . <i>Scientific Reports</i> , 2018, 8, 5781.	1.6	26
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7469	Phylogenomic and Comparative Analyses of Complete Plastomes of <i>Croomia</i> and <i>Stemona</i> (Stemonaceae). <i>International Journal of Molecular Sciences</i> , 2018, 19, 2383.	1.8	30
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7473	The evolutionary dynamics of H1N1/pdm2009 in India. <i>Infection, Genetics and Evolution</i> , 2018, 65, 276-282.	1.0	13

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7475	Genetic and climatic approaches reveal effects of Pleistocene refugia and climatic stability in an old giant of the Neotropical Dry Forest. <i>Biological Journal of the Linnean Society</i> , 2018, 125, 401-420.	0.7	26
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7507	Molecular identification of <i>Ascaris lumbricoides</i> and <i>Ascaris suum</i> recovered from humans and pigs in Thailand, Lao PDR, and Myanmar. <i>Parasitology Research</i> , 2018, 117, 2427-2436.	0.6	25
7508	Accurate authentication of <i>Dendrobium officinale</i> and its closely related species by comparative analysis of complete plastomes. <i>Acta Pharmaceutica Sinica B</i> , 2018, 8, 969-980.	5.7	52
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7524	Expansion and evolutionary patterns of GDSL-type esterases/lipases in Rosaceae genomes. <i>Functional and Integrative Genomics</i> , 2018, 18, 673-684.	1.4	37
7525	Using molecular markers to investigate genetic diversity, mating system and gene flow of Neotropical trees. <i>Revista Brasileira De Botanica</i> , 2018, 41, 481-496.	0.5	20
7526	Molecular heterogeneity of <i>Rhipicephalus sanguineus sensu lato</i> and screening for <i>Ehrlichia canis</i> in mainland Portugal. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 1383-1390.	1.1	10
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7531	Uneven recombination rate and linkage disequilibrium across a reference SNP map for common bean (<i>Phaseolus vulgaris</i> L.). <i>PLoS ONE</i> , 2018, 13, e0189597.	1.1	108
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7538	Complete chloroplast genome of seven <i>Fritillaria</i> species, variable DNA markers identification and phylogenetic relationships within the genus. <i>PLoS ONE</i> , 2018, 13, e0194613.	1.1	38
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7544	Morphological and molecular evidence for a new shrimp species, <i>Atyaephyra vladoi</i> sp. nov. (Decapoda), demographic history. <i>Zoologischer Anzeiger</i> , 2018, 275, 66-79.	0.4	11
7545	Connecting Amazonian, Cerrado, and Atlantic forest histories: Paraphyly, old divergences, and modern population dynamics in tyrant-manakins (<i>Neopelma/Tyrannetes</i> , Aves: Pipridae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 696-705.	1.2	26

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7550	Signatures of balancing selection in toll-like receptor (TLRs) genes – novel insights from a free-living rodent. <i>Scientific Reports</i> , 2018, 8, 8361.	1.6	38
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7557	Genetic structure and dispersal patterns in <i>Limnoria nagatai</i> (Limnoriidae, Isopoda) dwelling in non-buoyant kelps, <i>Eisenia bicyclis</i> and <i>E. arborea</i> , in Japan. <i>PLoS ONE</i> , 2018, 13, e0198451.	1.1	6
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7575	Algorithms for Graph and Network Analysis: Graph Indexes/Descriptors. , 2019, , 81-88.		0
7576	Evolution of MHC class I genes in Eurasian badgers, genus <i>Meles</i> (Carnivora, Mustelidae). <i>Heredity</i> , 2019, 122, 205-218.	1.2	9
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7578	A comparative evolutionary study reveals radically different scales of genetic structuring within two atyid shrimp species (Crustacea: Decapoda: Atyidae). <i>Zoological Journal of the Linnean Society</i> , 2019, 186, 200-212.	1.0	5
7579	Phylogenetic analysis and genetic structure of the seahorse, <i>Hippocampus fuscus</i> from the Arabian and Red Sea based on mitochondrial DNA sequences. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2019, 30, 165-171.	0.7	7
7580	European bridgehead effect in the worldwide invasion of the obscure mealybug. <i>Biological Invasions</i> , 2019, 21, 123-136.	1.2	8
7581	Lineage diversity and reproductive modes of the <i>Daphnia pulex</i> group in Chinese lakes and reservoirs. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 424-433.	1.2	26

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7584	Signals of local adaptation across an environmental gradient among highly connected populations of the Dead Sea Sparrow <i>Passer moabiticus</i> in Israel. <i>Ibis</i> , 2019, 161, 619-631.	1.0	4
7585	Complex patterns of genetic and phenotypic divergence in populations of the Lake Malawi cichlid <i>Maylandia zebra</i> . <i>Hydrobiologia</i> , 2019, 832, 135-151.	1.0	1
7586	Molecular edge effects in the Endangered golden-brown mouse lemur <i>Microcebus ravelobensis</i> . <i>Oryx</i> , 2019, 53, 716-726.	0.5	10
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7590	Genetic differentiation of the Malawi blue crab reflects Pleistocene desiccation of Lake Malawi (Brachyura, Potamonautidae: Potamonautes lirrangensis (Rathbun, 1904)). <i>Hydrobiologia</i> , 2019, 843, 1-11.	1.0	0
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7595	Population genetic studies of genus <i>Dicentrarchus</i> reveal loss of genetic diversity in Egyptian waters. <i>Regional Studies in Marine Science</i> , 2019, 31, 100783.	0.4	2
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7597	Inference from the analysis of genetic structure of <i>Helicobacter pylori</i> strains isolates from two paediatric patients with recurrent infection. <i>BMC Microbiology</i> , 2019, 19, 184.	1.3	12
7598	Trans-Species Polymorphism in Mitochondrial Genome of Camarodont Sea Urchins. <i>Genes</i> , 2019, 10, 592.	1.0	0
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7610	Contrasting selective patterns across the segmented genome of bluetongue virus in a global reassortment hotspot. Virus Evolution, 2019, 5, vez027.	2.2	17
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7616	Living on the edge: Assessing the diversity of South African <i>Pocillopora</i> on the margins of the Southwestern Indian Ocean. PLoS ONE, 2019, 14, e0220477.	1.1	4
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7619	Phylogeographic Analysis and Genetic Structure of an Endemic Sino-Japanese Disjunctive Genus <i>Diabelia</i> (Caprifoliaceae). <i>Frontiers in Plant Science</i> , 2019, 10, 913.	1.7	12
7620	Gradual Distance Dispersal Shapes the Genetic Structure in an Alpine Grasshopper. <i>Genes</i> , 2019, 10, 590.	1.0	4
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7624	Population Genetics of <i>Bactrocera minax</i> (Diptera: Tephritidae) in China Based on <i>nad4</i> Gene Sequence. <i>Insects</i> , 2019, 10, 236.	1.0	0
7625	Complete mitochondrial genome of <i>Stichaeus nozawae</i> Jordan & Snyder 1902 (Zoarcales: Tj ETQq1 1 0.784314 rgBT /Over	0.2	2
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7640	Two Y-chromosome-encoded genes determine sex in kiwifruit. <i>Nature Plants</i> , 2019, 5, 801-809.	4.7	148
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7653	Pan African phylogeography and palaeodistribution of rousettine fruit bats: Ecogeographic correlation with Pleistocene climate vegetation cycles. <i>Journal of Biogeography</i> , 2019, 46, 2336-2349.	1.4	14

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7658	Genome-wide identification and expression analysis of the BURP domain-containing genes in <i>Gossypium hirsutum</i> . BMC Genomics, 2019, 20, 558.	1.2	17
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7663	Population differentiation and genetic diversity of endangered <i>Brachymystax tsinlingensis</i> Li between Yangtze River and Yellow River in China based on mtDNA. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2019, 30, 695-701.	0.7	2
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7665	Quaternary climate change and habitat preference shaped the genetic differentiation and phylogeography of <i>Rhodiola</i> sect. <i>Prainia</i> in the southern Qinghai-Tibetan Plateau. Ecology and Evolution, 2019, 9, 8305-8319.	0.8	7
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7673	Messing about on the river: the role of geographic barriers in shaping the genetic structure of Bornean small mammals in a fragmented landscape. <i>Conservation Genetics</i> , 2019, 20, 691-704.	0.8	14
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7679	Historical demography of <i>Coereba flaveola</i> on Puerto Rico. <i>Auk</i> , 2019, 136, .	0.7	0
7680	Molecular identification and phylogenetic relationships of clinical <i>Nocardia</i> isolates. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 1755-1766.	0.7	10
7681	Genetic diversity of two mitochondrial DNA genes in <i>Spirometra erinaceieuropaei</i> (Cestoda). <i>Trends in Parasitology</i> , 2019, 35, 764-777.	0.6	13
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7707	Phylogeography suggest the Yili Valley being the glacial refuge of the genus <i>Ixiolirion</i> (Amaryllidaceae) in China. Systematics and Biodiversity, 2019, 17, 385-401.	0.5	6

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7709	Genome-Wide Identification, Characterization, and Expression Analysis of the NAC Transcription Factor in <i>Chenopodium quinoa</i> . <i>Genes</i> , 2019, 10, 500.	1.0	15
7710	Systematics, biogeography, and evolution of <i>Pristurus minimus</i> (Squamata, Sphaerodactylidae) with the discovery of the smallest Arabian vertebrate. <i>Systematics and Biodiversity</i> , 2019, 17, 349-366.	0.5	7
7711	Research Article Genetic assessment of a breeding population of black rhinoceros in Kenya using mitochondrial DNA D-loop sequencing. <i>Genetics and Molecular Research</i> , 2019, 18, .	0.3	1
7712	Conservation of genetic uniqueness in remaining populations of red squirrels (<i>Sciurus</i>). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 Td</i>	0.8	9
7713	Phylogeography of the endangered sand dune whiptail lizard <i>Glucomastix aabaetensis</i> (Dias, Rocha). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 0.2 8</i>	0.2	3
7714	Genetic, phenotypic and ecological differentiation suggests incipient speciation in two <i>Charadrius</i> plovers along the Chinese coast. <i>BMC Evolutionary Biology</i> , 2019, 19, 135.	3.2	30
7715	Multi-authority Attribute-Based Encryption with User Revocation and Outsourcing Decryption. <i>Journal of Physics: Conference Series</i> , 2019, 1302, 022026.	0.3	2
7716	Contribution of rice variety renewal and agronomic innovations to yield improvement and greenhouse gas mitigation in China. <i>Environmental Research Letters</i> , 2019, 14, 114020.	2.2	37
7717	Genetic variation and cryptic lineage diversity of the Nigerian red-headed rock agama <i>Agama agama</i> associate with eco-geographic zones. <i>Environmental Epigenetics</i> , 2019, 65, 713-724.	0.9	2
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7723	Land Invasion by the Mudskipper, <i>Periophthalmodon septemradiatus</i> , in Fresh and Saline Waters of the Mekong River. <i>Scientific Reports</i> , 2019, 9, 14227.	1.6	10
7724	Mitochondrial DNA diversity and origin of indigenous pigs in South China and their contribution to western modern pig breeds. <i>Journal of Integrative Agriculture</i> , 2019, 18, 2338-2350.	1.7	14
7725	Characterization of the complete mitochondrial genomes of two species of the genus <i>Aphaena</i> Guâ€rin-Mâ€neville (Hemiptera: Fulgoridae) and its phylogenetic implications. <i>International Journal of Biological Macromolecules</i> , 2019, 141, 29-40.	3.6	20

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7731	Efficient Identification of <i>Pulsatilla</i> (Ranunculaceae) Using DNA Barcodes and Micro-Morphological Characters. <i>Frontiers in Plant Science</i> , 2019, 10, 1196.	1.7	18
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7735	Genetic diversity and phylogenetic relationships in feral pig populations from Argentina. <i>Mammalian Biology</i> , 2019, 99, 27-36.	0.8	5
7736	Morphological and genetic characterizations of <i>Avitellina</i> tapeworms from domestic ruminants in Senegal: An evidence of specificity among sheep and cattle host. <i>Veterinary Parasitology: Regional Studies and Reports</i> , 2019, 18, 100337.	0.3	0
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7741	Genetic Diversity and <i>Wolbachia</i> Infection Patterns in a Globally Distributed Invasive Ant. <i>Frontiers in Genetics</i> , 2019, 10, 838.	1.1	25
7742	Mitochondrial DNA Mutations and Rheumatic Heart Diseases. <i>Journal of Cardiovascular Development and Disease</i> , 2019, 6, 36.	0.8	1
7743	The complete mitochondrial genomes of two vent squat lobsters, <i>Munidopsis lauensis</i> and <i>M. verrilli</i> : Novel gene arrangements and phylogenetic implications. <i>Ecology and Evolution</i> , 2019, 9, 12390-12407.	0.8	16

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7745	The first complete mitochondrial genome of the Indian Tent Turtle, <i>Pangshura tentoria</i> (Testudines: Geoemydidae): Characterization and comparative analysis. <i>Ecology and Evolution</i> , 2019, 9, 10854-10868.	0.8	8
7746	Population genetic structures of two ecologically distinct species <i>Betula platyphylla</i> and <i>B. Aermanii</i> inferred based on nuclear and chloroplast DNA markers. <i>Ecology and Evolution</i> , 2019, 9, 11406-11419.	0.8	1
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7749	Genetic Diversity and Demographic History of an Upper Hill Dipterocarp (<i>Shorea platyclados</i>): Implications for Conservation. <i>Journal of Heredity</i> , 2019, 110, 844-856.	1.0	5
7750	Integrated Heat and Electricity Coordinated Dispatch Considering Multiple Time-Scale Flexibility of CHP Based on Thermal Energy Storage of DHS. <i>IOP Conference Series: Earth and Environmental Science</i> , 2019, 252, 032208.	0.2	0
7751	Patterns of genetic diversity in African forest elephants living in a human-modified landscape in southwest Gabon. <i>Conservation Science and Practice</i> , 2019, 1, e76.	0.9	6
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7753	Knowledge Sharing and Co-Opetition: Turning Absorptive Capacity into Effectiveness in Consumer Electronics Industries. <i>Sustainability</i> , 2019, 11, 4694.	1.6	14
7754	Comparison of chloroplast genomes of <i>Gynura</i> species: sequence variation, genome rearrangement and divergence studies. <i>BMC Genomics</i> , 2019, 20, 791.	1.2	8
7755	Population genetics of <i>Aedes albopictus</i> (Diptera: Culicidae) in its native range in Lao People's Democratic Republic. <i>Parasites and Vectors</i> , 2019, 12, 477.	1.0	11
7756	Distribution and genetic diversity of <i>Beauveria</i> species at different soil depths in natural and agricultural ecosystems. <i>Mycological Progress</i> , 2019, 18, 1241-1252.	0.5	3
7757	Genetic diversification of <i>Panstrongylus geniculatus</i> (Reduviidae: Triatominae) in northern South America. <i>PLoS ONE</i> , 2019, 14, e0223963.	1.1	11
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7760	Genetic Differentiation and Origin of Naturalized Rainbow Trout Populations From Southern Chile, Revealed by the mtDNA Control Region Marker. <i>Frontiers in Genetics</i> , 2019, 10, 1212.	1.1	5
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7768	Genetic admixture despite ecological segregation in a North African sparrow hybrid zone (Aves). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50</i>	0.8	8
7769	Does geography, evolutionary history or ecology drive ploidy and genome size variation in the <i>Minuartia verna</i> group (Caryophyllaceae) across Europe?. <i>Plant Systematics and Evolution</i> , 2019, 305, 1019-1040.	0.3	5
7770	Fixation of genetic variation and optimization of gene expression: The speed of evolution in isolated lizard populations undergoing Reverse Island Syndrome. <i>PLoS ONE</i> , 2019, 14, e0224607.	1.1	10
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7772	Designation of flyways and genetic structure of Woodpigeon <i>Columba palumbus</i> in Europe and Morocco. <i>European Journal of Wildlife Research</i> , 2019, 65, 1.	0.7	4
7773	Genetic structure of <i>Mycoplasma ovipneumoniae</i> informs pathogen spillover dynamics between domestic and wild Caprinae in the western United States. <i>Scientific Reports</i> , 2019, 9, 15318.	1.6	20
7774	Complete chloroplast genomes of all six <i>Hosta</i> species occurring in Korea: molecular structures, comparative, and phylogenetic analyses. <i>BMC Genomics</i> , 2019, 20, 833.	1.2	36
7775	Phylogeographical Structure of <i>Liquidambar formosana</i> Hance Revealed by Chloroplast Phylogeography and Species Distribution Models. <i>Forests</i> , 2019, 10, 858.	0.9	4
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7777	Sow Thistle Chloroplast Genomes: Insights into the Plastome Evolution and Relationship of Two Weedy Species, <i>Sonchus asper</i> and <i>Sonchus oleraceus</i> (Asteraceae). <i>Genes</i> , 2019, 10, 881.	1.0	19
7778	Assessing cross-species transmission of hemoplasmas at the wild-domestic felid interface in Chile using genetic and landscape variables analysis. <i>Scientific Reports</i> , 2019, 9, 16816.	1.6	22
7779	Contrasting molecular diversity and demography patterns in two intertidal amphipod crustaceans reflect Atlantification of High Arctic. <i>Marine Biology</i> , 2019, 166, 1.	0.7	14

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7781	Conservation of freshwater wildlife in Hong Kong: A genetic perspective. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2019, 29, 2204-2218.	0.9	5
7782	Population structure, connectivity, and demographic history of an apex marine predator, the bull shark <i>Carcharhinus leucas</i> . <i>Ecology and Evolution</i> , 2019, 9, 12980-13000.	0.8	18
7783	Factors of Kinetics Processes in Lithium-Sulfur Reactions. <i>Energy Technology</i> , 2019, 7, 1900574.	1.8	18
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7786	Morphological and molecular divergence of Indian hill trout, <i>Barilius bendelisis</i> (Hamilton, 1822) stocks from different Rivers in Indo-Burma biodiversity hotspot: Does river altitude and Dam play a role?. <i>Journal of Applied Ichthyology</i> , 2019, 35, 1242-1248.	0.3	2
7787	Genomics detects population structure within and between ocean basins in a circumpolar seabird: The white-chinned petrel. <i>Molecular Ecology</i> , 2019, 28, 4552-4572.	2.0	21
7788	Mixing Genetically and Morphologically Distinct Populations in Translocations: Asymmetrical Introgression in A Newly Established Population of the Boodie (<i>Bettongia lesueur</i>). <i>Genes</i> , 2019, 10, 729.	1.0	25
7789	Phenotypically and Genotypically Heterogeneous Strains of <i>Pseudomonas syringae</i> Associated With Alfalfa Leaf Spot Disease in Iran. <i>Plant Disease</i> , 2019, 103, 3199-3208.	0.7	2
7790	Genetic diversity of <i>Cedrela fissilis</i> (Meliaceae) in the Brazilian Atlantic Forest reveals a complex phylogeographic history driven by Quaternary climatic fluctuations. <i>Journal of Systematics and Evolution</i> , 2019, 57, 655-669.	1.6	8
7791	Effects of dispersal barriers and geographic distance on the genetic structure of a narrowly distributed frog in a spatially structured landscape. <i>Journal of Zoology</i> , 2019, 309, 295-309.	0.8	4
7792	<i>Aeschynomene indica</i> -Nodulating Rhizobia Lacking Nod Factor Synthesis Genes: Diversity and Evolution in Shandong Peninsula, China. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	7
7793	Phylogenetics, patterns of genetic variation and population dynamics of <i>Trypanosoma terrestris</i> support both coevolution and ecological host-fitting as processes driving trypanosome evolution. <i>Parasites and Vectors</i> , 2019, 12, 473.	1.0	12
7794	The impact of genetic diversity on the accuracy of DNA barcoding to identify species: A study on the genus <i>Phellodendron</i> . <i>Ecology and Evolution</i> , 2019, 9, 10723-10733.	0.8	7
7795	The complete chloroplast genomes of two species in threatened monocot genus <i>Caldesia</i> in China. <i>Genetica</i> , 2019, 147, 381-390.	0.5	4
7796	Genetic diversity and structure of the binturong <i>Arctictis binturong</i> (Carnivora: Viverridae) – status of the elusive Palawan binturong and implications for conservation. <i>Zoological Journal of the Linnean Society</i> , 2019, , .	1.0	2
7797	Genome-Wide Mining and Identification of Protein Kinase Gene Family Impacts Salinity Stress Tolerance in Highly Dense Genetic Map Developed from Interspecific Cross between <i>G. hirsutum</i> L. and <i>G. darwinii</i> G. Watt. <i>Agronomy</i> , 2019, 9, 560.	1.3	21

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7799	The G119S Acetylcholinesterase (Ace-1) Target Site Mutation Confers Carbamate Resistance in the Major Malaria Vector <i>Anopheles gambiae</i> from Cameroon: A Challenge for the Coming IRS Implementation. <i>Genes</i> , 2019, 10, 790.	1.0	31
7800	Genetic analysis of populations of brown trout (<i>Salmo trutta</i> L.) from the Romanian Carpathians. <i>Aquatic Living Resources</i> , 2019, 32, 23.	0.5	8
7801	Introduction history and population genetics of intracontinental scotch broom (<i>Cytisus</i>) Tj ETQq1 1 0.784314 r _g BT /Overlock 10 T ₅	0.9	0
7802	Effects of intragenomic polymorphism in the SSU rRNA gene on estimating marine microeukaryotic diversity: A test for ciliates using single-cell high-throughput DNA sequencing. <i>Limnology and Oceanography: Methods</i> , 2019, 17, 533-543.	1.0	22
7803	Evaluating methodologies for species delimitation: the mismatch between phenotypes and genotypes in lichenized fungi (<i>Bryoria</i> sect. <i>Implexae</i> , <i>Parmeliaceae</i>). <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2019, 42, 75-100.	1.6	44
7804	Noda-Like RNA Viruses Infecting <i>Caenorhabditis</i> Nematodes: Sympatry, Diversity, and Reassortment. <i>Journal of Virology</i> , 2019, 93, .	1.5	17
7805	Dual DNA Barcoding for the Molecular Identification of the Agents of Invasive Fungal Infections. <i>Frontiers in Microbiology</i> , 2019, 10, 1647.	1.5	40
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7807	Biogeographical history of the genus <i>Atherina</i> (Pisces: Atherinidae) in the central Eastern Atlantic. <i>Marine Biodiversity</i> , 2019, 49, 2633-2639.	0.3	0
7808	Molecular Typing Reveals High Genetic Diversity of <i>Xanthomonas translucens</i> Strains Infecting Small-Grain Cereals in Iran. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	37
7809	Genetic Variability of Three Isolated Populations of the Muya Valley Vole <i>Alexandromys mujanensis</i> Orlov et Kovalskaja, 1978 (Rodentia, Arvicolinae). <i>Russian Journal of Genetics</i> , 2019, 55, 978-992.	0.2	4
7810	Beyond balancing selection: frequent mitochondrial recombination contributes to high female frequencies in gynodioecious <i>Lobelia siphilitica</i> (Campanulaceae). <i>New Phytologist</i> , 2019, 224, 1381-1393.	3.5	6
7811	Genetic variation and survival of <i>Erysiphe necator</i> in tropical India. <i>Tropical Plant Pathology</i> , 2019, 44, 438-451.	0.8	2
7812	Do mosses really exhibit so large distribution ranges? Insights from the integrative taxonomic study of the <i>Lewinskya affinis</i> complex (Orthotrichaceae, Bryopsida). <i>Molecular Phylogenetics and Evolution</i> , 2019, 140, 106598.	1.2	23
7813	Using internal transcribed spacers 2 (ITS2) to identify seaweed species from Tomini Bay and Banten Bay. <i>IOP Conference Series: Earth and Environmental Science</i> , 2019, 278, 012017.	0.2	0
7814	Population Structure and Microevolution of Pacific Cod <i>Gadus macrocephalus</i> Based on the Analysis of the Control Region (mtDNA) Polymorphism. <i>Russian Journal of Genetics</i> , 2019, 55, 580-591.	0.2	8
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7817	Revision of the species composition and distribution of Turkish sand flies using DNA barcodes. <i>Parasites and Vectors</i> , 2019, 12, 410.	1.0	24
7818	Convergent reduction of V1R genes in subterranean rodents. <i>BMC Evolutionary Biology</i> , 2019, 19, 176.	3.2	13
7819	Global invasion genetics of two parasitic copepods infecting marine bivalves. <i>Scientific Reports</i> , 2019, 9, 12730.	1.6	5
7820	Genetic diversity of Bangladeshi native chickens based on complete sequence of mitochondrial DNA D-loop region. <i>British Poultry Science</i> , 2019, 60, 628-637.	0.8	6
7821	Phylogeographic Analyses of the East Asian Endemic Genus <i>Prinsepia</i> and the Role of the East Asian Monsoon System in Shaping a North-South Divergence Pattern in China. <i>Frontiers in Genetics</i> , 2019, 10, 128.	1.1	11
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7823	Long-term isolation at a low effective population size greatly reduced genetic diversity in Gulf of California fin whales. <i>Scientific Reports</i> , 2019, 9, 12391.	1.6	7
7824	Abundant Genetic Diversity of Yunling Cattle Based on Mitochondrial Genome. <i>Animals</i> , 2019, 9, 641.	1.0	22
7825	Distribution and phylogenetic analysis of the 3'UTR and coat protein gene of Iranian Beet black scorch virus. <i>Journal of Plant Diseases and Protection</i> , 2019, 126, 535-542.	1.6	0
7826	Phylogenetic structure of <i>Holbrookia lacerata</i> (Cope 1880) (Squamata: Phrynosomatidae): one species or two?. <i>Zootaxa</i> , 2019, 4619, zootaxa.4619.1.6.	0.2	6
7827	Genome characterization of citrus yellow vein-clearing virus: limited heterogeneity of viral genomes in Mandarivirus-infecting different citrus species. <i>3 Biotech</i> , 2019, 9, 348.	1.1	11
7828	Characterization of VQ motif-containing protein family and their expression patterns under phytohormones and abiotic stresses in melon (<i>Cucumis melo</i> L.). <i>Plant Growth Regulation</i> , 2019, 89, 273-285.	1.8	8
7829	Biogeography and population structure of predominant macrofaunal taxa (Annelida and Isopoda) in abyssal polymetallic nodule fields: implications for conservation and management. <i>Marine Biodiversity</i> , 2019, 49, 2641-2658.	0.3	28
7830	Shallow genetic divergence and distinct phenotypic differences between two Andean hummingbirds: Speciation with gene flow?. <i>Auk</i> , 2019, 136, .	0.7	18
7831	Species or population? Systematic status of <i>Vieja coatlicue</i> (Teleostei: Cichlidae). <i>Neotropical Ichthyology</i> , 2019, 17, .	0.5	3
7832	Landscape Features and Climatic Forces Shape the Genetic Structure and Evolutionary History of an Oak Species (<i>Quercus chenii</i>) in East China. <i>Frontiers in Plant Science</i> , 2019, 10, 1060.	1.7	26
7833	Multilocus approach reveals a complex evolutionary history of the invasive mile-a-minute plant, <i>Mikania micrantha</i> (Asteraceae), in its natural habitat. <i>Botanical Journal of the Linnean Society</i> , 2019, 191, 188-215.	0.8	1

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7869	Plastid phylogeography of <i>Delphinium fissum</i> subsp. <i>sordidum</i> and the series <i>Fissa</i> (Ranunculaceae) in the Iberian Peninsula: implications for conservation. <i>Botany Letters</i> , 2019, 166, 345-355.	0.7	3

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7920	Both Alpha- and Beta-Rhizobia Occupy the Root Nodules of <i>Vachellia karroo</i> in South Africa. <i>Frontiers in Microbiology</i> , 2019, 10, 1195.	1.5	25
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7933	The plastomes of <i>Astrocaryum aculeatum</i> G. Mey. and <i>A. murumuru</i> Mart. show a flip-flop recombination between two short inverted repeats. <i>Planta</i> , 2019, 250, 1229-1246.	1.6	20
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7939	Evolutionary forces at work in partitiviruses. <i>Virus Genes</i> , 2019, 55, 563-573.	0.7	14
7940	Natural Killer Cell Receptor Genes in Camels: Another Mammalian Model. <i>Frontiers in Genetics</i> , 2019, 10, 620.	1.1	12
7941	Genetic characteristics and phylogenetic relationship of <i>Parascaris</i> spp. from <i>Equus zebra</i> , <i>E. caballus</i> , and <i>E. asinus</i> . <i>Veterinary Parasitology</i> , 2019, 271, 76-79.	0.7	5
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7945	Comparative analysis of the complete chloroplast genomes of seven <i>Populus</i> species: Insights into alternative female parents of <i>Populus tomentosa</i> . <i>PLoS ONE</i> , 2019, 14, e0218455.	1.1	15
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7949	Molecular and Morphological Characterization of <i>Cysticercus tenuicollis</i> in Red Deer (<i>Cervus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502	0.4	13
7950	Genetic structure of <i>Amphioctopus fangsiao</i> (Mollusca, Cephalopoda) in Chinese waters inferred from variation in three mtDNA genes (ATPase 6, ND2, and ND5). <i>Hydrobiologia</i> , 2019, 838, 111-119.	1.0	6
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7952	Comprehensive Analysis of SnRK Gene Family and their Responses to Salt Stress in <i>Eucalyptus grandis</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 2786.	1.8	29
7953	High Plasmodium infection and multiple insecticide resistance in a major malaria vector <i>Anopheles coluzzii</i> from Sahel of Niger Republic. <i>Malaria Journal</i> , 2019, 18, 181.	0.8	15
7954	Anthropogenic Factors Driving Recent Range Expansion of the Malaria Vector <i>Anopheles stephensi</i> . <i>Frontiers in Public Health</i> , 2019, 7, 53.	1.3	52
7955	Evolutionary Analyses Reveal Diverged Patterns of SQUAMOSA Promoter Binding Protein-Like (SPL) Gene Family in <i>Oryza</i> Genus. <i>Frontiers in Plant Science</i> , 2019, 10, 565.	1.7	37
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7957	Genetic variability of an orange-shell line of the Pacific oyster <i>Crassostrea gigas</i> during artificial selection inferred from microsatellites and mitochondrial COI sequences. <i>Aquaculture</i> , 2019, 508, 159-166.	1.7	31
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7959	Wx Gene in <i>Hordeum chilense</i> : Chromosomal Location and Characterisation of the Allelic Variation in the Two Main Ecotypes of the Species. <i>Agronomy</i> , 2019, 9, 261.	1.3	10
7960	Genetic diversity and host relationships of endosymbiotic bacteria in the Asian cryptic species of <i>Bemisia tabaci</i> from Bangladesh. <i>Symbiosis</i> , 2019, 79, 75-87.	1.2	3

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7961	Rapid divergence, molecular evolution, and morphological diversification of coastal host-parasite systems from southern Brazil. <i>Parasitology</i> , 2019, 146, 1313-1332.	0.7	3
7962	A combination of metabolic resistance and high frequency of the 1014F <i>kdr</i> mutation is driving pyrethroid resistance in <i>Anopheles coluzzii</i> population from Guinea savanna of Cameroon. <i>Parasites and Vectors</i> , 2019, 12, 263.	1.0	34
7963	The popular model annelid <i>Enchytraeus albidus</i> is only one species in a complex of seashore white worms (Clitellata, Enchytraeidae). <i>Organisms Diversity and Evolution</i> , 2019, 19, 105-133.	0.7	13
7964	A comparative genomic and evolutionary analysis of circulating strains of Avian avulavirus 1 in Pakistan. <i>Molecular Genetics and Genomics</i> , 2019, 294, 1289-1309.	1.0	3
7965	Genetic diversity and host relationships of endosymbiotic bacteria in the Asian cryptic species of <i>Bemisia tabaci</i> from Bangladesh. <i>Symbiosis</i> , 2019, 79, 75.	1.2	0
7966	Prevalence, geographic distribution and phylogenetic relationships among cryptic species of <i>Plasmopara viticola</i> in grape-producing regions of Georgia and Florida, USA. <i>Journal of Phytopathology</i> , 2019, 167, 422-429.	0.5	5
7967	Natural variation in the <i>THICK TASSEL DWARF1</i> (<i>TD1</i>) gene in the regulation of maize (<i>Zea mays</i> L.) ear-related traits. <i>Breeding Science</i> , 2019, 69, 323-331.	0.9	7
7968	A novel rice grain size gene <i>OsSNB</i> was identified by genome-wide association study in natural population. <i>PLoS Genetics</i> , 2019, 15, e1008191.	1.5	72
7969	Genetic variation, demographic history and phylogeography of tire track eel, <i>Mastacembelus favus</i> (Synbranchiformes: Mastacembelidae) in Southeast Asia. <i>Hydrobiologia</i> , 2019, 838, 163-182.	1.0	3
7970	Phylogeography and ecological niche modeling unravel the evolutionary history of the Yarkand hare, <i>Lepus yarkandensis</i> (Mammalia: Leporidae), through the Quaternary. <i>BMC Evolutionary Biology</i> , 2019, 19, 113.	3.2	5
7971	A New Case of Recombination between Nuclear and Mitochondrial Genomes in the Genus <i>Calliope</i> Gould, 1836 (Muscicapidae, Aves): The Hypothesis of Origin <i>Calliope pectoralis</i> Gould, 1837. <i>Russian Journal of Genetics</i> , 2019, 55, 89-99.	0.2	2
7972	Uncovering of natural allelic variants of key yield contributing genes by targeted resequencing in rice (<i>Oryza sativa</i> L.). <i>Scientific Reports</i> , 2019, 9, 8192.	1.6	5
7973	Strong genetic isolation despite wide distribution in a commercially exploited coastal shark. <i>Hydrobiologia</i> , 2019, 838, 121-137.	1.0	6
7974	Assessing the genetic diversity of catface grouper <i>Epinephelus andersoni</i> in the subtropical Western Indian Ocean. <i>Fisheries Research</i> , 2019, 218, 186-197.	0.9	10
7975	Genetic diversity and structure of striped snakehead (<i>Channa striata</i>) in the Lower Mekong Basin: Implications for aquaculture and fisheries management. <i>Fisheries Research</i> , 2019, 218, 166-173.	0.9	12
7976	From mountains to towns: DNA from ancient reindeer antlers as proxy for domestic procurement networks in medieval Norway. <i>Journal of Archaeological Science: Reports</i> , 2019, 26, 101860.	0.2	3
7977	DNA barcoding inferred maternal philopatric affinity of ocean maskray (<i>Neotrygon indica</i>) in the Bay of Bengal. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1924-1929.	0.2	0
7978	Intra-species variation and geographic differentiation among the populations of the quarantine agricultural pest <i>leucinoides orbonalis</i> (Lepidoptera: Crambidae) in the global assemblage – a prospective of DNA barcoding. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2019, 30, 682-693.	0.7	4

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7979	First Molecular Phylogenetic Analysis of the Lagothrix Taxon Living in Southern Peru and Northern Bolivia: <i>Lagothrix lagothricha tschudii</i> (Atelidae, Primates), a New Subspecies. <i>Folia Primatologica</i> , 2019, 90, 215-239.	0.3	8
7980	Comparative analysis of B-BOX genes and their expression pattern analysis under various treatments in <i>Dendrobium officinale</i> . <i>BMC Plant Biology</i> , 2019, 19, 245.	1.6	31
7981	Selective use of primate CD4 receptors by HIV-1. <i>PLoS Biology</i> , 2019, 17, e3000304.	2.6	10
7982	Mitochondrial variation in small brown planthoppers linked to multiple traits and probably reflecting a complex evolutionary trajectory. <i>Molecular Ecology</i> , 2019, 28, 3306-3323.	2.0	16
7983	Genetic Differentiation of Eastern Honey Bee (<i>Apis cerana</i>) Populations Across Qinghai-Tibet Plateau-Valley Landforms. <i>Frontiers in Genetics</i> , 2019, 10, 483.	1.1	18
7984	Sugar Transporter Proteins (STPs) in Gramineae Crops: Comparative Analysis, Phylogeny, Evolution, and Expression Profiling. <i>Cells</i> , 2019, 8, 560.	1.8	30
7985	Mitochondrial genome of <i>Chthamalus challengerii</i> (Crustacea: Sessilia): gene order comparison within Chthamalidae and phylogenetic consideration within Balanomorpha. <i>Acta Oceanologica Sinica</i> , 2019, 38, 25-31.	0.4	9
7986	Wheat domestication in light of haplotype analyses of the Brittle rachis 1 genes (BTR1-A and BTR1-B). <i>Plant Science</i> , 2019, 285, 193-199.	1.7	23
7987	Knockon community impacts of a novel vector: spillover of emerging DWV from <i>Varroa</i> -infested honeybees to wild bumblebees. <i>Ecology Letters</i> , 2019, 22, 1306-1315.	3.0	68
7988	Genetic and morphological divergence at a biogeographic break in the beach-dwelling brooder <i>Excirrolana hirsuticauda</i> Menzies (Crustacea, Peracarida). <i>BMC Evolutionary Biology</i> , 2019, 19, 118.	3.2	15
7989	Genetic and morphological divergence among three closely related <i>Phrynocephalus</i> species (Agamidae). <i>BMC Evolutionary Biology</i> , 2019, 19, 114.	3.2	15
7990	Two Divergent Genetic Lineages within the Horned Passalus Beetle, <i>Odontotaenius disjunctus</i> (Coleoptera: Passalidae): An Emerging Model for Insect Behavior, Physiology, and Microbiome Research. <i>Insects</i> , 2019, 10, 159.	1.0	4
7991	Forensic analysis reveals fraud in fillets from the <i>Gurijuba</i> (<i>Sciades parkeri</i>) (Ariidae) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Sequencing, and Analysis, 2019, 30, 721-729.	0.7	6
7992	Genetic diversity and metapopulation structures of two intertidal species along the coast of Zhejiang, China: implications for conservation. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2019, 30, 674-681.	0.7	4
7993	Genetic Diversity of atp6 and cox3 Gene in Wild <i>Drosophila melanogaster</i> . <i>Russian Journal of Genetics</i> , 2019, 55, 360-367.	0.2	0
7994	Genetic diversity and population structure of <i>Brycon nattereri</i> (Characiformes: Bryconidae): a Neotropical fish under threat of extinction. <i>Neotropical Ichthyology</i> , 2019, 17, .	0.5	1
7995	A glycan shield on chimpanzee CD4 protects against infection by primate lentiviruses (HIV/SIV). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11460-11469.	3.3	11
7996	Multigene phylogeny, phylogeography and population structure of <i>Podarcis cretensis</i> species group in south Balkans. <i>Molecular Phylogenetics and Evolution</i> , 2019, 138, 193-204.	1.2	13

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7997	Historical climate changes and hybridization shaped the evolution of Atlantic Forest spinetails (Aves: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.2	12
7998	Preliminary report on the genetic structure of <i>Glyphoglossus molossus</i> (Anura: Microhylidae) from the Khorat Plateau, north-eastern Thailand. <i>Journal of Natural History</i> , 2019, 53, 849-861.	0.2	1
7999	A mayfly's rapid transition toward unisexual populations. <i>Biological Journal of the Linnean Society</i> , 2019, 127, 472-478.	0.7	5
8000	<i>Sanguina nivaloides</i> and <i>Sanguina aurantia</i> gen. et spp. nov. (Chlorophyta): the taxonomy, phylogeny, biogeography and ecology of two newly recognised algae causing red and orange snow. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	80
8001	Phylogeographic and evolutionary history analyses of the warty crab <i>Eriphia verrucosa</i> (Decapoda,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Gibraltar Strait, erased by postglacial expansion and admixture among refugial lineages. <i>BMC Evolutionary Biology</i> , 2019, 19, 105.	3.2	13
8002	Population genetic differentiation of the hydrothermal vent crab <i>Austinograea alayseae</i> (Crustacea:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.1	11
8003	Winter temperature correlates with mtDNA genetic structure of yellow-necked mouse population in NE Poland. <i>PLoS ONE</i> , 2019, 14, e0216361.	1.1	2
8004	Hiding in plain sight: invasive coral <i>Tubastraea tagusensis</i> (Scleractinia:Hexacorallia) in the Gulf of Mexico. <i>Coral Reefs</i> , 2019, 38, 395-403.	0.9	16
8005	Genome-Wide Identification and Expression Analyses of the bZIP Transcription Factor Genes in moso bamboo (<i>Phyllostachys edulis</i>). <i>International Journal of Molecular Sciences</i> , 2019, 20, 2203.	1.8	26
8006	Inferring boundaries among fish species of the new world silversides (Atherinopsidae; genus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 <i>Odontesthes argentinensis</i> . <i>Genetica</i> , 2019, 147, 217-229.	0.5	9
8007	Different speciation processes in a cryptobenthic reef fish from the Western Tropical Atlantic. <i>Hydrobiologia</i> , 2019, 837, 133-147.	1.0	11
8008	Mitochondrial genomes of three kissing bugs (Reduviidae: Triatominae) and their phylogenetic implications. <i>International Journal of Biological Macromolecules</i> , 2019, 134, 36-42.	3.6	19
8009	Incomplete lineage sorting and introgression in the diversification of Chinese spot-billed ducks and mallards. <i>Environmental Epigenetics</i> , 2019, 65, 589-597.	0.9	19
8010	Morphological and Genetic Structure of Two Equivalent <i>Astyanax</i> Species (Characiformes:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.8	2
8011	Genome-wide association analysis identifies a natural variation in basic helix-loop-helix transcription factor regulating ascorbate biosynthesis via D-mannose/L-galactose pathway in tomato. <i>PLoS Genetics</i> , 2019, 15, e1008149.	1.5	66
8012	Genetic population structure and demography of an apex predator, the tiger shark <i>Galeocerdo cuvier</i> . <i>Ecology and Evolution</i> , 2019, 9, 5551-5571.	0.8	22
8013	Arms races with mitochondrial genome soft sweeps in a gynodioecious plant, <i>Plantago lanceolata</i> . <i>Molecular Ecology</i> , 2019, 28, 2772-2785.	2.0	3
8014	Cryptic speciation in the Chinese white pine (<i>Pinus armandii</i>): Implications for the high species diversity of conifers in the Hengduan Mountains, a global biodiversity hotspot. <i>Molecular Phylogenetics and Evolution</i> , 2019, 138, 114-125.	1.2	27

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8015	Genetic diversity and population structure of goliath frogs (<i>Conraua goliath</i>) from Cameroon. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2019, 30, 657-663.	0.7	3
8016	Found, forgotten, and found again: systematics and distribution of Cooper's Rocky Mountain snail (<i>Oreohelix cooperi</i>) on a sky island in the Canadian Prairies. Canadian Journal of Zoology, 2019, 97, 833-840.	0.4	6
8017	Comparative Chloroplast Genomes of <i>Sorghum</i> Species: Sequence Divergence and Phylogenetic Relationships. BioMed Research International, 2019, 2019, 1-11.	0.9	29
8018	<i>DREB</i> Genes from Common Bean (<i>Phaseolus vulgaris</i> L.) Show Broad to Specific Abiotic Stress Responses and Distinct Levels of Nucleotide Diversity. International Journal of Genomics, 2019, 2019, 1-28.	0.8	17
8019	Expansion and Evolutionary Patterns of Glycosyltransferase Family 8 in Gramineae Crop Genomes and Their Expression under Salt and Cold Stresses in <i>Oryza sativa</i> ssp. japonica. Biomolecules, 2019, 9, 188.	1.8	30
8020	<i>kn1</i> , a major quantitative trait locus for kernel row number in maize. New Phytologist, 2019, 223, 1634-1646.	3.5	47
8021	Molecular identification of natural hybridization between <i>Melastoma malabathricum</i> and <i>Melastoma beccarianum</i> in Sarawak, Malaysia. Ecology and Evolution, 2019, 9, 5766-5776.	0.8	8
8022	Evolution and Genetic Diversity of the <i>k13</i> Gene Associated with Artemisinin Delayed Parasite Clearance in <i>Plasmodium falciparum</i> . Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	15
8023	Uncovering population structure in the Humboldt penguin (<i>Spheniscus humboldti</i>) along the Pacific coast at South America. PLoS ONE, 2019, 14, e0215293.	1.1	3
8024	Phylogeography of <i>Potamon ibericum</i> (Brachyura: Potamidae) identifies Quaternary glacial refugia within the Caucasus biodiversity hot spot. Ecology and Evolution, 2019, 9, 4749-4759.	0.8	15
8025	High genetic diversity in a "recent outbreak" spider mite, <i>Tetranychus pueraricola</i> , in mainland China. Experimental and Applied Acarology, 2019, 78, 15-27.	0.7	4
8026	Updating the saga of the small hive beetle (<i>Aethina tumida</i>): molecular inference of the origin of the South American invasion. Apidologie, 2019, 50, 273-276.	0.9	7
8027	Analysis of the genetic diversity of genome sequences of variants of apple hammerhead viroid. Canadian Journal of Plant Pathology, 2019, 41, 551-559.	0.8	7
8028	Genetic basis of amphibian larval development along a latitudinal gradient: Gene diversity, selection and links with phenotypic variation in transcription factor <i>C/EBPβ</i> . Molecular Ecology, 2019, 28, 2786-2801.	2.0	5
8029	Widespread gene duplication and adaptive evolution in the RNA interference pathways of the <i>Drosophila obscura</i> group. BMC Evolutionary Biology, 2019, 19, 99.	3.2	15
8030	Ancient habitat shifts and organismal diversification are decoupled in the African viper genus <i>Bitis</i> (Serpentes: Viperidae). Journal of Biogeography, 2019, 46, 1234-1248.	1.4	26
8031	Mitochondrial Gene Heterogeneity and Population Genetics of <i>Haemaphysalis longicornis</i> (Acari: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.4	5
8032	Unveiling the Diversity of Immunoglobulin Heavy Constant Gamma (IGHC) Gene Segments in Brazilian Populations Reveals 28 Novel Alleles and Evidence of Gene Conversion and Natural Selection. Frontiers in Immunology, 2019, 10, 1161.	2.2	31

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8034	Identification and analysis of tRNA genes provide new insights into oil biosynthesis in tung tree (<i>Vernicia fordii</i> Hemsl.). <i>Industrial Crops and Products</i> , 2019, 137, 74-80.	2.5	8
8035	Improved subtyping affords better discrimination of <i>Trichomonas gallinae</i> strains and suggests hybrid lineages. <i>Infection, Genetics and Evolution</i> , 2019, 73, 234-241.	1.0	12
8036	Phylogeny of Chinese <i>Allium</i> Species in Section <i>Daghestanica</i> and Adaptive Evolution of <i>Allium</i> (<i>Amaryllidaceae</i> , <i>Allioideae</i>) Species Revealed by the Chloroplast Complete Genome. <i>Frontiers in Plant Science</i> , 2019, 10, 460.	1.7	64
8037	Genome-wide analysis of HSP70 family genes in cabbage (<i>Brassica oleracea</i> var. <i>capitata</i>) reveals their involvement in floral development. <i>BMC Genomics</i> , 2019, 20, 369.	1.2	16
8038	Complete chloroplast genome of <i>Camellia japonica</i> genome structures, comparative and phylogenetic analysis. <i>PLoS ONE</i> , 2019, 14, e0216645.	1.1	53
8039	Molecular Data Reveal Multiple Lineages in Piranhas of the Genus <i>Pygocentrus</i> (Teleostei). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502 Td</i>	1.0	10
8040	Ethnogenetic analysis reveals that Kohistanis of Pakistan were genetically linked to west Eurasians by a probable ancestral genepool from Eurasian steppe in the bronze age. <i>Mitochondrion</i> , 2019, 47, 82-93.	1.6	2
8041	<i>Plasmodium knowlesi</i> clinical isolates from Malaysia show extensive diversity and strong differential selection pressure at the merozoite surface protein 7D (MSP7D). <i>Malaria Journal</i> , 2019, 18, 150.	0.8	9
8042	A novel multilocus sequence typing scheme identifying genetic diversity amongst <i>Leishmania donovani</i> isolates from a genetically homogeneous population in the Indian subcontinent. <i>International Journal for Parasitology</i> , 2019, 49, 555-567.	1.3	15
8043	Measuring the impact of European colonization on Native American populations in Southern Brazil and Uruguay: Evidence from mtDNA. <i>American Journal of Human Biology</i> , 2019, 31, e23243.	0.8	10
8044	Conservation genetics of the pond bat (<i>Myotis dasycneme</i>) with special focus on the populations in northwestern Germany and in Jutland, Denmark. <i>Ecology and Evolution</i> , 2019, 9, 5292-5308.	0.8	5
8045	Two new mitogenomes of Picidae (Aves, Piciformes): Sequence, structure and phylogenetic analyses. <i>International Journal of Biological Macromolecules</i> , 2019, 133, 683-692.	3.6	13
8046	Genetics and evidence for balancing selection of a sex-linked colour polymorphism in a songbird. <i>Nature Communications</i> , 2019, 10, 1852.	5.8	47
8047	Genetic diversity of mango leafhopper, <i>Amritodus atkinsoni</i> (Hemiptera: Cicadellidae) based on mtCOI gene sequences from India. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 261-264.	0.2	2
8048	Species reassessment congruent with the phylogeographical study of the <i>Biston falcata</i> species group. <i>Systematic Entomology</i> , 2019, 44, 886-898.	1.7	6
8049	Complete plastome sequences of <i>Picea asperata</i> and <i>P. crassifolia</i> and comparative analyses with <i>P. abies</i> and <i>P. morrisonicola</i> . <i>Genome</i> , 2019, 62, 317-328.	0.9	5
8050	Highly polymorphic mitochondrial DNA and deceiving haplotypic differentiation: implications for assessing population genetic differentiation and connectivity. <i>BMC Evolutionary Biology</i> , 2019, 19, 92.	3.2	7

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8052	Patterns of mtDNA variation reveal complex evolutionary history of relict and endangered peat bog pine (<i>Pinus uliginosa</i>). <i>AoB PLANTS</i> , 2019, 11, plz015.	1.2	8
8053	Phylogeography of the freshwater bivalve genus <i>Ensis</i> (Unionidae) in Thailand. <i>Journal of Molluscan Studies</i> , 2019, 85, 224-231.	0.4	10
8054	Multiple colonizations, hybridization and uneven diversification in <i>Cyrtandra</i> (Gesneriaceae) lineages on Hawai'i Island. <i>Journal of Biogeography</i> , 2019, 46, 1178-1196.	1.4	20
8055	On the Issue of <i>Larix lubarskii</i> Sukaczew Origin: Analysis of Polymorphism of Mitochondrial Genome Markers. <i>Russian Journal of Genetics</i> , 2019, 55, 197-203.	0.2	0
8056	Genome-wide diversity and demographic dynamics of Cameroon goats and their divergence from east African, north African, and Asian conspecifics. <i>PLoS ONE</i> , 2019, 14, e0214843.	1.1	6
8057	Comparative genomic and phylogenetic analyses of <i>Populus</i> section <i>Leuce</i> using complete chloroplast genome sequences. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	15
8058	Mechanisms of allopatric speciation in an Antillean damselfly genus (Odonata, Zygoptera): Vicariance or long-distance dispersal?. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 14-21.	1.2	5
8059	A Novel Insight into Functional Divergence of the MST Gene Family in Rice Based on Comprehensive Expression Patterns. <i>Genes</i> , 2019, 10, 239.	1.0	60
8060	No evidence for recent introgressive hybridization between the European and Siberian roe deer in Poland. <i>Mammalian Biology</i> , 2019, 97, 59-63.	0.8	5
8061	Species diversity of <i>Marmosa</i> subgenus <i>Micoureus</i> (Didelphimorphia, Didelphidae) and taxonomic evaluation of the white-bellied woolly mouse opossum, <i>Marmosa constantiae</i> . <i>Zoological Journal of the Linnean Society</i> , 2019, 187, 240-277.	1.0	27
8062	Evaluation of the multispecies coalescent method to explore intra- <i>Trypanosoma cruzi</i> relationships and genetic diversity. <i>Parasitology</i> , 2019, 146, 1063-1074.	0.7	8
8063	Genetic population structure of a highly migratory Hilsa Shad, <i>Tenualosa ilisha</i> , in three river systems, inferred from four mitochondrial genes analysis. <i>Environmental Biology of Fishes</i> , 2019, 102, 939-954.	0.4	8
8064	Identification and expression profiling analysis of NBS-LRR genes involved in <i>Fusarium oxysporum</i> f.sp. <i>conglutinans</i> resistance in cabbage. <i>3 Biotech</i> , 2019, 9, 202.	1.1	23
8065	Genetic variation of HvXYN1 associated with endoxylanase activity and TAX content in barley (<i>Hordeum vulgare</i> L.). <i>BMC Plant Biology</i> , 2019, 19, 170.	1.6	5
8066	Genome-Wide Identification and Transcriptional Expression Profiles of the F-box Gene Family in Common Walnut (<i>Juglans regia</i> L.). <i>Forests</i> , 2019, 10, 275.	0.9	8
8067	Increased habitat fragmentation leads to isolation among and low genetic diversity within populations of the imperiled Kentucky Arrow Darter (<i>Etheostoma sagitta spilotum</i>). <i>Conservation Genetics</i> , 2019, 20, 1009-1022.	0.8	11
8068	Current stocking program of the sterlet (<i>Acipenser ruthenus</i> , L.) can negatively shape its genetic variability in the Middle Danube. <i>Knowledge and Management of Aquatic Ecosystems</i> , 2019, , 19.	0.5	4

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8069	DNA barcoding reveals distinct population of <i>Plotosus canius</i> (Siluriformes: Plotosidae) in Sundarbans waters. Mitochondrial DNA Part B: Resources, 2019, 4, 1167-1171.	0.2	1
8070	Cloning of the Cytochrome b Gene From the Tomato Powdery Mildew Fungus <i>Leveillula taurica</i> Reveals High Levels of Allelic Variation and Heteroplasmy for the G143A Mutation. Frontiers in Microbiology, 2019, 10, 663.	1.5	13
8071	Genetic diversity of chemokine XCL1 and its receptor XCR1 in murine rodents. Developmental and Comparative Immunology, 2019, 98, 80-88.	1.0	3
8072	Conservation genomics of range disjunction in a global biodiversity hotspot: a case study of <i>Banksia biterax</i> (Proteaceae) in southwestern Australia. Biological Journal of the Linnean Society, 2019, 127, 390-406.	0.7	14
8073	Molecular characterization, comparative and evolutionary analysis of the recent Orf outbreaks among goats in the Eastern part of India (Odisha). Agri Gene, 2019, 12, 100088.	1.9	2
8074	New insights into Romanian Chilopoda: Redescription of <i>Clinopodes intermedius</i> DÄfrÄfbanÅ£u and Matic, 1969 (Geophilomorpha: Geophilidae). Biologia (Poland), 2019, 74, 1501-1507.	0.8	1
8075	The serotonin transporter gene could play a role in anti-predator behaviour in a forest passerine. Journal of Ethology, 2019, 37, 221-227.	0.4	7
8076	Intra-individual variation and transcribed pseudogenes in the ribosomal ITS1-5.8S-ITS2 rDNA of <i>Paraplagusia japonica</i> (Pleuronectiformes: Cynoglossidae). Biochemical and Biophysical Research Communications, 2019, 513, 726-731.	1.0	4
8077	Phylogeography of the Assassin Bug <i>Sphedanolestes impressicollis</i> in East Asia Inferred From Mitochondrial and Nuclear Gene Sequences. International Journal of Molecular Sciences, 2019, 20, 1234.	1.8	9
8078	The species identity and biogeography of <i>Blanus</i> (Amphisbaenia: Blanidae) in Lebanon. Zoology in the Middle East, 2019, 65, 208-214.	0.2	7
8079	Effect of low complexity regions within the PvMSP3 block II on the tertiary structure of the protein and implications to immune escape mechanisms. BMC Structural Biology, 2019, 19, 6.	2.3	10
8080	Clinical features and genetic background of the sympatric species <i>Paracoccidioides brasiliensis</i> and <i>Paracoccidioides americana</i> . PLoS Neglected Tropical Diseases, 2019, 13, e0007309.	1.3	31
8081	Evolution and phylogeography analysis of diploid and polyploid <i>Misgurnus anguillicaudatus</i> populations across China. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20190076.	1.2	17
8082	Contrasting patterns of phylogeographic structuring in two key beetle pests of stored grain in India and Australia. Journal of Pest Science, 2019, 92, 1249-1259.	1.9	14
8083	Phylogenetic patterns and molecular evolution among "True citrus fruit trees" group (Rutaceae family) Tj ETQq0 0 0 rgBT /Overlo	1.7	10
8084	Natural variation of OsGluA2 is involved in grain protein content regulation in rice. Nature Communications, 2019, 10, 1949.	5.8	82
8085	The highly divergent Jekyll genes, required for sexual reproduction, are lineage specific for the related grass tribes Triticeae and Bromeae. Plant Journal, 2019, 98, 961-974.	2.8	7
8086	The role of glacial-interglacial climate change in shaping the genetic structure of eastern subterranean termites in the southern Appalachian Mountains, USA. Ecology and Evolution, 2019, 9, 4621-4636.	0.8	10

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8088	Global phylogeography reveals the origin and the evolutionary history of the gypsy moth (Lepidoptera, Erebidae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 1-13.	1.2	11
8089	Genome-wide identification and analysis of the WUSCHEL-related homeobox (WOX) gene family in allotetraploid <i>Brassica napus</i> reveals changes in WOX genes during polyploidization. <i>BMC Genomics</i> , 2019, 20, 317.	1.2	40
8090	The trihelix family of transcription factors: functional and evolutionary analysis in Moso bamboo (<i>Phyllostachys edulis</i>). <i>BMC Plant Biology</i> , 2019, 19, 154.	1.6	22
8091	Molecular systematics, biogeography and taxonomy of forest falcons in the <i>Micrastur ruficollis</i> species complex (Aves: Falconidae). <i>Journal of Avian Biology</i> , 2019, 50, .	0.6	6
8092	Update on the geographical distribution and prevalence of <i>Aedes aegypti</i> and <i>Aedes albopictus</i> (Diptera: Culicidae), two major arbovirus vectors in Cameroon. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007137.	1.3	47
8093	Molecular Phylogeography and Ecological Niche Modeling of <i>Sibbaldia procumbens</i> s.l. (Rosaceae). <i>Frontiers in Genetics</i> , 2019, 10, 201.	1.1	7
8094	Species Boundaries and Parapatric Speciation in the Complex of Alpine Shrubs, <i>Rosa sericea</i> (Rosaceae), Based on Population Genetics and Ecological Tolerances. <i>Frontiers in Plant Science</i> , 2019, 10, 321.	1.7	19
8095	Evolutionary Comparison of the Chloroplast Genome in the Woody <i>Sonchus</i> Alliance (Asteraceae) on the Canary Islands. <i>Genes</i> , 2019, 10, 217.	1.0	16
8096	Patterns of genetic variation reflect multiple introductions and pre-admixture sources of common ragweed (<i>Ambrosia artemisiifolia</i>) in China. <i>Biological Invasions</i> , 2019, 21, 2191-2209.	1.2	13
8097	A cytochrome P450 allele confers pyrethroid resistance on a major African malaria vector, reducing insecticide-treated bednet efficacy. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	121
8098	On and off the rocks: persistence and ecological diversification in a tropical Australian lizard radiation. <i>BMC Evolutionary Biology</i> , 2019, 19, 81.	3.2	13
8099	The complete chloroplast genome sequences of four <i>Viola</i> species (Violaceae) and comparative analyses with its congeneric species. <i>PLoS ONE</i> , 2019, 14, e0214162.	1.1	35
8100	<i>Calochortus gunnisonii</i> furthers evidence for the complex genetic legacy of historical climate change in the southern Rocky Mountains. <i>American Journal of Botany</i> , 2019, 106, 477-488.	0.8	1
8101	Genetic diversity and population structure of the blue jack mackerel <i>Trachurus picturatus</i> across its western distribution. <i>Journal of Fish Biology</i> , 2019, 94, 725-731.	0.7	20
8102	Phylogeography of <i>Bellamya</i> (Mollusca: Gastropoda: Viviparidae) snails on different continents: contrasting patterns of diversification in China and East Africa. <i>BMC Evolutionary Biology</i> , 2019, 19, 82.	3.2	14
8103	Genome-wide identification and analysis of the EIN3/EIL gene family in allotetraploid <i>Brassica napus</i> reveal its potential advantages during polyploidization. <i>BMC Plant Biology</i> , 2019, 19, 110.	1.6	21
8104	<i>Ferula paeoniifolia</i> sp. nov. (Apiaceae) from Sichuan, China. <i>Nordic Journal of Botany</i> , 2019, 37, .	0.2	2

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8106	Revisiting the North American freshwater mussel genus <i>Quadrula</i> sensu lato (Bivalvia). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10</i>	0.7	21
8107	Genetic diversity and population structure of a cyprinid fish (<i>Ancherythroculter nigrocauda</i>) in a highly fragmented river. <i>Journal of Applied Ichthyology</i> , 2019, 35, 701-708.	0.3	10
8108	Sequencing and Comparative Analysis of the Chloroplast Genome of <i>Angelica polymorpha</i> and the Development of a Novel Indel Marker for Species Identification. <i>Molecules</i> , 2019, 24, 1038.	1.7	38
8109	Molecular detection and identification of <i>Wolbachia</i> endosymbiont in fleas (Insecta: Siphonaptera). <i>Folia Microbiologica</i> , 2019, 64, 789-796.	1.1	8
8110	The mystery of the origins of <i>Cebus albifrons malitiosus</i> and <i>Cebus albifrons hypoleucus</i> : mitogenomics and microsatellite analyses revealed an amazing evolutionary history of the Northern Colombian white-fronted capuchins. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2019, 30, 525-547.	0.7	2
8111	Phylogeographic structure in the apparent absence of barriers: a case study of the Mexican land snail <i>Humboldtiana durangoensis</i> (Pulmonata: Humboldtianidae). <i>Journal of Molluscan Studies</i> , 2019, 85, 244-252.	0.4	3
8112	New insight into genetic variation and haplotype diversity of <i>Fasciola hepatica</i> from Algeria. <i>Parasitology Research</i> , 2019, 118, 1179-1192.	0.6	11
8113	Phylogeny, phylogeography and hybridization of Caucasian barbels of the genus <i>Barbus</i> (Actinopterygii, Cyprinidae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 31-44.	1.2	31
8114	The complete mitochondrial genomes of two sibling species of camellia weevils (Coleoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.8	9
8115	The roles of geography, climate and sexual selection in driving divergence among insect populations on mountaintops. <i>Journal of Biogeography</i> , 2019, 46, 784-795.	1.4	12
8116	Identification and Phylogenetic Analysis of the Complete Chloroplast Genomes of Three <i>Ephedra</i> Herbs Containing Ephedrine. <i>BioMed Research International</i> , 2019, 2019, 1-10.	0.9	18
8117	Genetic variation and phylogeography of the <i>Triatoma dimidiata</i> complex evidence a potential center of origin and recent divergence of haplogroups having differential <i>Trypanosoma cruzi</i> and DTU infections. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007044.	1.3	23
8118	Genetic outcomes of translocation of bighorn sheep in Arizona. <i>Journal of Wildlife Management</i> , 2019, 83, 838-854.	0.7	13
8119	Polymorphisms in genes associated with drug resistance of <i>Plasmodium vivax</i> in India. <i>Parasitology International</i> , 2019, 70, 92-97.	0.6	12
8120	Mitochondrial phylogeny and biogeography of the genus <i>Gobio</i> (Teleostei: Cyprinidae) in Turkey. <i>Zoology in the Middle East</i> , 2019, 65, 128-141.	0.2	10
8121	Phylogeography of the Chinese false gudgeon, <i>Abbottina rivularis</i> , in East Asia, with special reference to the origin and artificial disturbance of Japanese populations. <i>Ichthyological Research</i> , 2019, 66, 460-478.	0.5	16
8122	Low genetic diversity in the vulnerable Goitred Gazelle, <i>Gazella subgutturosa</i> (Cetartiodactyla). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10</i>	0.2	4

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8142	Multilocus Sequence Analysis, a Rapid and Accurate Tool for Taxonomic Classification, Evolutionary Relationship Determination, and Population Biology Studies of the Genus <i>Shewanella</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	13
8143	Natural variations of FT family genes in soybean varieties covering a wide range of maturity groups. <i>BMC Genomics</i> , 2019, 20, 230.	1.2	33
8144	Late Pleistocene climatic changes promoted demographic expansion and population reconnection of a Neotropical savanna-adapted bird, <i>Neothraupis fasciata</i> (Aves: Thraupidae). <i>PLoS ONE</i> , 2019, 14, e0212876.	1.1	11
8145	Population genetics of the capybara, <i>Hydrochoerus hydrochaeris</i> , in the Chaco-pampean region. <i>Mammalian Biology</i> , 2019, 96, 14-22.	0.8	5
8146	<i>Diaphorina citri</i> (Hemiptera: Psylloidea) in China: Two Invasion Routes and Three Transmission Paths. <i>Journal of Economic Entomology</i> , 2019, 112, 1418-1427.	0.8	6
8147	Genetic and morphological variations of the lichenized fungus <i>Steinera intricata</i> (Arctomiaceae, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5 907-918.	0.5	0
8148	The deubiquitinating gene <i>Usp29</i> is dispensable for fertility in male mice. <i>Science China Life Sciences</i> , 2019, 62, 544-552.	2.3	9
8149	Mitochondrial Genomics Reveals Shared Phylogeographic Patterns and Demographic History among Three Periodical Cicada Species Groups. <i>Molecular Biology and Evolution</i> , 2019, 36, 1187-1200.	3.5	92
8150	Living on the edge: Exploring the role of coastal refugia in the Alexander Archipelago of Alaska. <i>Ecology and Evolution</i> , 2019, 9, 1777-1797.	0.8	16
8151	Phylogenetic Studies on Red Junglefowl (<i>Gallus gallus</i>) and Native Chicken (<i>Gallus gallus domesticus</i>) in Samar Island, Philippines using the Mitochondrial DNA D-Loop Region. <i>Journal of Poultry Science</i> , 2019, 56, 237-244.	0.7	9
8152	Comparative transcriptome analysis reveals expression signatures of albino Russian sturgeon, <i>Acipenseriformes gueldenstaedtii</i> . <i>Marine Genomics</i> , 2019, 46, 1-7.	0.4	17
8153	Macaronesian islands as promoters of diversification in amphipods: The remarkable case of the family Hyalidae (Crustacea, Amphipoda). <i>Zoologica Scripta</i> , 2019, 48, 359-375.	0.7	26
8154	Lack of phylogeographic structure in the endangered Pickersgill's Reed Frog; <i>Hyperolius pickersgilli</i> (Raw, 1982). <i>African Journal of Herpetology</i> , 2019, 68, 1-17.	0.3	3
8155	Persistence of a Geographically-Stable Hybrid Zone in Puerto Rican Dwarf Geckos. <i>Journal of Heredity</i> , 2019, 110, 523-534.	1.0	14
8156	The phylogeny and evolutionary timescale of stoneflies (Insecta: Plecoptera) inferred from mitochondrial genomes. <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 123-135.	1.2	35
8157	Taming extreme morphological variability through coupling of molecular phylogeny and quantitative phenotype analysis as a new avenue for taxonomy. <i>Scientific Reports</i> , 2019, 9, 2429.	1.6	7
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8160	Analysis of genetic diversity and phylogeny of <i>Philosamia ricini</i> (Lepidoptera: Saturniidae) by using RAPD and internal transcribed spacer DNA1. <i>Molecular Biology Reports</i> , 2019, 46, 3035-3048.	1.0	1
8161	Matrix metalloproteinase gene polymorphisms in chronic periodontitis: a caseâ€“control study in the Indian population. <i>Journal of Genetics</i> , 2019, 98, 1.	0.4	8
8162	Selection for background matching drives sympatric speciation in Wall Gecko. <i>Scientific Reports</i> , 2019, 9, 1288.	1.6	8
8163	Plastid genome and composition analysis of two medical ferns: <i>Dryopteris crassirhizoma</i> Nakai and <i>Osmunda japonica</i> Thunb.. <i>Chinese Medicine</i> , 2019, 14, 9.	1.6	8
8164	Improved phylogeny of brown algae <i>Cystoseira</i> (Fucales) from the Atlantic-Mediterranean region based on mitochondrial sequences. <i>PLoS ONE</i> , 2019, 14, e0210143.	1.1	27
8165	Taxonomical over splitting in the <i>Rhodnius prolixus</i> (Insecta: Hemiptera: Reduviidae) clade: Are <i>R. taquarussuensis</i> (da Rosa et al., 2017) and <i>R. neglectus</i> (Lent, 1954) the same species?. <i>PLoS ONE</i> , 2019, 14, e0211285.	1.1	46
8166	Genetic diversity and population structure of naturally rare <i>Calibrachoa</i> species with small distribution in southern Brazil. <i>Genetics and Molecular Biology</i> , 2019, 42, 108-119.	0.6	11
8167	Evolutionary Toxicogenomics of the Striped Killifish (<i>Fundulus majalis</i>) in the New Bedford Harbor (Massachusetts, USA). <i>International Journal of Molecular Sciences</i> , 2019, 20, 1129.	1.8	7
8168	Demographic Expansion of the Predominant <i>Bemisia tabaci</i> (Gennadius) (Hemiptera: Aleyrodidae) Mitotypes Associated With the Cotton Leaf Curl Virus Epidemic in Pakistan. <i>Annals of the Entomological Society of America</i> , 2019, 112, 265-280.	1.3	19
8169	Population Genetics Analyses of the Endangered Proboscis Monkey from Malaysian Borneo. <i>Folia Primatologica</i> , 2019, 90, 139-152.	0.3	2
8170	A detection of benzimidazole resistance-associated SNPs in the isotype-1 β -tubulin gene in <i>Haemonchus contortus</i> from wild blue sheep (<i>Pseudois nayaur</i>) sympatric with sheep in Helan Mountains, China. <i>BMC Veterinary Research</i> , 2019, 15, 89.	0.7	5
8171	Genetic diversity and demography of the critically endangered Robertsâ€™ false brook salamander (<i>Pseudoeurycea robertsi</i>) in Central Mexico. <i>Genetica</i> , 2019, 147, 149-164.	0.5	8
8172	Molecular characterization of <i>Bathymodiolus</i> mussels and gill symbionts associated with chemosynthetic habitats from the U.S. Atlantic margin. <i>PLoS ONE</i> , 2019, 14, e0211616.	1.1	18
8173	Behavior and abundance of <i>Anopheles darlingi</i> in communities living in the Colombian Amazon riverside. <i>PLoS ONE</i> , 2019, 14, e0213335.	1.1	9
8174	Pliocene Origin, Ice Ages and Postglacial Population Expansion Have Influenced a Panmictic Phylogeography of the European Bee-Eater <i>Merops apiaster</i> . <i>Diversity</i> , 2019, 11, 12.	0.7	11
8175	Population structure and genetic diversity of <i>Vibrio parahaemolyticus</i> from a coastal area of China based on a multi-locus sequence typing (MLST) scheme. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 1199-1211.	0.7	3
8176	Genetic structure of Kho population from north-western Pakistan based on mtDNA control region sequences. <i>Genetica</i> , 2019, 147, 177-183.	0.5	5

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8178	Cryptic diversity in <i>Telestes pleurobipunctatus</i> (Actinopterygii; Leuciscidae) as a consequence of historical biogeography in the Ionian Freshwater Ecoregion (Greece, Albania). <i>Hydrobiologia</i> , 2019, 835, 147-163.	1.0	18
8179	New insights from nuclear and mitochondrial markers on the genetic diversity and structure of the Indian white shrimp <i>Fenneropenaeus indicus</i> among the marginal seas in the Indian Ocean. <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 53-64.	1.2	12
8180	Detection of alleles associated with resistance to chemical insecticide in the malaria vector <i>Anopheles arabiensis</i> in Santiago, Cabo Verde. <i>Malaria Journal</i> , 2019, 18, 120.	0.8	9
8181	Phenotypic Trait Variation as a Response to Altitude-Related Constraints in <i>Arabidopsis</i> Populations. <i>Frontiers in Plant Science</i> , 2019, 10, 430.	1.7	11
8182	Temporal correlation of population composition and environmental variables in the marine invader <i>Ciona robusta</i> . <i>Marine Ecology</i> , 2019, 40, e12543.	0.4	12
8183	Assessment of various genetic components through NCD-I and NCD-III designs of biparental mating in opium poppy. <i>Journal of Genetics</i> , 2019, 98, 1.	0.4	0
8184	The complete mitochondrial genome of <i>Mahanta tanyae</i> compared with other zygaenoid moths (Lepidoptera: Zygaenoidea). <i>Journal of Asia-Pacific Entomology</i> , 2019, 22, 513-521.	0.4	7
8185	A marker of glutathione S-transferase-mediated resistance to insecticides is associated with higher <i>Plasmodium</i> infection in the African malaria vector <i>Anopheles funestus</i> . <i>Scientific Reports</i> , 2019, 9, 5772.	1.6	42
8186	The complete mitochondrial genomes of three species of <i>Macridiscus</i> Dall, 1902 (Bivalvia: Veneroidea). <i>TJ ETQq1 1 0.784314 rgBT /Over 0,4</i>	0.4	4
8187	Phylogeographic diversification and postglacial range dynamics shed light on the conservation of the kelp <i>Saccharina japonica</i> . <i>Evolutionary Applications</i> , 2019, 12, 791-803.	1.5	22
8188	Alternated selection mechanisms maintain adaptive diversity in different demographic scenarios of a large carnivore. <i>BMC Evolutionary Biology</i> , 2019, 19, 90.	3.2	6
8189	Genetics and telemetry indicate unexpected movements among structured populations for <i>Brachyplatystoma platynemum</i> in the Amazon. <i>Journal of Fish Biology</i> , 2019, 95, 633-637.	0.7	7
8190	A high throughput deep amplicon sequencing method to show the emergence and spread of <i>Calicophoron daubneyi</i> rumen fluke infection in United Kingdom cattle herds. <i>Veterinary Parasitology</i> , 2019, 268, 9-15.	0.7	17
8191	A century of decline: Loss of genetic diversity in a southern African lion conservation stronghold. <i>Diversity and Distributions</i> , 2019, 25, 870-879.	1.9	26
8192	Genetic Profile of Hydatid Cysts in Patients with Multi-Organ Involvement: Mixed Infections by Different Strains. <i>Vector-Borne and Zoonotic Diseases</i> , 2019, 19, 724-730.	0.6	6
8193	A strategy for developing high-resolution DNA barcodes for species discrimination of wood specimens using the complete chloroplast genome of three <i>Pterocarpus</i> species. <i>Planta</i> , 2019, 250, 95-104.	1.6	40
8194	Genetic analysis of admixture and hybrid patterns of <i>Populus hopeiensis</i> and <i>P. tomentosa</i> . <i>Scientific Reports</i> , 2019, 9, 4821.	1.6	15

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8196	Identification and Expression Analysis of Snf2 Family Proteins in Tomato (<i>Solanum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 70 0.8	0.8	7
8197	Sourcing effective biological control agents of conical snails, <i>Cochlicella acuta</i> , in Europe and north Africa for release in southern Australia. <i>Biological Control</i> , 2019, 134, 1-14.	1.4	15
8198	The phylogeography and genetic diversity of the salt marsh species <i>Salicornia tegetaria</i> (S.Steffen.) Tj ETQq1 1 0.784314 rgBT /Overlock 1.2 1	1.2	1
8199	Phylogeographic structures of the host insects of <i>Ophiocordyceps sinensis</i> . <i>Zoology</i> , 2019, 134, 27-37.	0.6	7
8200	Genetic analysis of the endangered Hyacinth Macaw (<i>Anodorhynchus hyacinthinus</i>) based on mitochondrial markers: different conservation efforts are required for different populations. <i>Journal of Ornithology</i> , 2019, 160, 711-720.	0.5	4
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8202	The use of spatially explicit genetic variation data from four deep-sea sponges to inform the protection of Vulnerable Marine Ecosystems. <i>Scientific Reports</i> , 2019, 9, 5482.	1.6	12
8203	Intraspecific genetic diversity and distribution of North African hedgehogs (Mammalia: Erinaceidae). <i>Biological Journal of the Linnean Society</i> , 2019, 127, 156-163.	0.7	5
8204	Rigorous monitoring of a large-scale marine stock enhancement program demonstrates the need for comprehensive management of fisheries and nursery habitat. <i>Scientific Reports</i> , 2019, 9, 5290.	1.6	27
8205	Genetic structure, phylogeography, and demography of <i>Anadara tuberculosa</i> (Bivalvia) from East Pacific as revealed by mtDNA: Implications to conservation. <i>Ecology and Evolution</i> , 2019, 9, 4392-4402.	0.8	9
8206	Genetic variability and population structure of chamois in Greece (<i>Rupicapra rupicapra balcanica</i>). <i>Conservation Genetics</i> , 2019, 20, 939-945.	0.8	8
8207	A complex invasion story underlies the fast spread of the invasive box tree moth (<i>Cydalima</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 T 1.9 52	1.9	52
8208	Complete genome characterization and population dynamics of potato virus Y-NTN strain from India. <i>VirusDisease</i> , 2019, 30, 252-260.	1.0	3
8209	Genome-wide identification, characterization and in-silico profiling of genes encoding FAD (fatty acid) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 1.4 12	1.4	12
8210	DNA barcodes and their characteristic diagnostic sites analysis of Schizothoracinae fishes in Qinghai province. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2019, 30, 592-601.	0.7	2
8211	Host plant budburst and male-biased dispersal affect the genetic structure of the green oak leaf roller moth, <i>Tortrix viridana</i> (Lepidoptera: Tortricidae). <i>Biological Journal of the Linnean Society</i> , 2019, 127, 56-74.	0.7	1
8212	Population genetic diversity of an odorous frog <i>Odorrana grahami</i> (Amphibia: Anura: Ranidae) in relation to conservation based on mitochondrial DNA. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 57-61.	0.2	1

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8213	Metacaspase gene family in Rosaceae genomes: Comparative genomic analysis and their expression during pear pollen tube and fruit development. <i>PLoS ONE</i> , 2019, 14, e0211635.	1.1	9
8214	Prevalence and molecular characterisation of <i>Sarcocystis miescheriana</i> and <i>Sarcocystis suihominis</i> in wild boars (<i>Sus scrofa</i>) in Italy. <i>Parasitology Research</i> , 2019, 118, 1271-1287.	0.6	27
8215	Identification of an active miniature invertedâ€¢repeat transposable element <i><sc>M</sc>ing</i> in rice. <i>Plant Journal</i> , 2019, 98, 639-653.	2.8	11
8216	Genetic diversity and matrilineal genetic origin of fat-rumped sheep in Ethiopia. <i>Tropical Animal Health and Production</i> , 2019, 51, 1393-1404.	0.5	7
8217	Genetic diversity and phylogeny analysis of <i>Antheraea assamensis</i> Helfer (Lepidoptera: Saturniidae) based on mitochondrial DNA sequences. <i>Journal of Genetics</i> , 2019, 98, 1.	0.4	5
8218	Development of multi locus sequence typing (MLST) of <i>Rodentibacter pneumotropicus</i> . <i>Veterinary Microbiology</i> , 2019, 231, 11-17.	0.8	4
8219	Genetic diversity and population structure of native mitten crab (<i>Eriocheir sensu stricto</i>) by microsatellite markers and mitochondrial COI gene sequence. <i>Gene</i> , 2019, 693, 101-113.	1.0	15
8220	Sequence diversity studies of papaya ringspot virus isolates in South India reveal higher variability and recombination in the 5â€²-terminal gene sequences. <i>VirusDisease</i> , 2019, 30, 261-268.	1.0	9
8221	Phylogenetic analysis of haemagglutinin gene deciphering a new genetically distinct lineage of canine distemper virus circulating among domestic dogs in India. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 1252-1267.	1.3	36
8222	Multilocus Typing of <i>Enterocytozoon bienersi</i> in Pig Reveals the High Prevalence, Zoonotic Potential, Host Adaptation and Geographical Segregation in China. <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 707-718.	0.8	25
8223	The long journey of <i>Orthotrichum shevockii</i> (Orthotrichaceae, Bryopsida): From California to Macaronesia. <i>PLoS ONE</i> , 2019, 14, e0211017.	1.1	12
8224	Isolation by elevation: mitochondrial divergence among sky island populations of Sacramento Mountain salamander (<i>Aneides hardii</i>). <i>Conservation Genetics</i> , 2019, 20, 545-556.	0.8	6
8225	Neither <i>Diplectanum</i> nor specific: a dramatic twist to the taxonomic framework of <i>Diplectanum</i> (Monogenea: Diplectanidae). <i>International Journal for Parasitology</i> , 2019, 49, 365-374.	1.3	10
8226	Assessment of genetic diversity and population structure of <i>Magnaporthe oryzae</i> causing rice blast disease using SSR markers. <i>Physiological and Molecular Plant Pathology</i> , 2019, 106, 157-165.	1.3	16
8227	Phylogeographical Study of <i>Camellia japonica</i> Inferred from AFLP and Chloroplast DNA Haplotype Analyses. <i>Journal of Plant Biology</i> , 2019, 62, 14-26.	0.9	4
8228	Wild birds do not harbor higher diversity of influenza virus internal genes than poultry. <i>Virology</i> , 2019, 530, 59-64.	1.1	0
8229	Back to the wild: does feralization affect the mandible of non-commensal house mice (<i>Mus</i>). <i>Evolution</i> , 2019, 73, 1300-1310.	0.7	13
8230	Limited influence of landscape on the genetic structure of three small mammals in a heterogeneous arid environment. <i>Journal of Biogeography</i> , 2019, 46, 539-551.	1.4	8

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8231	First assessment of MHC diversity in wild Scottish red deer populations. <i>European Journal of Wildlife Research</i> , 2019, 65, 1.	0.7	7
8232	Chromosomal and molecular characterization of 5S rRNA genes in the North American abalones <i>Haliotis rufescens</i> Swainson (red abalone) and <i>H. fulgens</i> Philippi (blue abalone). <i>Gene</i> , 2019, 695, 65-74.	1.0	1
8233	Mitochondrial diversity and phylogeographic analysis of <i>Pediculus humanus</i> reveals a new Amazonian clade. <i>Infection, Genetics and Evolution</i> , 2019, 70, 1-8.	1.0	24
8234	A countrywide molecular survey leads to a seminal identification of the invasive cattle tick <i>Rhipicephalus (Boophilus) microplus</i> in Cameroon, a decade after it was reported in Cote d'Ivoire. <i>Ticks and Tick-borne Diseases</i> , 2019, 10, 585-593.	1.1	28
8235	Unravelling population processes over the Late Pleistocene driving contemporary genetic divergence in Palearctic buzzards. <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 269-281.	1.2	8
8236	New lineages and old species: Lineage diversity and regional distribution of <i>Moina</i> (Crustacea). <i>Trends in Ecology and Evolution</i> , 2019, 34, 119-124.	1.2	19
8237	Complex population evolutionary history of four cold-tolerant <i>Notopterygium</i> herb species in the Qinghai-Tibetan Plateau and adjacent areas. <i>Heredity</i> , 2019, 123, 242-263.	1.2	14
8238	Evolution and functional divergence of MADS-box genes in <i>Pyrus</i> . <i>Scientific Reports</i> , 2019, 9, 1266.	1.6	15
8239	Phylogenetic relationship and variation of alarm call traits of populations of red-cheeked ground squirrels (<i>Spermophilus erythrognys</i> sensu lato) suggest taxonomic delineation. <i>Integrative Zoology</i> , 2019, 14, 341-353.	1.3	11
8240	Inferring the demographic history of Japanese cedar, <i>Cryptomeria japonica</i> , using amplicon sequencing. <i>Heredity</i> , 2019, 123, 371-383.	1.2	7
8241	Genetic variation in field voles (<i>Microtus agrestis</i>) from the British Isles: selective sweeps or population bottlenecks?. <i>Biological Journal of the Linnean Society</i> , 2019, 126, 852-865.	0.7	3
8242	Secondary contact between diverged host lineages entails ecological speciation in a European hantavirus. <i>PLoS Biology</i> , 2019, 17, e3000142.	2.6	26
8243	Acclimation limits of <i>Fucus evanescens</i> along the salinity gradient of the southwestern Baltic Sea. <i>Botanica Marina</i> , 2019, 62, 31-42.	0.6	2
8244	Tomato Chlorotic Spot Virus (TCSV) Putatively Incorporated a Genomic Segment of Groundnut Ringspot Virus (GRSV) Upon a Reassortment Event. <i>Viruses</i> , 2019, 11, 187.	1.5	8
8245	Bidirectional mitochondrial introgression between Korean cobitid fish mediated by hybridogenetic hybrids. <i>Ecology and Evolution</i> , 2019, 9, 1244-1254.	0.8	18
8246	Genetic diversity and origin of the rare, narrow endemic <i>Asperula crassifolia</i> (Rubiaceae). <i>Plant Systematics and Evolution</i> , 2019, 305, 181-192.	0.3	2
8247	A high gene flow in populations of <i>Amblyomma ovale</i> ticks found in distinct fragments of Brazilian Atlantic rainforest. <i>Experimental and Applied Acarology</i> , 2019, 77, 215-228.	0.7	2
8248	The complete mitochondrial genome of <i>Tetrupleps aterrimus</i> (Hemiptera: Anthocoridae): Genomic comparisons and phylogenetic analysis of Cimicomorpha. <i>International Journal of Biological Macromolecules</i> , 2019, 130, 369-377.	3.6	12

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8250	Phylogeographic structuring of the amphidromous shrimp <i>Atya scabra</i> (Crustacea, Decapoda, Atyidae) unveiled by range-wide mitochondrial DNA sampling. <i>Marine and Freshwater Research</i> , 2019, 70, 1078.	0.7	11
8251	Haplotype diversity in medically important red scorpion (Scorpiones: Buthidae: <i>Hottentotta tamulus</i>) from India. <i>Journal of Genetics</i> , 2019, 98, 1.	0.4	3
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8261	<i>Plasmodium ovale curtisi</i> and <i>Plasmodium ovale wallikeri</i> in Chinese travelers: Prevalence of novel genotypes of circumsporozoite protein in the African continent. <i>Infection, Genetics and Evolution</i> , 2019, 70, 9-14.	1.0	3
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8265	Deep segregation in the open ocean: Macaronesia as an evolutionary hotspot for low dispersal marine invertebrates. <i>Molecular Ecology</i> , 2019, 28, 1784-1800.	2.0	20
8266	Genetic Diversity of <i>Apis</i> spp. in Thailand Inferred from 28S rRNA Nuclear and Cytochrome b Mitochondrial Gene Sequences. <i>Psyche: Journal of Entomology</i> , 2019, 2019, 1-11.	0.4	4

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8268	The evolutionary history of the white wagtail species complex, (Passeriformes: Motacillidae:). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf</i>	0.2	1
8269	Mitochondrial D-loop Sequence Variability in Three Native Insular Griffon Vulture (<i>Gyps</i>). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i>	0.9	5
8270	Deciphering the Factors for Nodulation and Symbiosis of <i>Mesorhizobium</i> Associated with <i>Cicer arietinum</i> in Northwest India. <i>Sustainability</i> , 2019, 11, 7216.	1.6	17
8271	The Complete Chloroplast Genome of <i>Trichopus zeylanicus</i> , And Phylogenetic Analysis with <i>Dioscoreales</i> . <i>Plant Genome</i> , 2019, 12, 1-11.	1.6	17
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8273	Redefining Dispersal Boundaries of <i>Siganus fuscescens</i> In The Coral Triangle Area. <i>Ilmu Kelautan: Indonesian Journal of Marine Sciences</i> , 2019, 24, 31.	0.3	0
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8276	Multiple Introductions of Tomato Pathogen <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> into Iran as Revealed by a Global-Scale Phylogeographic Analysis. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	30
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8278	Genetic Diversity of Copepod <i>Limnocalanus macrurus</i> from Russian Arctic Seas. <i>Oceanology</i> , 2019, 59, 903-911.	0.3	0
8279	Characterization of the Complete Chloroplast Genome of <i>Acer truncatum</i> Bunge (Sapindales:). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i>	0.9	12
8280	Extensive recombination challenges the utility of Sugarcane mosaic virus phylogeny and strain typing. <i>Scientific Reports</i> , 2019, 9, 20067.	1.6	13
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8282	A survey of the relationship between functional genes and acetaldehyde production characteristics in <i>Streptococcus thermophilus</i> by multilocus sequence typing. <i>Journal of Dairy Science</i> , 2019, 102, 9651-9662.	1.4	8
8283	Comparative genetic differentiation study of three coexisting mangrove crabs in western Atlantic. <i>Journal of Natural History</i> , 2019, 53, 2883-2903.	0.2	5
8284	The Diversity of the <i>Plasmodium falciparum</i> K13 Propeller Domain Did Not Increase after Implementation of Artemisinin-Based Combination Therapy in Uganda. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	9

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8286	Population genetics of <i>Anopheles koliensis</i> through Papua New Guinea: New cryptic species and landscape topography effects on genetic connectivity. <i>Ecology and Evolution</i> , 2019, 9, 13375-13388.	0.8	1
8287	Evidence for adaptive introgression of exons across a hybrid swarm in deer. <i>BMC Evolutionary Biology</i> , 2019, 19, 199.	3.2	12
8288	First insights into the population genetic structure and the phylogeographic status of the Mehelya's horseshoe bat <i>Rhinolophus mehelyi</i> (Chiroptera: Rhinolophidae) in Iran inferred from mitochondrial genes. <i>Mammalian Biology</i> , 2019, 99, 97-108.	0.8	4
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8290	Mitogenomic diversity in Sacred Ibis Mummies sheds light on early Egyptian practices. <i>PLoS ONE</i> , 2019, 14, e0223964.	1.1	14
8291	Morphological and genetic variation of <i>Leptopelis brevirostris</i> encompasses the little-known treefrogs <i>Leptopelis crystallinoron</i> from Gabon and <i>Leptopelis brevipes</i> from Bioko Island, Equatorial Guinea. <i>African Journal of Herpetology</i> , 2019, 68, 91-117.	0.3	3
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8295	Molecular phylogenetics of Black Cobra (<i>Naja naja</i>) in Pakistan. <i>Electronic Journal of Biotechnology</i> , 2019, 42, 23-29.	1.2	4
8296	Genetic identification of native populations of Mediterranean brown trout <i>Salmo trutta</i> L. complex (Osteichthyes: Salmonidae) in central Italy. , 2019, 86, 424-431.		15
8297	Development of 16 single-copy nuclear gene markers for <i>Oreocharis auricula</i> , a perennial herb in China. <i>Applications in Plant Sciences</i> , 2019, 7, e11304.	0.8	2
8298	Population genetic structure based on mitochondrial DNA analysis of Ikonnikov's whiskered bat (<i>Myotis ikonnikovi</i>) (Chiroptera: Vespertilionidae) from Korea. <i>Journal of Ecology and Environment</i> , 2019, 43, .	1.6	5
8299	Genetic variation across trophic levels: A test of the correlation between population size and genetic diversity in sympatric desert lizards. <i>PLoS ONE</i> , 2019, 14, e0224040.	1.1	2
8300	Characterization of the complete chloroplast genome sequence of <i>Dalbergia</i> species and its phylogenetic implications. <i>Scientific Reports</i> , 2019, 9, 20401.	1.6	46
8301	Biochemical and molecular differentiation of <i>Anacroneuria</i> species (Plecoptera, Insecta) in Andean National Park, Venezuela. <i>Systematics and Biodiversity</i> , 2019, 17, 669-678.	0.5	2
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8304	Genetic Analysis of Turkish lynx (<i>Lynx lynx</i>) Based on Mitochondrial DNA Sequences. <i>Russian Journal of Genetics</i> , 2019, 55, 1426-1437.	0.2	3
8305	Population genetics of <i>Liriomyza trifolii</i> (Diptera: Agromyzidae) and comparison with four <i>Liriomyza</i> species in China based on COI, EF-1a and microsatellites loci. <i>Scientific Reports</i> , 2019, 9, 17856.	1.6	2
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8307	GTn Repeat Microsatellite Instability in Uterine Fibroids. <i>Frontiers in Genetics</i> , 2019, 10, 810.	1.1	3
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8312	Genetic diversity, natural selection and haplotype grouping of <i>Plasmodium vivax</i> Duffy-binding protein genes from eastern and western Myanmar borders. <i>Parasites and Vectors</i> , 2019, 12, 546.	1.0	7
8313	Diversity pattern of <i>Plasmodium knowlesi</i> merozoite surface protein 4 (MSP4) in natural population of Malaysia. <i>PLoS ONE</i> , 2019, 14, e0224743.	1.1	14
8314	Phylogeography of <i>Excoecaria acerifolia</i> (Euphorbiaceae) suggests combined effects of historical drainage reorganization events and climatic changes on riparian plants in the Sino-Himalayan region. <i>Botanical Journal of the Linnean Society</i> , 2019, , .	0.8	1
8315	Phylogeography, Population Structure, and Species Delimitation in Rockhopper Penguins (<i>Eudyptes</i>)	1.0	3
8316	Diversity of PBI-Ddel satellite DNA in snakes correlates with rapid independent evolution and different functional roles. <i>Scientific Reports</i> , 2019, 9, 15459.	1.6	18
8317	From taxonomic deflation to newly detected cryptic species: Hidden diversity in a widespread African squeaker catfish. <i>Scientific Reports</i> , 2019, 9, 15748.	1.6	6
8318	Consequences of past climate change and recent human persecution on mitogenomic diversity in the arctic fox. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20190212.	1.8	12
8319	Maternal and paternal genetic variation in Estonian local horse breeds in the context of geographically adjacent and distant Eurasian breeds. <i>Animal Genetics</i> , 2019, 50, 757-760.	0.6	8
8320	Towards Improved Molecular Identification Tools in Fine Fescue (<i>Festuca L.</i> , Poaceae) Turfgrasses: Nuclear Genome Size, Ploidy, and Chloroplast Genome Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 1223.	1.1	14

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8322	Variation in plastid genomes in the gynodioecious species <i>Silene vulgaris</i> . <i>BMC Plant Biology</i> , 2019, 19, 568.	1.6	8
8323	Phylogeography of higher Diptera in glacial and postglacial grasslands in western North America. <i>BMC Ecology</i> , 2019, 19, 53.	3.0	4
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8325	Not so unique to Primates: The independent adaptive evolution of TRIM5 in Lagomorpha lineage. <i>PLoS ONE</i> , 2019, 14, e0226202.	1.1	7
8326	Complete chloroplast genomes of two <i>Siraitia</i> Merrill species: Comparative analysis, positive selection and novel molecular marker development. <i>PLoS ONE</i> , 2019, 14, e0226865.	1.1	30
8327	Molecular identification of Ehrlichia, Anaplasma, Babesia and Theileria in African elephants and their ticks. <i>PLoS ONE</i> , 2019, 14, e0226083.	1.1	5
8328	Phylogenetic position of two species of the <i>Liolaemus elongatus-kriegi</i> Complex and a new northern limit for <i>L. buergeri</i> (Squamata: Liolaemidae). <i>Phyllomedusa</i> , 2019, 18, 115-121.	0.2	1
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8331	Genetic Characterization and Molecular Evolution of Urban Seoul Virus in Southern China. <i>Viruses</i> , 2019, 11, 1137.	1.5	14
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8334	The tin1 gene retains the function of promoting tillering in maize. <i>Nature Communications</i> , 2019, 10, 5608.	5.8	44
8335	Fermentation innovation through complex hybridization of wild and domesticated yeasts. <i>Nature Ecology and Evolution</i> , 2019, 3, 1576-1586.	3.4	76
8336	High insecticide resistance in the major malaria vector <i>Anopheles coluzzii</i> in Chad Republic. <i>Infectious Diseases of Poverty</i> , 2019, 8, 100.	1.5	14
8337	Genome-Wide Identification and Expression Analysis of the Ascorbate Oxidase Gene Family in <i>Gossypium hirsutum</i> Reveals the Critical Role of GhAO1A in Delaying Dark-Induced Leaf Senescence. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6167.	1.8	11
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8344	Genetic analysis reveals the presence of frigate tuna (<i>Auxis thazard</i>) in the bullet tuna (<i>Auxis rochei</i>) fishery of the Iberian Peninsula and the western-central Mediterranean Sea. Bulletin of Marine Science, 2019, 95, 317-325.	0.4	7
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8350	Integrative taxonomy reveals a new <i>Gammarus</i> species (<i>Crustacea</i> , <i>Amphipoda</i>) surviving in a previously unknown southeast European glacial refugium. Journal of Zoological Systematics and Evolutionary Research, 2019, 57, 272-297.	0.6	18
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8352	Topography explains the distribution of genetic diversity in one of the most fragile European hotspots. Diversity and Distributions, 2019, 25, 74-89.	1.9	15
8353	Genetic connectivity and phylogeography of the night shark (<i>Carcharhinus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 Td (signature). Aquatic Conservation: Marine and Freshwater Ecosystems, 2019, 29, 102-114.	0.9	16
8354	Phylogeography of the black rat <i>Rattus rattus</i> in India and the implications for its dispersal history in Eurasia. Biological Invasions, 2019, 21, 417-433.	1.2	10
8355	High cryptic diversity of bitterling fish in the southern West Palearctic. Molecular Phylogenetics and Evolution, 2019, 133, 1-11.	1.2	18
8356	Game of clones: Is <i>Wolbachia</i> inducing speciation in a weevil with a mixed reproductive mode?. Molecular Phylogenetics and Evolution, 2019, 133, 42-53.	1.2	16

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8359	Genetic polymorphism of MHC class III \pm alleles and its association with resistance/susceptibility to viral nervous necrosis virus (VNNV) in golden pompano (<i>Trachinotus ovatus</i>). <i>Aquaculture</i> , 2019, 501, 144-152.	1.7	5
8360	DNA barcoding evidence for the first recorded transmission of <i>Neobenedenia</i> sp. from wild fish species to <i>Seriola lalandi</i> cultured in an open recirculating system on the Coast of Northern Chile. <i>Aquaculture</i> , 2019, 501, 239-246.	1.7	8
8361	Phylogenetic implications and secondary structure analyses of <i>Vigna mungo</i> (L.) Hepper genotypes based on nrDNA ITS2 sequences. <i>Computational Biology and Chemistry</i> , 2019, 78, 389-397.	1.1	4
8362	Avian haemosporidian infections in rufous-collared sparrows in an Andean dry forest: diversity and factors related to prevalence and parasitaemia. <i>Parasitology</i> , 2019, 146, 765-773.	0.7	13
8363	Genetic diversity and demographic analysis of an endangered tree species <i>Diplopanax stachyanthus</i> in subtropical China: implications for conservation and management. <i>Conservation Genetics</i> , 2019, 20, 315-327.	0.8	5
8364	Pathogenicity and molecular phylogenetic analysis reveal a distinct position of the banana fingertip rot pathogen among the <i>Burkholderia cenocepacia</i> genomovars. <i>Plant Pathology</i> , 2019, 68, 804-815.	1.2	6
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8366	Genetic and in silico analysis of plantaricin EFI locus in indigenous isolates of <i>Lactobacillus plantarum</i> . <i>Biotechnology Progress</i> , 2019, 35, e2773.	1.3	2
8367	Evaluation of the molecular variability and characteristics of <i>Paramecium polycaryum</i> and <i>Paramecium nephridiatum</i> , within subgenus <i>Cypriostomum</i> (Ciliophora, Protista). <i>Molecular Phylogenetics and Evolution</i> , 2019, 132, 296-306.	1.2	6
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8369	Challenging the European southern refugium hypothesis: Species-specific structures versus general patterns of genetic diversity and differentiation among small mammals. <i>Global Ecology and Biogeography</i> , 2019, 28, 262-274.	2.7	20
8370	The niches of nuthatches affect their lineage evolution differently across latitude. <i>Molecular Ecology</i> , 2019, 28, 803-817.	2.0	4
8371	Diversification of the genus <i>Apogon</i> (Lacepède, 1801) (Apogonidae: Perciformes) in the tropical eastern Pacific. <i>Molecular Phylogenetics and Evolution</i> , 2019, 132, 232-242.	1.2	11
8372	Genetic diversity of <i>Culicoides</i> species within the <i>Pulicaris</i> complex (Diptera: Ceratopogonidae) in Turkey inferred from mitochondrial COI gene sequences. <i>Acta Tropica</i> , 2019, 190, 380-388.	0.9	8
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8376	High-density quantitative trait locus mapping revealed genetic architecture of leaf angle and tassel size in maize. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	10
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8378	Genetic diversity and the origin of Mongolian native sheep. <i>Livestock Science</i> , 2019, 220, 17-25.	0.6	12
8379	Selective sweep and phylogenetic models for the emergence and spread of pyrimethamine resistance mutations in <i>Plasmodium vivax</i> . <i>Infection, Genetics and Evolution</i> , 2019, 68, 221-230.	1.0	10
8380	Sequence analysis and molecular evolution of Tunisian date palm cultivars (<i>Phoenix dactylifera</i> L.) based on the internal transcribed spacers (ITSs) region of the nuclear ribosomal DNA. <i>Scientia Horticulturae</i> , 2019, 247, 373-379.	1.7	7
8381	Multilocus phylogeography of the brown-spotted pitviper <i>Protobothrops mucrosquamatus</i> (Reptilia: Tj ETQq0 0 0 rgBT /Overlock 10 T and Evolution, 2019, 133, 82-91.	1.2	19
8382	Phylogeography of the New Zealand whelks <i>Cominella maculosa</i> and <i>C. virgata</i> (Gastropoda: Neogastropoda: Buccinoidea: Buccinidae). <i>Biological Journal of the Linnean Society</i> , 2019, 126, 178-202.	0.7	5
8383	The Expansion of Inosine at the Wobble Position of tRNAs, and Its Role in the Evolution of Proteomes. <i>Molecular Biology and Evolution</i> , 2019, 36, 650-662.	3.5	34
8384	<i>Daphnia galeata</i> and <i>D. dentifera</i> are geographically and ecologically separated whereas their hybrids occur in intermediate habitats: A survey of 44 Chinese lakes. <i>Molecular Ecology</i> , 2019, 28, 785-802.	2.0	26
8385	Relationships between mycobiont identity, photobiont specificity and ecological preferences in the lichen genus <i>Peltigera</i> (Ascomycota) in Estonia (northeastern Europe). <i>Fungal Ecology</i> , 2019, 39, 45-54.	0.7	26
8386	DNA barcoding identification and genetic diversity of bamboo shoot wireworms (Coleoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.4	6
8387	Mapping loci controlling fatty acid profiles, oil and protein content by genome-wide association study in <i>Brassica napus</i> . <i>Crop Journal</i> , 2019, 7, 217-226.	2.3	19
8388	Deep mitochondrial lineage divergence among populations of the southern stingray (<i>Hypanus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T Caribbean. <i>Marine Biodiversity</i> , 2019, 49, 1627-1634.	0.3	6
8389	Emergence of tomato leaf curl New Delhi virus in Italy: estimation of incidence and genetic diversity. <i>Plant Pathology</i> , 2019, 68, 601-608.	1.2	31
8390	Molecular divergence between <i>Iridaea cordata</i> (Turner) Bory de Saint-Vincent from the Antarctic Peninsula and the Magellan Region. <i>Journal of Applied Phycology</i> , 2019, 31, 939-949.	1.5	15
8391	The population genomics of multiple tsetse fly (<i>Glossina fuscipes fuscipes</i>) admixture zones in Uganda. <i>Molecular Ecology</i> , 2019, 28, 66-85.	2.0	11
8392	Haplotypic differentiation between seasonal populations of <i>Sargassum horneri</i> (Fucales.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.8	12

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8393	The Origin and Population History of the Endangered Golden Snub-Nosed Monkey (<i>Rhinopithecus</i>)	3.5	20
8394	Evolving in isolation: Genetic tests reject recent connections of Amazonian savannas with the central Cerrado. <i>Journal of Biogeography</i> , 2019, 46, 196-211.	1.4	18
8395	Genetic diversity and population demography of narrow-ridged finless porpoises from South Korea on the basis of mitochondrial DNA variation: Implications for its conservation in East Asia. <i>Marine Mammal Science</i> , 2019, 35, 574-594.	0.9	4
8396	Pleistocene glaciation explains the disjunct distribution of the Chestnut-backed Nuthatch (<i>Aves</i>)	0.7	12
8397	No genetic differentiation, but less diversity, in the Iberian breeding population of the Eurasian Curlew (<i>Numenius arquata</i>). <i>Journal of Ornithology</i> , 2019, 160, 17-25.	0.5	1
8398	The first two mitochondrial genomes of wood wasps (Hymenoptera: Symphyta): Novel gene rearrangements and higher-level phylogeny of the basal hymenopterans. <i>International Journal of Biological Macromolecules</i> , 2019, 123, 1189-1196.	3.6	17
8399	Comprehensive analysis of the mitochondrial DNA diversity in Chinese cattle. <i>Animal Genetics</i> , 2019, 50, 70-73.	0.6	35
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8401	Evolutionary history of the scorpionfly <i>Dicerapanorpa magna</i> (Mecoptera, Panorpidae). <i>Zoologica Scripta</i> , 2019, 48, 93-105.	0.7	8
8402	Morphological and molecular diagnoses of <i>Polydora brevipalpa</i> Zachs, 1933 (Annelida: Spionidae) from the shellfish along the coast of China. <i>Journal of Oceanology and Limnology</i> , 2019, 37, 713-723.	0.6	11
8403	Database establishment for the secondary fungal DNA barcode translational elongation factor 11 (TEF11). <i>Genome</i> , 2019, 62, 160-169.	0.9	41
8404	Natural variation of ZmHKT1 affects root morphology in maize at the seedling stage. <i>Planta</i> , 2019, 249, 879-889.	1.6	16
8405	Host associations and climate influence avian haemosporidian distributions in Benin. <i>International Journal for Parasitology</i> , 2019, 49, 27-36.	1.3	9
8406	Comparative phylogeography of two coastal species of <i>Perinereis</i> Kinberg, 1865 (Annelida, Polychaeta) in the South Atlantic. <i>Marine Biodiversity</i> , 2019, 49, 1537-1551.	0.3	14
8407	Persistence of phylogeographic footprints helps to understand cryptic diversity detected in two marine amphipods widespread in the Mediterranean basin. <i>Molecular Phylogenetics and Evolution</i> , 2019, 132, 53-66.	1.2	22
8408	Species delimitation in the presence of strong incomplete lineage sorting and hybridization: Lessons from <i>Ophioderma</i> (Ophiuroidea: Echinodermata). <i>Molecular Phylogenetics and Evolution</i> , 2019, 131, 138-148.	1.2	37
8409	Nucleotide polymorphisms associated with climate and physiological traits in silver fir (<i>Abies alba</i>)	0.6	6
8410	Molecular identification and genetic diversity analysis of Chocolate mahseer (<i>Neolissochilus</i>) DNA Part A: DNA Mapping, Sequencing, and Analysis, 2019, 30, 397-406.	0.7	7

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8412	The APETALA2-Like Transcription Factor SUPERNUMERARY BRACT Controls Rice Seed Shattering and Seed Size. <i>Plant Cell</i> , 2019, 31, 17-36.	3.1	93
8413	How many came home? Evaluating ex situ conservation of green turtles in the Cayman Islands. <i>Molecular Ecology</i> , 2019, 28, 1637-1651.	2.0	19
8414	Contrasting evolutionary histories in Neotropical birds: Divergence across an environmental barrier in South America. <i>Molecular Ecology</i> , 2019, 28, 1730-1747.	2.0	19
8415	High Levels of Variation Within Gene Sequences of <i>Olea europaea</i> L.. <i>Frontiers in Plant Science</i> , 2018, 9, 1932.	1.7	21
8416	The Complete Chloroplast Genomes of <i>Echinacanthus</i> Species (Acanthaceae): Phylogenetic Relationships, Adaptive Evolution, and Screening of Molecular Markers. <i>Frontiers in Plant Science</i> , 2018, 9, 1989.	1.7	38
8417	Complete mitochondrial genome of <i>Japalura flaviceps</i> : Deep insights into the phylogeny and gene rearrangements of Agamidae species. <i>International Journal of Biological Macromolecules</i> , 2019, 125, 423-431.	3.6	23
8418	Genetic Structure of <i>Liriomyza trifolii</i> (Diptera: Agromyzidae) Associated With Host Plants From Southeastern Mexico. <i>Environmental Entomology</i> , 2019, 48, 253-262.	0.7	2
8419	Molecular phylogeny and taxonomy of subgenus <i>Eothenomys</i> (Cricetidae: Arvicolinae: <i>Eothenomys</i>) with the description of four new species from Sichuan, China. <i>Zoological Journal of the Linnean Society</i> , 2019, 186, 569-598.	1.0	9
8420	How repeatable is microevolution on islands? Patterns of dispersal and colonization-related plant traits in a phylogeographical context. <i>Annals of Botany</i> , 2019, 123, 557-568.	1.4	20
8421	Intra-population genetic diversity and its effects on outlining genetic diversity of ciliate populations: Using <i>Paramecium multimicronucleatum</i> as an example. <i>European Journal of Protistology</i> , 2019, 67, 142-150.	0.5	10
8422	Geographic patterns of mtDNA and Z-linked sequence variation in the Common Chiffchaff and the <i>chiffchaff complex</i> . <i>PLoS ONE</i> , 2019, 14, e0210268.	1.1	14
8423	The Complete Plastid Genome of <i>Magnolia zenii</i> and Genetic Comparison to Magnoliaceae species. <i>Molecules</i> , 2019, 24, 261.	1.7	38
8424	Phylogeography of <i>Ixiolirion songaricum</i> , a spring ephemeral species endemic to Northwest China. <i>Plant Systematics and Evolution</i> , 2019, 305, 205-221.	0.3	5
8425	Molecular phylogeny and diversification timing of the Nemouridae family (Insecta, Plecoptera) in the Japanese Archipelago. <i>PLoS ONE</i> , 2019, 14, e0210269.	1.1	13
8426	A Phylogeographic Approach to the <i>Drosophila suzukii</i> (Diptera: Drosophilidae) Invasion in Brazil. <i>Journal of Economic Entomology</i> , 2019, 112, 425-433.	0.8	21
8427	Genome-wide identification and expression analyses of WRKY transcription factor family members from chickpea (<i>Cicer arietinum</i> L.) reveal their role in abiotic stress-responses. <i>Genes and Genomics</i> , 2019, 41, 467-481.	0.5	60
8428	Hepatitis B virus reverse transcriptase polymorphisms between treated and treatment-naïve chronically infected patients. <i>VirusDisease</i> , 2019, 30, 219-226.	1.0	4

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8430	Conservation implications of population genetic structure in a threatened orchid <i>Cypripedium tibeticum</i> . <i>Plant Diversity</i> , 2019, 41, 13-18.	1.8	9
8431	Genetic structure, phylogeography, and migration routes of <i>Bouteloua gracilis</i> (Kunth) Lag. ex Griffiths (Poaceae:Chloridoideae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 50-60.	1.2	9
8432	An integrative study of island diversification: Insights from the endemic <i>Haemodracon</i> geckos of the Socotra Archipelago. <i>Molecular Phylogenetics and Evolution</i> , 2019, 133, 166-175.	1.2	8
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8434	Enhanced agricultural sustainability through within-species diversification. <i>Nature Sustainability</i> , 2019, 2, 46-52.	11.5	63
8435	Genetic evidence for several cryptic species within the <i>Scarturus elater</i> species complex (Rodentia: Dipodoidea): when cryptic species are really cryptic. <i>Biological Journal of the Linnean Society</i> , 2019, 126, 16-39.	0.7	12
8436	Systematics and description of a new species of <i>Faxonius</i> Ortmann, 1905 (Decapoda: Astacidea): <i>Tj ETQq1 1 0.784314 rgBT /Over</i> 2019, 39, 40-53.	0.3	4
8437	Phylogeography and Population Structure of the Mediterranean Corn Borer, <i>Sesamia nonagrioides</i> (Lepidoptera: Noctuidae), Across Its Geographic Range. <i>Journal of Economic Entomology</i> , 2019, 112, 396-406.	0.8	3
8438	First complete chloroplast genomics and comparative phylogenetic analysis of <i>Commiphora gileadensis</i> and <i>C. foliacea</i> : Myrrh producing trees. <i>PLoS ONE</i> , 2019, 14, e0208511.	1.1	31
8439	Red deer in Iberia: Molecular ecological studies in a southern refugium and inferences on European postglacial colonization history. <i>PLoS ONE</i> , 2019, 14, e0210282.	1.1	29
8440	Multilocus sequence typing of <i>Cryptococcus neoformans</i> var. <i>grubii</i> from Laos in a regional and global context. <i>Medical Mycology</i> , 2019, 57, 557-565.	0.3	14
8441	Evolutionary history of a beautiful damselfly, <i>Matrona basilaris</i> , revealed by phylogeographic analyses: the first study of an odonate species in mainland China. <i>Heredity</i> , 2019, 122, 570-581.	1.2	4
8442	Characterization of the satellitome in lower vascular plants: the case of the endangered fern <i>Vandenboschia speciosa</i> . <i>Annals of Botany</i> , 2019, 123, 587-599.	1.4	20
8443	The evolutionary history of the goby <i>Elacatinus puncticulatus</i> in the tropical eastern pacific: Effects of habitat discontinuities and local environmental variability. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 269-285.	1.2	17
8444	Genetic divergence among <i>Bradyrhizobium</i> strains nodulating wild and cultivated <i>Kummerowia</i> spp. in China. <i>Systematic and Applied Microbiology</i> , 2019, 42, 223-231.	1.2	4
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8448	Phylogeography and genetic connectivity of the marine macroalga <i>Sargassum ilicifolium</i> (Phaeophyceae, Ochrophyta) in the northwestern Pacific. <i>Journal of Phycology</i> , 2019, 55, 7-24.	1.0	17
8449	Systematics of the Sahara-Arabian clade of the Palearctic naked-toed geckos with the description of a new species of <i>Tropicolotes</i> endemic to Oman. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2019, 57, 159-178.	0.6	7
8450	Phylogeography Approach of <i>Diloboderus abderus</i> (Coleoptera: Melolonthidae) in the Southern Cone of America. <i>Neotropical Entomology</i> , 2019, 48, 332-339.	0.5	1
8451	Antimicrobial resistance, virulence and genetic relationship of <i>Vibrio parahaemolyticus</i> in seafood from coasts of Bohai Sea and Yellow Sea, China. <i>International Journal of Food Microbiology</i> , 2019, 290, 116-124.	2.1	57
8452	Molecular diversity and phylogeny of Tunisian <i>Prunus armeniaca</i> L. by evaluating three candidate barcodes of the chloroplast genome. <i>Scientia Horticulturae</i> , 2019, 245, 99-106.	1.7	10
8453	<i>Albugo candida</i> race diversity, ploidy and host-associated microbes revealed using DNA sequence capture on diseased plants in the field. <i>New Phytologist</i> , 2019, 221, 1529-1543.	3.5	41
8454	Recombination and purifying and balancing selection determine the evolution of major antigenic protein 1 (map 1) family genes in <i>Ehrlichia ruminantium</i> . <i>Gene</i> , 2019, 683, 216-224.	1.0	8
8455	Genetic diversity and patterns of demographic expansion in natural populations of milkfish, <i>Chanos chanos</i> (Forsskål, 1775), in the Philippines. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2019, 30, 312-324.	0.7	3
8456	Frequency and genetic diversity of <i>Echinococcus granulosus sensu stricto</i> in sheep and cattle from the steppe region of Djelfa, Algeria. <i>Parasitology Research</i> , 2019, 118, 89-96.	0.6	20
8457	Genetic diversity and effective population size in successive mass selected generations of black shell strain Pacific oyster (<i>Crassostrea gigas</i>) based on microsatellites and mtDNA data. <i>Aquaculture</i> , 2019, 500, 338-346.	1.7	21
8458	Evolutionary and ecological patterns within the South African Bathyergidae: Implications for taxonomy. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 181-197.	1.2	8
8459	<i>Phenacoccus madeirensis</i> Green (Hemiptera: Pseudococcidae): New geographic records and rapid identification using a species-specific PCR assay. <i>Crop Protection</i> , 2019, 116, 68-76.	1.0	7
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8461	A novel approach for the identification and phylogenetic delineation of human <i>Mycoplasma</i> species and strains using genomic segment sequence analysis. <i>Infection, Genetics and Evolution</i> , 2019, 68, 68-76.	1.0	2
8462	Life in sympatry: coexistence of native <i>Eurytemora affinis</i> and invasive <i>Eurytemora carollelee</i> in the Gulf of Finland (Baltic Sea). <i>Oceanologia</i> , 2019, 61, 227-238.	1.1	19
8463	Multilocus phylogeny and taxonomy of pikas of the subgenus <i>Ochotona</i> (Lagomorpha, Ochotonidae). <i>Zoologica Scripta</i> , 2019, 48, 1-16.	0.7	15
8464	Species dilemma of musk deer (<i>Moschus</i> spp) in India: molecular data on cytochrome oxidase I suggests distinct genetic lineage in Uttarakhand compared to other <i>Moschus</i> species. <i>Animal Biotechnology</i> , 2019, 30, 193-201.	0.7	8

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8466	Evolutionary and demographic correlates of Pleistocene coastline changes in the Sicilian wall lizard <i>Podarcis wagleriana</i> . <i>Journal of Biogeography</i> , 2019, 46, 224-237.	1.4	18
8467	The genetic diversity, individual relatedness and possible mating system of an isolated population of the Cyprinid species <i>Megalobrama pellgrini</i> in upper reaches of the Changjiang (Yangtze) River, China. <i>Journal of Oceanology and Limnology</i> , 2019, 37, 1042-1050.	0.6	4
8468	Molecular evidence for repeated recruitment of wild Christmas poinsettia (<i>Euphorbia pulcherrima</i>) into traditional horticulture in Mexico. <i>Genetic Resources and Crop Evolution</i> , 2019, 66, 481-490.	0.8	1
8469	<i>Crassostrea talonata</i> , a new threat to native oyster (<i>Bivalvia: Ostreidae</i>) culture in the Southwest Atlantic. <i>Journal of Experimental Marine Biology and Ecology</i> , 2019, 511, 91-99.	0.7	9
8470	Mitochondrial DNA reveals species composition and phylogenetic relationships of hookworms in northeastern Brazil. <i>Infection, Genetics and Evolution</i> , 2019, 68, 105-112.	1.0	9
8471	Cryptic diversity in Brazilian endemic monkey frogs (<i>Hylidae, Phyllomedusinae, Pithecopus</i>) revealed by multispecies coalescent and integrative approaches. <i>Molecular Phylogenetics and Evolution</i> , 2019, 132, 105-116.	1.2	19
8472	Oceanographic processes shape genetic signatures of planktonic cephalopod paralarvae in two upwelling regions. <i>Progress in Oceanography</i> , 2019, 170, 11-27.	1.5	34
8473	From the Himalayas to a continental Island: Integrative species delimitation in the Brownish-flanked Bush Warbler <i>Horornis fortipes</i> complex. <i>Molecular Phylogenetics and Evolution</i> , 2019, 131, 219-227.	1.2	7
8474	Characterizing patterns of introgressive hybridization between two species of <i>Tyrannus</i> following concurrent range expansion. <i>Ibis</i> , 2019, 161, 770-780.	1.0	3
8475	Comparative Mitogenomic Analysis of Forensically Important Sarcophagid Flies (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 347 Td (392-407.	0.9	16
8476	How rivers and historical climate oscillations impact on genetic structure in Chinese Muntjac (<i>Muntiacus reevesi</i>)?. <i>Diversity and Distributions</i> , 2019, 25, 116-128.	1.9	4
8477	Genetic evidence for regional philopatry of the Bull Shark (<i>Carcharhinus leucas</i>), to nursery areas in estuaries of the Gulf of Mexico and western North Atlantic ocean. <i>Fisheries Research</i> , 2019, 209, 67-74.	0.9	22
8478	Morphological and Molecular Identification of <i>Phlebotomus mascittii</i> Grassi, 1908 Populations From Slovenia. <i>Journal of Medical Entomology</i> , 2019, 56, 565-568.	0.9	8
8479	Phylogeographic structure in the chromosomally polymorphic rodent <i>Cricetulus barabensis</i> sensu lato (Mammalia, Cricetidae). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2019, 57, 679-694.	0.6	9
8480	<i>ZmMADS69</i> functions as a flowering activator through the <i>ZmRap2.7</i> regulatory module and contributes to maize flowering time adaptation. <i>New Phytologist</i> , 2019, 221, 2335-2347.	3.5	100
8481	Analysis of the contribution of landscape attributes on the genetic diversity of <i>Artibeus jamaicensis</i> Leach, 1821. <i>Mammal Research</i> , 2019, 64, 223-233.	0.6	1
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8484	Genetic diversity of MHC class II<i>DRB</i> alleles in the marbled polecat, <i>Vormela peregusna</i>, in Bulgaria. <i>Ethology Ecology and Evolution</i> , 2019, 31, 59-72.	0.6	2
8485	A short LysM protein with high molecular diversity from an arbuscular mycorrhizal fungus, <i>Rhizophagus irregularis</i> . <i>Mycoscience</i> , 2019, 60, 63-70.	0.3	15
8486	Ecological Divergence with Gene Flow in a Thermophilic Cyanobacterium. <i>Microbial Ecology</i> , 2019, 78, 33-41.	1.4	4
8487	Genetic Variation and Differentiation of <i>Hylesia metabus</i> (Lepidoptera: Saturniidae): Moths of Public Health Importance in French Guiana and in Venezuela. <i>Journal of Medical Entomology</i> , 2019, 56, 137-148.	0.9	2
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8490	Molecular characterization of human echinococcosis in Sichuan, Western China. <i>Acta Tropica</i> , 2019, 190, 45-51.	0.9	20
8491	Genetic and Genome Analyses Reveal Genetically Distinct Populations of the Bee Pathogen <i>Nosema ceranae</i> from Thailand. <i>Microbial Ecology</i> , 2019, 77, 877-889.	1.4	8
8492	Origin of the widely and discontinuously distributed mitochondrial genotypes of <i>Oryzias latipes</i> : introduced or native genotypes?. <i>Ichthyological Research</i> , 2019, 66, 183-188.	0.5	1
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8496	Post-glacial colonization of Western Europe brown bears from a cryptic Atlantic refugium out of the Iberian Peninsula. <i>Historical Biology</i> , 2019, 31, 618-630.	0.7	12
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8499	Revisiting the genetic diversity and population structure of the critically endangered leatherback turtles in the South-west Atlantic Ocean: insights for species conservation. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2019, 99, 31-41.	0.4	5
8500	Deciphering demographic history and fine-scale population structure of cobia, <i>Rachycentron canadum</i> (Pisces: Rachycentridae) using microsatellite and mitochondrial markers. <i>Marine Biodiversity</i> , 2019, 49, 381-393.	0.3	3

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8502	Did maize domestication and early spread mediate the population genetics of corn leafhopper?. <i>Insect Science</i> , 2019, 26, 569-586.	1.5	16
8503	Population genetic evidence for positive and purifying selection acting at the human IFN- β locus in Africa. <i>Genes and Immunity</i> , 2019, 20, 143-157.	2.2	4
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8507	Extensive sharing of mitochondrial <i>COI</i> and <i>CYB</i> haplotypes among reef-building staghorn corals (<i>Acropora</i> spp.) in Sabah, North Borneo. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2019, 30, 16-23.	0.7	2
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8509	Genetic diversity and population genetic structure of the only population of Aoluguya Reindeer (<i>Rangifer tarandus</i>) in China. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2019, 30, 24-29.	0.7	11
8510	Genetic structure of intertidal shimofuri goby in the Zhejiang Coastal Sea, China: implications for management. <i>Marine Biodiversity</i> , 2019, 49, 923-931.	0.3	1
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8512	Historical explanation of genetic variation in the Mediterranean horseshoe bat <i>Rhinolophus euryale</i> (Chiroptera: Rhinolophidae) inferred from mitochondrial cytochrome-b and D-loop genes in Iran. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2019, 30, 135-147.	0.7	11
8513	High genetic connectivity among morphologically differentiated populations of the black sea urchin <i>Arbacia lixula</i> (Echinoidea: Arbacioida) across the central African Mediterranean coast. <i>Marine Biodiversity</i> , 2019, 49, 603-620.	0.3	5
8514	Population genetic structure and phylogeography of sterlet (<i>Acipenser ruthenus</i>), Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 and Analysis, 2019, 30, 156-164.	0.7	5
8515	Impact of Orogeny and Environmental Change on Genetic Divergence and Demographic History of <i>Dipus sagitta</i> (Dipodoidea, Dipodinae) since the Pliocene in Inland East Asia. <i>Journal of Mammalian Evolution</i> , 2019, 26, 253-266.	1.0	12
8516	Genetic structure among <i>Charadrius</i> plovers on the African mainland and islands of Madagascar and St. Helena. <i>Ibis</i> , 2020, 162, 104-118.	1.0	4
8517	Molecular systematics of the Amazonian endemic genus <i>Hylexetastes</i> (Aves: Dendrocolaptidae): taxonomic and conservation implications. <i>Ibis</i> , 2020, 162, 119-136.	1.0	9
8518	Lineages of Tuco-Tucos (Ctenomyidae: Rodentia) from Midwest and Northern Brazil: Late Irradiations of Subterranean Rodents Towards the Amazon Forest. <i>Journal of Mammalian Evolution</i> , 2020, 27, 161-176.	1.0	17

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8520	Evidence of doubly uniparental inheritance of the mitochondrial DNA in <i>Polititapes rhomboides</i> (Bivalvia, Veneridae): Evolutionary and population genetic analysis of F and M mitotypes. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 541-560.	0.6	7
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8523	A complex pattern of post-divergence expansion, contraction, introgression, and asynchronous responses to Pleistocene climate changes in two <i>Dipeltaster</i> species from western China. <i>Journal of Systematics and Evolution</i> , 2020, 58, 247-262.	1.6	13
8524	Ribosome profiling analysis identified a KRAS-interacting microprotein that represses oncogenic signaling in hepatocellular carcinoma cells. <i>Science China Life Sciences</i> , 2020, 63, 529-542.	2.3	36
8525	Mitochondrial DNA enrichment reduced NUMT contamination in porcine NGS analyses. <i>Briefings in Bioinformatics</i> , 2020, 21, 1368-1377.	3.2	5
8526	Genetic analysis reveals strong phylogeographical divergences within the Scarlet Macaw <i>Ara macao</i> . <i>Ibis</i> , 2020, 162, 735-748.	1.0	6
8527	Molecular Phylogenetics of <i>Bradypus</i> (Three-Toed Sloth, Pilosa: Bradypodidae, Mammalia) and Phylogeography of <i>Bradypus variegatus</i> (Brown-Throated Three-Toed Sloth) with Mitochondrial Gene Sequences. <i>Journal of Mammalian Evolution</i> , 2020, 27, 461-482.	1.0	4
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8529	The mitochondrial genomes of three skippers: Insights into the evolution of the family Hesperiiidae (Lepidoptera). <i>Genomics</i> , 2020, 112, 432-441.	1.3	22
8530	Molecular characterization of arabis mosaic virus from grapevines in Iran. <i>Journal of Plant Pathology</i> , 2020, 102, 179-181.	0.6	2
8531	Adaptive signals of flowering time pathways in wild barley from Israel over 28 generations. <i>Heredity</i> , 2020, 124, 62-76.	1.2	13
8532	Genetic and morphological characterization of <i>Ixodes apronophorus</i> from Western Siberia, Russia. <i>Ticks and Tick-borne Diseases</i> , 2020, 11, 101284.	1.1	8
8533	DNA barcoding and fauna of phlebotomine sand flies (Diptera: Psychodidae: Phlebotominae) from Los Tuxtlas, Veracruz, Mexico. <i>Acta Tropica</i> , 2020, 201, 105220.	0.9	15
8534	Plastid phylogenomic insights into the evolution of the Caprifoliaceae s.l. (Dipsacales). <i>Molecular Phylogenetics and Evolution</i> , 2020, 142, 106641.	1.2	52
8535	Satellite DNA content of B chromosomes in the characid fish <i>Characidium gomesi</i> supports their origin from sex chromosomes. <i>Molecular Genetics and Genomics</i> , 2020, 295, 195-207.	1.0	22
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8538	Evolutionary history of mountain voles of the subgenus <i>Aschizomys</i> (Cricetidae, Rodentia), inferred from mitochondrial and nuclear markers. <i>Integrative Zoology</i> , 2020, 15, 187-201.	1.3	3
8539	Navigating the southern seas with small fins: Genetic connectivity of seahorses (<i>Hippocampus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 60	1.4	6
8540	Evolutionary biogeography on <i>Ophiocordyceps sinensis</i> : An indicator of molecular phylogeny to geochronological and ecological exchanges. <i>Geoscience Frontiers</i> , 2020, 11, 807-820.	4.3	10
8541	Phylogenetic relationships and phylogeography of the genus <i>Sinocyrtaspis</i> Liu, 2000 (Orthoptera: Tettigoniidae: Meconematinae) reveal speciation processes related to climate change. <i>Systematic Entomology</i> , 2020, 45, 144-159.	1.7	11
8542	Population genetic structure and demographic history of the scallop <i>Argopecten purpuratus</i> from Peru and Northern Chile: implications for management and conservation of natural beds. <i>Hydrobiologia</i> , 2020, 847, 11-26.	1.0	4
8543	Mitochondrial genes associated with pyrethroid resistance revealed by mitochondrial genome and transcriptome analyses in the malaria vector <i>Anopheles sinensis</i> (Diptera: Culicidae). <i>Pest Management Science</i> , 2020, 76, 769-778.	1.7	7
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8546	A Mitochondrial Phylogeny of the Sand Cat (<i>Felis margarita</i> Loche, 1858). <i>Journal of Mammalian Evolution</i> , 2020, 27, 525-534.	1.0	6
8547	Allopatric divergence drives the genetic structuring of an endangered alpine endemic lizard with a skyâ€island distribution. <i>Animal Conservation</i> , 2020, 23, 104-118.	1.5	13
8548	Upliftâ€driven diversification revealed by the historical biogeography of the cockroach <i>Cryptocercus</i> Scudder (Blattodea: Cryptocercidae) in eastern Asia. <i>Systematic Entomology</i> , 2020, 45, 60-72.	1.7	7
8549	A comprehensive approach uncovers hidden diversity in freshwater mussels (Bivalvia: Unionidae) with the description of a novel species. <i>Cladistics</i> , 2020, 36, 88-113.	1.5	23
8550	Habitat loss, fragmentation, and the genetic status of Roanoke bass. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2020, 77, 375-387.	0.7	2
8551	<i>Fasciola hepatica</i> in Brazil: genetic diversity provides insights into its origin and geographic dispersion. <i>Journal of Helminthology</i> , 2020, 94, e83.	0.4	14
8552	Comparative phylogeography of two hemipteran species (<i>Geisha distinctissima</i> and <i>Megacopta</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 60 concordant historical demographies. <i>Heredity</i> , 2020, 124, 207-222.	1.2	3
8553	Identification and Characterization of <i>Colletotrichum</i> Species Associated with Anthracnose Disease of <i>Camellia oleifera</i> in China. <i>Plant Disease</i> , 2020, 104, 474-482.	0.7	27
8554	Genetic assessment of the invasion history of <i>Drosophila suzukii</i> in Argentina. <i>Journal of Pest Science</i> , 2020, 93, 63-75.	1.9	22

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8556	Genetic variability on worldwide populations of the scale insect <i>Pulvinariella mesembryanthemi</i> . <i>Biological Invasions</i> , 2020, 22, 735-748.	1.2	2
8557	Origin and dissemination route of pear accessions from Western China to abroad based on combined analysis of SSR and cpDNA markers. <i>Genetic Resources and Crop Evolution</i> , 2020, 67, 107-128.	0.8	1
8558	Spatial distribution and genetic structure of loliginid paralarvae along the Galician coast (NW Spain). <i>Fisheries Research</i> , 2020, 222, 105406.	0.9	10
8559	Genetic data support speciation between <i>Panstrongylus howardi</i> and <i>Panstrongylus chinai</i> , vectors of Chagas disease in Ecuador. <i>Infection, Genetics and Evolution</i> , 2020, 78, 104103.	1.0	5
8560	Diversity and phenotypic analyses of salt- and heat-tolerant wild bean <i>Phaseolus filiformis</i> rhizobia native of a sand beach in Baja California and description of <i>Ensifer aridi</i> sp. nov.. <i>Archives of Microbiology</i> , 2020, 202, 309-322.	1.0	8
8561	Genetic variability and functional implication of HPV16 from cervical intraepithelial neoplasia in Shanghai women. <i>Journal of Medical Virology</i> , 2020, 92, 372-381.	2.5	8
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8563	Secondary contact after allopatric divergence explains avian speciation and high species diversity in the Himalayan-Hengduan Mountains. <i>Molecular Phylogenetics and Evolution</i> , 2020, 143, 106671.	1.2	14
8564	Vulnerability to climate change for two endemic high-elevation, low-dispersive <i>Annitella</i> species (Trichoptera) in Sierra Nevada, the southernmost high mountain in Europe. <i>Insect Conservation and Diversity</i> , 2020, 13, 283-295.	1.4	13
8565	Population structure and species delimitation of rice white tip nematode, <i>Aphelenchoides besseyi</i> (Nematoda: Aphelenchoididae), in China. <i>Plant Pathology</i> , 2020, 69, 159-167.	1.2	16
8566	Characterization of a hybrid zone between two annual killifish genus <i>Austrolebias</i> from the Biosphere Reserve and Ramsar Sites in South America. <i>Hydrobiologia</i> , 2020, 847, 421-442.	1.0	4
8567	Geography alone cannot explain <i>Tetranychus truncatus</i> (Acari: Tetranychidae) population abundance and genetic diversity in the context of the center-periphery hypothesis. <i>Heredity</i> , 2020, 124, 383-396.	1.2	9
8568	The evolution of polymorphism in the warning coloration of the Amazonian poison frog <i>Adelphobates galactonotus</i> . <i>Heredity</i> , 2020, 124, 439-456.	1.2	11
8569	Male-male competition and repeated evolution of terrestrial breeding in Atlantic Coastal Forest frogs*. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 459-475.	1.1	9
8570	Genetic diversity and population structure of burbot <i>Lota lota</i> in Germany: Implications for conservation and management. <i>Fisheries Management and Ecology</i> , 2020, 27, 170-184.	1.0	8
8571	Population diversity of <i>Cistopus indicus</i> inferred from mitochondrial DNA (Cytochrome b) variation from China and Vietnam. <i>Molluscan Research</i> , 2020, 40, 1-7.	0.2	4
8572	Widespread prevalence but contrasting patterns of intragenomic rRNA polymorphisms in nematodes: Implications for phylogeny, species delimitation and life history inference. <i>Molecular Ecology Resources</i> , 2020, 20, 318-332.	2.2	16

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8574	Host Abundance and Identity Determine the Epidemiology and Evolution of a Generalist Plant Virus in a Wild Ecosystem. <i>Phytopathology</i> , 2020, 110, 94-105.	1.1	6
8575	Lack of gene flow between <i>Phytophthora infestans</i> populations of two neighboring countries with the largest potato production. <i>Evolutionary Applications</i> , 2020, 13, 318-329.	1.5	15
8576	Time-averaged serum uric acid and 10-year incident diabetic kidney disease: A prospective study from China. <i>Journal of Diabetes</i> , 2020, 12, 169-178.	0.8	5
8577	Long-term within-basin isolation patterns, different conservation units, and interspecific mitochondrial DNA introgression in an amphipod endemic to the ancient Lake Skadar system, Balkan Peninsula. <i>Freshwater Biology</i> , 2020, 65, 209-225.	1.2	9
8578	Genetic structure and demographic histories of two sympatric <i>Culter</i> species in eastern China. <i>Journal of Oceanology and Limnology</i> , 2020, 38, 408-426.	0.6	1
8579	New and Old World phylogeography of pumpkinseed <i>Lepomis gibbosus</i> (Linnaeus, 1758): the North American origin of introduced populations in Europe. <i>Hydrobiologia</i> , 2020, 847, 345-364.	1.0	13
8580	Effects of climate and geography on spatial patterns of genetic structure in tropical skinks. <i>Molecular Phylogenetics and Evolution</i> , 2020, 143, 106661.	1.2	6
8581	Effects of dams and their environmental impacts on the genetic diversity and connectivity of freshwater mussel populations in Poyang Lake Basin, China. <i>Freshwater Biology</i> , 2020, 65, 264-277.	1.2	15
8582	Molecular and morphological evidence reveals hybridisation between two endemic cyprinid fishes. <i>Journal of Fish Biology</i> , 2020, 96, 1234-1250.	0.7	7
8583	Nucleotide diversity and demographic history of <i>Pinus bungeana</i> , an endangered conifer species endemic in China. <i>Journal of Systematics and Evolution</i> , 2020, 58, 282-294.	1.6	10
8584	Non-SMC Condensin I Complex Subunit D2 Is a Prognostic Factor in Triple-Negative Breast Cancer for the Ability to Promote Cell Cycle and Enhance Invasion. <i>American Journal of Pathology</i> , 2020, 190, 37-47.	1.9	16
8585	Hybridization with natives augments the threats of introduced species in <i>Sonneratia</i> mangroves. <i>Aquatic Botany</i> , 2020, 160, 103166.	0.8	8
8586	A Spirit of Trust: A Reading of Hegel's Phenomenology, by Robert Brandom. <i>Mind</i> , 2020, 129, 990-999.	0.2	1
8587	Seasonality of interactions between a plant virus and its host during persistent infection in a natural environment. <i>ISME Journal</i> , 2020, 14, 506-518.	4.4	45
8588	The Complete Chloroplast Genomes of Two <i>Lespedeza</i> Species: Insights into Codon Usage Bias, RNA Editing Sites, and Phylogenetic Relationships in <i>Desmodieae</i> (Fabaceae: Papilionoideae). <i>Plants</i> , 2020, 9, 51.	1.6	40
8589	Population subdivision and hybridization in a species complex of <i>Gentiana</i> in the Qinghai-Tibetan Plateau. <i>Annals of Botany</i> , 2020, 125, 677-690.	1.4	14
8590	Phylogeography of the Siberian weasel (<i>Mustela sibirica</i>), based on a mitochondrial DNA analysis. <i>Biological Journal of the Linnean Society</i> , 2020, 129, 587-593.	0.7	6

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8592	Native bighead carp <i>Hypophthalmichthys nobilis</i> and silver carp <i>Hypophthalmichthys molitrix</i> populations in the Pearl River are threatened by Yangtze River introductions as revealed by mitochondrial DNA. <i>Journal of Fish Biology</i> , 2020, 96, 651-662.	0.7	12
8593	Genetic diversity of a widespread annual killifish from coastal Tanzania. <i>BMC Evolutionary Biology</i> , 2020, 20, 1.	3.2	92
8594	Living on the edge: comparative phylogeography and phylogenetics of <i>Oreohelix</i> land snails at their range edge in Western Canada. <i>BMC Evolutionary Biology</i> , 2020, 20, 3.	3.2	5
8595	Phylogenetic divergence between <i>Rickettsia amblyommatis</i> strains from Argentina. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2020, 69, 101418.	0.7	4
8596	Subspecific identity and a comparison of genetic diversity between wild and ex situ wildebeest. <i>Zoo Biology</i> , 2020, 39, 129-140.	0.5	0
8597	Chloroplast genome of an extremely endangered conifer <i>Thuja sutchuenensis</i> Franch.: gene organization, comparative and phylogenetic analysis. <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 409-418.	1.4	10
8598	A comprehensive phylogeographic study of <i>Arion vulgaris</i> Moquin-Tandon, 1855 (Gastropoda: Tj ETQq1 1 0.784314 rgBT /Oyerlock 10	0.7	11
8599	Variable outcomes of hybridization between declining <i>Alosa alosa</i> and <i>Alosa fallax</i> . <i>Evolutionary Applications</i> , 2020, 13, 636-651.	1.5	12
8600	Wing morphology of the butterfly <i>Coenonympha arcania</i> in Europe: Traces of both historical isolation in glacial refugia and current adaptation. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 929-943.	0.6	6
8601	The virome of maize rough dwarf disease: Molecular genome diversification, phylogeny and selection. <i>Annals of Applied Biology</i> , 2020, 176, 192-202.	1.3	3
8602	First report on <i>Wolbachia</i> endosymbiosis in freshwater <i>Aphelocheirus aestivalis</i> (Heteroptera: Aphelocheiridae) and its potential impact on genetic diversity of host. <i>Entomological Science</i> , 2020, 23, 44-56.	0.3	2
8603	Identification and evolutionary analysis of polycistronic miRNA clusters in domesticated and wild wheat. <i>Genomics</i> , 2020, 112, 2334-2348.	1.3	12
8604	Datamining, Genetic Diversity Analyses, and Phylogeographic Reconstructions Redefine the Worldwide Evolutionary History of <i>Grapevine Pinot gris virus</i> and <i>Grapevine berry inner necrosis virus</i> . <i>Phytobiomes Journal</i> , 2020, 4, 165-177.	1.4	33
8605	Phylogeny of European Anodontini (Bivalvia: Unionidae) with a redescription of <i>Anodonta exulcerata</i> . <i>Zoological Journal of the Linnean Society</i> , 2020, 189, 745-761.	1.0	13
8606	Are striped mullet (<i>Mugil cephalus</i>) philopatric?. <i>Marine Biology</i> , 2020, 167, 1.	0.7	8
8607	Molecular evidence for three genetic species of <i>Dipteryx</i> in the Peruvian Amazon. <i>Genetica</i> , 2020, 148, 1-11.	0.5	5
8608	Complex phylogeographic relationships among the Eurasian perch (<i>Perca fluviatilis</i>) populations in the eastern part of the Baltic Sea Region. <i>Hydrobiologia</i> , 2020, 847, 925-938.	1.0	3

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8610	Genetic diversity of TLR3 and TLR8 genes among five Chinese native cattle breeds from southwest China. <i>Livestock Science</i> , 2020, 232, 103895.	0.6	4
8611	Extremely diversified haplotypes observed among assemblage B population of <i>Giardia intestinalis</i> in Kenya. <i>Parasitology International</i> , 2020, 75, 102038.	0.6	7
8612	Phylogeographic evidence that the distribution of cryptic euryhaline species in the <i>Gambusia punctata</i> species group in Cuba was shaped by the archipelago geological history. <i>Molecular Phylogenetics and Evolution</i> , 2020, 144, 106712.	1.2	5
8613	The roles of vicariance and dispersal in the differentiation of two species of the <i>Rhinella marina</i> species complex. <i>Molecular Phylogenetics and Evolution</i> , 2020, 145, 106723.	1.2	12
8614	The enigmatic Leosaurae clade: Phylogeography, species delimitation, phylogeny and historical biogeography of its southernmost species. <i>Molecular Phylogenetics and Evolution</i> , 2020, 144, 106725.	1.2	10
8615	Multilocus phylogenetic analysis helps to untangle the taxonomic puzzle of chubs (genus <i>Squalius</i> .) <i>Journal of the Linnean Society</i> , 2020, 189, 953-974.	1.0	12
8616	Complete Genome Characterization and Coat Protein Genealogy of Isolates of Maize dwarf mosaic virus from Johnsongrass and Maize in Oklahoma and Missouri. <i>Plant Disease</i> , 2020, 104, 1214-1223.	0.7	4
8617	Chloroplast and nuclear DNA analyses provide insight into the phylogeography and conservation genetics of <i>Camellia nitidissima</i> (Theaceae) in southern Guangxi, China. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	7
8618	Genetic structure and geographical variation of <i>Bithynia siamensis goniomphalos sensu lato</i> (Gastropoda: Bithyniidae), the snail intermediate host of <i>Opisthorchis viverrini sensu lato</i> (Digenea.) <i>Journal for Parasitology</i> , 2020, 50, 55-62.	1.3	12
8619	Genetic diversity and lack of molecular evidence for hemoplasma cross-species transmission between wild and synanthropic mammals from Central-Western Brazil. <i>Acta Tropica</i> , 2020, 203, 105303.	0.9	25
8620	A new species of <i>Cambeva</i> (Siluriformes, Trichomycteridae) from the Rio Ivaã-basin, Upper Rio Paranã basin, Paranã State, Brazil. <i>Journal of Fish Biology</i> , 2020, 96, 350-363.	0.7	12
8621	Invasion dynamics of the white piranha (<i>Serrasalmus brandtii</i>) in a Neotropical river basin. <i>Biological Invasions</i> , 2020, 22, 983-995.	1.2	8
8622	Genetic structure of natural populations of endangered <i>Tor mahseer</i> , <i>Tor tor</i> (Hamilton, 1822) inferred from two mitochondrial DNA markers. <i>Meta Gene</i> , 2020, 23, 100635.	0.3	6
8623	Population genetics and phenotypic differentiation of cotton leafhoppers (Hemiptera: Cicadellidae) from Pakistan. <i>Ecoscience</i> , 2020, 27, 33-43.	0.6	0
8624	Multilocus data of a manakin species reveal cryptic diversification moulded by vicariance. <i>Zoologica Scripta</i> , 2020, 49, 129-144.	0.7	15
8625	Molecular characterisation of five <i>Sarcocystis</i> species in domestic sheep (<i>Ovis aries</i>) from Spain. <i>Parasitology Research</i> , 2020, 119, 215-231.	0.6	21
8626	Systematics and evolution of the libyan jird based on molecular and morphometric data. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 439-458.	0.6	4

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8628	Development and field evaluation of a species-specific mt-COI targeted SYBR-Green Real Time PCR for detection and quantification of <i>Haemonchus contortus</i> in cattle in Turkey. <i>Veterinary Parasitology</i> , 2020, 277, 109020.	0.7	1
8629	European minnows through time: museum collections aid genetic assessment of species introductions in freshwater fishes (Cyprinidae: Phoxinus species complex). <i>Heredity</i> , 2020, 124, 410-422.	1.2	25
8630	Historical decline of genetic diversity in a range-periphery population of Spruce Grouse (<i>Falcapennis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.8	3
8631	High-Throughput Sequencing Reveals Bell Pepper Endornavirus Infection in Pepper (<i>Capsicum annum</i>) in Slovakia and Enables Its Further Molecular Characterization. <i>Plants</i> , 2020, 9, 41.	1.6	17
8632	<i>Leptoglossus occidentalis</i> (Hemiptera: Coreidae) occurrence, potential habitats, and COI diversity in South Korea. <i>Journal of Asia-Pacific Biodiversity</i> , 2020, 13, 35-45.	0.2	11
8633	Phylogeography and population dynamics of an endemic oak (<i>Quercus fabri</i> Hance) in subtropical China revealed by molecular data and ecological niche modeling. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	11
8634	Genetic and phylogenetic structure of <i>Hynobius quelpaertensis</i> , an endangered endemic salamander species on the Korean Peninsula. <i>Genes and Genomics</i> , 2020, 42, 165-178.	0.5	5
8635	Morphological and genetic characterization of Mount Kenya brush-furred rats (<i>Lophuromys Peters</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.6	1
8636	Genetic variability in the parasitic fly, <i>Sarcophaga villeneuveana</i> , in south-western Europe and Morocco. <i>BioControl</i> , 2020, 65, 59-70.	0.9	6
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8638	Phylogeography of the specialist plant <i>Mandirola hirsuta</i> (Gesneriaceae) suggests ancient habitat fragmentation due to savanna expansion. <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2020, 262, 151522.	0.6	3
8639	Molecular detection and identification of <i>Bartonella</i> in the cat flea <i>Ctenocephalides felis felis</i> collected from companion animals in a border area in northeastern Argentina. <i>Veterinary Parasitology: Regional Studies and Reports</i> , 2020, 19, 100361.	0.3	1
8640	Utility of genetic variation in coat color genes to distinguish wild, domestic and hybrid South American camelids for forensic and judicial applications. <i>Forensic Science International: Genetics</i> , 2020, 45, 102226.	1.6	12
8641	Conservation and innovation: Plastome evolution during rapid radiation of <i>Rhodiola</i> on the Qinghai-Tibetan Plateau. <i>Molecular Phylogenetics and Evolution</i> , 2020, 144, 106713.	1.2	30
8642	Dogs are reservoir hosts for possible transmission of human strongyloidiasis in Thailand: molecular identification and genetic diversity of causative parasite species. <i>Journal of Helminthology</i> , 2020, 94, e110.	0.4	17
8643	Mitochondrial genomes of four satyrine butterflies and phylogenetic relationships of the family Nymphalidae (Lepidoptera: Papilionoidea). <i>International Journal of Biological Macromolecules</i> , 2020, 145, 272-281.	3.6	17
8644	The Anatolian glacial refugium and human-mediated colonization: a phylogeographical study of the stone marten (<i>Martes foina</i>) in Turkey. <i>Biological Journal of the Linnean Society</i> , 2020, 129, 470-491.	0.7	5

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8646	Contrasting impacts of a novel specialist vector on multihost viral pathogen epidemiology in wild and managed bees. <i>Molecular Ecology</i> , 2020, 29, 380-393.	2.0	20
8647	Out of Africa: The origins of the protozoan blood parasites of the <i>Trypanosoma cruzi</i> clade found in bats from Africa. <i>Molecular Phylogenetics and Evolution</i> , 2020, 145, 106705.	1.2	23
8648	A simple molecular identification method of the <i>Thrips tabaci</i> (Thysanoptera: Thripidae) cryptic species complex. <i>Bulletin of Entomological Research</i> , 2020, 110, 397-405.	0.5	15
8649	A tale of four bears: Environmental signal on the phylogeographical patterns within the extant <i>Ursus</i> species. <i>Journal of Biogeography</i> , 2020, 47, 472-486.	1.4	10
8650	Spatio-temporal formation of the genetic diversity in the Mediterranean dwelling lichen during the Neogene and Quaternary epochs. <i>Molecular Phylogenetics and Evolution</i> , 2020, 144, 106704.	1.2	7
8651	Widespread Gene Flow Model Explains the Geneticâ€“Morphological Variation in a Giant Water Bug Species Under Fine-Scale Spatial Sampling. <i>Annals of the Entomological Society of America</i> , 2020, 113, 160-170.	1.3	1
8652	Unraveling the diversification and systematic puzzle of the highly polymorphic <i>Psammobates tentorius</i> (Bell, 1828) complex (Reptilia: Testudinidae) through phylogenetic analyses and species delimitation approaches. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 308-326.	0.6	7
8653	Polyphasic phenotypic and genetic analysis reveals clonal nature of <i>Xanthomonas axonopodis</i> pv. <i>punicae</i> causing pomegranate bacterial blight. <i>Plant Pathology</i> , 2020, 69, 347-359.	1.2	14
8654	Phylogeography, speciation and demographic history: Contrasting evidence from mitochondrial and nuclear markers of the <i>Odorrana graminea</i> sensu lato (Anura, Ranidae) in China. <i>Molecular Phylogenetics and Evolution</i> , 2020, 144, 106701.	1.2	14
8655	Investigation of PIC1 (permease in chloroplasts 1) geneâ€™s role in iron homeostasis: bioinformatics and expression analyses in tomato and sorghum. <i>BioMetals</i> , 2020, 33, 29-44.	1.8	9
8656	Genetic diversity in potato mop-top virus populations in the United States and a global analysis of the PMTV genome. <i>European Journal of Plant Pathology</i> , 2020, 156, 333-342.	0.8	2
8657	Sympatric lineages in the <i>Mantidactylus ambreensis</i> complex of Malagasy frogs originated allopatrically rather than by in-situ speciation. <i>Molecular Phylogenetics and Evolution</i> , 2020, 144, 106700.	1.2	12
8658	Detection and molecular characterization of canine circovirus circulating in northeastern China during 2014â€“2016. <i>Archives of Virology</i> , 2020, 165, 137-143.	0.9	21
8659	Analysis of Genetic Variation Among Cowpea Aphid (Hemiptera: Aphididae) Populations Evidenced from Mitochondrial and Nuclear DNA Sequences. <i>Annals of the Entomological Society of America</i> , 2020, 113, 149-159.	1.3	0
8660	The mitochondrial genomes of ladybird beetles and implications for evolution and phylogeny. <i>International Journal of Biological Macromolecules</i> , 2020, 147, 1193-1203.	3.6	9
8661	Genetic Characterization of Exotic Commercial Honey Bee (Hymenoptera: Apidae) Populations in Thailand Reveals High Genetic Diversity and Low Population Substructure. <i>Journal of Economic Entomology</i> , 2020, 113, 34-42.	0.8	1
8662	Genetic variability and demographic history of <i>Anguilla mossambica</i> (Peters, 1852) from continental Africa and Madagascar. <i>Journal of Fish Biology</i> , 2020, 96, 1251-1259.	0.7	4

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8664	Phylogeographic pattern and population structure of the Persian stone loach, <i>Oxynoemacheilus persa</i> (Heckel 1847) (family: Nemacheilidae) in southern Iran with implications for conservation. <i>Environmental Biology of Fishes</i> , 2020, 103, 77-88.	0.4	4
8665	Double control regions of some flatfish mitogenomes evolve in a concerted manner. <i>International Journal of Biological Macromolecules</i> , 2020, 142, 11-17.	3.6	1
8666	Seed germination schedule and environmental context shaped the population genetic structure of subtropical evergreen oaks on the Yun-Gui Plateau, Southwest China. <i>Heredity</i> , 2020, 124, 499-513.	1.2	10
8667	Genetic homogeneity in the face of morphological heterogeneity in the harbor porpoise from the Black Sea and adjacent waters (<i>Phocoena phocoena relicta</i>). <i>Heredity</i> , 2020, 124, 469-484.	1.2	5
8668	Low innate immune-gene diversity in the critically endangered orange-bellied parrot (<i>Neophema</i>)	0.2	11
8669	Evolutionary history of a relict conifer, <i>Pseudotaxus chienii</i> (Taxaceae), in south-east China during the late Neogene: old lineage, young populations. <i>Annals of Botany</i> , 2020, 125, 105-117.	1.4	27
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8671	Drivers of bromeliad leaf and floral bract variation across a latitudinal gradient in the Atlantic Forest. <i>Journal of Biogeography</i> , 2020, 47, 261-274.	1.4	6
8672	Oil induces chlorophyll deficient propagules in mangroves. <i>Marine Pollution Bulletin</i> , 2020, 150, 110667.	2.3	7
8673	Genetic diversity of Aoluguya Reindeer based on D-loop region of mtDNA and its conservation implications. <i>Gene</i> , 2020, 733, 144271.	1.0	4
8674	Optimal markers for the identification of <i>Colletotrichum</i> species. <i>Molecular Phylogenetics and Evolution</i> , 2020, 143, 106694.	1.2	51
8675	Significant population genetic structuring in <i>Rhizopertha dominica</i> across Turkey: Biogeographic and practical implications. <i>Journal of Stored Products Research</i> , 2020, 85, 101536.	1.2	3
8676	Phylogeography and population history of the least weasel (<i>Mustela nivalis</i>) in the Palearctic based on multilocus analysis. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 408-426.	0.6	4
8677	Crayfish populations genetically fragmented in streams impounded for 36–104 years. <i>Freshwater Biology</i> , 2020, 65, 768-785.	1.2	14
8678	Plastome phylogenomic insights into the Sino-Japanese biogeography of <i>Diabelia</i> (Caprifoliaceae). <i>Journal of Systematics and Evolution</i> , 2020, 58, 972-987.	1.6	18
8679	Integrative taxonomy uncovers hidden species diversity in the rheophilic genus <i>Potamometra</i> (Hemiptera: Gerridae). <i>Zoologica Scripta</i> , 2020, 49, 174-186.	0.7	26
8680	Mitogenome Diversity and Maternal Origins of Guangxi Cattle Breeds. <i>Animals</i> , 2020, 10, 19.	1.0	12

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8683	Diversification and evolutionary history of brush-tailed mice, Calomyscidae (Rodentia), in southwestern Asia. <i>Organisms Diversity and Evolution</i> , 2020, 20, 155-170.	0.7	8
8684	Molecular analysis of the invasive populations of <i>Urochloa</i> (Poaceae) in a large Neotropical reservoir. <i>Aquatic Botany</i> , 2020, 161, 103183.	0.8	4
8685	Morphological and molecular analyses of Leafhopper, <i>Amrasca biguttula</i> (Ishida) (Hemiptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 587 Asia-Pacific Entomology, 2020, 23, 260-268.	0.4	1
8686	Phylogeography highlights two different Atlantic/Mediterranean lineages and a phenotypic latitudinal gradient for the deep-sea morid codling <i>Lepidion lepidion</i> (Gadiformes: Moridae). <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2020, 157, 103212.	0.6	3
8687	Five new mitogenomes of <i>Phylloscopus</i> (Passeriformes, Phylloscopidae): Sequence, structure, and phylogenetic analyses. <i>International Journal of Biological Macromolecules</i> , 2020, 146, 638-647.	3.6	25
8688	Integrative description of bisexual <i>Paramacrobotus experimentalis</i> sp. nov. (Macrobotidae) from republic of Madagascar (Africa) with microbiome analysis. <i>Molecular Phylogenetics and Evolution</i> , 2020, 145, 106730.	1.2	34
8689	The ghost of connections past: A role for mainland vicariance in the isolation of an insular population of the red-billed chough (Aves: Corvidae). <i>Journal of Biogeography</i> , 2020, 47, 2567-2583.	1.4	4
8690	Testing species hypotheses for <i>Fridericia magna</i> , an enchytraeid worm (Annelida: Clitellata) with great mitochondrial variation. <i>BMC Evolutionary Biology</i> , 2020, 20, 116.	3.2	6
8691	The molecular taxonomy of three endemic Central Asian species of <i>Ranunculus</i> (Ranunculaceae). <i>PLoS ONE</i> , 2020, 15, e0240121.	1.1	9
8692	Cystic Echinococcosis of Camels: 12S rRNA Gene Variation Revealed Changing Pattern of Genetic Diversity Within <i>Echinococcus granulosus sensu lato</i> in the Middle East and North/Sub-Saharan Africa. <i>Frontiers in Veterinary Science</i> , 2020, 7, 618.	0.9	4
8693	A Genetic Window on Sardinian Native Horse Breeds through Uniparental Molecular Systems. <i>Animals</i> , 2020, 10, 1544.	1.0	7
8694	Exploring the Genetic Background of the Differences in Nest-Building Behavior in European Rabbit. <i>Animals</i> , 2020, 10, 1579.	1.0	4
8695	Cryptic species in White Cloud Mountain minnow, <i>Tanichthys albonubes</i> : Taxonomic and conservation implications. <i>Molecular Phylogenetics and Evolution</i> , 2020, 153, 106950.	1.2	8
8696	Transit From Autotrophism to Heterotrophism: Sequence Variation and Evolution of Chloroplast Genomes in Orobanchaceae Species. <i>Frontiers in Genetics</i> , 2020, 11, 542017.	1.1	6
8697	Molecular and morphometric divergence of four species of butterflies (Nymphalidae and Pieridae) from the Western Himalaya, India. <i>Molecular Biology Reports</i> , 2020, 47, 8687-8699.	1.0	1
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8700	Population Genetic Structure and Demography of the Critically Endangered Chequered Blue Butterfly (<i>Scolitantides orion</i>) in a Highly Isolated Part of Its Distribution Range. <i>Insects</i> , 2020, 11, 608.	1.0	2
8701	Chromoblastomycosis in an Endemic Area of Brazil: A Clinical-Epidemiological Analysis and a Worldwide Haplotype Network. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 204.	1.5	11
8702	Molecular Characterization and Genomic Function of Grapevine Geminivirus A. <i>Frontiers in Microbiology</i> , 2020, 11, 555194.	1.5	7
8703	Low adaptive and neutral genetic diversity in the endangered Antioquia wren (<i>Thryophilus sernai</i>). <i>Conservation Genetics</i> , 2020, 21, 1051-1065.	0.8	0
8704	Hidden in plain sight: Systematic investigation of Leucine-rich repeat containing genes unveil the their regulatory network in response to <i>Fusarium</i> wilt in tung tree. <i>International Journal of Biological Macromolecules</i> , 2020, 163, 1759-1767.	3.6	10
8705	Strict allopatric speciation of sky island <i>Pyrrhula erythaca</i> species complex. <i>Molecular Phylogenetics and Evolution</i> , 2020, 153, 106941.	1.2	5
8706	Maternal Origins and Haplotype Diversity of Seven Russian Goat Populations Based on the D-loop Sequence Variability. <i>Animals</i> , 2020, 10, 1603.	1.0	6
8707	Mitogenome diversity of <i>Aedes (Stegomyia) albopictus</i> : Detection of multiple introduction events in Portugal. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008657.	1.3	12
8708	Mitogenomic architecture of the multivalent endemic black clam (<i>Villorita cyprinoides</i>) and its phylogenetic implications. <i>Scientific Reports</i> , 2020, 10, 15438.	1.6	2
8709	Spatial genetic structure in <i>Themisto libellula</i> (Amphipoda: Hyperiididae) from the coastal Gulf of Alaska, Bering and Chukchi seas. <i>Polar Biology</i> , 2020, 43, 1795-1804.	0.5	2
8710	Mitochondrial DNA markers reveal genetic connectivity among populations of Osteoglossiform fish <i>Chitala chitala</i> . <i>Molecular Biology Reports</i> , 2020, 47, 8579-8592.	1.0	4
8711	Phylogeography and potential glacial refugia of terrestrial gastropod <i>Faustina faustina</i> (Rossm�ssler.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf models. <i>Organisms Diversity and Evolution</i> , 2020, 20, 747-762.	0.7	8
8712	Identificaci�n de polimorfismos en el gen <i>RXAM1</i> de yuca y su asociaci�n con la resistencia a la bacteriosis vascular. <i>Acta Biologica Colombiana</i> , 2020, 25, 185-193.	0.1	0
8713	Genetic diversity of Merozoite surface protein 1�42 (MSP1-42) fragment of <i>Plasmodium vivax</i> from Indonesian isolates: Rationale implementation of candidate MSP1 vaccine. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104573.	1.0	6
8714	Population demographic history and adaptability of the vulnerable Lolokou Sucker Frog. <i>Genetica</i> , 2020, 148, 207-213.	0.5	1
8715	Distribution of genetic diversity reveals colonization patterns and philopatry of the loggerhead sea turtles across geographic scales. <i>Scientific Reports</i> , 2020, 10, 18001.	1.6	20
8716	Dorsal Pigmentation and Its Association with Functional Variation in <i>MC1R</i> in a Lizard from Different Elevations on the Qinghai� Tibetan Plateau. <i>Genome Biology and Evolution</i> , 2020, 12, 2303-2313.	1.1	10

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8718	The Complete Chloroplast Genome Sequence of the <i>Speirantha gardenii</i> : Comparative and Adaptive Evolutionary Analysis. <i>Agronomy</i> , 2020, 10, 1405.	1.3	14
8719	First molecular characterization of the facultative myiasis agent <i>Eristalis tenax</i> in Turkey using mitochondrial cytochrome c oxidase subunit I DNA barcoding sequences. <i>Turkish Journal of Veterinary and Animal Sciences</i> , 2020, 44, 449-455.	0.2	0
8720	Nucleotide diversity analysis of candidate genes for <i>Verticillium</i> wilt resistance in olive. <i>Scientia Horticulturae</i> , 2020, 274, 109653.	1.7	6
8721	Phylogeography of <i>Schizopygopsis malacanthus</i> Herzenstein (Cypriniformes, Cyprinidae) in relation to the tectonic events and Quaternary climatic oscillations in the Shaluli Mountains Region. <i>Zoology</i> , 2020, 143, 125835.	0.6	1
8722	Genetic structure and demographic history of <i>Indirana semipalmata</i> , an endemic frog species of the Western Ghats, India. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2020, 31, 365-378.	0.7	3
8723	Genetic diversity and conservation of the endemic tuco-tuco <i>Ctenomys ibicuiensis</i> (Rodentia: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.6	4
8724	Genetic Evidence for a Mixed Composition of the Genus <i>Myoxocephalus</i> (Cottoidei: Cottidae) Necessitates Generic Realignment. <i>Genes</i> , 2020, 11, 1071.	1.0	5
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8726	Using multiple lines of evidence to delimit protogynes and deutogynes of four-legged mites: a case study on <i>Epitrimerus sabinae</i> s.l. (Acari : Eriophyidae). <i>Invertebrate Systematics</i> , 2020, , .	0.5	5
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8730	Human-associated migration of Holarctic <i>Saccharomyces uvarum</i> strains to Patagonia. <i>Fungal Ecology</i> , 2020, 48, 100990.	0.7	4
8731	A multifaceted approach towards investigating childbirth deaths in double burials: Anthropology, paleopathology and ancient DNA. <i>Journal of Archaeological Science</i> , 2020, 122, 105219.	1.2	11
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8734	Ancient divergence, a crisis of salt and another of ice shaped the evolution of the west Mediterranean butterfly <i>Euchloe tagis</i> . <i>Biological Journal of the Linnean Society</i> , 2020, 131, 487-504.	0.7	2

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8737	The phylogeographic structure of the mountain coati (<i>Nasuella olivacea</i> ; Procyonidae, Carnivora), and its phylogenetic relationships with other coati species (<i>Nasua nasua</i> and <i>Nasua narica</i>) as inferred by mitochondrial DNA. <i>Mammalian Biology</i> , 2020, 100, 521-548.	0.8	4
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8741	Molecular systematics and phylogeography of the genus <i>Alburnus</i> Rafinesque, 1820 (Teleostei). <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i> 273-284.	0.7	15
8742	First insights into the phylogeography and demographic history of the common hermit crab <i>Pagurus bernhardus</i> (Linnaeus, 1758) (Decapoda: Anomura: Paguridae) across the Eastern Atlantic and North Sea. <i>Journal of Crustacean Biology</i> , 2020, 40, 435-449.	0.3	1
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8746	Allelic Variation and Selection in Effector Genes of <i>Phytophthora infestans</i> (Mont.) de Bary. <i>Pathogens</i> , 2020, 9, 551.	1.2	4
8747	Diversity of <i>Taenia</i> and <i>Hydatigera</i> (Cestoda: Taeniidae) in domestic dogs in Kenya. <i>Parasitology Research</i> , 2020, 119, 2863-2875.	0.6	5
8748	Taeniid cestodes in Tibetan foxes (<i>Vulpes Ferrilata</i>) detected by copro-PCR: Applications and challenges. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2020, 12, 242-249.	0.6	1
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8750	Population structure and genetic diversity of <i>Aedes aegypti</i> and <i>Aedes albopictus</i> in Penang as revealed by mitochondrial DNA cytochrome oxidase I. <i>Saudi Journal of Biological Sciences</i> , 2020, 27, 953-967.	1.8	29
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8752	A journey through the Amazon Middle Earth reveals <i>Aspidoras azaghal</i> (Siluriformes). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 T</i> Biology, 2020, 97, 1072-1086.	0.7	4

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8754	Relationship between mitochondrial DNA haplogroup and litter size in the pig. <i>Reproduction, Fertility and Development</i> , 2020, 32, 267.	0.1	4
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8757	The Andaman day gecko paradox: an ancient endemic without pronounced phylogeographic structure. <i>Scientific Reports</i> , 2020, 10, 11745.	1.6	3
8758	<i>Parastagonospora nodorum</i> and Related Species in Western Canada: Genetic Variability and Effector Genes. <i>Phytopathology</i> , 2020, 110, 1946-1958.	1.1	15
8759	Advances in Computational and Bio-Engineering. <i>Learning and Analytics in Intelligent Systems</i> , 2020, , .	0.5	1
8760	The genetic structure and recombination analyses of Sweetpotato leaf curl virus (SPLCV) population in China. <i>Journal of Plant Diseases and Protection</i> , 2020, 127, 741-751.	1.6	2
8761	Genome-wide characterization of Toll-like receptors in black rockfish <i>Sebastes schlegelii</i> : Evolution and response mechanisms following <i>Edwardsiella tarda</i> infection. <i>International Journal of Biological Macromolecules</i> , 2020, 164, 949-962.	3.6	28
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8767	Insights into the molecular diversity of <i>Plasmodium vivax</i> merozoite surface protein-3 ³ (pvmSP3 ³), a polymorphic member in the msp3 multi-gene family. <i>Scientific Reports</i> , 2020, 10, 10977.	1.6	5
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8769	Biogeography and ecology of geographically distant populations of sibling <i>Cryptocephalus</i> leaf beetles. , 2020, 87, 223-234.		3
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8774	Genetic diversity analysis of papaya leaf distortion mosaic virus isolates infecting transgenic papaya 'Huanong No. 1' in South China. <i>Ecology and Evolution</i> , 2020, 10, 11671-11683.	0.8	0
8775	DNA barcoding reveals cryptic diversity in the underestimated genus <i>Triplophysa</i> (Cypriniformes: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50). <i>Ecology and Evolution</i> , 2020, 20, 151.	3.2	19
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8777	The Genetic Structure of Chinese Hui Ethnic Group Revealed by Complete Mitochondrial Genome Analyses Using Massively Parallel Sequencing. <i>Genes</i> , 2020, 11, 1352.	1.0	13
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8780	Migration of <i>Sogatella furcifera</i> between the Greater Mekong Subregion and northern China revealed by mtDNA and SNP. <i>BMC Evolutionary Biology</i> , 2020, 20, 154.	3.2	6
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8784	Morphological and genetic variability associated with environmental variation in two species of <i>Pseudodiploria</i> Fukami, Budd & Knowlton, 2012 (Cnidaria: Anthozoa: Scleractinia). <i>Marine Biodiversity</i> , 2020, 50, 1.	0.3	1
8785	First confirmed record of <i>Trichobilharzia franki</i> MÅ¼ller & Kimmig, 1994, from <i>Radix auricularia</i> (Linnaeus, 1758) for Austria. <i>Parasitology Research</i> , 2020, 119, 4135-4141.	0.6	5
8786	Chloroplast-based DNA barcode analysis indicates high discriminatory potential of <i>matK</i> locus in Himalayan temperate bamboos. <i>3 Biotech</i> , 2020, 10, 534.	1.1	2
8787	Intra- and Inter-Host Assessment of <i>Bartonella</i> Diversity with Focus on Non-Hematophagous Bats and Associated Ectoparasites from Brazil. <i>Microorganisms</i> , 2020, 8, 1822.	1.6	16
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8805	Chloroplast genomes elucidate diversity, phylogeny, and taxonomy of Pulsatilla (Ranunculaceae). Scientific Reports, 2020, 10, 19781.	1.6	20
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8809	Insights from Population Genomics to Enhance and Sustain Biological Control of Insect Pests. <i>Insects</i> , 2020, 11, 462.	1.0	19
8810	Comparative analysis of mitochondrial DNA datasets indicates that <i>Cylicostephanus minutus</i> represents a species complex. <i>Infection, Genetics and Evolution</i> , 2020, 84, 104487.	1.0	3
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8815	Phylogeography of feral Monteiro pig in the Brazilian Pantanal Ecosystem. <i>Genetica</i> , 2020, 148, 183-193.	0.5	3
8816	Comparative genotyping of <i>Blastocystis</i> infecting cattle and human in the south of Iran. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2020, 72, 101529.	0.7	19
8817	Comparative genetic diversity of <i>Cryptosporidium</i> species causing human infections. <i>Parasitology</i> , 2020, 147, 1532-1537.	0.7	8
8818	Genetic Diversity Among SARS-CoV2 Strains in South America may Impact Performance of Molecular Detection. <i>Pathogens</i> , 2020, 9, 580.	1.2	28
8819	The Complete Chloroplast Genome Sequences of 14 <i>Curcuma</i> Species: Insights Into Genome Evolution and Phylogenetic Relationships Within Zingiberales. <i>Frontiers in Genetics</i> , 2020, 11, 802.	1.1	43
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8827	Phylogeography and Phylogenetic Evolution in Tibetan Sheep Based on MT-CYB Sequences. <i>Animals</i> , 2020, 10, 1177.	1.0	6
8828	Assessing Genome-Wide Diversity in European Hantaviruses through Sequence Capture from Natural Host Samples. <i>Viruses</i> , 2020, 12, 749.	1.5	11
8829	Ecology and Genetic Structure of the Parasitoid <i>Phobocampe confusa</i> (Hymenoptera: Ichneumonidae) in Relation to Its Hosts, <i>Aglais</i> Species (Lepidoptera: Nymphalidae). <i>Insects</i> , 2020, 11, 478.	1.0	9
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8831	Complete chloroplast genomes of <i>Zingiber montanum</i> and <i>Zingiber zerumbet</i> : Genome structure, comparative and phylogenetic analyses. <i>PLoS ONE</i> , 2020, 15, e0236590.	1.1	17
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8835	Genome-wide identification and characterization of HSP70 gene family in four species of cotton. <i>Genomics</i> , 2020, 112, 4442-4453.	1.3	12
8836	Fourteen complete mitochondrial genomes of butterflies from the genus <i>Lethe</i> (Lepidoptera, Tj ETQq1 1 0.784314 1.3 BT / Overlock 10	1.3	28
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8838	Genetic Diversity and Phylogenetic Analyses of Turkish Cotton (<i>Gossypium hirsutum</i> L.) Lines using ISSR Markers and Chloroplast <i>trnL-F</i> Regions. <i>Journal of Natural Fibers</i> , 2022, 19, 1837-1850.	1.7	13
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8841	Adult survival in migratory caribou is negatively associated with MHC functional diversity. <i>Heredity</i> , 2020, 125, 290-303.	1.2	5
8842	Characterisation of arginine kinase intron regions and their potential as molecular markers for population genetic studies of <i>Bithynia</i> snails (Gastropoda: Bithyniidae) in Thailand. <i>Molluscan Research</i> , 2020, 40, 354-362.	0.2	3

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8845	DNA Barcoding and Phylogenetic Analysis Sugarcane (<i>Saccharum officinarum</i> L.) Based on m<i>it</i>atK <i>(m</i>at<i>urase K</i>) Gene. <i>Key Engineering Materials</i> , 0, 840, 162-170.	0.4	0
8846	Structural diversity, natural selection and intragenic recombination in the <i>Plasmodium vivax</i> merozoite surface protein 9 locus in Thailand. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104467.	1.0	3
8847	A Genomewide Scan for Genetic Structure and Demographic History of Two Closely Related Species, <i>Rhododendron dauricum</i> and <i>R. mucronulatum</i> (<i>Rhododendron</i> , Ericaceae). <i>Frontiers in Plant Science</i> , 2020, 11, 1093.	1.7	7
8848	Phylogenetic relationships between different raccoon dog (<i>Nyctereutes procyonoides</i>) populations based on four nuclear and Y genes. <i>Genes and Genomics</i> , 2020, 42, 1075-1085.	0.5	4
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8850	First report of freshwater atyid shrimp, <i>Caridina formosae</i> (Decapoda: Caridea) as a host of ectosymbiotic branchiobdellidan, <i>Holtodrilus truncatus</i> (Annelida, Citellata). <i>Knowledge and Management of Aquatic Ecosystems</i> , 2020, , 33.	0.5	4
8851	Hidden diversity in Antarctica: Molecular and morphological evidence of two different species within one of the most conspicuous ascidian species. <i>Ecology and Evolution</i> , 2020, 10, 8127-8143.	0.8	6
8852	<i>Wolbachia</i> have made it twice: Hybrid introgression between two sister species of <i>Eurema</i> butterflies. <i>Ecology and Evolution</i> , 2020, 10, 8323-8330.	0.8	8
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8854	Phylogeography of the Japanese scad, <i>Decapterus maruadsi</i> (Teleostei; Carangidae) across the Central Indo-West Pacific: evidence of strong regional structure and cryptic diversity. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2020, 31, 298-310.	0.7	10
8855	Mitochondrial DNA Diversity in Large White Pigs in Russia. <i>Animals</i> , 2020, 10, 1365.	1.0	8
8856	Molecular identification of head lice collected in Franceville (Gabon) and their associated bacteria. <i>Parasites and Vectors</i> , 2020, 13, 410.	1.0	13
8857	Chloroplast DNA phylogeography of the Holly mangrove <i>Acanthus ilicifolius</i> in the Indo-West Pacific. <i>Hydrobiologia</i> , 2020, 847, 3591-3608.	1.0	7
8858	DNA barcoding supports existence of morphospecies complex in endemic bamboo genus <i>Ochlandra</i> Thwaites of the Western Ghats, India. <i>Journal of Genetics</i> , 2020, 99, 1.	0.4	1
8859	Investigation of <i>Anisakis</i> larvae in different products of ready-to-eat fish meat and imported frozen fish in Turkey. <i>International Journal of Food Microbiology</i> , 2020, 333, 108829.	2.1	1
8860	DNA barcoding coupled with secondary structure information enhances <i>Achyranthes</i> species resolution. <i>Journal of Applied Research on Medicinal and Aromatic Plants</i> , 2020, 19, 100269.	0.9	0

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8861	Systematic considerations on two species of nectarivorous bats (<i>Anoura caudifer</i> and <i>A. Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>)	0.1	3
8862	Genome-wide analysis of evolution and expression profiles of NAC transcription factor gene family in <i>Juglans regia</i> L.. <i>Annals of Forest Science</i> , 2020, 77, 1.	0.8	6
8863	Remarkably low genetic diversity and shallow population structure detected of the spiny eel (<i>Sinobdella sinensis</i>) in Eastern China. <i>Genes and Genomics</i> , 2020, 42, 1251-1257.	0.5	2
8864	SNP barcodes provide higher resolution than microsatellite markers to measure <i>Plasmodium vivax</i> population genetics. <i>Malaria Journal</i> , 2020, 19, 375.	0.8	25
8865	Ecotypes of <i>Hypnea pseudomusciformis</i> (Cystocloniaceae, Rhodophyta) revealed by physiological, morphological, and molecular data. <i>Journal of Applied Phycology</i> , 2020, 32, 4399-4409.	1.5	8
8866	Evolution of <i>Poecilimon jonicus</i> group (Orthoptera: Tettigoniidae): a history linked to the Aegean Neogene paleogeography. <i>Organisms Diversity and Evolution</i> , 2020, 20, 803-819.	0.7	6
8867	Molecular species identification of red shrimp (Crustacea: Decapoda: Barbouriidae) from Tanjung Sanjangan (Tolitoli, Central Sulawesi) through 16S rRNA mitochondrial gene. <i>AIP Conference Proceedings</i> , 2020, , .	0.3	0
8868	Genetic characterization of red shrimp (<i>Parhippolyte uveae</i> Borradaile, 1900) from Tanjung Sanjangan (Tolitoli, Central Sulawesi) using COI mitochondrial gene as a barcoding marker. <i>AIP Conference Proceedings</i> , 2020, , .	0.3	1
8869	Composition of mitochondrial DNA 16S and COI nucleotide of red shrimp (<i>Parhippolyte uveae</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2020, , .	0.3	0
8870	Complete Mitochondrial Genomes Reveal Population-Level Patterns in the Widespread Red Alga <i>Gelidiella fanii</i> (Gelidiales, Rhodophyta). <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	8
8871	Comparative Analysis of Sequence Polymorphism in Complete Organelle Genomes of the "Golden Tide"™ Seaweed <i>Sargassum horneri</i> between Korean and Chinese Forms. <i>Sustainability</i> , 2020, 12, 7280.	1.6	6
8872	Myco- and photobiont associations in crustose lichens in the McMurdo Dry Valleys (Antarctica) reveal high differentiation along an elevational gradient. <i>Polar Biology</i> , 2020, 43, 1967-1983.	0.5	14
8873	Potential biological mechanisms underlying the endangered status of <i>Glehnia littoralis</i> revealed by nrDNA ITS and RAPD analyses. <i>Biotechnology and Biotechnological Equipment</i> , 2020, 34, 1243-1251.	0.5	0
8874	Origins of cultivars of <i>Chrysanthemum</i> "Evidence from the chloroplast genome and nuclear LFY gene. <i>Journal of Systematics and Evolution</i> , 2020, 58, 925-944.	1.6	30
8875	Molecular Survey and Genetic Diversity of Hemoplasmas in Rodents from Chile. <i>Microorganisms</i> , 2020, 8, 1493.	1.6	8
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8877	Genetic characterization of the invasive Blue crab, <i>Callinectes sapidus</i> (Rathbun, 1896), in the Black Sea. <i>Regional Studies in Marine Science</i> , 2020, 39, 101412.	0.4	4
8878	mtDNA genetic characterization of an isolated sheep breed in South of Moroccan Atlas. <i>Small Ruminant Research</i> , 2020, 193, 106250.	0.6	3

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8880	Characterization of Chloroplast Genomes From Two <i>Salvia</i> Medicinal Plants and Gene Transfer Among Their Mitochondrial and Chloroplast Genomes. <i>Frontiers in Genetics</i> , 2020, 11, 574962.	1.1	19
8881	Amphitropical variation of the algal partners of <i>Pseudephebe</i> (Parmeliaceae, lichenized fungi). <i>Symbiosis</i> , 2020, 82, 35-48.	1.2	9
8882	Genetic diversification of acanthocephalans of the genus <i>Floridosentis</i> Ward 1953 (Acanthocephala: Tj ETQq1 1 0.784314 rgBT /Overlock 10 2020, 85, 104535.	1.0	10
8883	Genome-Wide Characterization and Expression of Two-Component System Genes in Cytokinin-Regulated Gall Formation in <i>Zizania latifolia</i> . <i>Plants</i> , 2020, 9, 1409.	1.6	14
8884	Monuments Unveiled: Genetic Characterization of Large Old Chestnut (<i>Castanea sativa</i> Mill.) Trees Using Comparative Nuclear and Chloroplast DNA Analysis. <i>Forests</i> , 2020, 11, 1118.	0.9	8
8885	The Quaternary range dynamics of <i>Noccaea iberidea</i> (Brassicaceae), a typical representative of subalpine/alpine steppe communities of Anatolian mountains. <i>Biological Journal of the Linnean Society</i> , 2020, 131, 986-1001.	0.7	7
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8887	Genetic characterization of striped snakehead (<i>Channa striata</i> Bloch, 1793) from Arut River, Central Kalimantan inferred from COI mitochondrial gene. <i>AIP Conference Proceedings</i> , 2020, , .	0.3	1
8888	Composition of mitochondrial DNA COI nucleotide of striped snakehead (<i>Channa striata</i> bloch, 1793) collected from three rivers in Sumatra and Kalimantan. <i>AIP Conference Proceedings</i> , 2020, , .	0.3	0
8889	Low Genetic Diversity in Turkish Populations of Wels Catfish <i>Silurus glanis</i> L., 1758 (Siluridae, Pisces) Revealed by Mitochondrial Control Region Sequences. <i>Turkish Journal of Fisheries and Aquatic Sciences</i> , 2020, 20, 767-776.	0.4	2
8890	Molecular investigation of zoonotic intracellular bacteria in Chilean bats. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2020, 73, 101541.	0.7	13
8891	Does marine bioregionalisation provide a framework for the conservation of genetic structure?. <i>Regional Studies in Marine Science</i> , 2020, 40, 101505.	0.4	1
8892	Scale(s) matter: Deconstructing an area of endemism for Middle American freshwater fishes. <i>Journal of Biogeography</i> , 2020, 47, 2483-2501.	1.4	18
8893	<i>Vanmanenia intermedia</i> Fang, 1935, a valid hill-stream species of loach (Teleostei: Tj ETQq0 0 0 rgBT /Overlock 10 4819, 109-127.	0.2	2
8894	Genome-Wide Analysis of the PIN Auxin Efflux Carrier Gene Family in Coffee. <i>Plants</i> , 2020, 9, 1061.	1.6	10
8895	Comparative Genomics and Phylogenetic Analyses of <i>Christia vespertilionis</i> and <i>Urariopsis brevissima</i> in the Tribe Desmodieae (Fabaceae: Papilionoideae) Based on Complete Chloroplast Genomes. <i>Plants</i> , 2020, 9, 1116.	1.6	8
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8899	Genome-wide survey, characterization, and expression analysis of bZIP transcription factors in <i>Chenopodium quinoa</i> . <i>BMC Plant Biology</i> , 2020, 20, 405.	1.6	16
8900	Genetic polymorphism and natural selection of circumsporozoite protein in Myanmar <i>Plasmodium vivax</i> . <i>Malaria Journal</i> , 2020, 19, 303.	0.8	11
8901	Population genetics of the African wolf (<i>Canis lupaster</i>) across its range: first evidence of hybridization with domestic dogs in Africa. <i>Mammalian Biology</i> , 2020, 100, 645-658.	0.8	7
8902	Prion Protein Gene (<i>PRNP</i>) Sequences Suggest Differing Vulnerability to Chronic Wasting Disease for Florida Key Deer (<i>Odocoileus virginianus clavium</i>) and Columbian White-Tailed Deer (<i>O. v. leucurus</i>). <i>Journal of Heredity</i> , 2020, 111, 564-572.	1.0	7
8903	Multilocus and morphological analysis of southeastern Iberian Wall lizards (Squamata, Podarcis). <i>Zoologica Scripta</i> , 2020, 49, 668-683.	0.7	7
8904	Molecular-genetic identification of chameleon goby <i>Tridentiger trigonocephalus</i> (Gill, 1859) in the Black Sea. <i>Ecologica Montenegrina</i> , 2020, 32, 46-52.	0.5	2
8905	Morphological and Genetic Variability of Sympatric Whitefishes of the <i>Coregonus lavaretus pidschian</i> Complex from Lake Kutaramakan of the Khantaisk Drainage System (Taymyr Peninsula). <i>Russian Journal of Genetics</i> , 2020, 56, 580-591.	0.2	5
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8907	Comparative and Phylogenetic Analysis of the Complete Chloroplast Genomes of Three <i>Paeonia</i> Section Moutan Species (Paeoniaceae). <i>Frontiers in Genetics</i> , 2020, 11, 980.	1.1	32
8908	<i>Orostachys spinosa</i> (Crassulaceae) origin and diversification: East Asia or South Siberian Mountains? Chloroplast DNA data. <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	0
8909	Evidence of genetic isolation between two Mediterranean morphotypes of <i>Parazoanthus axinellae</i> . <i>Scientific Reports</i> , 2020, 10, 13938.	1.6	8
8910	Next generation sequencing-aided comprehensive geographic coverage sheds light on the status of rare and extinct populations of <i>Aporia</i> butterflies (Lepidoptera: Pieridae). <i>Scientific Reports</i> , 2020, 10, 13970.	1.6	4
8911	Characterization of glycerol-3-phosphate acyltransferase 9 (<i>AhGPAT9</i>) genes, their allelic polymorphism and association with oil content in peanut (<i>Arachis hypogaea</i> L.). <i>Scientific Reports</i> , 2020, 10, 14648.	1.6	9
8912	Morphologic and genetic characterisation of Corsican and Sardinian trout with comments on <i>Salmo</i> taxonomy. <i>Knowledge and Management of Aquatic Ecosystems</i> , 2020, , 21.	0.5	12
8913	Phylogenetic and Comparative Analyses of Complete Chloroplast Genomes of Chinese <i>Viburnum</i> and <i>Sambucus</i> (Adoxaceae). <i>Plants</i> , 2020, 9, 1143.	1.6	11
8914	Asia-wide phylogeography of wild boar (<i>Sus scrofa</i>) based on mitochondrial DNA and Y-chromosome: Revising the migration routes of wild boar in Asia. <i>PLoS ONE</i> , 2020, 15, e0238049.	1.1	23

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8916	Connection, isolation and reconnection: Quaternary climatic oscillations and the Andes shaped the phylogeographical patterns of the Patagonian bee <i>Centris cineraria</i> (Apidae). <i>Biological Journal of the Linnean Society</i> , 2020, 131, 396-416.	0.7	10
8917	The genetic structure of the spectacled bear (<i>Tremarctos ornatus</i> ; Ursidae, Carnivora) in Colombia by means of mitochondrial and microsatellite markers. <i>Journal of Mammalogy</i> , 2020, 101, 1072-1090.	0.6	39
8918	First report of <i>Onchocerca lupi</i> from Israel and confirmation of two genotypes circulating among canine, feline and human hosts. <i>Parasitology</i> , 2020, 147, 1723-1727.	0.7	9
8919	Genomic evidence of recent hybridization between sea turtles at Abrolhos Archipelago and its association to low reproductive output. <i>Scientific Reports</i> , 2020, 10, 12847.	1.6	9
8920	Association of chronic wasting disease susceptibility with prion protein variation in white-tailed deer (<i>Odocoileus virginianus</i>). <i>Prion</i> , 2020, 14, 214-225.	0.9	11
8921	Molecular evidence confirms occurrence of <i>Rhipicephalus microplus</i> Clade A in Kenya and sub-Saharan Africa. <i>Parasites and Vectors</i> , 2020, 13, 432.	1.0	21
8922	The receptor binding domain of SARS-CoV-2 spike protein is the result of an ancestral recombination between the bat-CoV RaTG13 and the pangolin-CoV MP789. <i>BMC Research Notes</i> , 2020, 13, 398.	0.6	31
8923	Classification of <i>Takifugu rubripes</i> , <i>T. chinensis</i> and <i>T. pseudommus</i> by genotyping-by-sequencing. <i>PLoS ONE</i> , 2020, 15, e0236483.	1.1	4
8924	Distinct haplotypes and free movement of <i>Aedes aegypti</i> in Port Sudan, Sudan. <i>Journal of Applied Entomology</i> , 2020, 144, 817-823.	0.8	6
8925	ddRAD Sequencing-Based Identification of Genomic Boundaries and Permeability in <i>Quercus ilex</i> and <i>Q. suber</i> Hybrids. <i>Frontiers in Plant Science</i> , 2020, 11, 564414.	1.7	19
8926	Cryptic differentiation in the Manx shearwater hinders the identification of a new endemic subspecies. <i>Journal of Avian Biology</i> , 2020, 51, .	0.6	14
8927	Pollinators drive floral evolution in an Atlantic Forest genus. <i>AoB PLANTS</i> , 2020, 12, plaa046.	1.2	10
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8929	Assessment of the dunnocks™ introduction to New Zealand using innate immune-gene diversity. <i>Evolutionary Ecology</i> , 2020, 34, 803-820.	0.5	4
8930	Phylogeny and species reassessment of <i>Hyalopterus</i> (Aphididae, Aphidinae). <i>Zoologica Scripta</i> , 2020, 49, 755-767.	0.7	3
8931	The speciation and adaptation of the polyploids: a case study of the Chinese Isoetes L. diploid-polyploid complex. <i>BMC Evolutionary Biology</i> , 2020, 20, 118.	3.2	12
8932	The Climate-Driven Genetic Diversity Has a Higher Impact on the Population Structure of <i>Plasmopara viticola</i> Than the Production System or QoI Fungicide Sensitivity in Subtropical Brazil. <i>Frontiers in Microbiology</i> , 2020, 11, 575045.	1.5	5

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8934	Association between host wing morphology polymorphism and <i>Wolbachia</i> infection in <i>Vollenhovia emeryi</i> (Hymenoptera: Myrmicinae). <i>Ecology and Evolution</i> , 2020, 10, 8827-8837.	0.8	4
8935	Sequence diversity of cytotoxic T cell antigens and satellite marker analysis of <i>Theileria parva</i> informs the immunization against East Coast fever in Rwanda. <i>Parasites and Vectors</i> , 2020, 13, 452.	1.0	5
8936	Genetic diversity of the coat protein gene and biological variation of citrus yellow vein clearing virus infecting different citrus species. <i>Tropical Plant Pathology</i> , 2020, 45, 467-475.	0.8	3
8937	Diatom DNA barcodes for forensic discrimination of drowning incidents. <i>FEMS Microbiology Letters</i> , 2020, 367, .	0.7	15
8938	Phenotypic characterization and phylogenetic analysis of <i>Pseudomonas syringae</i> strains associated with canker disease on apricot in Iran within the context of the global genetic diversity of the <i>P. syringae</i> complex. <i>European Journal of Plant Pathology</i> , 2020, 158, 545-560.	0.8	0
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8940	<i>Ehrlichia</i> spp. and <i>Anaplasma</i> spp. in <i>Xenarthra</i> mammals from Brazil, with evidence of novel <i>Candidatus Anaplasma</i> spp.™. <i>Scientific Reports</i> , 2020, 10, 12615.	1.6	21
8941	Mitochondrial genetic diversity of the invasive drosophilid <i>Zaprionus indianus</i> (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50,422 Td (D	1.2	2
8942	Comparative population genetics of the federally endangered Relict Darter, and its sister taxon the Clarks Darter (Teleostei: Percidae). <i>Conservation Genetics</i> , 2020, 21, 957-970.	0.8	2
8943	Investigation of the relationship between CE cyst characteristics and genetic diversity of <i>Echinococcus granulosus sensu lato</i> in humans from Turkey. <i>Parasitology</i> , 2020, 147, 1712-1717.	0.7	5
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8946	Genetic diversity and phenotypic variation of the red swamp crayfish, <i>Procambarus clarkii</i> (Cirard), Tj ETQq1 1 0.784314 rgBT ₁ /Overlock 0.3	0.3	1
8947	New Genetic Insights About Hybridization and Population Structure of Hawksbill and Loggerhead Turtles From Brazil. <i>Journal of Heredity</i> , 2020, 111, 444-456.	1.0	13
8948	Cryptic variation in mole voles <i>Ellobius</i> (Arvicolinae, Rodentia) of Mongolia. <i>Zoologica Scripta</i> , 2020, 49, 535-548.	0.7	10
8949	Multi-Species Phylogeography of Arid-Zone Sminthopsinae (Marsupialia: Dasyuridae) Reveals Evidence of Refugia and Population Expansion in Response to Quaternary Change. <i>Genes</i> , 2020, 11, 963.	1.0	10
8950	Identification of <i>Aedes</i> (Diptera: Culicidae) Species and Arboviruses Circulating in Arauca, Eastern Colombia. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	9

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8953	Fine-Scale Patterns of Genetic Structure in the Host Plant <i>Chamaecrista fasciculata</i> (Fabaceae) and Its Nodulating Rhizobia Symbionts. <i>Plants</i> , 2020, 9, 1719.	1.6	2
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8955	Population Genetic Structure and Connectivity of the European Lobster <i>Homarus gammarus</i> in the Adriatic and Mediterranean Seas. <i>Frontiers in Genetics</i> , 2020, 11, 576023.	1.1	5
8956	Low Genetic Diversity of the Endangered Franciscana (<i>Pontoporia blainvillei</i>) in Its Northernmost, Isolated Population (FMAIa, Espírito Santo, Brazil). <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	9
8957	Biometry, Distribution and Genetic Characterization of Blue Jack Mackerel <i>Trachurus picturatus</i> (Bowdich, 1825), a Rare Pelagic Fish Species in the Adriatic Sea. <i>Diversity</i> , 2020, 12, 463.	0.7	1
8958	Fusarium Consortium Populations Associated with Asparagus Crop in Spain and Their Role on Field Decline Syndrome. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 336.	1.5	18
8959	Phylogenetic Analysis of Mitogenomic Data Sets Resolves the Relationship of Seven <i>Macropostrongyloides</i> Species from Australian Macropodid and Vombatid Marsupials. <i>Pathogens</i> , 2020, 9, 1042.	1.2	5
8960	Strong Sexual Selection Does Not Induce Population Differentiation in a Fish Species with High Dispersal Potential: The Curious Case of the Worm Pipefish <i>Nerophis lumbriciformis</i> (Teleostei). <i>Tj ETQq1 1 0.784314 rgBT /Ove</i>		
8961	Population Dynamics in Italian Canids between the Late Pleistocene and Bronze Age. <i>Genes</i> , 2020, 11, 1409.	1.0	13
8962	Integrative Approach to <i>Phlebotomus mascittii</i> Grassi, 1908: First Record in Vienna with New Morphological and Molecular Insights. <i>Pathogens</i> , 2020, 9, 1032.	1.2	8
8963	Assessing the Diversity and Population Substructure of Sarda Breed Bucks by Using Mtdna and Y-Chromosome Markers. <i>Animals</i> , 2020, 10, 2194.	1.0	0
8964	In situ glacial survival maintains high genetic diversity of <i>Mussaenda kwangtungensis</i> on continental islands in subtropical China. <i>Ecology and Evolution</i> , 2020, 10, 11304-11321.	0.8	1
8965	Species integrity, introgression, and genetic variation across a coral reef fish hybrid zone. <i>Ecology and Evolution</i> , 2020, 10, 11998-12014.	0.8	8
8966	The genetic differentiation of a cricket (<i>Velarifictorus micado</i>) with two modes of life cycle in East Asia after the middle Pleistocene and the invasion origin of the United States of America. <i>Ecology and Evolution</i> , 2020, 10, 13767-13786.	0.8	2
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8968	Colour variation of the intertidal hermit crab <i>Clibanarius virescens</i> considering growth stage, geographic area in the Indo-West Pacific Ocean, and molecular phylogeny. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2020, 100, 1107-1121.	0.4	1

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8970	Weedy Rice From South Korea Arose From Two Distinct De-domestication Events. Frontiers in Agronomy, 2020, 2, .	1.5	2
8971	Tomato Yellow Leaf Curl Virus-Resistant and -Susceptible Tomato Genotypes Similarly Impact the Virus Population Genetics. Frontiers in Plant Science, 2020, 11, 599697.	1.7	22
8972	Genomic Identification, Evolution and Sequence Analysis of the Heat-Shock Protein Gene Family in Buffalo. Genes, 2020, 11, 1388.	1.0	29
8973	Microsatellite and mitochondrial DNA analyses unveil the genetic structure of native sheep breeds from three major agro-ecological regions of India. Scientific Reports, 2020, 10, 20422.	1.6	24
8974	Chaotic genetic structure and past demographic expansion of the invasive gastropod Tritia neritea in its native range, the Mediterranean Sea. Scientific Reports, 2020, 10, 21624.	1.6	2
8975	Population genetics of the brown marmorated stink bug <i>Halyomorpha halys</i> in the early phase of invasion in South Tyrol (Northern Italy). Bulletin of Entomological Research, 2021, 111, 394-401.	0.5	4
8976	Mitogenomic features of <i>Pteronarcys sachalina</i> (Plecoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 2020, 4860, 401-412.	0.2	0
8977	Genetic Differentiation of an Endangered Megalobrama terminalis Population in the Heilong River within the Genus Megalobrama. Diversity, 2020, 12, 404.	0.7	2
8978	Cryptic Diversity in the Monotypic Neotropical Micromoth Genus Angelabella (Lepidoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 2020, 11, 1086.	1.0	3
8979	Characterization of the Complete Mitochondrial Genomes of Two Species with Preliminary Investigation on Phylogenetic Status of Zygineellini (Hemiptera: Cicadellidae: Typhlocybinae). Insects, 2020, 11, 684.	1.0	21
8980	Recent Apareiodon species evolutionary divergence (Characiformes: Parodontidae) evidenced by chromosomal and molecular inference. Zoologischer Anzeiger, 2020, 289, 166-176.	0.4	5
8981	Global Biodiversity Patterns of the Photobionts Associated with the Genus Cladonia (Lecanorales,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2020, 11, 1086.	1.4	26
8982	Genetic Consequences of Hybridization in Relict Isolated Trees Pinus sylvestris and the Pinus mugo Complex. Forests, 2020, 11, 1086.	0.9	8
8984	Evaluating taxonomic inflation: towards evidence-based species delimitation in Eurasian vipers (Serpentes: Viperinae). Amphibia - Reptilia, 2020, 41, 285-311.	0.1	45
8985	Alborz Heritage: geographic distribution and genetic differentiation of the Iranian Paradactylodon (Amphibia: Hynobiidae). Amphibia - Reptilia, 2020, 41, 519-534.	0.1	13
8986	The Stummer's Racrunner (Eremias stummeri Wettstein, 1940) does occur in Northwest China. Amphibia - Reptilia, 2020, 42, 93-105.	0.1	1
8987	Intra-genomic variability and pseudogenes in ribosomal ITS regions of Paraplagusia blochii (Pleuronectiformes: Cynoglossidae). Animal Biology, 2020, 70, 145-158.	0.6	2

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8988	Lineage diversity, morphological and genetic divergence in <i>Daphnia magna</i> (Crustacea) among Chinese lakes at different altitudes. <i>Contributions To Zoology</i> , 2020, 89, 450-470.	0.2	10
8989	Comparative mitochondrial phylogeography of two legless lizards (Pygopodidae) from Queensland's fragmented woodlands. <i>Israel Journal of Ecology and Evolution</i> , 2020, 66, 142-150.	0.2	2
8990	Complete Plastid Genome Sequencing of Eight Species from <i>Hansenia</i> , <i>Haplospira</i> and <i>Sinodielsia</i> (Apiaceae): Comparative Analyses and Phylogenetic Implications. <i>Plants</i> , 2020, 9, 1523.	1.6	18
8991	Identification, Association of Natural Variation and Expression Analysis of <i>ZmNAC9</i> Gene Response to Low Phosphorus in Maize Seedling Stage. <i>Plants</i> , 2020, 9, 1447.	1.6	1
8992	Phylogenetic differentiation between Awassi and Hamdani sheep using the mitochondrial 12S rRNA. <i>Animal Biotechnology</i> , 2022, 33, 801-809.	0.7	5
8993	Genetic interactions among <i>Pto-miR319</i> family members and their targets influence growth and wood properties in <i>Populus tomentosa</i> . <i>Molecular Genetics and Genomics</i> , 2020, 295, 855-870.	1.0	2
8994	The honeybee (<i>Apis mellifera</i>) developmental state shapes the genetic composition of the deformed wing virus-A quasispecies during serial transmission. <i>Scientific Reports</i> , 2020, 10, 5956.	1.6	15
8995	In the rivers: Multiple adaptive radiations of cyprinid fishes (<i>Labeobarbus</i>) in Ethiopian Highlands. <i>Scientific Reports</i> , 2020, 10, 7192.	1.6	25
8996	Co-varying patterns of genetic diversity and structure with life-history traits of freshwater mussel species (<i>Bivalvia:Unionidae</i>) in the Poyang Lake drainage, China. <i>Freshwater Science</i> , 2020, 39, 213-227.	0.9	2
8997	PCR-based molecular identification of two intermediate snail hosts of <i>Schistosoma mansoni</i> in Cameroon. <i>Parasites and Vectors</i> , 2020, 13, 158.	1.0	1
8998	Implications of plastome evolution in the true lilies (monocot order Liliales). <i>Molecular Phylogenetics and Evolution</i> , 2020, 148, 106818.	1.2	23
8999	Species delimitation and phylogenetic relationships in the genus <i>Trypoxylon</i> (Hymenoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5 Biodiversity, 2020, 18, 315-327.	0.5	5
9000	Malaria in Venezuela: changes in the complexity of infection reflects the increment in transmission intensity. <i>Malaria Journal</i> , 2020, 19, 176.	0.8	24
9001	Genetic diversity in <i>Pangasius</i> spp. collected in Bangladesh based on mitochondrial cytochrome b gene sequence analysis. <i>Aquaculture Reports</i> , 2020, 17, 100351.	0.7	7
9002	Great journey of Great Tits (<i>Parus major</i> group): Origin, diversification and historical demographics of a broadly distributed bird lineage. <i>Journal of Biogeography</i> , 2020, 47, 1585-1598.	1.4	15
9003	Genomic footprints of an old affair: Single nucleotide polymorphism data reveal historical hybridization and the subsequent evolution of reproductive barriers in two recently diverged grasshoppers with partly overlapping distributions. <i>Molecular Ecology</i> , 2020, 29, 2254-2268.	2.0	17
9004	Paleoclimatic distribution and phylogeography of <i>Mussismilia braziliensis</i> (Anthozoa, Scleractinia), an endemic Brazilian reef coral. <i>Marine Biodiversity</i> , 2020, 50, 1.	0.3	3
9005	Complex variation in the <i>KLRA</i> (<i>LY49</i>) immunity-related genomic region in horses. <i>Hla</i> , 2020, 96, 257-267.	0.4	4

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9006	Genetic Homogeneity of the Black-Billed Capercaillie Subspecies <i>Tetrao parvirostris parvirostris</i> Bonaparte, 1856 and <i>T. p. kamtschaticus</i> Kittlitz, 1858 (Tetraonidae, Aves) Based on the Mitochondrial and Nuclear DNA Data. <i>Russian Journal of Genetics</i> , 2020, 56, 454-459.	0.2	0
9007	Taxonomic revision of <i>Aegla lata</i> Bond-Buckup & Buckup, 1994 (Decapoda: Anomura: Aeglididae), with the description of a new species of <i>Aegla</i> Leach, 1820 from the Upper Paraná Ecoregion, Brazil. <i>Journal of Crustacean Biology</i> , 2020, 40, 425-434.	0.3	8
9008	Spatial genetic structuring in a widespread wetland plant on a plateau: Effects of elevation-driven geographic isolation and environmental heterogeneity. <i>Freshwater Biology</i> , 2020, 65, 1596-1607.	1.2	4
9009	Genetic polymorphism of merozoite surface protein-3 in Myanmar <i>Plasmodium falciparum</i> field isolates. <i>Malaria Journal</i> , 2020, 19, 184.	0.8	6
9010	Genetic evidence of multiple introductions and mixed reproductive strategy in the peregrine earthworm <i>Pontoscolex corethrurus</i> . <i>Biological Invasions</i> , 2020, 22, 2545-2557.	1.2	2
9011	Genetic analyses reveal female philopatric behavior and nest usage by multiple females of the solitary oil-collecting bee <i>Tetrapedia diversipes</i> (Hymenoptera: Apidae). <i>Apidologie</i> , 2020, 51, 815-825.	0.9	3
9012	Target-enriched DNA sequencing from historical type material enables a partial revision of the Madagascar giant stream frogs (genus <i>Mantidactylus</i>). <i>Journal of Natural History</i> , 2020, 54, 87-118.	0.2	16
9013	<i>Sarcocheilichthys vittatus</i> , a new species of gudgeon (Teleostei: Tj ETQq1 1 0.784314 rgBT /Overlooked) 201-220.	0.2	1
9014	Isolation and identification of <i>Phytophthora cinnamomi</i> collected in avocado (<i>Persea americana</i>) from Northeast Colombia. <i>Tropical Plant Pathology</i> , 2020, 45, 402-414.	0.8	1
9015	A new cryptic species of fringe-toed lizards from southwestern Arizona with revised taxonomy of the <i>Uma notata</i> species complex (Squamata: Phrynosomatidae). <i>Zootaxa</i> , 2020, 4778, 67-100.	0.2	2
9016	Genetic Diversity and Population Structure of <i>Acanthochiton rubrolineatus</i> (Polyplacophora) Based on Mitochondrial and Nuclear Gene Markers. <i>Diversity</i> , 2020, 12, 159.	0.7	4
9017	Genetic Characterization of Porcine Circovirus 3 Strains Circulating in Sardinian Pigs and Wild Boars. <i>Pathogens</i> , 2020, 9, 344.	1.2	21
9018	High functionality of DNA barcodes and revealed cases of cryptic diversity in Korean curved-horn moths (Lepidoptera: Gelechioidea). <i>Scientific Reports</i> , 2020, 10, 6208.	1.6	10
9019	Distribution and genetic diversity of the toxic benthic dinoflagellate genus <i>Ostreopsis</i> in Korea. <i>Harmful Algae</i> , 2020, 96, 101820.	2.2	10
9020	DNA barcode based species-specific marker for <i>Ocimum tenuiflorum</i> and its applicability in quantification of adulteration in herbal formulations using qPCR. <i>Journal of Herbal Medicine</i> , 2020, 23, 100376.	1.0	8
9021	Mitochondrial diversity of Yoruba and Fulani chickens: A biodiversity reservoir in Nigeria. <i>Poultry Science</i> , 2020, 99, 2852-2860.	1.5	9
9022	First record and DNA barcodes of the invasive blue-coloured spiny-cheek crayfish <i>Faxonius limosus</i> (Rafinesque, 1817) (Decapoda: Cambaridae). <i>Knowledge and Management of Aquatic Ecosystems</i> , 2020, , 20.	0.5	0
9023	Phylogeography and palaeomodelling of <i>Duseniella patagonica</i> (Barnadesioideae), an early-diverging member of Asteraceae endemic to the Argentinean Monte and Patagonia. <i>Biological Journal of the Linnean Society</i> , 2020, 130, 726-750.	0.7	4

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9025	Identification of CSP Types and Genotypic Variability of Clinical and Environmental Isolates of <i>Aspergillus fumigatus</i> from Different Geographic Origins. <i>Microorganisms</i> , 2020, 8, 688.	1.6	7
9026	Genetic diversity and connectivity of <i>Flaccisagitta enflata</i> (Chaetognatha: Sagittidae) in the tropical Atlantic ocean (northeastern Brazil). <i>PLoS ONE</i> , 2020, 15, e0231574.	1.1	7
9027	Population Genetic Analysis of <i>Sillago nigrofasciata</i> (Perciformes: Sillaginidae) Along the Coast of China by Sequencing Mitochondrial DNA Control Region. <i>Journal of Ocean University of China</i> , 2020, 19, 707-716.	0.6	0
9028	Potato-Infecting <i>Ralstonia solanacearum</i> Strains in Iran Expand Knowledge on the Global Diversity of Brown Rot Ecotype of the Pathogen. <i>Phytopathology</i> , 2020, 110, 1647-1656.	1.1	8
9029	Genetic diversity and phylogenetic relationships of tsetse flies of the palpalis group in Congo Brazzaville based on mitochondrial <i>cox1</i> gene sequences. <i>Parasites and Vectors</i> , 2020, 13, 253.	1.0	5
9030	Comparison of molecular and morphological characterization and haplotype analysis of cattle and sheep isolates of cystic echinococcosis. <i>Veterinary Parasitology</i> , 2020, 282, 109132.	0.7	13
9031	A minor QTL, SG3, encoding an R2R3-MYB protein, negatively controls grain length in rice. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2387-2399.	1.8	25
9032	Genetics of the Andean bear (<i>Tremarctos ornatus</i> ; Ursidae, Carnivora) in Ecuador: when the Andean Cordilleras are not an Obstacle. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2020, 31, 190-208.	0.7	36
9033	Different efficiencies in organic P exploitation of two Italian alfalfa (<i>Medicago sativa</i>) landraces involving a possible adaptation pattern of the phytase encoding <i>MsPHY1</i> gene. <i>Plant Breeding</i> , 2020, 139, 834-844.	1.0	0
9034	Epidemiology and genetic diversity of zoonotic pathogens in urban rats (<i>Rattus</i> spp.) from a subtropical city, Guangzhou, southern China. <i>Zoonoses and Public Health</i> , 2020, 67, 534-545.	0.9	15
9035	Modeling <i>Aceria tosichella</i> biotype distribution over geographic space and time. <i>PLoS ONE</i> , 2020, 15, e0233507.	1.1	6
9036	<i>Dugesia hepta</i> and <i>Dugesia benazzii</i> (Platyhelminthes: Tricladida): two sympatric species with occasional sex?. <i>Organisms Diversity and Evolution</i> , 2020, 20, 369-386.	0.7	8
9037	Comparative analysis of <i>Plasmodium falciparum</i> dihydrofolate-reductase gene sequences from different regions of India. <i>Heliyon</i> , 2020, 6, e03715.	1.4	4
9038	Tracking diversity and evolutionary pathways of Lebanese oak taxa through plastome analyses. <i>Botany Letters</i> , 2020, 167, 315-330.	0.7	5
9039	Evolution, characterization and phylogenetic utility of ITS2 gene in Orthoptera and some Polyneoptera: Highly variable at the order level and highly conserved at the species level. <i>Zootaxa</i> , 2020, 4780, 54-76.	0.2	4
9040	Genetic diversity and geographic distribution of <i>Bemisia tabaci</i> species complex in Nepal. <i>Journal of Asia-Pacific Entomology</i> , 2020, 23, 509-515.	0.4	7
9041	Molecular identification of seven new Zygopteran genera from South China through partial cytochrome oxidase subunit I (COI) gene. <i>Meta Gene</i> , 2020, 25, 100739.	0.3	2

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9042	Characterization of centromeric satellite DNAs (MALREP) in the Asian swamp eel (<i>Monopterus albus</i>) suggests the possible origin of repeats from transposable elements. <i>Genomics</i> , 2020, 112, 3097-3107.	1.3	11
9043	A new species of <i>Brachiella</i> (Copepoda, Siphonostomatoida, Lernaeopodidae) from Peninsular Malaysia, with relegation of two genera <i>Charopinopsis</i> and <i>Eobrachiella</i> to junior synonyms of <i>Brachiella</i> . <i>Parasite</i> , 2020, 27, 40.	0.8	4
9044	Genetic structure of bloodworm, <i>Arenicola loveni</i> (Annelida; Arenicolidae) suggests risk of local extinction in the face of overexploitation is lower than expected. <i>African Zoology</i> , 2020, 55, 175-183.	0.2	5
9045	Phylogeography and genetic structure of an iconic tree of the Sonoran Desert, the Cirio (<i>Fouquieria columnaris</i>), based on chloroplast DNA. <i>Biological Journal of the Linnean Society</i> , 2020, 130, 433-446.	0.7	7
9046	First come, first served: Possible role for priority effects in marine populations under different degrees of dispersal potential. <i>Journal of Biogeography</i> , 2020, 47, 1649-1662.	1.4	4
9047	Genome-Wide Identification and Evolutionary Analysis of NBS-LRR Genes From <i>Dioscorea rotundata</i> . <i>Frontiers in Genetics</i> , 2020, 11, 484.	1.1	38
9048	Large-Scale Hybridisation as an Extinction Threat to the Suweon Treefrog (Hylidae: Dryophytes) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50	1.0	8
9049	Comparative Analyses of Five Complete Chloroplast Genomes from the Genus <i>Pterocarpus</i> (Fabaceae). <i>International Journal of Molecular Sciences</i> , 2020, 21, 3758.	1.8	52
9050	Genome-wide data reveal discordant mitonuclear introgression in the intermediate horseshoe bat (<i>Rhinolophus affinis</i>). <i>Molecular Phylogenetics and Evolution</i> , 2020, 150, 106886.	1.2	18
9051	Disentangling the interplay of positive and negative selection forces that shaped mitochondrial genomes of <i>Gammarus pisinnus</i> and <i>Gammarus lacustris</i> . <i>Royal Society Open Science</i> , 2020, 7, 190669.	1.1	7
9052	Identification and genetic analysis of qCL1.2, a novel allele of the "œgreen revolution" gene SD1 from wild rice (<i>Oryza rufipogon</i>) that enhances plant height. <i>BMC Genetics</i> , 2020, 21, 62.	2.7	14
9053	Evolutionary analysis of chemokine CXCL16 and its receptor CXCR6 in murine rodents. <i>Developmental and Comparative Immunology</i> , 2020, 109, 103718.	1.0	1
9054	Long-term monoculture reduces the symbiotic rhizobial biodiversity of peanut. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126101.	1.2	18
9055	Molecular phylogeny and biogeography of <i>Triplophysa</i> stone loaches in the Central Chinese Mountains. <i>Biological Journal of the Linnean Society</i> , 2020, 130, 563-577.	0.7	11
9056	Complete chloroplast genome sequence of <i>Barleria prionitis</i> , comparative chloroplast genomics and phylogenetic relationships among Acanthoideae. <i>BMC Genomics</i> , 2020, 21, 393.	1.2	42
9057	Is there low maternal genetic variation in West Asian populations of leopard?. <i>Mammal Research</i> , 2020, 65, 701-708.	0.6	3
9058	Mitochondrial DNA intra-individual variation in a bumblebee species: A challenge for evolutionary studies and molecular identification. <i>Mitochondrion</i> , 2020, 53, 243-254.	1.6	9
9059	Molecular identification of <i>Trichogramma</i> species parasitizing <i>Ostrinia nubilalis</i> in corn and pepper in south-east border of Europe. <i>International Journal of Pest Management</i> , 2021, 67, 346-357.	0.9	6

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9060	Comprehensive analysis of mitochondrial DNA based genetic diversity in Indian goats. <i>Gene</i> , 2020, 756, 144910.	1.0	13
9061	Genetic diversity and population structure of <i>Camellia huana</i> (Theaceae), a limestone species with narrow geographic range, based on chloroplast DNA sequence and microsatellite markers. <i>Plant Diversity</i> , 2020, 42, 343-350.	1.8	26
9062	Tracing temporal and geographic distribution of resistance to pyrethroids in the arboviral vector <i>Aedes albopictus</i> . <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008350.	1.3	13
9063	Phylogeographic investigation of <i>Elaeagnus mollis</i> revealed potential glacial refugia and allopatric divergence in central China. <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	4
9064	Spatial genetic structure in the rock hyrax (<i>Procavia capensis</i>) across the Namaqualand and western Fynbos areas of South Africa – a mitochondrial and microsatellite perspective. <i>Canadian Journal of Zoology</i> , 2020, 98, 557-571.	0.4	4
9065	Genetic Diversity of the root-knot nematode <i>Meloidogyne enterolobii</i> in Mulberry Based on the Mitochondrial COI Gene. <i>Ecology and Evolution</i> , 2020, 10, 5391-5401.	0.8	5
9066	Identification, association, and expression analysis of ZmNAC134 gene response to phosphorus deficiency tolerance traits in maize at seedling stage. <i>Euphytica</i> , 2020, 216, 1.	0.6	3
9067	Signals of selection in the mitogenome provide insights into adaptation mechanisms in heterogeneous habitats in a widely distributed pelagic fish. <i>Scientific Reports</i> , 2020, 10, 9081.	1.6	14
9068	Cryptic speciation in gentoo penguins is driven by geographic isolation and regional marine conditions: Unforeseen vulnerabilities to global change. <i>Diversity and Distributions</i> , 2020, 26, 958-975.	1.9	17
9069	Differentiation, evolution and utilization of natural alleles for cold adaptability at the reproductive stage in rice. <i>Plant Biotechnology Journal</i> , 2020, 18, 2491-2503.	4.1	27
9070	New records and DNA barcoding of deer flies, Chrysops (Diptera: Tabanidae) in Thailand. <i>Acta Tropica</i> , 2020, 210, 105532.	0.9	6
9071	Molecular Phylogenetic Analysis of the Endemic Far Eastern Closely Related <i>Oxytropis</i> Species of Section <i>Orobia</i> (Fabaceae). <i>Russian Journal of Genetics</i> , 2020, 56, 429-440.	0.2	5
9072	Morphometrics and genetics highlight the complex history of Eastern Mediterranean spiny mice. <i>Biological Journal of the Linnean Society</i> , 2020, 130, 599-614.	0.7	8
9073	The influence of host dispersal on the gene flow and genetic diversity of generalist and specialist ectoparasites. <i>African Zoology</i> , 2020, 55, 119-126.	0.2	7
9074	Genetic diversity and structure of the Chinese lake gudgeon (<i>Sarcocheilichthys sinensis</i>). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2020, 31, 228-237.	0.7	2
9075	Porcine circovirus type 2 (PCV2) genotyping in Austrian pigs in the years 2002 to 2017. <i>BMC Veterinary Research</i> , 2020, 16, 198.	0.7	15
9076	Evaluation of the effect of longitudinal connectivity in population genetic structure of endangered golden mahseer, <i>Tor putitora</i> (Cyprinidae), in Himalayan rivers: Implications for its conservation. <i>PLoS ONE</i> , 2020, 15, e0234377.	1.1	8
9077	Mitochondrial COI Sequence Variations within and among Geographic Samples of the Hemp Pest <i>Psylliodes attenuata</i> from China. <i>Insects</i> , 2020, 11, 370.	1.0	4

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9078	Substantial differences in genetic diversity and spatial structuring among (cryptic) amphipod species in a mountainous river basin. <i>Freshwater Biology</i> , 2020, 65, 1641-1656.	1.2	14
9079	Micro-Evolution Analysis Reveals Diverged Patterns of Polyol Transporters in Seven Gramineae Crops. <i>Frontiers in Genetics</i> , 2020, 11, 565.	1.1	13
9080	Molecular Characterization and Antimicrobial Susceptibilities of <i>Nocardia</i> Species Isolated from the Soil; A Comparison with Species Isolated from Humans. <i>Microorganisms</i> , 2020, 8, 900.	1.6	4
9081	Complete mitogenome data for the Serbian population: the contribution to high-quality forensic databases. <i>International Journal of Legal Medicine</i> , 2020, 134, 1581-1590.	1.2	7
9082	Patterns of mtDNA introgression suggest population replacement in Palaearctic whiskered bat species. <i>Royal Society Open Science</i> , 2020, 7, 191805.	1.1	15
9083	Morphological characterization and genetic identity of crop wild relatives of rice (<i>Oryza sativa</i> L.) collected from different ecological niches of India. <i>Genetic Resources and Crop Evolution</i> , 2020, 67, 2037-2055.	0.8	8
9084	Spatial genetic structure and historical demography of East Asian wild boar. <i>Animal Genetics</i> , 2020, 51, 557-567.	0.6	9
9085	Phylogenetic structure of Neotropical annual fish of the genus <i>Cynopoeilus</i> (Cyprinodontiformes: Tj ETQq1 1 0.784314 rgBT /Overlook Evolutionary Research, 2020, 58, 1123-1134.	0.6	3
9086	Pathways of Pelagic Connectivity: <i>Eukrohnia hamata</i> (Chaetognatha) in the Arctic Ocean. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	8
9087	The Gene Flow Direction of Geographically Distinct <i>Phytophthora infestans</i> Populations in China Corresponds With the Route of Seed Potato Exchange. <i>Frontiers in Microbiology</i> , 2020, 11, 1077.	1.5	7
9088	Population connectivity and genetic structure of Asian green mussel, <i>Perna viridis</i> along Indian waters assessed using mitochondrial markers. <i>Molecular Biology Reports</i> , 2020, 47, 5061-5072.	1.0	5
9089	Plastome sequences of the subgenus <i>Passiflora</i> reveal highly divergent genes and specific evolutionary features. <i>Plant Molecular Biology</i> , 2020, 104, 21-37.	2.0	13
9090	DNA barcoding for identification of fish species from freshwater in Enugu and Anambra States of Nigeria. <i>Conservation Genetics Resources</i> , 2020, 12, 643-658.	0.4	17
9091	Molecular data supports monophyly of <i>Triatoma dispar</i> complex within genus <i>Triatoma</i> . <i>Infection, Genetics and Evolution</i> , 2020, 85, 104429.	1.0	2
9092	Signatures of TRI5, TRI8 and TRI11 Protein Sequences of <i>Fusarium incarnatum-equiseti</i> Species Complex (FIESC) Indicate Differential Trichothecene Analogue Production. <i>Toxins</i> , 2020, 12, 386.	1.5	1
9093	Coalescence-based species delimitation using genome-wide data reveals hidden diversity in a cosmopolitan group of lichens. <i>Organisms Diversity and Evolution</i> , 2020, 20, 189-218.	0.7	7
9094	Expanded inverted repeat region with large scale inversion in the first complete plastid genome sequence of <i>Plantago ovata</i> . <i>Scientific Reports</i> , 2020, 10, 3881.	1.6	34
9095	The maternal origin of indigenous domestic chicken from the Middle East, the north and the horn of Africa. <i>BMC Genetics</i> , 2020, 21, 30.	2.7	19

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9096	Evidence for population expansion of Cotton pink bollworm <i>Pectinophora gossypiella</i> (Saunders) (Lepidoptera: Gelechiidae) in India. <i>Scientific Reports</i> , 2020, 10, 4740.	1.6	19
9097	Chitinolytic activity of phylogenetically diverse <i>Bacillus cereus sensu lato</i> from natural environments. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126075.	1.2	15
9098	Antigen gene and variable number tandem repeat (VNTR) diversity in <i>Theileria parva</i> parasites from Ankole cattle in south-western Uganda: Evidence for conservation in antigen gene sequences combined with extensive polymorphism at VNTR loci. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 99-107.	1.3	1
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9206	Comparative Chloroplast Genomics of Endangered <i>Euphorbia</i> Species: Insights into Hotspot Divergence, Repetitive Sequence Variation, and Phylogeny. <i>Plants</i> , 2020, 9, 199.	1.6	12
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9220	Evidence of strong population bottleneck in genetics of endangered Brazilian Merganser (<i>Mergus</i>)	0.5	4
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9222	Genetic diversity and multiplicity of infection in <i>Fasciola gigantica</i> isolates of Pakistani livestock. <i>Parasitology International</i> , 2020, 76, 102071.	0.6	12
9223	Genetic relatedness and novel sequence types of clinical <i>Aeromonas dhakensis</i> from Malaysia. <i>Brazilian Journal of Microbiology</i> , 2020, 51, 909-918.	0.8	9
9224	Phylogeographic analyses of a migratory freshwater fish (<i>Megalobrama terminalis</i>) reveal a shallow genetic structure and pronounced effects of sea-level changes. <i>Gene</i> , 2020, 737, 144478.	1.0	19
9225	Geological and Climatic Factors Affect the Population Genetic Connectivity in <i>Mirabilis himalaica</i> (Nyctaginaceae): Insight From Phylogeography and Dispersal Corridors in the Himalaya-Hengduan Biodiversity Hotspot. <i>Frontiers in Plant Science</i> , 2019, 10, 1721.	1.7	21
9226	Phylogeographic and population genetic analyses of <i>Cucurbita moschata</i> reveal divergence of two mitochondrial lineages linked to an elevational gradient. <i>American Journal of Botany</i> , 2020, 107, 510-525.	0.8	10
9227	Genomic analysis of Sweet potato feathery mottle virus from East Africa. <i>Physiological and Molecular Plant Pathology</i> , 2020, 110, 101473.	1.3	6
9228	Prevalence of <i>Fasciola hepatica</i> infection in <i>Galba cousini</i> and <i>Galba schirazensis</i> from an Andean region of Ecuador. <i>Veterinary Parasitology: Regional Studies and Reports</i> , 2020, 20, 100390.	0.3	5
9229	Lasting through the ice age: The role of the proglacial refugia in the maintenance of genetic diversity, population growth, and high dispersal rate in a widespread freshwater crustacean. <i>Freshwater Biology</i> , 2020, 65, 1028-1046.	1.2	26
9230	Genome-wide analysis of ethylene-insensitive3 (EIN3/EIL) in <i>Triticum aestivum</i> . <i>Crop Science</i> , 2020, 60, 2019-2037.	0.8	23
9231	Genetic diversity within and between British and Irish breeds: The maternal and paternal history of native ponies. <i>Ecology and Evolution</i> , 2020, 10, 1352-1367.	0.8	4
9232	Global transmission and evolutionary dynamics of the Chikungunya virus. <i>Epidemiology and Infection</i> , 2020, 148, e63.	1.0	12
9233	The persimmon genome reveals clues to the evolution of a lineage-specific sex determination system in plants. <i>PLoS Genetics</i> , 2020, 16, e1008566.	1.5	54
9234	Population history of a social spider reveals connection between South American tropical forests. <i>Zoologischer Anzeiger</i> , 2020, 285, 139-146.	0.4	1
9235	Genetic analysis and population structure of the <i>Anopheles gambiae</i> complex from different ecological zones of Burkina Faso. <i>Infection, Genetics and Evolution</i> , 2020, 81, 104261.	1.0	4
9236	Phenotypic and genetic differentiation between diadromous and landlocked puyen <i>Galaxias maculatus</i> . <i>Journal of Fish Biology</i> , 2020, 96, 956-967.	0.7	18
9237	Molecular detection and genetic diversity of <i>Bartonella</i> species in large ruminants and associated ectoparasites from the Brazilian Cerrado. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 1888.	1.3	4
9238	Phylogeography and demographic history of <i>Gyrodactylus konovalovi</i> (Monogenoidea: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 Td (Gyrodactylidae)). <i>Evolution</i> , 2020, 10, 1454-1468.	0.8	2
9239	Genetic diversity and differentiation in the blackflies <i>Simulium cheongi</i> , <i>Simulium jeffreyi</i> and <i>Simulium vanluni</i> (Diptera: Simuliidae) in Peninsular Malaysia. <i>Acta Tropica</i> , 2020, 205, 105415.	0.9	1

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9240	Bemisia tabaci in Iraq: Population structure, endosymbiont diversity and putative species. Journal of Applied Entomology, 2020, 144, 297-307.	0.8	3
9241	DNA taxonomy of the potamid freshwater crabs from Northern Africa (Decapoda, Potamidae). Zoologica Scripta, 2020, 49, 473-487.	0.7	9
9242	Evidence of an ancient connectivity and biogeodispersal of a bitterling species, Rhodeus notatus, across the Korean Peninsula. Scientific Reports, 2020, 10, 1011.	1.6	11
9243	Worldwide Phylogeography of Ceratitis capitata (Diptera: Tephritidae) Using Mitochondrial DNA. Journal of Economic Entomology, 2020, 113, 1455-1470.	0.8	12
9244	Morphotypes or distinct species? A multilocus assessment of two East Asian scimitar babblers (Aves, Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.7	4
9245	Population differentiation and historical demography of the threatened snowy plover Charadrius nivosus (Cassin, 1858). Conservation Genetics, 2020, 21, 387-404.	0.8	6
9246	What should we call the Levant mole? Unravelling the systematics and demography of Talpa levantis Thomas, 1906 sensu lato (Mammalia: Talpidae). Mammalian Biology, 2020, 100, 1-18.	0.8	4
9247	Genetic differentiation and evolutionary history of the circumpolar species Ophiura sarsii and subspecies Ophiura sarsii vadicola (Ophiurida: Ophiuridae). Continental Shelf Research, 2020, 197, 104085.	0.9	4
9248	Distribution patterns of two co-existing oyster species in the northern Adriatic Sea: The native European flat oyster Ostrea edulis and the non-native Pacific oyster Magallana gigas. Ecological Indicators, 2020, 113, 106233.	2.6	16
9249	Deep mitochondrial DNA phylogeographic divergence in the threatened aoudad Ammotragus lervia (Bovidae, Caprini). Gene, 2020, 739, 144510.	1.0	5
9250	Molecular systematics of the genus Necromys (Rodentia: Cricetidae: Sigmodontinae) reveals two cryptic and syntopic species in western Cerrado of Brazil. Zoologischer Anzeiger, 2020, 285, 147-158.	0.4	5
9251	Mass appearance of the Ponto-Caspian invader <i>Pontogammarus robustoides</i> in the River Tisza catchment: bypass in the southern invasion corridor?. Knowledge and Management of Aquatic Ecosystems, 2020, , 9.	0.5	11
9252	Plastid-encoded gene comparison reveals usefulness of <i>atp</i>B, <i>psa</i>A, and <i>rbc</i>L for identification and phylogeny of plastid-containing cryptophyte clades. Phycologia, 2020, 59, 154-164.	0.6	1
9253	DNA Barcoding Subtropical Aphids and Implications for Population Differentiation. Insects, 2020, 11, 11.	1.0	10
9254	Population genetic structure and maternal lineage of South African crossbred Nguni cattle using the cytochrome b gene in mtDNA. Tropical Animal Health and Production, 2020, 52, 2079-2089.	0.5	1
9255	Phylogeographical structure of the pygmy shrew: revisiting the roles of southern and northern refugia in Europe. Biological Journal of the Linnean Society, 2020, 129, 901-917.	0.7	12
9256	Evolution of the Plasmodium vivax multidrug resistance 1 gene in the Greater Mekong Subregion during malaria elimination. Parasites and Vectors, 2020, 13, 67.	1.0	13
9257	The Mitochondrial Genome of Amara aulica (Coleoptera, Carabidae, Harpalinae) and Insights into the Phylogeny of Ground Beetles. Genes, 2020, 11, 181.	1.0	8

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9258	Invasion History of <i>Sirex noctilio</i> Based on COI Sequence: The First Six Years in China. <i>Insects</i> , 2020, 11, 111.	1.0	4
9259	Evolutionary history of two cryptic species of northern African jerboas. <i>BMC Evolutionary Biology</i> , 2020, 20, 26.	3.2	16
9260	Molecular phylogenetics and mitogenomics of three avian dicrocoeliids (Digenea: Dicrocoeliidae) and comparison with mammalian dicrocoeliids. <i>Parasites and Vectors</i> , 2020, 13, 74.	1.0	16
9261	A comparative approach for species delimitation based on multiple methods of multi-locus DNA sequence analysis: A case study of the genus <i>Giraffa</i> (Mammalia, Cetartiodactyla). <i>PLoS ONE</i> , 2020, 15, e0217956.	1.1	37
9262	Spatiotemporal Differentiation of Alpine Butterfly <i>Parnassius glacialis</i> (Papilionidae: Parnassiinae) in China: Evidence from Mitochondrial DNA and Nuclear Single Nucleotide Polymorphisms. <i>Genes</i> , 2020, 11, 188.	1.0	9
9263	Isolation and characterization of two satellite DNAs in <i>Atlantolacerta andreanskyi</i> (Werner,) <i>Tj ETQq1 1 0.784314 rgBT /Overlock Evolution</i> , 2020, 334, 178-191.	0.6	4
9264	Evolution of self-compatibility by a mutant Sm-RNase in citrus. <i>Nature Plants</i> , 2020, 6, 131-142.	4.7	85
9265	Divergence across mitochondrial genomes of sympatric members of the <i>Schistosoma indicum</i> group and clues into the evolution of <i>Schistosoma spindale</i> . <i>Scientific Reports</i> , 2020, 10, 2480.	1.6	16
9266	Comparison of the complete plastomes and the phylogenetic analysis of <i>Paulownia</i> species. <i>Scientific Reports</i> , 2020, 10, 2225.	1.6	25
9267	Cellular Innovation of the Cyanobacterial Heterocyst by the Adaptive Loss of Plasticity. <i>Current Biology</i> , 2020, 30, 344-350.e4.	1.8	11
9268	Highly divergent mitogenomes of <i>Geukensia demissa</i> (Bivalvia, Mytilidae) with extreme AT content. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 571-580.	0.6	8
9269	Biotic and abiotic drivers of evolution in some Australian thornbills (Passeriformes: Acanthiza) in allopatry, sympatry, and parapatry including a case of character displacement. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 1290-1302.	0.6	0
9270	Sky islands as foci for divergence of fig trees and their pollinators in southwest China. <i>Molecular Ecology</i> , 2020, 29, 762-782.	2.0	18
9271	Population genomics of three deep-sea cephalopod species reveals connectivity between the Gulf of Mexico and northwestern Atlantic Ocean. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2020, 158, 103222.	0.6	21
9272	New records and genetic diversity of <i>Mycoplasma ovis</i> in free-ranging deer in Brazil. <i>Epidemiology and Infection</i> , 2020, 148, e6.	1.0	7
9273	Comparative phylogeography of two sister species of snowcock: impacts of species-specific altitude preference and life history. <i>Avian Research</i> , 2020, 11, .	0.5	4
9274	Conservation Genetics in Mammals. , 2020, , .		6
9275	Getting off on the right foot: Integration of spatial distribution of genetic variability for aquaculture development and regulations, the European perch case. <i>Aquaculture</i> , 2020, 521, 734981.	1.7	11

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9276	Multilocus approach reveals discordant molecular markers and corridors for gene flow between North African populations of <i>Fasciola hepatica</i> . <i>Veterinary Parasitology</i> , 2020, 278, 109035.	0.7	8
9277	A helitron-induced RabGD1± variant causes quantitative recessive resistance to maize rough dwarf disease. <i>Nature Communications</i> , 2020, 11, 495.	5.8	45
9278	Revising the taxonomy of <i>Proceratophrys</i> Miranda&Ribeiro, 1920 (Anura: Odontophrynidae) from the Brazilian semiarid Caatinga: Morphology, calls and molecules support a single widespread species. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 1151-1172.	0.6	13
9279	Use of species delimitation approaches to assess biodiversity in freshwater planaria (Platyhelminthes). <i>Tj ETQq1 1 0.784314 rgBT /Ove</i> 209-218.	0.9	10
9280	Sequence and functional analysis of cis-elements associated with MIR159 loci from <i>Brassica juncea</i> reveal functional diversification and complex transcriptional regulation. <i>Plant Growth Regulation</i> , 2020, 90, 279-306.	1.8	4
9281	DNA barcoding for identification of marine gastropod species from Hainan island, China. <i>Fisheries Research</i> , 2020, 225, 105504.	0.9	14
9282	Quaternary ice sheets and sea level regression drove divergence in a marine gastropod along Eastern and Western coasts of South America. <i>Scientific Reports</i> , 2020, 10, 844.	1.6	12
9283	Genetic structure and recent population expansion in the commercially harvested deep-sea decapod, <i>Metanephrops challengeri</i> (Crustacea: Decapoda). <i>New Zealand Journal of Marine and Freshwater Research</i> , 2020, 54, 251-270.	0.8	2
9284	Genetic structure and phylogeographic relationships of the <i>Bellamya</i> complex: A nascent aquacultural snail in the Pearl River basin, China. <i>Aquaculture Research</i> , 2020, 51, 1323-1335.	0.9	4
9285	<i>Barbus xanthos</i> , a new barbel from the Southern Aegean basin (Teleostei: Cyprinidae). <i>Journal of Fish Biology</i> , 2020, 96, 1309-1319.	0.7	7
9286	Molecular detection and genetic diversity of <i>Anaplasma marginale</i> based on the major surface protein genes in Thailand. <i>Acta Tropica</i> , 2020, 205, 105338.	0.9	20
9287	Artificial Selection in Domestication and Breeding Prevents Speciation in Rice. <i>Molecular Plant</i> , 2020, 13, 650-657.	3.9	12
9288	Type specimens matter: new insights on the systematics, taxonomy and nomenclature of the subalpine warbler (<i>Sylvia cantillans</i>) complex. <i>Zoological Journal of the Linnean Society</i> , 2020, 190, 314-341.	1.0	14
9289	Comparative phylogeography of two free-living cosmopolitan cyanobacteria: Insights on biogeographic and latitudinal distribution. <i>Journal of Biogeography</i> , 2020, 47, 1106-1118.	1.4	8
9290	Impact of past climate warming on genomic diversity and demographic history of collared lemmings across the Eurasian Arctic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 3026-3033.	3.3	19
9291	Population Genetic Diversity and Structure of <i>Thrips tabaci</i> (Thysanoptera: Thripidae) on <i>Allium</i> Hosts in China, Inferred From Mitochondrial COI Gene Sequences. <i>Journal of Economic Entomology</i> , 2020, 113, 1426-1435.	0.8	11
9292	Genome-wide nuclear data confirm two species in the Alpine endemic land snail <i>Noricella oreinoss</i> .l. (Gastropoda, Hygromiidae). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 982-1004.	0.6	3
9293	Impact of Suboptimal APOBEC3G Neutralization on the Emergence of HIV Drug Resistance in Humanized Mice. <i>Journal of Virology</i> , 2020, 94, .	1.5	11

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9294	Genetic diversity hotspot of the amphi-Pacific macroalga <i>Gloiopeltis furcata</i> sensu lato (Gigartinales,) Tj ETQq0 0 0 1.5 / Overlock 10 Tf		
9295	Comparative Analysis of the Complete Chloroplast Genomes in <i>Allium</i> Subgenus <i>Cyathophora</i> (Amaryllidaceae): Phylogenetic Relationship and Adaptive Evolution. BioMed Research International, 2020, 2020, 1-17.	0.9	16
9296	Genome-wide identification of BXL genes in <i>Populus trichocarpa</i> and their expression under different nitrogen treatments. 3 Biotech, 2020, 10, 57.	1.1	5
9297	Morphology and genetic investigation of flatfish interspecies hybrids (<i>Pleuronectes platessa</i> X) Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf	0.9	5
9298	Subterranean <i>Deuteraphorura</i> Absolon, 1901, (Hexapoda, Collembola) of the Western Carpathians – Troglomorphy at the northern distributional limit in Europe. PLoS ONE, 2020, 15, e0226966.	1.1	6
9299	Phylogenetic relationships of <i>Atractylodes lancea</i> , <i>A. chinensis</i> and <i>A. macrocephala</i> , revealed by complete plastome and nuclear gene sequences. PLoS ONE, 2020, 15, e0227610.	1.1	10
9300	Resequencing 200 Flax Cultivated Accessions Identifies Candidate Genes Related to Seed Size and Weight and Reveals Signatures of Artificial Selection. Frontiers in Plant Science, 2019, 10, 1682.	1.7	32
9301	Understanding Historical Demographic Processes to Inform Contemporary Conservation of an Arid Zone Specialist: The Yellow-Footed Rock-Wallaby. Genes, 2020, 11, 154.	1.0	2
9302	High genetic variability of clinical and environmental <i>Cryptococcus gattii</i> isolates from Brazil. Medical Mycology, 2020, 58, 1126-1137.	0.3	18
9303	Climatic refugia boosted allopatric diversification in Western Mediterranean vipers. Journal of Biogeography, 2020, 47, 1698-1713.	1.4	37
9304	Comparative Plastome Analyses and Phylogenetic Applications of the <i>Acer</i> Section <i>Platanoidea</i> . Forests, 2020, 11, 462.	0.9	10
9305	Comparative genetic analysis of grayling (<i>Thymallus</i> spp. Salmonidae) across the paleohydrologically dynamic river drainages of the Altai-Sayan mountain region. Hydrobiologia, 2020, 847, 2823-2844.	1.0	6
9306	Adaptive genetic diversity and evidence of population genetic structure in the endangered Sierra Madre Sparrow (<i>Xenospiza baileyi</i>). PLoS ONE, 2020, 15, e0232282.	1.1	4
9307	Molecular investigation and genetic diversity of <i>Pediculus</i> and <i>Pthirus</i> lice in France. Parasites and Vectors, 2020, 13, 177.	1.0	15
9308	Single-strand conformation polymorphism (SSCP) of mitochondrial genes helps to estimate genetic differentiation, demographic parameters and phylogeny of <i>Glossina palpalis palpalis</i> populations from West and Central Africa. Infection, Genetics and Evolution, 2020, 82, 104303.	1.0	1
9309	A Tale of Two Families: Whole Genome and Segmental Duplications Underlie Glutamine Synthetase and Phosphoenolpyruvate Carboxylase Diversity in Narrow-Leafed Lupin (<i>Lupinus angustifolius</i> L.). International Journal of Molecular Sciences, 2020, 21, 2580.	1.8	7
9310	The origin of allotetraploid <i>Lepisorus inaequibasis</i> (Polypodiaceae) and paternal bias in its morphology and abiotic niche. Taxon, 2020, 69, 43-55.	0.4	4
9311	Population genetics of the wolverine in Finland: the road to recovery?. Conservation Genetics, 2020, 21, 481-499.	0.8	12

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9312	Population genetic structures of <i>Puccinia triticina</i> in five provinces of China. <i>European Journal of Plant Pathology</i> , 2020, 156, 1135-1145.	0.8	9
9313	Purifying selection shaping the evolution of the Toll-like receptor 2 TIR domain in brown hares (<i>Lepus</i>) Tj ETQq1 1 0,784314 rgBT /Overl	1.0	4
9314	Effect of temperature and oxygen regime on growth and physiology of juvenile <i>Salvelinus fontinalis</i> Å– <i>Salvelinus alpinus</i> hybrids. <i>Aquaculture</i> , 2020, 522, 735119.	1.7	7
9315	Complete chloroplast genome sequencing of sago palm (<i>Metroxylon sagu</i> Rottb.): Molecular structures, comparative analysis and evolutionary significance. <i>Gene Reports</i> , 2020, 19, 100662.	0.4	8
9316	New insights into the haplotype diversity of the cosmopolitan cat flea <i>Ctenocephalides felis</i> (Siphonaptera: Pulicidae). <i>Veterinary Parasitology</i> , 2020, 281, 109102.	0.7	15
9317	Cryptic diversity and ancient diversification in the northern Atlantic Forest <i>Pristimantis</i> (Amphibia,) Tj ETQq1 1 0,784314 rgBT /Overl	1.2	19
9318	Vicariance, dispersal, extinction and hybridization underlie the evolutionary history of Atlantic forest fire-eye antbirds (<i>Aves: Thamnophilidae</i>). <i>Molecular Phylogenetics and Evolution</i> , 2020, 148, 106820.	1.2	5
9319	Mitochondrial sequenceâ€based evolutionary analysis of riverineâ€swamp hybrid buffaloes of India indicates novel maternal differentiation and domestication patterns. <i>Animal Genetics</i> , 2020, 51, 476-482.	0.6	10
9320	Population expansion and genomic adaptation to agricultural environments of the soybean looper, <i>Chrysodeixis includens</i> . <i>Evolutionary Applications</i> , 2020, 13, 2071-2085.	1.5	30
9321	Isolation and characterization of a new <i>MATE</i> gene located in the same chromosome arm of the aluminium tolerance (<i>Alt1</i>) rye locus. <i>Plant Biology</i> , 2020, 22, 691-700.	1.8	5
9322	Hemoplasmas Are Endemic and Cause Asymptomatic Infection in the Endangered Darwinâ€™s Fox (<i>Lycalopex fulvipes</i>). <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	16
9323	Whole Genome Scan Reveals Molecular Signatures of Divergence and Selection Related to Important Traits in Durum Wheat Germplasm. <i>Frontiers in Genetics</i> , 2020, 11, 217.	1.1	50
9324	Evolutionary Dynamics of Multigene Families in <i>Triportheus</i> (Characiformes, Triporthidae): A Transposon Mediated Mechanism?. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	14
9325	New insights on the geographical origins of the Caribbean raccoons. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2020, 58, 1303-1322.	0.6	8
9326	Low genetic diversity of cultivated spotted hard clam (<i>Meretrix petechialis</i>) in Taiwan. <i>Aquaculture Research</i> , 2020, 51, 2962-2972.	0.9	3
9327	Influence of the 2011 Tohoku tsunami on the genetic structure of wild sea urchin (<i>Mesocentrotus</i>) Tj ETQq1 1 0,784314 rgBT /Overl	0,4	4
9328	Genetically â€pureâ€™ <i>Fasciola gigantica</i> discovered in Algeria: DNA multimarker characterization, transâ€Saharan introduction from a Sahel origin and spreading risk into northâ€western Maghreb countries. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 2190.	1.3	13
9329	Exploring the Mechanisms of Multiple Insecticide Resistance in a Highly Plasmodium-Infected Malaria Vector <i>Anopheles funestus</i> Sensu Stricto from Sahel of Northern Nigeria. <i>Genes</i> , 2020, 11, 454.	1.0	9

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9330	Comparative Analysis of the Complete Plastid Genome of Five <i>Bupleurum</i> Species and New Insights into DNA Barcoding and Phylogenetic Relationship. <i>Plants</i> , 2020, 9, 543.	1.6	26
9331	Invalidation of taxa within the silvery wooly monkey (<i>Lagothrix lagothricha poeppigii</i> , Atelidae.) <i>Tj ETQq1 1 0.784314,rgBT /Overlock 10</i>	0.7	1
9332	Toward a preliminary assessment of the diversity and origin of Cyprinid fish genus <i>Carassius</i> in Iran. <i>Journal of Applied Ichthyology</i> , 2020, 36, 422-430.	0.3	6
9333	How many species of angulate tortoises occur in Southern Africa? (Testudines: Testudinidae.) <i>Tj ETQq1 1 0.784314,rgBT /Overlock 10</i>	0.7	6
9334	Lineage-specific evolution of mangrove plastid genomes. <i>Plant Genome</i> , 2020, 13, e20019.	1.6	4
9335	DNA barcoding of selected Zingiberaceae species from North-East India. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2020, 29, 494-502.	0.9	1
9336	DNA Barcoding Silver Butter Catfish (<i>Schilbe intermedius</i>) Reveals Patterns of Mitochondrial Genetic Diversity Across African River Systems. <i>Scientific Reports</i> , 2020, 10, 7097.	1.6	8
9337	Cryptic speciation in the ectocommensal <i>Bdelloura candida</i> (Platyhelminthes, Tricladida, Maricola) follows habitat specialization of the American horseshoe crab, <i>Limulus polyphemus</i> . <i>Invertebrate Biology</i> , 2020, 139, e12284.	0.3	2
9338	Multilocus phylogeny and systematics of Iberian endemic <i>Squalius</i> (Actinopterygii, Leuciscidae). <i>Zoologica Scripta</i> , 2020, 49, 440-457.	0.7	5
9339	Plastome Evolution in Saxifragaceae and Multiple Plastid Capture Events Involving <i>Heuchera</i> and <i>Tiarella</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 361.	1.7	34
9340	Retrospective study of porcine circovirus 3 (PCV3) in swine tissue from Brazil (1967–2018). <i>Brazilian Journal of Microbiology</i> , 2020, 51, 1391-1397.	0.8	16
9341	Inconspicuous genetic and morphological patterns challenge the taxonomic status of endemic species <i>Bodianus insularis</i> (Labridae). <i>Zoologischer Anzeiger</i> , 2020, 286, 43-51.	0.4	2
9342	Antimicrobial peptide and sequence variation along a latitudinal gradient in two anurans. <i>BMC Genetics</i> , 2020, 21, 38.	2.7	6
9343	Dispersal and genetic structure in a tropical small mammal, the Bornean tree shrew (<i>Tupaia longipes</i>), in a fragmented landscape along the Kinabatangan River, Sabah, Malaysia. <i>BMC Genetics</i> , 2020, 21, 43.	2.7	5
9344	Insights into phylogeny, age and evolution of <i>Allium</i> (Amaryllidaceae) based on the whole plastome sequences. <i>Annals of Botany</i> , 2020, 125, 1039-1055.	1.4	49
9345	Chloroplast genomes of seven species of Coryloideae (Betulaceae): structures and comparative analysis. <i>Genome</i> , 2020, 63, 337-348.	0.9	11
9346	Phylogeography and genetic diversity of the copepod family Cyclopidae (Crustacea: Cyclopoida) from freshwater ecosystems of Southeast Nigeria. <i>BMC Evolutionary Biology</i> , 2020, 20, 45.	3.2	2
9347	Molecular assessment of the distribution and taxonomy of the Lesser Whitethroat <i>Sylvia curruca</i> complex in Iran, with particular emphasis on the identity of the contentious taxon, <i>zagrossiensis</i> Sarudny, 1911. <i>Journal of Ornithology</i> , 2020, 161, 665-676.	0.5	4

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9348	Phylogeography and species distribution modeling reveal a historic disjunction for the conifer <i>Podocarpus lambertii</i> . <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	1
9350	Multiple invasions of a generalist herbivore—Secondary contact between two divergent lineages of <i>Nezara viridula</i> Linnaeus in Australia. <i>Evolutionary Applications</i> , 2020, 13, 2113-2129.	1.5	5
9351	Pleistocene expansion and connectivity of mesic forests inside the South American Dry Diagonal supported by the phylogeography of a small lizard*. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 1988-2004.	1.1	7
9352	Genetic diversity and differentiation of populations of <i>Chlorops oryzae</i> (Diptera, Chloropidae). <i>BMC Ecology</i> , 2020, 20, 22.	3.0	10
9353	Distribution and pyrethroid resistance status of <i>Aedes aegypti</i> and <i>Aedes albopictus</i> populations and possible phylogenetic reasons for the recent invasion of <i>Aedes aegypti</i> in Nepal. <i>Parasites and Vectors</i> , 2020, 13, 213.	1.0	12
9354	Revisiting the Woolly wolf (<i>Canis lupus chanco</i>) phylogeny in Himalaya: Addressing taxonomy, spatial extent and distribution of an ancient lineage in Asia. <i>PLoS ONE</i> , 2020, 15, e0231621.	1.1	14
9355	Characteristic features of the SERA multigene family in the malaria parasite. <i>Parasites and Vectors</i> , 2020, 13, 170.	1.0	15
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9357	Molecular Phylogeography and Evolutionary History of the Endemic Species <i>Corydalis hendersonii</i> (Papaveraceae) on the Tibetan Plateau Inferred From Chloroplast DNA and ITS Sequence Variation. <i>Frontiers in Plant Science</i> , 2020, 11, 436.	1.7	11
9358	New Records of Antarctic Tardigrada with Comments on Interpopulation Variability of the <i>Paramacrotus fairbanksi</i> Schill, Förster, Dandekar and Wolf, 2010. <i>Diversity</i> , 2020, 12, 108.	0.7	18
9359	Genome-Wide Identification, Classification, and Expression Profiling Reveals R2R3-MYB Transcription Factors Related to Monoterpenoid Biosynthesis in <i>Osmanthus fragrans</i> . <i>Genes</i> , 2020, 11, 353.	1.0	20
9360	Characterization of Nuclear and Mitochondrial Genomes of Two Tobacco Endophytic Fungi <i>Leptosphaerulina chartarum</i> and <i>Curvularia trifolii</i> and Their Contributions to Phylogenetic Implications in the Pleosporales. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2461.	1.8	7
9361	Complete Mitogenomic Structure and Phylogenetic Implications of the Genus <i>Ostrinia</i> (Lepidoptera: Tortricidae). <i>Genetics and Molecular Biology</i> , 2020, 43, 190-200.	1.9	20
9362	Phylogenetic relationship of <i>Picea mongolica</i> with other <i>Picea</i> species in the same area based on chloroplast gene variations. <i>Journal of Forestry Research</i> , 2021, 32, 297-305.	1.7	0
9363	Polyphyly and species delimitation of <i>Picea brachytyla</i> (Pinaceae) based on population genetic data. <i>Journal of Systematics and Evolution</i> , 2021, 59, 515-523.	1.6	2
9364	Landscape genetic analyses reveal host association of mitochondrial haplotypes in the Asian corn borer, <i>Ostrinia furnacalis</i> . <i>Insect Science</i> , 2021, 28, 1169-1178.	1.5	3
9365	Genotyping of mitochondrial D-loop sequences in three breeds of sheep. <i>Biologia (Poland)</i> , 2021, 76, 203-211.	0.8	8
9366	First records raise questions: DNA barcoding of Odonata in the middle of the Mediterranean. <i>Genome</i> , 2021, 64, 196-206.	0.9	10

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9367	Evolutionary history of the reef fish <i>Anisotremus interruptus</i> (Perciformes: Haemulidae) throughout the Tropical Eastern Pacific. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 148-162.	0.6	6
9368	<i>Candidatus</i> <i>Mycoplasma haemoalbiventris</i> TM , a novel hemoplasma species in white-eared opossums (<i>Didelphis albiventris</i>) from Brazil. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 565-572.	1.3	16
9369	Geoclimatic factors influence the population genetic connectivity of <i>Incarvillea arguta</i> (Bignoniaceae) in the Himalaya-Hengduan Mountains biodiversity hotspot. <i>Journal of Systematics and Evolution</i> , 2021, 59, 151-168.	1.6	28
9370	Molecular identification and population differentiation of <i>Aurelia</i> spp. ephyrae in sea cucumber aquaculture ponds of northern China. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 989-996.	0.6	2
9371	Up in the air: Threats to Afromontane biodiversity from climate change and habitat loss revealed by genetic monitoring of the Ethiopian Highlands bat. <i>Evolutionary Applications</i> , 2021, 14, 794-806.	1.5	13
9372	Regional-scale aquifer hydrogeology as a driver of phylogeographic structure in the Neotropical catfish <i>Rhamdia guatemalensis</i> (Siluriformes: Heptapteridae) from cenotes of the Yucatán Peninsula, Mexico. <i>Freshwater Biology</i> , 2021, 66, 332-348.	1.2	5
9373	Genetic and phenotypic displacement of an endemic <i>Barbus</i> complex by invasive European barbel <i>Barbus barbus</i> in central Italy. <i>Biological Invasions</i> , 2021, 23, 521-535.	1.2	9
9374	Lineage diversity and gene introgression in freshwater cladoceran crustaceans of the <i>Chydorus sphaericus</i> species complex. <i>Limnology and Oceanography</i> , 2021, 66, 95-107.	1.6	12
9375	Genetic population structure of the striped venus clam <i>Chamelea gallina</i> across its range. <i>Fisheries Research</i> , 2021, 234, 105758.	0.9	3
9376	Multilocus phylogeny of African striped grass mice (<i>Lemniscomys</i>): Stripe pattern only partly reflects evolutionary relationships. <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 107007.	1.2	11
9377	Expression and localization of SWEETs in <i>Populus</i> and the effect of <i>SWEET7</i> overexpression in secondary growth. <i>Tree Physiology</i> , 2021, 41, 882-899.	1.4	20
9378	Grapevine Asteroid Mosaic-Associated Virus is Resident and Prevalent in Wild, Noncultivated Grapevine of New York State. <i>Plant Disease</i> , 2021, 105, 758-763.	0.7	4
9379	Biological, epidemiological and population structure analyses of vitiviruses in Iran. <i>European Journal of Plant Pathology</i> , 2021, 159, 117-129.	0.8	2
9380	Genome-wide investigation and expression analysis of APETALA-2 transcription factor subfamily reveals its evolution, expansion and regulatory role in abiotic stress responses in Indica Rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgB2/Overlaid		
9381	High connectivity and migration potentiate the invasion of <i>Limnoperna fortunei</i> (Mollusca: Mytilidae) in South America. <i>Hydrobiologia</i> , 2021, 848, 499-513.	1.0	11
9382	Genetic Polymorphism and Lineage of Pigeon Pea [<i>Cajanus cajan</i> (L.) Millsp.] inferred from Chloroplast and Nuclear DNA gene regions. <i>Arabian Journal for Science and Engineering</i> , 2021, 46, 5285-5297.	1.7	0
9383	Variability analyses of the maternal lineage of horses and donkeys. <i>Gene</i> , 2021, 769, 145231.	1.0	3
9384	Mitochondrial heteroplasmy and pseudogenes in the freshwater prawn, <i>Macrobrachium amazonicum</i> (Heller, 1862): DNA barcoding and phylogeographic implications. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2021, 32, 1-11.	0.7	4

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9386	Almost never you get what you pay for: Widespread mislabeling of commercial "amburi" in northern Spain. <i>Food Control</i> , 2021, 120, 107541.	2.8	8
9387	Phylogeographical history of the Olive Woodpecker (<i>Dendropicos griseocephalus</i>), a species widely distributed across Africa. <i>Ibis</i> , 2021, 163, 417-428.	1.0	2
9388	Widespread mislabeling of nonnative apple snails (Ampullariidae: Pomacea) as native field snails (Viviparidae: Cipangopaludina) on the Chinese food markets. <i>Aquaculture</i> , 2021, 530, 735756.	1.7	9
9389	Origin, selection, and spread of diamide insecticide resistance allele in field populations of diamondback moth in east and southeast Asia. <i>Pest Management Science</i> , 2021, 77, 313-324.	1.7	10
9390	Geographical distribution and ecological niche modeling of the etiological agents of human sporotrichosis in Venezuela. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 63-71.	0.8	4
9391	Comparative plastomic analysis and insights into the phylogeny of <i>Salvia</i> (Lamiaceae). <i>Plant Diversity</i> , 2021, 43, 15-26.	1.8	19
9392	Conservation genetics of native and European-introduced Chinese water deer (<i>Hydropotes inermis</i>). <i>Zoological Journal of the Linnean Society</i> , 2021, 191, 1181-1191.	1.0	5
9393	Phenotypic and molecular characterisation of <i>Sporothrix globosa</i> of diverse origin from India. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 91-100.	0.8	14
9394	Bioecology of false codling moth, <i>Thaumatotibia leucotreta</i> (Meyrick) (Lepidoptera: Tortricidae) within citrus orchards in Kenya and Tanzania. <i>Agricultural and Forest Entomology</i> , 2021, 23, 13-22.	0.7	1
9395	Evolution and Transcriptional Modulation of Lipoxygenase Genes Under Heat, Drought, and Combined Stress in <i>Brassica rapa</i> . <i>Plant Molecular Biology Reporter</i> , 2021, 39, 60-71.	1.0	5
9396	GNP6, a novel allele of MOC1, regulates panicle and tiller development in rice. <i>Crop Journal</i> , 2021, 9, 57-67.	2.3	22
9397	Patagonian glacial effects on the endemic Green-backed Firecrown, <i>Sephanoides sephanoides</i> (Aves: Tj ETQq0 0 0 rgBT /Overlock 10 Tf). <i>Evolution</i> , 2021, 162, 289-301.	0.5	6
9398	Genome-wide SNP analysis of Siamese cobra (<i>Naja kaouthia</i>) reveals the molecular basis of transitions between Z and W sex chromosomes and supports the presence of an ancestral super-sex chromosome in amniotes. <i>Genomics</i> , 2021, 113, 624-636.	1.3	18
9399	Systematics, biogeography and evolution of the Saharo-Arabian naked-toed geckos genus <i>Tropicolotes</i> . <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 106969.	1.2	8
9400	Subspecies divergence and pronounced phylogenetic incongruence in the East-Asia-endemic shrub <i>Magnolia sieboldii</i> . <i>Annals of Botany</i> , 2021, 127, 75-90.	1.4	7
9401	House mouse <i>Mus musculus</i> dispersal in East Eurasia inferred from 98 newly determined complete mitochondrial genome sequences. <i>Heredity</i> , 2021, 126, 132-147.	1.2	26
9402	Comprehensive evidence for subspecies designations in Cook's Petrel <i>Pterodroma cookii</i> with implications for conservation management. <i>Bird Conservation International</i> , 2021, 31, 1-13.	0.7	2

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9403	De novo assembly of chloroplast genomes of <i>Corchorus capsularis</i> and <i>C. olitorius</i> yields species-specific InDel markers. <i>Crop Journal</i> , 2021, 9, 216-226.	2.3	4
9404	Genetic diversity, phylogenetic position and morphometric analysis of <i>Astacus colchicus</i> (Decapoda, Tj ETQq1 1 0.784314 rgBT /Ove	1.3	18
9405	Discovery of a morphologically and genetically distinct population of Black-tailed Godwits in the East Asian-Australasian Flyway. <i>Ibis</i> , 2021, 163, 448-462.	1.0	8
9406	Genetic diversity of the naked mole-rat (<i>Heterocephalus glaber</i>). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 323-340.	0.6	4
9407	Extended phenotypes on coral reefs: cryptic phenotypes modulate coral-vermetid interactions. <i>Ecology</i> , 2021, 102, e03215.	1.5	1
9408	Genetic and morphological assessment of a vulnerable large catfish, <i>Silonia silondia</i> (Hamilton, 1822), in natural populations from India. <i>Journal of Fish Biology</i> , 2021, 98, 430-444.	0.7	5
9409	Plastome evolution and phylogenetic relationships among Malvaceae subfamilies. <i>Gene</i> , 2021, 765, 145103.	1.0	27
9410	Phylogenetic Network of Mitochondrial COI Gene Sequences Distinguishes 10 Taxa Within the Neotropical Albitarsis Group (Diptera: Culicidae), Confirming the Separate Species Status of <i>Anopheles albitarsis</i> H (Diptera: Culicidae) and Revealing a Novel Lineage, <i>Anopheles albitarsis</i> L. <i>Journal of Medical Entomology</i> , 2021, 58, 599-607.	0.9	8
9411	Low genetic variation of cinereous vultures (<i>Aegypius monachus</i>) revealed by the mitochondrial COI gene in central Mongolia. <i>Journal of Asia-Pacific Biodiversity</i> , 2021, 14, 93-97.	0.2	1
9412	Genetic Variability and Molecular Evolution of Maize Yellow Mosaic Virus Populations from Different Geographic Origins. <i>Plant Disease</i> , 2021, 105, 896-903.	0.7	9
9413	Regional population genetics and global phylogeography of the endangered highly migratory shark <i>Lamna nasus</i> : Implications for fishery management and conservation. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2021, 31, 620-634.	0.9	7
9414	Morphological and genetic diversity of <i>Sabanejewia balcanica</i> (Cobitidae, Actinopterygii) in Bosnia and Herzegovina. <i>Journal of Applied Ichthyology</i> , 2021, 37, 89-98.	0.3	0
9415	New resources for genetic studies in maize (<i>Zea mays</i> L.): a genome-wide Maize60K single nucleotide polymorphism array and its application. <i>Plant Journal</i> , 2021, 105, 1113-1122.	2.8	13
9416	First molecular detection of piroplasmids in non-hematophagous bats from Brazil, with evidence of putative novel species. <i>Parasitology Research</i> , 2021, 120, 301-310.	0.6	14
9417	Genome-wide diversity analysis of TCP transcription factors revealed cases of selection from wild to cultivated barley. <i>Functional and Integrative Genomics</i> , 2021, 21, 31-42.	1.4	9
9418	Revisiting Pholidopterini (Orthoptera, Tettigoniidae): Rapid radiation causes homoplasy and phylogenetic instability. <i>Zoologica Scripta</i> , 2021, 50, 225-240.	0.7	6
9419	Variations in the conserved 18S and 5.8S reveal the putative pseudogenes in 18S-ITS1-5.8S rDNA of <i>Cynoglossus melampetalus</i> (Pleuronectiformes: Cynoglossidae). <i>Biochemical and Biophysical Research Communications</i> , 2021, 534, 233-239.	1.0	5
9420	Vicariance and ecological adaptation drive genetic and morphological diversification of a widely distributed bug, <i>Carbula crassiventris</i> (Insecta: Hemiptera: Pentatomidae), in South China. <i>Ecological Entomology</i> , 2021, 46, 368-382.	1.1	2

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9421	High diversity and strong variation in host specificity of seed parasitic acorn weevils. <i>Insect Conservation and Diversity</i> , 2021, 14, 367-376.	1.4	5
9422	Genetic management of a water monitor lizard (<i>Varanus salvator macromaculatus</i>) population at Bang Kachao Peninsula as a consequence of urbanization with Varanus Farm Kamphaeng Saen as the first captive research establishment. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 484-497.	0.6	8
9423	Contrasting population genetics of co-endemic cattle- and buffalo- derived <i>Theileria annulata</i> . <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101595.	1.1	7
9424	Phylogeography of a widespread Palaearctic forest bird species: The White-backed Woodpecker (Aves.) <i>Tj ETQq1 1 0.784314 rgBT / 0.7 6</i>	0.7	6
9425	Phylogeographic analyses and taxonomic inconsistencies of the Neotropical annual fish <i>Austrolebias minuano</i> , <i>Austrolebias charrua</i> and <i>Austrolebias pongondo</i> (Cyprinodontiformes: Rivulidae). <i>Environmental Biology of Fishes</i> , 2021, 104, 1-14.	0.4	2
9426	Sargassum blooms in the East China Sea and Yellow Sea: Formation and management. <i>Marine Pollution Bulletin</i> , 2021, 162, 111845.	2.3	23
9427	DNA barcoding of commercially important groupers (Epinephelidae) in Aceh, Indonesia. <i>Fisheries Research</i> , 2021, 234, 105796.	0.9	6
9428	Contrasting biogeographical patterns in <i>Margarella</i> (Gastropoda: Calliostomatidae: Margarellinae) across the Antarctic Polar Front. <i>Molecular Phylogenetics and Evolution</i> , 2021, 156, 107039.	1.2	14
9429	An invasive pest of bumblebee: A new record of the tracheal mite <i>Locustacarus buchneri</i> (Acari:) <i>Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 42</i> <i>Journal of Asia-Pacific Entomology</i> , 2021, 24, 136-140.	0.4	3
9430	Phylogeographic analyses of poplar revealed potential glacial refugia and allopatric divergence in southwest China. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2021, 32, 66-72.	0.7	0
9431	Identifying multiple geographically restricted phylogeographic lineages of <i>Moggel</i> (Cyprinidae:) <i>Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 34</i>	0.5	6
9432	Isolation by environment and recurrent gene flow shaped the evolutionary history of a continentally distributed Neotropical treefrog. <i>Journal of Biogeography</i> , 2021, 48, 760-772.	1.4	18
9433	Effects of urbanization on population genetic structure of western gray squirrels. <i>Conservation Genetics</i> , 2021, 22, 67-81.	0.8	3
9434	Rapid peripatric speciation linked with drainage evolution in a rare African rodent, <i>Mastomys shortridgei</i> (Rodentia: Muridae). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 522-542.	0.6	4
9435	Phylogeography of the widespread fern <i>Lemmaphyllum</i> in East Asia: species differentiation and population dynamics in response to change in climate and geography. <i>Journal of Systematics and Evolution</i> , 2022, 60, 411-432.	1.6	5
9436	Correlation of <i>Trichosporon asahii</i> Genotypes with Anatomical Sites and Antifungal Susceptibility Profiles: Data Analyses from 284 Isolates Collected in the Last 22 Years across 24 Medical Centers. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	1.4	13
9437	Genetic and Geographic Patterns of Duplicate DPL Genes Causing Genetic Incompatibility Within Rice: Implications for Multiple Domestication Events in Rice. <i>Rice Science</i> , 2021, 28, 58-68.	1.7	2
9438	Genetic polymorphism of vir genes of <i>Plasmodium vivax</i> in Myanmar. <i>Parasitology International</i> , 2021, 80, 102233.	0.6	2

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9439	Development of genomic resources for the genus <i>Celtis</i> (Cannabaceae) based on genome skimming data. <i>Plant Diversity</i> , 2021, 43, 43-53.	1.8	13
9440	Distribution pattern of the brackish <i>Apocorophium lacustre</i> (Vanhoffen, 1911) (Amphipoda): Tj ETQq1 1 0.784314 rgBT /Overlock 10 <i>International Review of Hydrobiology</i> , 2021, 106, 149-163.	0.5	0
9441	Systematics and cryptic diversification of <i>Leptodactylus</i> frogs in the Brazilian campo rupestre. <i>Zoologica Scripta</i> , 2021, 50, 300-317.	0.7	4
9442	Analyses of mitogenomic markers shed light on the divergence, population dynamics, and demographic history of Pakistani chickens. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2021, 32, 34-42.	0.7	0
9443	Recurrent hybridization underlies the evolution of novelty in <i>Gentiana</i> (Gentianaceae) in the Qinghai-Tibetan Plateau. <i>AoB PLANTS</i> , 2021, 13, plaa068.	1.2	14
9444	Cross-species transmission of retroviruses among domestic and wild felids in human-occupied landscapes in Chile. <i>Evolutionary Applications</i> , 2021, 14, 1070-1082.	1.5	13
9445	Geographic restriction, genetic divergence, and morphological disparity in the Brazilian Atlantic Forests: Insights from <i>Leposoma</i> lizards (Gymnophthalmidae, Squamata). <i>Molecular Phylogenetics and Evolution</i> , 2021, 154, 106993.	1.2	2
9446	Blow to the Northeast? Intraspecific differentiation of <i>Populus davidiana</i> suggests a north-eastward skew of a phylogeographic break in East Asia. <i>Journal of Biogeography</i> , 2021, 48, 187-201.	1.4	10
9447	Parasites in a hotspot: diversity and specificity patterns of apicomplexans infecting reptiles from the Socotra Archipelago. <i>Parasitology</i> , 2021, 148, 42-52.	0.7	7
9448	Molecular and morphological diversity in species of <i>Kronichthys</i> (Teleostei, Loricariidae) from Atlantic coastal rivers of Brazil. <i>Journal of Fish Biology</i> , 2021, 98, 668-679.	0.7	2
9449	Morphologies and population genetic structures of the eight-barbel loach of the genus <i>Lefua</i> on southern Sakhalin. <i>Ichthyological Research</i> , 2021, 68, 239-248.	0.5	5
9450	De novo assembly and comparative analysis of the complete mitochondrial genome sequence of the pistachio psyllid, <i>Agonoscena pistaciae</i> (Hemiptera: Aphalaridae). <i>International Journal of Tropical Insect Science</i> , 2021, 41, 1387-1396.	0.4	1
9451	Plitvice Lakes National park harbors ancient, yet endangered diversity of trout (genus <i>Salmo</i>). <i>Journal of Applied Ichthyology</i> , 2021, 37, 20-37.	0.3	6
9452	No genetic signature of glacial refugia in current European fallow deer (<i>Dama dama dama</i> L., 1758) populations: a comment on Baker et al. (2017). <i>Mammalian Biology</i> , 2021, 101, 305-312.	0.8	5
9453	<i>Anaplasma marginale</i> in goats from a multispecies grazing system in northeastern Brazil. <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101592.	1.1	13
9454	Detecting no natural hybridization and predicting range overlap in <i>Saccharina angustata</i> and <i>Saccharina japonica</i> . <i>Journal of Applied Phycology</i> , 2021, 33, 693-702.	1.5	3
9455	Habitat fragmentation differentially shapes neutral and immune gene variation in a tropical bird species. <i>Heredity</i> , 2021, 126, 148-162.	1.2	11
9456	Mitogenomics of the endangered Mediterranean monk seal (<i>Monachus monachus</i>) reveals dramatic loss of diversity and supports historical gene-flow between Atlantic and eastern Mediterranean populations. <i>Zoological Journal of the Linnean Society</i> , 2021, 191, 1147-1159.	1.0	8

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9457	When phylogeography meets niche suitability to unravel the evolutionary history of a shrub from the Brazilian Atlantic Forest. <i>Botanical Journal of the Linnean Society</i> , 2021, 195, 77-92.	0.8	3
9458	Dispersal as a result of asymmetrical hybridization between two closely related oak species in China. <i>Molecular Phylogenetics and Evolution</i> , 2021, 154, 106964.	1.2	4
9459	Evolutionary insights into <i>Rhinolophus episcopus</i> (Chiroptera, Rhinolophidae) in China: Isolation by distance, environment, or sensory system?. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 294-310.	0.6	5
9460	DNA barcoding of <i>Oryza</i> : conventional, specific, and super barcodes. <i>Plant Molecular Biology</i> , 2021, 105, 215-228.	2.0	29
9461	Identification of Suitable Barcodes for Specifically Detecting Adulterants of Turnip (<i>Brassica rapa</i>) and Radish (<i>Raphanus sativus</i>) in Maca (<i>Lepidium meyenii</i>). <i>Food Analytical Methods</i> , 2021, 14, 66-73.	1.3	2
9462	Microgeographic Epidemiology of Malaria Parasites in an Irrigated Area of Western Kenya by Deep Amplicon Sequencing. <i>Journal of Infectious Diseases</i> , 2021, 223, 1456-1465.	1.9	4
9463	Highly conserved TaPstol5AS-1, a wheat ortholog of OsPstol1 has undergone a high selection pressure. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2021, 30, 297-303.	0.9	0
9464	Genetic variation of a freshwater snail <i>Hydrobioides nassa</i> (Gastropoda: Bithyniidae) in Thailand examined by mitochondrial DNA sequences. <i>Hydrobiologia</i> , 2021, 848, 2965-2976.	1.0	12
9465	Nucleotide sequence analysis of mitochondrial DNA hypervariable region II and inter HVR in Thais. <i>Australian Journal of Forensic Sciences</i> , 2021, 53, 138-146.	0.7	1
9466	Characterization and comparison of chloroplast genomes from two sympatric Hippophae species (Elaeagnaceae). <i>Journal of Forestry Research</i> , 2021, 32, 307-318.	1.7	9
9467	Origins of weedy rice revealed by polymorphisms of chloroplast DNA sequences and nuclear microsatellites. <i>Journal of Systematics and Evolution</i> , 2021, 59, 316-325.	1.6	4
9468	In-vitro anti-fungal assay and association analysis reveal a role for the <i>Pinus monticola</i> PR10 gene (PmPR10-3.1) in quantitative disease resistance to white pine blister rust. <i>Genome</i> , 2021, 64, 693-704.	0.9	7
9469	Complete mitogenome of <i>Treron sphenurus</i> (Aves, Columbiformes): the first representative from the genus <i>Treron</i> , genomic comparisons and phylogenetic analysis of Columbidae. <i>Animal Biotechnology</i> , 2021, , 1-11.	0.7	0
9470	Variability of Chloroplast DNA in <i>Oxytropis</i> Section <i>Polyadena</i> (Fabaceae) from Asian Russia: Population Analysis and Phylogenetic Relationships. <i>Biology Bulletin</i> , 2021, 48, 16-25.	0.1	4
9471	Molecular characterization of spiny hedgehogs of the Iberian Peninsula: the missing link in the postglacial colonization of the western European hedgehog. <i>Mammal Research</i> , 2021, 66, 187-200.	0.6	1
9472	Charrs of the genus <i>Salvelinus</i> (Salmonidae): hybridization, phylogeny and evolution. <i>Hydrobiologia</i> , 2021, 848, 705-726.	1.0	7
9473	Metagenomic analyses and genetic diversity of Tomato leaf curl Arusha virus affecting tomato plants in Kenya. <i>Virology Journal</i> , 2021, 18, 2.	1.4	3
9474	Polymorphism Analysis of pfmdr1 and pfcr1 from Plasmodium falciparum Isolates in Northwestern Nigeria Revealed the Major Markers Associated with Antimalarial Resistance. <i>Diseases (Basel)</i> , TJ ETQq1 1 0.784314.igBT /Ovarlock 10		

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9478	Plastid genome evolution in Amazonian aÃ§aÃ¸-palm (<i>Euterpe oleracea</i> Mart.) and Atlantic forest aÃ§aÃ¸-palm (<i>Euterpe edulis</i> Mart.). <i>Plant Molecular Biology</i> , 2021, 105, 559-574.	2.0	12
9479	Genome wide identification and expression pattern analysis of the GRAS family in quinoa. <i>Functional Plant Biology</i> , 2021, 48, 948-962.	1.1	9
9480	Genome-wide analysis and characterization of GRAS family in switchgrass. <i>Bioengineered</i> , 2021, 12, 6096-6114.	1.4	5
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9487	Evolutionary Rescue of an Environmental <i>Pseudomonas otitidis</i> in Response to Anthropogenic Perturbation. <i>Frontiers in Microbiology</i> , 2020, 11, 563885.	1.5	5
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9490	The systematics of the amphidromous shrimp <i>Macrobrachium americanum</i> Spence Bate, 1868 (Decapoda:) Tj ETQq1,1 0.784314 rgB / 0,3 0	0.3	0
9491	Low genetic diversity and population differentiation in <i>Thuja sutchuenensis</i> Franch., an extremely endangered rediscovered conifer species in southwestern China. <i>Global Ecology and Conservation</i> , 2021, 25, e01430.	1.0	9
9492	Comparative genomic analysis of Polypodiaceae chloroplasts reveals fine structural features and dynamic insertion sequences. <i>BMC Plant Biology</i> , 2021, 21, 31.	1.6	14

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9494	Phylogeography and ecological niche modeling reveal evolutionary history of <i>Leiolepis ocellata</i> (Squamata, Leiolepidae). Ecology and Evolution, 2021, 11, 2221-2233.	0.8	4
9495	Effects of Sample Size in the Determination of the True Number of Haplogroups or ESUs Within a Species with Phylogeographic and Conservation Purposes: The Case of <i>Cebus albifrons</i> in Ecuador, and the Kinkajous and Coatis Throughout Latin America. , 2021, , 101-148.		0
9496	Current and Historical Genetic Structure of the White-Footed Tamarin (<i>Saguinus leucopus</i>). , 2021, , 171-197.		0
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9499	Quasispecies of SARS-CoV-2 revealed by single nucleotide polymorphisms (SNPs) analysis. Virulence, 2021, 12, 1209-1226.	1.8	16
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9506	Correlated Population Genetic Structure in a Three-Tiered Host-Parasite System: The Potential for Coevolution and Adaptive Divergence. Journal of Heredity, 2021, 112, 590-601.	1.0	6
9507	<i>Phlebotomus (Adlerius) simici</i> NITZULESCU, 1931: first record in Austria and phylogenetic relationship with other <i>Adlerius</i> species. Parasites and Vectors, 2021, 14, 20.	1.0	5
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9510	Genetic structure of the endangered Irrawaddy dolphin (<i>Orcaella brevirostris</i>) in the Gulf of Thailand. Genetics and Molecular Biology, 2021, 44, e20200365.	0.6	3

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9518			

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9531	Candidate genes and SNPs associated with stomatal conductance under drought stress in <i>Vitis</i> . <i>BMC Plant Biology</i> , 2021, 21, 7.	1.6	12
9532	Climatic Refugia and Geographical Isolation Contribute to the Speciation and Genetic Divergence in Himalayan-Hengduan Tree Peonies (<i>Paeonia delavayi</i> and <i>Paeonia ludlowii</i>). <i>Frontiers in Genetics</i> , 2020, 11, 595334.	1.1	9
9533	Distribution and Genetic Diversity of <i>Aedes aegypti</i> Subspecies across the Sahelian Belt in Sudan. <i>Pathogens</i> , 2021, 10, 78.	1.2	8
9534	Phylogeography, population connectivity and demographic history of the Stoplight parrotfish, <i>Sparisoma viride</i> (Teleostei: Labridae), in the Greater Caribbean. <i>Coral Reefs</i> , 2022, 41, 753-765.	0.9	3
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9536	Evidence on the paleodrainage connectivity during Pleistocene: Phylogeography of a hypoptopomatine endemic to southeastern Brazilian coastal drainages. <i>Neotropical Ichthyology</i> , 2021, 19, .	0.5	3
9537	Population history of the Blue-backed Manakin (<i>Chiroxiphia pareola</i>) supports Plio-Pleistocene diversification in the Amazon and shows a recent connection with the Atlantic Forest. <i>Journal of Ornithology</i> , 2021, 162, 549-563.	0.5	7
9538	Greater Bandicoot Rats (<i>Bandicota indica</i>) are Not Native to Sundaland Based on Deoxyribonucleic Acid (DNA) Analyses. <i>Journal of Mammalian Evolution</i> , 2021, 28, 929-938.	1.0	2
9539	Ant crickets and their secrets: <i>Myrmecophilus acervorum</i> is not always parthenogenetic (Insecta: Orthoptera: Myrmecophilidae). <i>Zoological Journal of the Linnean Society</i> , 2023, 197, 211-228.	1.0	3
9540	Genetic variation of blue-tongue skinks of the genus <i>Tiliqua</i> (Squamata: Scincidae) from New Guinea and Wallacea. <i>Biologia (Poland)</i> , 2021, 76, 1445.	0.8	1
9541	Haplotypes traceability and genetic variability of the breeding population of pacu (<i>Piaractus</i>) Tj ETQq1 1 0.784314 $\frac{rgBT}{0.6}$ /Overlock 10 Tf		
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9546	New Haplotypes of <i>Trypanosoma evansi</i> Identified in Dromedary Camels from Algeria. <i>Acta Parasitologica</i> , 2021, 66, 294-302.	0.4	5
9547	Re-description of the loach species <i>Leptobotia citraurata</i> (Teleostei, Botiidae), with the description of <i>L. brachycephala</i> from southern Zhejiang Province, China. <i>ZooKeys</i> , 2021, 1017, 89-109.	0.5	2

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9550	Introgression of phylogeography lineages of <i>Convolvulus gortschakovii</i> (Convolvulaceae) in the northwest China. Plant Systematics and Evolution, 2021, 307, 1.	0.3	1
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9554	Comparative plastome genomics and phylogenetic analyses of Liliaceae. Botanical Journal of the Linnean Society, 2021, 196, 279-293.	0.8	19
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9556	Mitochondrial DNA revealed the validation of <i>Quasipaa robertingeri</i> (Amphibia: Anura). Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 427 668-671.	0.2	2
9557	High Genetic Diversity of an Invasive Alien Species: Comparison between Fur-Farmed and Feral American Mink (<i>Neovison vison</i>) in China. Animals, 2021, 11, 472.	1.0	5
9558	Comparisons of fall armyworm haplotypes between the Galápagos Islands and mainland Ecuador indicate limited migration to and between islands. Scientific Reports, 2021, 11, 3457.	1.6	5
9559	Genetic Diversity of Hard Ticks (Acari: Ixodidae) in the South and East Regions of Kazakhstan and Northwestern China. Korean Journal of Parasitology, 2021, 59, 103-108.	0.5	4
9560	Characterization of the complete mitochondrial genome of <i>Notocotylus</i> sp. (Trematoda). Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 Td (0.6	0.6	4
9561	The nearly complete mitogenome of the Southeast Asian firefly <i>Pteroptyx tener</i> (Coleoptera). Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 107 1.8	1.8	1
9562	Assessment of genetic diversity, detection of strain-specific single nucleotide polymorphisms and identification of the Bangladesh and Vietnam strain of <i>Channa striata</i> by PCR-RFLP analysis of the mitochondrial COI gene fragment. Aquaculture and Fisheries, 2022, 7, 287-295.	1.2	3
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9564	Cytochrome <i>b</i> as a more promising marker for analysing the distribution vector for <i>Metagonimus suifunensis</i> (Trematoda: Heterophyidae). Parasitology, 2021, 148, 760-766.	0.7	2
9565	Characterization of the complete mitochondrial genomes of <i>Coronocycclus labiatus</i> and <i>Cylicodontophorus bicoronatus</i> : Comparison with Strongylidae species and phylogenetic implication. Veterinary Parasitology, 2021, 290, 109359.	0.7	5

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9567	Identification and Characterization of the APX Gene Family and Its Expression Pattern under Phytohormone Treatment and Abiotic Stress in <i>Populus trichocarpa</i> . <i>Genes</i> , 2021, 12, 334.	1.0	19
9568	Molecular Epidemiology Surveillance of SARS-CoV-2: Mutations and Genetic Diversity One Year after Emerging. <i>Pathogens</i> , 2021, 10, 184.	1.2	29
9569	Mitochondrial Genome Structures and Phylogenetic Analyses of Two Tropical Characidae Fishes. <i>Frontiers in Genetics</i> , 2021, 12, 627402.	1.1	21
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9571	Complete Mitochondrial Genome of <i>Trichuristrichiura</i> from <i>Macaca sylvanus</i> and <i>Papio papio</i> . <i>Life</i> , 2021, 11, 126.	1.1	5
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9573	Chloroplast genome variation and phylogenetic relationships of <i>Atractylodes</i> species. <i>BMC Genomics</i> , 2021, 22, 103.	1.2	54
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9575	Cryptic speciation in the <i>Marshallora nigrocincta</i> species complex (Gastropoda, Triphoridae) from the Western Atlantic. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 819-838.	0.6	2
9576	Genetic characterization of <i>Plasmodium vivax</i> isolates from Pakistan using circumsporozoite protein (pvcsp) and merozoite surface protein-1 (pvmsp-1) genes as genetic markers. <i>Malaria Journal</i> , 2021, 20, 112.	0.8	5
9577	Complete mitochondrial genome of the hemp borer, <i>Grapholita delineaana</i> (Lepidoptera: Tortricidae): Gene variability and phylogeny among <i>Grapholita</i> . <i>Journal of Asia-Pacific Entomology</i> , 2021, 24, 250-258.	0.4	4
9578	Genome-wide identification and expression analysis of the GhIQD gene family in upland cotton (<i>Gossypium hirsutum</i> L.). <i>Journal of Cotton Research</i> , 2021, 4, .	1.0	0
9579	The Independent Domestication of Timopheev's Wheat: Insights from Haplotype Analysis of the Brittle rachis 1 (BTR1-A) Gene. <i>Genes</i> , 2021, 12, 338.	1.0	11
9580	Comparative Analyses of <i>Euonymus</i> Chloroplast Genomes: Genetic Structure, Screening for Loci With Suitable Polymorphism, Positive Selection Genes, and Phylogenetic Relationships Within Celastrineae. <i>Frontiers in Plant Science</i> , 2020, 11, 593984.	1.7	25
9581	<i>Spirometra</i> species from Asia: Genetic diversity and taxonomic challenges. <i>Parasitology International</i> , 2021, 80, 102181.	0.6	26
9582	Mitochondrial DNA and microsatellite analyses reveal strong genetic differentiation between two types of estuarine tapertail anchovies (<i>Coilia</i>) in Yangtze River Basin, China. <i>Hydrobiologia</i> , 2021, 848, 1409-1431.	1.0	8
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9585	High genetic diversity and strong genetic structure of <i>Strongylodes variegatus</i> populations in oilseed rape production areas of China. <i>Bmc Ecology and Evolution</i> , 2021, 21, 18.	0.7	3
9586	Detection of high heteroplasmy in complete loggerhead and hawksbill sea turtles mitochondrial genomes using RNAseq. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2021, 32, 106-114.	0.7	1
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9588	Genetic Characterization of Fungal Biodiversity in Storage Grains: Towards Enhancing Food Safety in Northern Uganda. <i>Microorganisms</i> , 2021, 9, 383.	1.6	4
9589	Understanding the diversification pattern of three subspecies of swamp deer (<i>Rucervus duvaucelii</i>) during the Pleistocene–Holocene based on mitochondrial and Y chromosome markers. <i>Mammalian Biology</i> , 2021, 101, 217-232.	0.8	5
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9595	Species delimitation and hybridization history of a hazel species complex. <i>Annals of Botany</i> , 2021, 127, 875-886.	1.4	6
9596	Current genetic conservation of Chinese indigenous horses revealed with Y-chromosomal and mitochondrial DNA polymorphisms. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	6
9597	Rich maternal and paternal genetic diversity and divergent lineage composition in wild yak (<i>Bos</i>) Tj ETQq1 1 0.784314 rgBT /Overl	0.7	4
9598	Comparative chloroplast genomes: insights into the evolution of the chloroplast genome of <i>Camellia sinensis</i> and the phylogeny of <i>Camellia</i> . <i>BMC Genomics</i> , 2021, 22, 138.	1.2	46
9599	Comparative analysis of the complete plastid genomes of <i>Mangifera</i> species and gene transfer between plastid and mitochondrial genomes. <i>PeerJ</i> , 2021, 9, e10774.	0.9	6
9600	Identification of <i>Vicia</i> Species Native to South Korea Using Molecular and Morphological Characteristics. <i>Frontiers in Plant Science</i> , 2021, 12, 608559.	1.7	10
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9604	Molecular data suggest the worldwide introduction of the bryozoan <i>Amathia verticillata</i> (Ctenostomata, Vesiculariidae). <i>Marine Biology</i> , 2021, 168, 1.	0.7	5
9605	Characteristic and evolution of HAT and HDAC genes in Gramineae genomes and their expression analysis under diverse stress in <i>Oryza sativa</i> . <i>Planta</i> , 2021, 253, 72.	1.6	12
9606	Striking habitat reduction, decreased genetic diversity, and imperilled conservation of natural populations of <i>Terrapene</i> <i>coahuila</i> . <i>Freshwater Biology</i> , 2021, 66, 842-858.	1.2	4
9607	Phylogeography of <i>Patelloida pygmaea</i> along the China coast. <i>Marine Biodiversity</i> , 2021, 51, 1.	0.3	3
9608	Low levels of genetic differentiation with isolation by geography and environment in populations of <i>Drosophila melanogaster</i> from across China. <i>Heredity</i> , 2021, 126, 942-954.	1.2	5
9610	Molecular Evolution of Infectious Pancreatic Necrosis Virus in China. <i>Viruses</i> , 2021, 13, 488.	1.5	12
9611	Genetic Diversity of Symbiotic Green Algae of <i>Paramecium bursaria</i> Syngens Originating from Distant Geographical Locations. <i>Plants</i> , 2021, 10, 609.	1.6	4
9612	Evaluating the DNA barcodes for identification of butterflies from Western Himalayas, Uttarakhand, India. <i>Journal of Asia-Pacific Entomology</i> , 2021, 24, 118-118.	0.4	1
9613	High pyrethroid/DDT resistance in major malaria vector <i>Anopheles coluzzii</i> from Niger-Delta of Nigeria is probably driven by metabolic resistance mechanisms. <i>PLoS ONE</i> , 2021, 16, e0247944.	1.1	7
9614	Genetic diversity analysis of <i>Dermacentor nuttalli</i> within Inner Mongolia, China. <i>Parasites and Vectors</i> , 2021, 14, 131.	1.0	12
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9751	Time or Space? Relative Importance of Geographic Distribution and Interannual Variation in Three Lineages of the Ascidian <i>Pyura chilensis</i> in the Southeast Pacific Coast. <i>Frontiers in Marine Science</i> , 0, 8, .	1.2	4
9752	Distinct phylogeographic patterns in populations of two oribatid mite species from the genus <i>Pantelozetes</i> (Acari, Oribatida, Thyrisomidae) in Central Europe. <i>Experimental and Applied Acarology</i> , 2021, 83, 493-511.	0.7	1
9753	A complement to DNA barcoding reference library for identification of fish from the Northeast Pacific. <i>Genome</i> , 2021, 64, 927-936.	0.9	2
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9756	Analysis of the relationship between geography and body color with the genetic diversity in the Echiura worm <i>Urechis unicinctus</i> based on the mitochondrial COI and D-loop sequences. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1380-1386.	0.2	2
9757	Molecular Characterization of Potato Virus Y (PVY) Using High-Throughput Sequencing: Constraints on Full Genome Reconstructions Imposed by Mixed Infection Involving Recombinant PVY Strains. <i>Plants</i> , 2021, 10, 753.	1.6	6
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9760	Population genetic patterns of a mangrove-associated frog reveal its colonization history and habitat connectivity. <i>Diversity and Distributions</i> , 2021, 27, 1584-1600.	1.9	6
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9764	Diversification, selective sweep, and body size in the invasive Paelearctic alfalfa weevil infected with <i>Wolbachia</i> . <i>Scientific Reports</i> , 2021, 11, 9664.	1.6	3
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9766	A survival story: evolutionary history of the Iberian <i>Algyroides</i> (Squamata: Lacertidae), an endemic lizard relict. <i>Biodiversity and Conservation</i> , 2021, 30, 2707-2729.	1.2	4
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9768	Genome-Wide Characterization of WRKY Transcription Factors Revealed Gene Duplication and Diversification in Populations of Wild to Domesticated Barley. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5354.	1.8	11
9769	Mitochondrial DNA phylogeography of the Guizhou odorous frog: limited population genetic structure and evidence for recent population size expansion. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1592-1596.	0.2	1
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9775	Still time for action: genetic conservation of imperiled South Canadian River fishes, Arkansas River Shiner (<i>Notropis girardi</i>), Peppered Chub (<i>Macrhybopsis tetranema</i>) and Plains Minnow (<i>Hybognathus</i>) Tj ETQq1 1 0.784314rgBT /Ov	0.7	1
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9784	Allopatric differentiation in the <i>Enteromius anoplus</i> complex in South Africa, with the revalidation of <i>Enteromius cernuus</i> and <i>Enteromius oraniensis</i> , and description of a new species, <i>Enteromius mandelai</i> (Teleostei: Cyprinidae). Journal of Fish Biology, 2021, 99, 931-954.	0.7	10
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9786	Identification of <i>Saccostrea mordax</i> and a New Species <i>Saccostrea mordoides</i> sp. nov. (Bivalvia:) Tj ETQq0 0 0 rgBT /Qverlock_10 Tf 50 2 0.3 8	0.3	8
9787	Taxonomy, Population Structure and Genetic Diversity of Iranian Leishmania Strains of Cutaneous and Visceral Leishmaniasis. Acta Parasitologica, 2021, 66, 1274-1284.	0.4	0
9788	Europe as a bridgehead in the worldwide invasion history of grapevine downy mildew, <i>Plasmopara viticola</i> . Current Biology, 2021, 31, 2155-2166.e4.	1.8	36
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9790	Molecular diversity within the genus <i>Laeonereis</i> (Annelida, Nereididae) along the west Atlantic coast: paving the way for integrative taxonomy. PeerJ, 2021, 9, e11364.	0.9	9
9791	Mitochondrial DNA diversity of the alpine newt (<i>Ichthyosaura alpestris</i>) in the Carpathian Basin: evidence for multiple cryptic lineages associated with Pleistocene refugia. Acta Zoologica Academiae Scientiarum Hungaricae, 2021, 67, 177-197.	0.1	3

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9793	Molecular Insights into the Genetic Variability of ORF Virus in a Mediterranean Region (Sardinia, Italy). <i>Life</i> , 2021, 11, 416.	1.1	5
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9795	Identification, evolution, expression analysis of phospholipase D (PLD) gene family in tea (<i>Camellia</i>). <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i>	1.4	10
9796	Dynamic landscapes in northwestern North America structured populations of wolverines (<i>Gulo</i>). <i>Tj ETQq0 0 0 rgBT /Overlock</i>	0.6	7
9797	The complete mitogenome of <i>Phymorhynchus</i> sp. (Neogastropoda, Conoidea, Raphitomidae) provides insights into the deep-sea adaptive evolution of Conoidea. <i>Ecology and Evolution</i> , 2021, 11, 7518-7531.	0.8	10
9798	Past and recent connectivity of white mullet between the Gulf of Mexico and the Mexican Pacific inferred through sequences of the gene cytochrome c oxidase I and microsatellites. <i>Marine Biology</i> , 2021, 168, 1.	0.7	2
9799	Population Genetic Structure Analysis Reveals Decreased but Moderate Diversity for the Oriental Fire-Bellied Toad Introduced to Beijing after 90 Years of Independent Evolution. <i>Animals</i> , 2021, 11, 1429.	1.0	1
9800	Genome-Wide Analysis of RAV Transcription Factors and Functional Characterization of Anthocyanin-Biosynthesis-Related RAV Genes in Pear. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5567.	1.8	7
9801	Rich maternal and paternal genetic diversity and divergent lineage composition in wild yak (<i>Bos</i>). <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i>	0.7	5
9802	<i>GTR1</i> and <i>GTR2</i> transporters differentially regulate tissue-specific glucosinolate contents and defence responses in the oilseed crop <i>Brassica juncea</i> .	2.8	22
9803	Comparative analysis of chloroplast genome structure and molecular dating in Myrtales. <i>BMC Plant Biology</i> , 2021, 21, 219.	1.6	25
9804	DNA barcoding of bats (Chiroptera) from the Colombian northern region. <i>Mammalia</i> , 2021, 85, 462-470.	0.3	1
9805	Biodiversity and Geographic Distribution of Rhizobia Nodulating With <i>Vigna minima</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 665839.	1.5	0
9806	Phylogenetic relationships and genetic diversity of <i>Monilinia</i> spp. isolated in Poland based on housekeeping and pathogenicity-related gene sequence analysis. <i>Plant Pathology</i> , 2021, 70, 1640-1650.	1.2	4
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9808	Effects of Mountain Uplift and Climatic Oscillations on Phylogeography and Species Divergence of <i>Chamaesium</i> (Apiaceae). <i>Frontiers in Plant Science</i> , 2021, 12, 673200.	1.7	9
9809	Genome-wide identification and analysis of cytokinin dehydrogenase/oxidase (CKX) family genes in <i>Brassica oleracea</i> L. reveals their involvement in response to <i>Plasmodiophora brassicae</i> infections. <i>Horticultural Plant Journal</i> , 2022, 8, 68-80.	2.3	15

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9811	Molecular characterization and population genetics of <i>Theileria parva</i> in Burundi's unvaccinated cattle: Towards the introduction of East Coast fever vaccine. <i>PLoS ONE</i> , 2021, 16, e0251500.	1.1	4
9812	Comparative analysis of mitochondrial genomes of Nirvanini and Evacanthini (Hemiptera: Cicadellidae) reveals an explicit evolutionary relationship. <i>Genomics</i> , 2021, 113, 1378-1385.	1.3	9
9813	Genome-wide assessment elucidates connectivity and the evolutionary history of the highly dispersive marine invertebrate <i>Littoraria flava</i> (Littorinidae: Gastropoda). <i>Biological Journal of the Linnean Society</i> , 2021, 133, 999-1015.	0.7	2
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9815	Complete chloroplast genome sequencing and comparative analysis reveals changes to the chloroplast genome after allopolyploidization in <i>Cucumis</i> . <i>Genome</i> , 2021, 64, 627-638.	0.9	6
9816	Global changes explain the long-term demographic trend of the Eurasian common lizard (Squamata: Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.9	1
9817	Genome-Wide Analysis of MYB Gene Family in Chinese Bayberry (<i>Morella rubra</i>) and Identification of Members Regulating Flavonoid Biosynthesis. <i>Frontiers in Plant Science</i> , 2021, 12, 691384.	1.7	40
9818	An approach for estimating haplotype diversity from sequences with unequal lengths. <i>Methods in Ecology and Evolution</i> , 2021, 12, 1658-1667.	2.2	3
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9820	Genetic diversity, population structure and historical demography of the two-spined yellowtail stargazer (<i>Uranoscopus cognatus</i>). <i>Scientific Reports</i> , 2021, 11, 13357.	1.6	8
9821	First Record of the Alien Species <i>Procambarus virginalis</i> Lyko, 2017 in Fresh Waters of Sardinia and Insight into Its Genetic Variability. <i>Life</i> , 2021, 11, 606.	1.1	4
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9823	Dispersal and mating patterns determine the fate of naturally dispersed populations: evidence from <i>Bombina orientalis</i> . <i>Bmc Ecology and Evolution</i> , 2021, 21, 111.	0.7	2
9824	Demographic history, not larval dispersal potential, explains differences in population structure of two New Zealand intertidal species. <i>Marine Biology</i> , 2021, 168, 1.	0.7	7
9825	Molecular characterization and phylogeography of Mediterranean picarels (<i>Spicara flexuosa</i> , S.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf <i>Marine Science</i> , 2021, 45, 101836.	0.4	4
9826	Vendace (<i>Coregonus albula</i>) and least cisco (<i>Coregonus sardinella</i>) are a single species: evidence from revised data on mitochondrial and nuclear DNA polymorphism. <i>Hydrobiologia</i> , 2021, 848, 4241-4262.	1.0	9
9827	High genetic divergence but low morphological differences in a keelback snake <i>Rhabdophis subminiatus</i> (Reptilia, Colubridae). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 1371.	0.6	7

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9828	Mitochondrial Genomes of the United States Distribution of Gray Fox (<i>Urocyon cinereoargenteus</i>) Reveal a Major Phylogeographic Break at the Great Plains Suture Zone. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	10
9829	Molecular Survey and Genetic Diversity of <i>Bartonella</i> spp. in Small Indian Mongooses (<i>Urva</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 662 T	1.6	5
9830	Phylogeographic genetic variation of <i>Indoplanorbis exustus</i> (Deshayes, 1834) (Gastropoda:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662 T	1.5	9
9831	Occurrence and Genetic Diversity of <i>Babesia caballi</i> and <i>Theileria equi</i> in Chilean Thoroughbred Racing Horses. <i>Pathogens</i> , 2021, 10, 714.	1.2	6
9832	Enhancing rice grain production by manipulating the naturally evolved cis-regulatory element-containing inverted repeat sequence of <i>OsREM20</i> . <i>Molecular Plant</i> , 2021, 14, 997-1011.	3.9	19
9833	<i>Aedes albopictus</i> diversity and relationships in south-western Europe and Brazil by rDNA/mtDNA and phenotypic analyses: ITS-2, a useful marker for spread studies. <i>Parasites and Vectors</i> , 2021, 14, 333.	1.0	13
9834	Phylogenomic Analyses of <i>Hepatica</i> Species and Comparative Analyses Within Tribe Anemoneae (Ranunculaceae). <i>Frontiers in Plant Science</i> , 2021, 12, 638580.	1.7	2
9835	Contrasting Phylogeographic Patterns in <i>Lumnitzera</i> Mangroves Across the Indo-West Pacific. <i>Frontiers in Plant Science</i> , 2021, 12, 637009.	1.7	1
9836	Genome-Wide Identification and Transcript Analysis of TCP Gene Family in Banana (<i>Musa acuminata</i> L.). <i>Biochemical Genetics</i> , 2021, , 1.	0.8	10
9837	Genetic Diversity and Population Structure of <i>Metaphire vulgaris</i> Based on the Mitochondrial COI Gene and Microsatellites. <i>Frontiers in Genetics</i> , 2021, 12, 686246.	1.1	6
9838	Current Classification of the <i>Bacillus pumilus</i> Group Species, the Rubber-Pathogenic Bacteria Causing Trunk Bulges Disease in Malaysia as Assessed by MLSA and Multi rep-PCR Approaches. <i>Plant Pathology Journal</i> , 2021, 37, 243-257.	0.7	2
9839	Southern introgression increases adaptive immune gene variability in northern range margin populations of Firebellied toad. <i>Ecology and Evolution</i> , 2021, 11, 9776-9790.	0.8	2
9840	Landscape configuration of an Amazonian island-like ecosystem drives population structure and genetic diversity of a habitat-specialist bird. <i>Landscape Ecology</i> , 2021, 36, 2565-2582.	1.9	4
9842	Characterization of metapopulation of <i>Ellobium chinense</i> through Pleistocene expansions and four covariate COI guanine-hotspots linked to G-quadruplex conformation. <i>Scientific Reports</i> , 2021, 11, 12239.	1.6	7
9843	Molecular population genetics of <i>Sex-lethal</i> (<i>Sxl</i>) in the <i>Drosophila melanogaster</i> species group: a locus that genetically interacts with <i>Wolbachia pipientis</i> in <i>Drosophila melanogaster</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	2
9844	Evidence for two types of <i>Aquilegia ecalcarata</i> and its implications for adaptation to new environments. <i>Plant Diversity</i> , 2021, 44, 153-162.	1.8	1
9845	The riverine thruway hypothesis: rivers as a key mediator of gene flow for the aquatic paradoxical frog <i>Pseudis tocantins</i> (Anura, Hylidae). <i>Landscape Ecology</i> , 2021, 36, 3049-3060.	1.9	11
9846	The Pleistocene species pump past its prime: Evidence from European butterfly sister species. <i>Molecular Ecology</i> , 2021, 30, 3575-3589.	2.0	35

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9847	Pathogen-mediated selection favours the maintenance of innate immunity gene polymorphism in a widespread wild ungulate. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1156-1166.	0.8	13
9848	Change of soluble acid invertase gene (SAI-1) haplotype in hybrid sorghum breeding program in China. <i>Molecular Breeding</i> , 2021, 41, 1.	1.0	2
9849	Comparative mitogenomics and phylogenetics of the stinging wasps (Hymenoptera: Aculeata). <i>Molecular Phylogenetics and Evolution</i> , 2021, 159, 107119.	1.2	13
9850	Insights into the evolution and dispersion of pyrethroid resistance among sylvatic Andean <i>Triatoma infestans</i> from Bolivia. <i>Infection, Genetics and Evolution</i> , 2021, 90, 104759.	1.0	6
9851	Identification and phylogenetic analysis of five <i>Crataegus</i> species (Rosaceae) based on complete chloroplast genomes. <i>Planta</i> , 2021, 254, 14.	1.6	27
9852	Phylogeography of <i>Habia fuscicauda</i> (Cardinalidae) indicates population isolation, genetic divergence and demographic changes during the Quaternary climate shifts in the Mesoamerican rainforest. <i>Journal of Ornithology</i> , 2021, 162, 961.	0.5	2
9853	Genetic differentiation of Southeast Asian <i>Paragonimus Braun, 1899</i> (Digenea: Paragonimidae) and genetic variation in the <i>Paragonimus heterotremus</i> complex examined by nuclear DNA sequences. <i>Infection, Genetics and Evolution</i> , 2021, 90, 104761.	1.0	3
9854	Characterization of the First Complete Mitochondrial Genome of <i>Cyphonocerinae</i> (Coleoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.0	9
9855	SOFT COMPUTING BASED IDENTIFICATION AND ASSESSMENT OF POTENTIAL DNA BARCODES OF SOLANACEOUS SPECIES USING cpDNA SEQUENCES. <i>Indian Journal of Computer Science and Engineering</i> , 2021, 12, 641-652.	0.2	0
9856	The role of internal transcribed spacer 2 secondary structures in classifying mycoparasitic <i>Ampelomyces</i> . <i>PLoS ONE</i> , 2021, 16, e0253772.	1.1	4
9857	Complete plastomes of six species of <i>Wikstroemia</i> (Thymelaeaceae) reveal paraphyly with the monotypic genus <i>Stellera</i> . <i>Scientific Reports</i> , 2021, 11, 13608.	1.6	5
9858	Parasitic copepods <i>Caligus lacustris</i> (Copepoda: Caligidae) on the rainbow trout <i>Oncorhynchus mykiss</i> in cage aquaculture: morphology, population demography, and first insights into phylogenetic relationships. <i>Parasitology Research</i> , 2021, 120, 2455-2467.	0.6	2
9859	<i>Histoplasma capsulatum</i> Isolated from <i>Tadarida brasiliensis</i> Bats Captured in Mexico Form a Sister Group to North American Class 2 Clade. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 529.	1.5	7
9860	Phylogeographic Investigation of an Endangered Longhorn Beetle, <i>Callipogon relictus</i> (Coleoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.0	1
9861	High genetic diversity of immunity genes in an expanding population of a highly mobile carnivore, the grey wolf <i>Canis lupus</i> , in Central Europe. <i>Diversity and Distributions</i> , 2021, 27, 1680-1695.	1.9	1
9862	Molecular characterization and phylogenetic analyses of <i>Fasciola gigantica</i> of buffaloes and goats in Punjab, Pakistan. <i>Parasitology International</i> , 2021, 82, 102288.	0.6	3
9863	Shennongjia "Wushan Mountains" One cryptic glacial refugium introduced by the phylogeographical study of the Geometridae moth <i>Ourapteryx szechuana</i> Wehrli. <i>Ecology and Evolution</i> , 2021, 11, 10066-10076.	0.8	3
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9866	Matrilineal diversity and population history of Norwegians. <i>American Journal of Physical Anthropology</i> , 2021, 176, 120-133.	2.1	3
9867	Historical and social-cultural processes as drivers for genetic structure in Nordic domestic reindeer. <i>Ecology and Evolution</i> , 2021, 11, 8910-8922.	0.8	4
9868	Distribution and Diversity of <i>Beauveria</i> in Boreal Forests of Northern European Russia. <i>Microorganisms</i> , 2021, 9, 1409.	1.6	3
9869	Phylogeography of <i>Aphanius fasciatus</i> (Osteichthyes: Aphaniidae) in the Mediterranean Sea, with a focus on its conservation in Cyprus. <i>Hydrobiologia</i> , 2021, 848, 4093-4114.	1.0	4
9870	Stepwise selection of natural variations at <i>CTB2</i> and <i>CTB4a</i> improves cold adaptation during domestication of <i>japonica</i> rice. <i>New Phytologist</i> , 2021, 231, 1056-1072.	3.5	30
9872	Phylogeny and Comparative Analysis for the Plastid Genomes of Five <i>Tulipa</i> (Liliaceae). <i>BioMed Research International</i> , 2021, 2021, 1-10.	0.9	7
9873	Characterization of transcriptomic response in ovules derived from inter-subgeneric hybridization in <i>Prunus</i> (Rosaceae) species. <i>Plant Reproduction</i> , 2021, 34, 255-266.	1.3	1
9874	Underlying microevolutionary processes parallel macroevolutionary patterns in ancient neotropical mountains. <i>Journal of Biogeography</i> , 2021, 48, 2312-2327.	1.4	8
9875	<i>GmRAV</i> confers ecological adaptation through photoperiod control of flowering time and maturity in soybean. <i>Plant Physiology</i> , 2021, 187, 361-377.	2.3	19
9876	Phylogeography of the <i>Dendrocolaptes picumnus</i> (Aves: Dendrocolaptidae) species complex: new insights on the diversification of a trans-American lineage. <i>Journal of Avian Biology</i> , 2021, 52, .	0.6	0
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9878	Genetic diversity and population structure of the native Western African honeybee (<i>Apis mellifera</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2021, 293, 17-25.	0.4	6
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9880	Characterization of expansin genes and their transcriptional regulation by histone modifications in strawberry. <i>Planta</i> , 2021, 254, 21.	1.6	8
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9885	Comparative Analysis of Mitogenomes among Five Species of <i>Filchnerella</i> (Orthoptera: Acridoidea: Tj ETQq1 1 0.784314 rgBT /Overlock 3 Tf 50	1.0	3
9886	Phylogeography of <i>Prunus armeniaca</i> L. revealed by chloroplast DNA and nuclear ribosomal sequences. <i>Scientific Reports</i> , 2021, 11, 13623.	1.6	3
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9897	Comparative phylogeography of <i>Juglans regia</i> and <i>J. mandshurica</i> combining organellar and nuclear DNA markers to assess genetic diversity and introgression in regions of sympatry. <i>Trees - Structure and Function</i> , 0, , 1.	0.9	3
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9899	Genome-wide analysis of MYB transcription factors and their responses to salt stress in <i>Casuarina equisetifolia</i> . <i>BMC Plant Biology</i> , 2021, 21, 328.	1.6	36
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9912	Species diversity of freshwater shrimp in Henan Province, China, based on morphological characters and <i>COI</i> mitochondrial gene. <i>Ecology and Evolution</i> , 2021, 11, 10502-10514.	0.8	5
9913	Impact of Colonization of an Invasive Species on Genetic Differentiation in New Environments: A Study on American <i>Artemia franciscana</i> (Crustacea: Anostraca) in the United Arab Emirates. <i>Journal of Ocean University of China</i> , 2021, 20, 911-920.	0.6	8
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9919	Speciation of the cold-adapted scorpionfly <i>Cerapanorpa brevicornis</i> (Mecoptera: Panorpidae) via interglacial refugia. <i>Insect Conservation and Diversity</i> , 2022, 15, 114-127.	1.4	6
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9922	Species delimitation in <i>Noccaea densiflora</i> species complex (Brassicaceae) based on morphological and molecular data. <i>Botany</i> , 2021, 99, 389-402.	0.5	0
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9937	Threadfin Porgy (<i>Evynnis Cardinalis</i>) Haplotype Pattern and Genetic Structure in Beibu Gulf, South China Sea. <i>Frontiers in Environmental Science</i> , 2021, 9, .	1.5	1
9938	Paraphyly and evolutionary independent lineages in <i>Gymnotus pantherinus</i> (Gymnotiformes: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 2021, 161, 107159.	1.2	1
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9952	Blood meal analysis of tsetse flies (<i>Glossina pallidipes</i> : Glossinidae) reveals higher host fidelity on wild compared with domestic hosts. Wellcome Open Research, 2021, 6, 213.	0.9	5
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9960	Metagenomic analysis of nepoviruses: diversity, evolution and identification of a genome region in members of subgroup A that appears to be important for host range. <i>Archives of Virology</i> , 2021, 166, 2789-2801.	0.9	5
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9962	Single nucleotide polymorphism-based methodology for authentication of bovine, caprine, ovine, camel, and donkey meat cuts. <i>Journal of Food Science</i> , 2021, 86, 4444-4456.	1.5	3
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9968	Genome-wide identification and analysis of NOD-like receptors and their potential roles in response to <i>Edwardsiella tarda</i> infection in black rockfish (<i>Sebastes schlegelii</i>). <i>Aquaculture</i> , 2021, 541, 736803.	1.7	12
9969	Phylogeography of <i>Baryancistrus xanthellus</i> (Siluriformes: Loricariidae), a rheophilic catfish endemic to the Xingu River basin in eastern Amazonia. <i>PLoS ONE</i> , 2021, 16, e0256677.	1.1	1
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9971	Variation in Ribosomal DNA in the Genus <i>Trifolium</i> (Fabaceae). <i>Plants</i> , 2021, 10, 1771.	1.6	4
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9973	Analysis of the genetic diversity and molecular phylogeography of the endangered wild rose (<i>Rosa</i>)	1.0	7
9974	Morphometric and molecular identification of the female castes of <i>Bombus ignitus</i> and <i>B. ardens</i> (Apidae: Hymenoptera). <i>Journal of Asia-Pacific Entomology</i> , 2021, 24, 918-924.	0.4	1
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9979	Phylogeographic structure of the dwarf snakehead (<i>Channa gachua</i>) around Gulf of Tonkin: Historical biogeography and pronounced effects of sea-level changes. <i>Ecology and Evolution</i> , 2021, 11, 12583-12595.	0.8	9
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9985	Congruence between ocean dispersal modelling and phylogeography explains recent evolutionary history of <i>Cycas</i> species with buoyant seeds. <i>New Phytologist</i> , 2021, 232, 1863-1875.	3.5	15
9986	Development of nuclear and chloroplast polymorphic microsatellites for <i>Crossostephium chinense</i> (Asteraceae). <i>Molecular Biology Reports</i> , 2021, 48, 6259-6267.	1.0	2
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9990	Backbone phylogeny and evolution of Apioideae (Apiaceae): New insights from phylogenomic analyses of plastome data. <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107183.	1.2	47
9992	Use of ITS-1 to Identify <i>Bactrocera dorsalis</i> and <i>Bactrocera occipitalis</i> (Diptera: Tephritidae): A Case Study Using Flies Trapped in California from 2008 to 2018. <i>Florida Entomologist</i> , 2021, 104, .	0.2	4
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9995	Detection and molecular characteristics of <i>Pyelosomum cochlear</i> (Digenea: Pronocephalidae) in the urinary bladder of the green sea turtle (<i>Chelonia mydas</i>) in the Northwest Pacific Ocean. <i>Infection, Genetics and Evolution</i> , 2021, 93, 104962.	1.0	0
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9999	rbcl, a potential candidate DNA barcode loci for aconites: conservation of himalayan aconites. <i>Molecular Biology Reports</i> , 2021, 48, 6769-6777.	1.0	7
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10001	Genetic diversity of <i>Glycaspis brimblecombei</i> (Hemiptera: Aphalaridae) and its parasitoid <i>Psyllaephagus bliteus</i> (Hymenoptera: Encyrtidae) in Brazil. <i>Brazilian Journal of Biology</i> , 2021, 81, 838-841.	0.4	4
10002	Intracellular DNA transfer events restricted to the genus <i>Convallaria</i> within the Asparagaceae family: Possible mechanisms and potential as genetic markers for biographical studies. <i>Genomics</i> , 2021, 113, 2906-2918.	1.3	8
10003	Taxonomic diversity and distribution of the genus <i>Proterorhinus</i> (Teleostei: Gobiidae) in the Caucasus biodiversity hotspot with conservation implications. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2022, 32, 129-138.	0.9	6
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10005	<i>BnaC7.ROT3</i> , the causal gene of <i>cqSL-C7</i> , mediates silique length by affecting cell elongation in <i>Brassica napus</i> . <i>Journal of Experimental Botany</i> , 2022, 73, 154-167.	2.4	11
10006	Relationships Among Trophic Niche Width, Morphological Variation, and Genetic Diversity of <i>Hemiculter leucisculus</i> in China. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	4
10007	Molecular phylogeny of the <i>Anopheles hyrcanus</i> group (Diptera: Culicidae) based on rDNA-ITS2 and mtDNA-COII. <i>Parasites and Vectors</i> , 2021, 14, 454.	1.0	5
10008	Butterfly Biodiversity on Isla Socorro, Mexico, with Comments on the Taxonomic Status of the Endemic Hairstreak <i>Strymon istapa socorroica</i> (Lycaenidae). <i>Journal of the Lepidopterists' Society</i> , 2021, 75, .	0.0	1
10009	A melting pot in the Arctic: Analysis of mitogenome variation in Arctic char (<i>Salvelinus alpinus</i>) reveals a 1000-km contact zone between highly divergent lineages. <i>Ecology of Freshwater Fish</i> , 2022, 31, 330-346.	0.7	8
10010	Diversity and distribution of cytochrome oxidase I (COI) haplotypes of the brown marmorated stink bug, <i>Halyomorpha halys</i> Stål (Hemiptera, Pentatomidae), along the eastern front of its invasive range in Eurasia. <i>NeoBiota</i> , 0, 68, 53-77.	1.0	11
10011	Pathogenomic analyses of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> supports a close genetic relationship between South and East Africa. <i>Plant Pathology</i> , 2022, 71, 279-288.	1.2	5
10012	Unraveling the Hidden Diversity of the Native White Claw Crayfish in the Iberian Peninsula. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	2
10013	A Global Invader Is Possibly Two: First Genetic Investigation of Native Populations of the Estuarine Bivalve <i>Mytilopsis leucophaeata</i> (Dreissenidae). <i>Estuaries and Coasts</i> , 2022, 45, 812-826.	1.0	4
10014	Genetic structure and ecological niche segregation of Indian gray mongoose (<i>Urva edwardsii</i>) in Iran. <i>Ecology and Evolution</i> , 2021, 11, 14813-14827.	0.8	3
10015	Pragmatic Assignment of Species Groups Based on Primary Species Hypotheses: The Case of a Dominant Component of the Southern Ocean Benthic Fauna. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	5

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10016	Genetic variation of avirulence genes (<i>AVR-Pi9</i> , <i>AVR-Pik</i> , <i>AVR-Pita1</i>) and genetic diversity of rice blast fungus, <i>Pyricularia oryzae</i> , in Thailand. <i>Plant Pathology</i> , 2022, 71, 322-333.	1.2	4
10017	Population genetics and phylogeography of <i>Tabanus bromius</i> (Diptera: Tabanidae). <i>Parasites and Vectors</i> , 2021, 14, 453.	1.0	5
10018	Genome-wide analysis of OSCA gene family members in <i>Vigna radiata</i> and their involvement in the osmotic response. <i>BMC Plant Biology</i> , 2021, 21, 408.	1.6	19
10019	Genome-Wide Investigation of SBT Family Genes in Pineapple and Functional Analysis of AcoSBT1.12 in Floral Transition. <i>Frontiers in Genetics</i> , 2021, 12, 730821.	1.1	6
10020	Maternal genetic diversity, differentiation and phylogeny of three white yak breeds/populations in China. <i>Animal Biotechnology</i> , 2023, 34, 728-733.	0.7	4
10021	Evolutionary history of the roan antelope across its African range. <i>Journal of Biogeography</i> , 2021, 48, 2812-2827.	1.4	4
10022	Authentication of medicinal herb <i>Wikstroemia indica</i> using novel DNA markers derived from the chloroplast genome sequences. <i>Journal of Applied Research on Medicinal and Aromatic Plants</i> , 2021, 24, 100315.	0.9	3
10023	Molecular Features of <i>Probopyrus</i> sp. (Isopoda: Bopyridae) from Brazilian Amazonia and the Parasitism of Inland Populations of <i>Macrobrachium amazonicum</i> (Decapoda: Palaemonidae). <i>Parasitology</i> , 2022, 149, 1-24.	0.7	2
10024	A Phylogeographic Contact Zone for Arctic Grayling in Alberta, Canada. <i>North American Journal of Fisheries Management</i> , 2021, 41, 1619-1630.	0.5	0
10025	Historical biogeography of the Gondwanan freshwater genus <i>Boeckella</i> (Crustacea): Timing and modes of speciation in the Southern Hemisphere. <i>Diversity and Distributions</i> , 2021, 27, 2330-2343.	1.9	8
10026	Isolation and endemism in subterranean aquatic snails: unexpected case of <i>Montenegrospeum bogici</i> (Pérez et al., 2012) (Gastropoda: Truncatelloidea: Hydrobiidae). <i>Hydrobiologia</i> , 2021, 848, 4967-4990.	1.0	7
10027	Comprehensive analysis and expression profiles of cassava UDP-glycosyltransferases (UGT) family reveal their involvement in development and stress responses in cassava. <i>Genomics</i> , 2021, 113, 3415-3429.	1.3	13
10028	Modified expression of <i>TaCYP78A5</i> enhances grain weight with yield potential by accumulating auxin in wheat (<i>Triticum aestivum</i> L.). <i>Plant Biotechnology Journal</i> , 2022, 20, 168-182.	4.1	29
10029	A holocenic and dynamic hybrid zone between two cactophilic <i>Drosophila</i> species in a coastal lowland plain of the Brazilian Atlantic Forest. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1737-1751.	0.8	1
10030	Distribution and Molecular Diversity of Whitefly Species Colonizing Cassava in Kenya. <i>Insects</i> , 2021, 12, 875.	1.0	9
10031	Higher Genetic Diversity of the Common Sea Cucumber <i>Holothuria (Halodeima) atra</i> in Marine Protected Areas of the Central and Southern Ryukyu Islands. <i>Frontiers in Conservation Science</i> , 2021, 2, .	0.9	8
10032	The role of Sahara highlands in the diversification and desert colonization of the Bosc's fringe-toed lizard. <i>Journal of Biogeography</i> , 2021, 48, 2891-2906.	1.4	8
10033	Evolutionary study of maize dwarf mosaic virus using nearly complete genome sequences acquired by next-generation sequencing. <i>Scientific Reports</i> , 2021, 11, 18786.	1.6	5

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10034	Patterns of Cryptic Diversity and Phylogeography in Four Freshwater Copepod Crustaceans in European Lakes. <i>Diversity</i> , 2021, 13, 448.	0.7	12
10035	Evolution of Methyltransferase-Like (METTL) Proteins in Metazoa: A Complex Gene Family Involved in Epitranscriptomic Regulation and Other Epigenetic Processes. <i>Molecular Biology and Evolution</i> , 2021, 38, 5309-5327.	3.5	21
10036	Low mitochondrial genetic diversity in the Indian Ocean humpback dolphin <i>Sousa plumbea</i> in South African waters. <i>Endangered Species Research</i> , 2021, 46, 91-103.	1.2	3
10037	The Complete Mitochondrial Genome Comparison between <i>Pelecanus occidentalis</i> and <i>Pelecanus crispus</i> . <i>Russian Journal of Genetics</i> , 2021, 57, 1073-1081.	0.2	0
10038	Historic dispersal barriers determine genetic structure and connectivity in a supratidal sandy-beach brooder. <i>Marine Ecology - Progress Series</i> , 2021, 674, 1-13.	0.9	2
10039	Resolving the origins of invertebrate colonists in the Yangtze River Estuary with molecular markers: Implications for ecological connectivity. <i>Ecology and Evolution</i> , 2021, 11, 13898-13911.	0.8	3
10040	Molecular characterization of <i>Anaplasma marginale</i> based on the <i>msp1a</i> and <i>msp1b</i> genes. <i>Veterinary Microbiology</i> , 2021, 262, 109236.	0.8	7
10041	Heterogeneous Genetic Diversity Estimation of a Promising Domestication Medicinal Motherwort <i>Leonurus Cardiaca</i> Based on Chloroplast Genome Resources. <i>Frontiers in Genetics</i> , 2021, 12, 721022.	1.1	7
10042	Discordance in maternal and paternal genetic markers in lesser long-nosed bat <i>Leptonycteris yerbabuenae</i> , a migratory bat: recent expansion to the North and male phylopatry. <i>PeerJ</i> , 2021, 9, e12168.	0.9	5
10043	Phylogeography of the smooth greensnake, <i>Opheodrys vernalis</i> (Squamata: Colubridae): divergent lineages and variable demographics in a widely distributed yet enigmatic species. <i>Biological Journal of the Linnean Society</i> , 2021, 134, 940-957.	0.7	3
10044	Low genetic variation in <i>Echinococcus multilocularis</i> from the Western Sichuan Plateau of China revealed by microsatellite and mitochondrial DNA markers. <i>Acta Tropica</i> , 2021, 221, 105989.	0.9	2
10045	Genetic structure and evidence for coexistence of three taxa of <i>Bithynia</i> (Gastropoda: Bithyniidae), the intermediate host of <i>Opisthorchis viverrini sensu lato</i> (Digenea: Opisthorchiidae) in Thailand examined by mitochondrial DNA sequences analyses. <i>Acta Tropica</i> , 2021, 221, 105980.	0.9	5
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10047	Phylogeography of the Oriental dobsonfly, <i>Neoneuromus ignobilis</i> (Navás), suggests Pleistocene allopatric isolation and glacial dispersal shaping its wide distribution. <i>Systematic Entomology</i> , 0, .	1.7	3
10048	Phylogeography and demographic inference of the endangered sei whale, with implications for conservation. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2021, 31, 3554-3563.	0.9	3
10049	Phylogenetic Relationships of the Species of Asian Russia of the Subgenera <i>Phacoxytropis</i> and <i>Tragacanthoxytropis</i> Genus <i>Oxytropis</i> Based on the Polymorphism of Markers of the Chloroplast and Nuclear Genomes. <i>Russian Journal of Genetics</i> , 2021, 57, 1042-1056.	0.2	3
10050	Conservation genetics of two critically endangered island dwarf carnivores. <i>Conservation Genetics</i> , 2022, 23, 35-49.	0.8	7
10051	Major biogeographic barriers in eastern Australia have shaped the population structure of widely distributed <i>Eucalyptus moluccana</i> and its putative subspecies. <i>Ecology and Evolution</i> , 2021, 11, 14828-14842.	0.8	4

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10052	DNA barcoding of <i>Lutzomyia longipalpis</i> species complex (Diptera: Psychodidae), suggests the existence of 8 candidate species. <i>Acta Tropica</i> , 2021, 221, 105983.	0.9	10
10053	Connectivity, diversity, and hybridization between two endemic fish species (<i>Percilia</i> spp.) in a complex temperate landscape. <i>Conservation Genetics</i> , 2022, 23, 23-33.	0.8	3
10054	Genetic Diversity of Microneme Protein 2 and Surface Antigen 1 of <i>Eimeria tenella</i> . <i>Genes</i> , 2021, 12, 1418.	1.0	7
10055	Lost, forgotten, and overlooked: systematic reassessment of two lesser-known toad species (Anura.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 Evolution</i> , 2021, 97, 451-470.	0.4	8
10056	Variation and Selection in the Putative Sperm-Binding Region of ZP3 in Muroid Rodents: A Comparison between Cricetids and Murines. <i>Genes</i> , 2021, 12, 1450.	1.0	0
10057	The taxonomy of two uncultivated fungal mammalian pathogens is revealed through phylogeny and population genetic analyses. <i>Scientific Reports</i> , 2021, 11, 18119.	1.6	22
10058	Disentangling the complex alpha taxonomy of Andean populations of <i>Ctenomys</i> (Rodentia): <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Journal of Mammalogy</i> , 2021, 102, 1405-1425.	0.6	8
10059	Identification, evolution and expression analysis of <i>WRKY</i> gene family in <i>Eucommia ulmoides</i> . <i>Genomics</i> , 2021, 113, 3294-3309.	1.3	20
10060	Comparative Chloroplast Genomics and Phylogenetic Analysis of <i>Zygophyllum</i> (Zygophyllaceae) of China. <i>Frontiers in Plant Science</i> , 2021, 12, 723622.	1.7	12
10061	High molecular diversity and divergent subpopulations of the begomovirus <i>cnidoscolus</i> mosaic leaf deformation virus associated with <i>Cnidoscolus urens</i> . <i>Archives of Virology</i> , 2021, 166, 3289-3299.	0.9	0
10062	Multiple Mechanisms Drive the Evolutionary Adaptation of <i>Phytophthora infestans</i> Effector <i>Avr1</i> to Host Resistance. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 789.	1.5	4
10063	Genetic Diversity and Population Structure Analysis of Wild <i>Cymbidium tortisepalum</i> Based on Chloroplast DNA in Yunnan Province of China. <i>Journal of the American Society for Horticultural Science</i> , 2021, 146, 424-434.	0.5	0
10064	A genotyping assay to determine geographic origin and transmission potential of <i>Plasmodium falciparum</i> malaria cases. <i>Communications Biology</i> , 2021, 4, 1145.	2.0	7
10065	Spatial genetic structure and <i>Ovis</i> haplogroup as a tool for an adaptive conservation management of the endangered <i>Cyprus mouflon</i> . <i>Zoology</i> , 2021, 148, 125959.	0.6	4
10066	Genetic monitoring of Himalayan goral (<i>Naemorhedus goral</i>) from Western Himalayas, India. <i>Molecular Biology Reports</i> , 2021, 48, 7609-7615.	1.0	2
10067	The biogeography of <i>Dromiciops</i> in southern South America: Middle Miocene transgressions, speciation and associations with <i>Nothofagus</i> . <i>Molecular Phylogenetics and Evolution</i> , 2021, 163, 107234.	1.2	16
10068	Genetic diversity and Multilocus Sequence Typing Analysis of <i>Bartonella henselae</i> in domestic cats from Southeastern Brazil. <i>Acta Tropica</i> , 2021, 222, 106037.	0.9	21
10069	Chinese eel products in EU markets imply the effectiveness of trade regulations but expose fraudulent labelling. <i>Marine Policy</i> , 2021, 132, 104651.	1.5	5

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10070	Population genetic structure of the pen shell <i>Atrina pectinata</i> sensu lato (Bivalvia: Pinnidae) throughout East Asia. <i>Regional Studies in Marine Science</i> , 2021, 48, 102024.	0.4	1
10071	The interaction between Tu-Izumo1 and Tu-JUNO is involved in turtles hybridization. <i>Reproduction</i> , 2021, 162, 249-257.	1.1	1
10072	Comparative fruit morphology and its systematic significance in <i>Ferula</i> (Apiaceae) species from different growth habitats. <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2021, 283, 151899.	0.6	1
10073	Genotyping of <i>Ascaris</i> spp. infecting humans and pigs in Italy, Slovakia and Colombia. <i>Infection, Genetics and Evolution</i> , 2021, 94, 104997.	1.0	2
10074	High-throughput sequencing of <i>Fasciola</i> spp. shows co-infection and intermediate forms in Balochistan, but only <i>Fasciola gigantica</i> in the Punjab province of Pakistan. <i>Infection, Genetics and Evolution</i> , 2021, 94, 105012.	1.0	7
10075	DNA Barcode is Efficient for Identifying Bat Species. <i>Journal of Mammalian Evolution</i> , 2022, 29, 63-75.	1.0	1
10076	Geography-Driven Evolution of Potato Virus A Revealed by Genetic Diversity Analysis of the Complete Genome. <i>Frontiers in Microbiology</i> , 2021, 12, 738646.	1.5	0
10077	Molecular survey and genetic characterization of <i>Candidatus Mycoplasma haemolamae</i> ™ in llamas (<i>Lama glama</i>) and alpacas (<i>Vicugna pacos</i>) from Southern Chile.. <i>Acta Tropica</i> , 2021, 222, 106046.	0.9	4
10078	First molecular characterization of <i>Blastocystis</i> subtypes from animals and animal-keepers stool in Algeria. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2021, 78, 101695.	0.7	10
10079	Genetic Diversity and Population Structure of the <i>Xanthomonas campestris</i> pv. <i>campestris</i> Strains Affecting Cabbages in China Revealed by MLST and Rep-PCR Based Genotyping. <i>Plant Pathology Journal</i> , 2021, 37, 476-488.	0.7	7
10080	Nuclear phylogenies and genomics of a contact zone establish the species rank of <i>Podarcis lusitanicus</i> (Squamata, Lacertidae). <i>Molecular Phylogenetics and Evolution</i> , 2021, 164, 107270.	1.2	10
10081	Genetic diversity and population structure of <i>Haemonchus contortus</i> in goats from Thailand. <i>Infection, Genetics and Evolution</i> , 2021, 95, 105021.	1.0	4
10082	Characterization of the complete mitochondrial genomes of six horseflies (Diptera: Tabanidae). <i>Infection, Genetics and Evolution</i> , 2021, 95, 105054.	1.0	9
10083	Genetic diversity, genetic structure, and demographic history of <i>Cinnamomum chago</i> , a plant species with extremely small populations in China. <i>Global Ecology and Conservation</i> , 2021, 31, e01808.	1.0	1
10084	Phylogeography of two widespread C4 grass species suggest that tableland and valley grassy biome in southwestern China pre-date human modification. <i>Global Ecology and Conservation</i> , 2021, 31, e01835.	1.0	5
10085	The Complete Chloroplast Genome Sequences of <i>Anisodus acutangulus</i> and a Comparison with Other Solanaceae Species. <i>Clinical Complementary Medicine and Pharmacology</i> , 2021, 1, 100002.	0.9	2
10086	DNA Barcoding unveils cryptic lineages of <i>Hoplias malabaricus</i> from Northeastern Brazil. <i>Brazilian Journal of Biology</i> , 2021, 81, 917-927.	0.4	3
10087	Environmental preferences of <i>Longitarsus jacobaeae</i> , a biocontrol agent of <i>Jacobaea vulgaris</i> , in northern Germany. <i>Biological Control</i> , 2021, 164, 104740.	1.4	1

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10088	Genetic lineage of the Amami islanders inferred from classical genetic markers. <i>Meta Gene</i> , 2021, 30, 100956.	0.3	1
10089	The importance of the genetic diversity of the HcRNAV ssRNA virus in the viral-based bloom control of the dinoflagellate <i>Heterocapsa circularisquama</i> . <i>Aquaculture</i> , 2022, 546, 737318.	1.7	6
10090	Phenotypic and molecular characterization of fluoroquinolone resistant <i>Pseudomonas aeruginosa</i> isolates in Palestine. <i>Brazilian Journal of Biology</i> , 2021, 82, e239868.	0.4	4
10091	Molecular classification and comparative phylogeographic study of insectivorous bat species (<i>Pipistrellus coromandra</i>) from Punjab, Pakistan. <i>Brazilian Journal of Biology</i> , 2021, 82, e240725.	0.4	0
10092	A multi-locus approach to elucidating the evolutionary history of the clingfish <i>Tomicodon petersii</i> (Gobiesocidae) in the Tropical Eastern Pacific. <i>Molecular Phylogenetics and Evolution</i> , 2022, 166, 107316.	1.2	7
10093	Integrative taxonomy and biogeography of Asian yellow house bats (<i>Vespertilionidae</i> : <i>Scotophilus</i>) in the Indomalayan Region. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 772-795.	0.6	2
10094	Phylogeography and systematics of <i>Algyroides</i> (Sauria: Lacertidae) of the Balkan Peninsula. <i>Zoologica Scripta</i> , 2021, 50, 282-299.	0.7	4
10095	TLR4 and TLR8 variability in Amazonian and West Indian manatee species from Brazil. <i>Genetics and Molecular Biology</i> , 2021, 44, e20190252.	0.6	0
10096	First molecular evidence for two new associate copepods of genus <i>Clausidium</i> Kossmann, 1874 (Copepoda: Cyclopoida: Clausidiidae) from the Persian Gulf and Gulf of Oman. <i>Nauplius</i> , 0, 29, .	0.3	1
10097	Extensive hybridization between two Andean warbler species with shallow divergence in mtDNA. <i>Auk</i> , 2021, 138, .	0.7	8
10098	Demographic consequences of foraging ecology explain genetic diversification in Neotropical bird species. <i>Ecology Letters</i> , 2021, 24, 563-571.	3.0	18
10099	Integrative description of <i>Macrobiotus porifini</i> sp. nov. (Macrobiotidae) from Madagascar and its phylogenetic position within the <i>hufelandi</i> group. , 2021, 88, 375-389.		7
10100	Molecular identification and temporal genetic differentiation of <i>Cyprinus carpio</i> (Cypriniformes: Cyprinidae) from the Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50 2	0.4	2
10101	Matrilineal evidence for genetic structure and Late Pleistocene demographic expansion of the Ornate goby <i>Istigobius ornatus</i> (Teleostei: Gobiidae) in the Persian Gulf and Oman Sea. <i>Marine Ecology</i> , 2021, 42, .	0.4	3
10102	First Complete Mitochondrial Genome of <i>Melyridae</i> (Coleoptera, Cleroidea): Genome Description and Phylogenetic Implications. <i>Insects</i> , 2021, 12, 87.	1.0	9
10103	Helminths of the mallard <i>Anas platyrhynchos</i> Linnaeus, 1758 from Austria, with emphasis on the morphological variability of <i>Polymorphus minutus</i> Goeze, 1782. <i>Journal of Helminthology</i> , 2021, 95, e16.	0.4	2
10104	Genetic characterisation of the spiny dogfish <i>Squalus acanthias</i> in the Adriatic Sea: evidence for high genetic diversity and an Atlantic-South Pacific origin. <i>Marine and Freshwater Research</i> , 2021, 72, 131.	0.7	0
10106	Differentiation in the eastern Asian <i>Periphyllus koelreuteriae</i> (Hemiptera: Aphididae) species complex driven by climate and host plant. <i>Biological Journal of the Linnean Society</i> , 2021, 132, 509-520.	0.7	2

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10107	Sucrose-phosphate phosphatase from sugarcane reveals an ancestral tandem duplication. <i>BMC Plant Biology</i> , 2021, 21, 23.	1.6	28
10108	Redescription of Antarctic eutardigrade <i>Dastychius improvisus</i> (Dastych, 1984) and some remarks on phylogenetic relationships within Isohypsibioidea. , 2021, 88, 117-131.		5
10109	Chloroplast genomic diversity in <i>Bulbophyllum</i> section <i>Macrocaulia</i> (Orchidaceae, Epidendroideae,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.8	21
10110	Mitochondrial DNA suggests Hybridization in Freshwater Stingrays <i>Potamotrygon</i> (POTAMOTRYGONIDAE: MYLIOBATIFORMES) from the Xingu river, Amazonia and reveals speciation in <i>Paratrygon aireba</i> . <i>Anais Da Academia Brasileira De Ciencias</i> , 2021, 93, .	0.3	3
10111	First record and DNA barcodes of non-native shrimp, <i>Caridina babaulti</i> (Bouvier, 1918) in Europe. , 2021, 88, 816-823.		3
10112	Multiple haplotypes of <i>Chelonia mydas</i> juveniles in a threatened hotspot area in Southern Brazil. <i>Genetics and Molecular Biology</i> , 2021, 44, e20200410.	0.6	1
10113	Comparative study on the chloroplast genomes of five <i>Larix</i> species from the Qinghai-Tibet Plateau and the screening of candidate DNA markers. <i>Journal of Forestry Research</i> , 2021, 32, 2219-2226.	1.7	6
10114	Chloroplast DNA Variation and Phylogeography of Pedunculate Oak <i>Quercus robur</i> L. in the Eastern Part of the Range. <i>Russian Journal of Genetics</i> , 2021, 57, 47-60.	0.2	12
10115	The phylogeny, phylogeography, and diversification history of the westernmost Asian cobra (Serpentes: Elapidae: <i>Naja oxiana</i>) in the Trans-Caspian region. <i>Ecology and Evolution</i> , 2021, 11, 2024-2039.	0.8	9
10116	Computational Methods of Identification of Pseudogenes Based on Functionality: Entropy and GC Content. <i>Methods in Molecular Biology</i> , 2014, 1167, 41-62.	0.4	2
10117	Multilocus Sequence Typing (MLST) of <i>Chlamydiales</i> . <i>Methods in Molecular Biology</i> , 2019, 2042, 69-86.	0.4	8
10118	Conservation Genetics, Demographic History, and Climatic Distribution of the Nine-Banded Armadillo (<i>Dasyus novemcinctus</i>): An Analysis of Its Mitochondrial Lineages. , 2020, , 141-163.		4
10119	Molecular Evolution (Mitochondrial and Nuclear Microsatellites Markers) in the Andean Bear (<i>Tremarctos ornatus</i> ; Ursidae, Carnivora): How Many ESUs Are There?. , 2020, , 165-194.		5
10120	<i>Trichinella</i> and Other Foodborne Nematodes. , 2018, , 175-215.		2
10121	Comparative phylogeography of meroplanktonic species, <i>Aurelia</i> spp. and <i>Rhizostoma pulmo</i> (Cnidaria:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5		5
10122	Diverse Genomic Backgrounds Vs. Highly Conserved Symbiotic Genes in <i>Sesbania</i> -Nodulating Bacteria: Shaping of the Rhizobial Community by Host and Soil Properties. <i>Microbial Ecology</i> , 2020, 80, 158-168.	1.4	6
10123	Morphology and molecular phylogeny of <i>Paragorgia rubra</i> sp. nov. (Cnidaria: Octocorallia), a new bubblegum coral species from a seamount in the tropical Western Pacific. <i>Chinese Journal of Oceanology and Limnology</i> , 2017, 35, 803-814.	0.7	21
10124	Molecular systematics of <i>Rosoideae</i> (Rosaceae). <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	12

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10125	Unveiling cryptic diversity among Müllerian co-mimics: insights from the Western Palearctic <i>Syntomis</i> moths (Lepidoptera: Erebiidae: Arctiinae). <i>Organisms Diversity and Evolution</i> , 2021, 21, 119-133.	0.7	1
10126	Clinal variation along precipitation gradients in Patagonian temperate forests: unravelling demographic and selection signatures in three <i>Nothofagus</i> spp.. <i>Annals of Forest Science</i> , 2020, 77, 1.	0.8	5
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10423	Evidence for Cryptic Speciation in Directly Transmitted Gyrodactylid Parasites of Trinidadian Guppies. PLoS ONE, 2015, 10, e0117096.	1.1	27
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10434	Evidence for Positive Selection within the PgiC1 Locus in the Grass <i>Festuca ovina</i> . PLoS ONE, 2015, 10, e0125831.	1.1	4
10435	Hitting an Unintended Target: Phylogeography of <i>Bombus brasiliensis</i> Lepeletier, 1836 and the First New Brazilian Bumblebee Species in a Century (Hymenoptera: Apidae). PLoS ONE, 2015, 10, e0125847.	1.1	30
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10437	Biogeography and Genetic Structure in Populations of a Widespread Lichen (<i>Parmelina tiliacea</i>). Tj ETQq1 1 0.784314 rgBT /Overlock 12 e0126657.	1.1	12
10438	Origin, Divergence, and Phylogeny of Asexual <i>Epichloa</i> Endophyte in <i>Elymus</i> Species from Western China. PLoS ONE, 2015, 10, e0127096.	1.1	21
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10442	Range-Wide Genetic Analysis of Little Brown Bat (<i>Myotis lucifugus</i>) Populations: Estimating the Risk of Spread of White-Nose Syndrome. PLoS ONE, 2015, 10, e0128713.	1.1	36
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10446	Demographic History of Indigenous Populations in Mesoamerica Based on mtDNA Sequence Data. PLoS ONE, 2015, 10, e0131791.	1.1	29
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10585	Phylogenetic Taxonomy of <i>Artemisia</i> L. Species from Kazakhstan Based on MatK Analyses. <i>Proceedings of the Latvian Academy of Sciences</i> , 2018, 72, 29-37.	0.0	6
10586	Identification of SNPs in candidate genes potentially involved in bud burst in European beech (<i>Fagus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.4	8
10587	Phylogeography of the gray red-backed vole <i>Craseomys rufocanus</i> (Rodentia: Cricetidae) across the distribution range inferred from nonrecombining molecular markers. <i>Russian Journal of Theriology</i> , 2012, 11, 137-156.	0.5	20
10588	Conserved gene arrangement in the mitochondrial genomes of barklouse families Stenopsocidae and Psocidae. <i>Frontiers of Agricultural Science and Engineering</i> , 2017, 4, 358.	0.9	6
10589	A population genetic study on the relationship between medaka fish and the spread of wet-rice cultivation across the Japanese archipelago. <i>Anthropological Science</i> , 2012, 120, 81-89.	0.2	5
10590	Aproximaci3n a la filogenia de Spodoptera (Lepidoptera: Noctuidae) con el uso de un fragmento del gen de la citocromo oxidasa I (COI). <i>Revista De Biologia Tropical</i> , 2012, 60, .	0.1	6
10591	Genealogical approaches to the temporal origins of the Central American gap: Speciation and divergence in Pacific & Chthamalus (Sessilia: Chthamalidae). <i>Revista De Biologia Tropical</i> , 2013, 61, 75-88.	0.1	13
10592	Pathogenicity in <i>Plasmopara halstedii</i> (Sunflower downy mildew) races 710, 714 and 704. <i>Acta Phytopathologica Et Entomologica Hungarica</i> , 2014, 49, 11-24.	0.1	2
10593	First record of genus <i>Cryptonanus</i> (Didelphimorphia) in the state of Rio de Janeiro, Brazil. <i>Check List</i> , 2016, 12, 1827.	0.1	8

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10594	Molecular characterization of the invasive aquatic macrophyte <i>Hydrilla verticillata</i> (Hydrocharitaceae) in Brazil. <i>Anais Da Academia Brasileira De Ciencias</i> , 2019, 91, e20180494.	0.3	3
10595	Genetic diversity and structuring in the arapaima (<i>Osteoglossiformes</i> , <i>Osteoglossidae</i>) population reveal differences between the Amazon and the Tocantins-Araguaia basins. <i>Anais Da Academia Brasileira De Ciencias</i> , 2020, 92, e20180496.	0.3	3
10596	Multilocus sequence typing (MLST) of clinical and environmental isolates of <i>Cryptococcus neoformans</i> and <i>Cryptococcus gattii</i> in six departments of Colombia reveals high genetic diversity. <i>Revista Da Sociedade Brasileira De Medicina Tropical</i> , 2020, 53, e20190422.	0.4	7
10597	Phylogenetic niche conservatism and plant diversification in South American subtropical grasslands along multiple climatic dimensions. <i>Genetics and Molecular Biology</i> , 2020, 43, e20180291.	0.6	14
10598	Combined use of mitochondrial and nuclear genetic markers further reveal immature marine turtle hybrids along the South Western Atlantic. <i>Genetics and Molecular Biology</i> , 2020, 43, e20190098.	0.6	10
10599	Global phylogeography of the critically endangered hawksbill turtle (<i>Eretmochelys imbricata</i>). <i>Genetics and Molecular Biology</i> , 2020, 43, e20190264.	0.6	12
10600	The complete chloroplast genome of <i>Papaver setigerum</i> and comparative analyses in <i>Papaveraceae</i> . <i>Genetics and Molecular Biology</i> , 2020, 43, e20190272.	0.6	12
10601	Mitochondrial genetic structure of two populations of <i>Uca uruguayensis</i> fails to reveal an impact of the Rio de la Plata on gene flow. <i>Nauplius</i> , 2012, 20, 15-25.	0.3	21
10602	Cytogenetic and DNA barcoding reveals high divergence within the trahira, <i>Hoplias malabaricus</i> (Characiformes: Erythrinidae) from the lower Amazon River. <i>Neotropical Ichthyology</i> , 2013, 11, 459-466.	0.5	27
10603	A new evolutionary unit in the <i>Excirolana braziliensis</i> species complex. <i>Brazilian Journal of Oceanography</i> , 2016, 64, 197-202.	0.6	10
10604	Genetic variability of papaya lethal yellowing virus isolates from Ceará and Rio Grande do Norte States, Brazil. <i>Tropical Plant Pathology</i> , 2012, 37, 37-43.	0.8	8
10605	Survey of vector-borne and nematode parasites involved in the etiology of anemic syndrome in sheep from Southern Brazil. <i>Brazilian Journal of Veterinary Parasitology</i> , 2020, 29, e007320.	0.2	17
10606	Genetic profile and molecular resistance of <i>Aedes (Stegomyia) aegypti</i> (Diptera: Culicidae) in Foz do Iguaçu (Brazil), at the border with Argentina and Paraguay. <i>Zoologia</i> , 2012, 29, 540-548.	0.5	10
10607	Comparative Analysis of Genetic and Morphological Variation within the <i>Platanthera hyperborea</i> Complex (Orchidaceae). <i>Systematic Botany</i> , 2020, 45, 767-778.	0.2	5
10608	Phylogeography of the Pacific Red Snapper (<i>Lutjanus peru</i>) and Spotted Rose Snapper (<i>Lutjanus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 1	1.4	5
10609	Feline Giardiasis in Turkey: Prevalence and Genetic and Haplotype Diversity of <i>Giardia duodenalis</i> Based on the β -Giardin Gene Sequence in Symptomatic Cats. <i>Journal of Parasitology</i> , 2020, 106, 699-706.	0.3	9
10610	Diversity of Nitrogen-Fixing Symbionts of <i>Chamaecrista fasciculata</i> (Partridge Pea) Across Variable Soils. <i>Southeastern Naturalist</i> , 2019, 18, 147.	0.2	3
10611	Phylogeographic Analysis of Mudpuppies (<i>Necturus maculosus</i>). <i>Journal of Herpetology</i> , 2020, 54, 78.	0.2	2

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10613	Phylogenetics of <i>Buchnera aphidicola</i> Munson et al., 1991 based on 16S rRNA amplified from seven aphid species. <i>Turkiye Entomoloji Dergisi</i> , 0, , 227-237.	0.1	2
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10615	Impact of Late Pleistocene-Holocene climatic fluctuations on the phylogeographic structure and historical demographics of <i>Zamia prasina</i> (Cycadales: Zamiaceae). <i>Botanical Sciences</i> , 2019, 97, 588-608.	0.3	3
10616	Population Genetic Analysis of Oceanic Paddle Crab (<i>Varuna litterata</i>) in Thailand. <i>Sains Malaysiana</i> , 2017, 46, 2251-2261.	0.3	5
10617	Phylogenetic analysis of S-RNase-like genes from <i>Fragaria</i> provides evidence for ancestral S-RNase duplication in the Rosaceae lineage. <i>Acta Horticulturae</i> , 2019, , 365-370.	0.1	1
10618	Genetic analysis of paleo-colombians from Nemocán, Cundinamarca provides insights on the early peopling of northwestern South America. <i>Revista De La Academia Colombiana De Ciencias Exactas, Fisicas Y Naturales</i> , 2016, 40, 461.	0.0	8
10619	Insights to the genetic structure of <i>Calanus helgolandicus</i> (Calanoida: Copepoda) from deep-sea specimens in the Balearic Sea. <i>Crustacean Research</i> , 2019, 48, 119-132.	0.2	2
10620	Hepatitis B virus (HBV) X gene mutations and their association with liver disease progression in HBV-infected patients. <i>Oncotarget</i> , 2017, 8, 105115-105125.	0.8	23
10621	The Demoiselle crane (<i>Anthropoides virgo</i>) population genetic structure in Russia. <i>Vavilovskii Zhurnal Genetiki I Seleksii</i> , 2018, 22, 586-592.	0.4	5
10622	GENETIC IMPLICATIONS OF RESTOCKING PROGRAMS ON WILD POPULATIONS OF STREAKED PROCHILOD & Prochilodus lineatus. <i>Boletim Do Instituto De Pesca</i> , 2019, 45, .	0.5	2
10623	Population Structure of Two Flightless Weevils of Genus <i>Scepticus</i> Roelofs (Coleoptera.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 107 Td (C</i>	0.3	2
10624	The Sicilian Wolf: Genetic Identity of a Recently Extinct Insular Population. <i>Zoological Science</i> , 2019, 36, 189.	0.3	14
10625	Phylogeographic Analysis of Madagascan Goats Using mtDNA Control Region and SRY Gene Sequences. <i>Zoological Science</i> , 2019, 36, 294.	0.3	5
10626	DNA Taxonomy Confirms the Identity of the Widely-Disjunct Mediterranean and Atlantic Populations of the Tufted Ghost Crab <i>Ocypode cursor</i> (Crustacea: Decapoda: Ocypodidae). <i>Zoological Science</i> , 2019, 36, 322.	0.3	8
10627	Low Coverage Whole Genome Sequencing Yields the Complete Mitogenome of <i>Hypselodoris bullocki</i> and <i>Hypselodoris apolegma</i> (Mollusca: Chromodorididae). <i>Journal of Coastal Research</i> , 2019, 97, 23.	0.1	3
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10629	ON IDENTIFICATION OF SPECIES IN THE FEATHER MITE GENUS <i>LAMINALLOPTES</i> DUBININ, 1955 (ACARI:) <i>Tj ETQq1 1 0.784314 rgBT /Ov</i>	0.1	4

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10631	Comparison of Patterns of Genetic Variation and Demographic History in the Greater Sage-Grouse (<i>Centrocercus urophasianus</i>): Relevance for Conservation. <i>Open Ornithology Journal</i> , 2014, 7, 19-29.	0.4	4
10632	Allele Mining Strategies: Principles and Utilisation for Blast Resistance Genes in Rice (<i>Oryza</i>) Overlock 10 Tf 50 66	1.0	9
10633	Centros de origen, domesticación y diversidad genética de la ciruela mexicana, <i>Spondias purpurea</i> (Anacardiaceae). <i>Acta Botanica Mexicana</i> , 2017, , 7-38.	0.1	7
10634	El uso ornamental de <i>Guarianthe skinneri</i> (Orchidaceae), en Chiapas y Guatemala, determina parcialmente su diversidad y estructura genética. <i>Acta Botanica Mexicana</i> , 2018, , 35-48.	0.1	2
10635	Variación en la captura de machos de <i>Neoleucinodes elegantalis</i> Guenée (Lepidoptera: Crambidae) usando feromonas sexuales comerciales en tres hospederos solanáceos. <i>Ciencia Tecnología Agropecuaria</i> , 2017, 18, 583-597.	0.3	3
10636	Molecular Identification and Phylogenetic Analysis of Multidrug-resistant Bacteria using 16S rDNA Sequencing. <i>Journal of Pure and Applied Microbiology</i> , 2018, 12, 489-496.	0.3	5
10637	Global evolution and expression analysis of BTB-containing ankyrin repeat genes in plants. <i>Archives of Biological Sciences</i> , 2018, 70, 249-258.	0.2	1
10638	Molecular characterization and evolution studies of a SERK like gene transcriptionally induced during somatic embryogenesis in <i>Phoenix Dactylifera</i> L v Deglet Nour. <i>Genetika</i> , 2015, 47, 323-337.	0.1	2
10639	ADOPS--Automatic Detection Of Positively Selected Sites. <i>Journal of Integrative Bioinformatics</i> , 2012, 9, 200.	1.0	25
10640	<i>Poecilimon zonatus</i> Bolívar (ORTHOPTERA, TETTIGONIIDAE) REVISITED: GENETIC DATA REVEALED TWO NEW SPECIES AND ONE NEW SUBSPECIES. <i>Trakya University Journal of Natural Sciences</i> , 2018, 19, 85-99.	0.4	3
10641	è'jè,é°, (<i>Muntiacus putaoensis</i>)ç°;ç²'ä½"á...äÿ°â»ç»„çš„æµ«á@šá'CEé°,á±žáŠ'ç%©ç³»ç»ÿâè,²ç"ç©¶. <i>Zoological Research</i> , 2017, 38, 31		
10642	è,ã°¼4ä°šâ±±éžéžè¡CEä°âž<á...½ç±»âšæ·æ€Šâšâ...¶âž,ç'â^fæ¼á±€. <i>Zoological Research</i> , 2019, 40, 53-60.	0.9	10
10643	Genetic diversity and temporal changes of an endemic cyprinid fish species, <i>Ancherythroculter nigrocauda</i> , from the upper reaches of Yangtze River. <i>Zoological Research</i> , 2019, 40, 427-438.	0.9	13
10644	Non-invasive genetic analysis indicates low population connectivity in vulnerable Chinese gorals: concerns for segregated population management. <i>Zoological Research</i> , 2019, 40, 439-448.	0.9	12
10645	Mitochondrial Diversity of the East Balkan Swine (<i>Sus scrofa</i> f. <i>domestica</i>) in South-Eastern Bulgaria. <i>Acta Veterinaria</i> , 2019, 69, 229-236.	0.2	1
10646	Phylogeny and phylogeography of arvicoline and lagurine voles of Mongolia. <i>Folia Zoologica</i> , 2019, 68, 100.	0.9	8
10647	Filling the gap: the common hamster, <i>Cricetus cricetus</i> , phylogeography â€“ a case study of Ukraine as potential refugial area. <i>Folia Zoologica</i> , 2019, 68, 48.	0.9	3

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10649	Genetic diversity and origins of invasive black rats (<i>Rattus rattus</i>) in Benin, West Africa. <i>Journal of Vertebrate Biology</i> , 2020, 69, 1.	0.4	6
10650	Genomic non-coding regions reveal hidden patterns of mumps virus circulation in Spain, 2005 to 2015. <i>Eurosurveillance</i> , 2018, 23, .	3.9	13
10651	Complete Mitochondrial Genomes of Two Pearl Oyster Species (Bivalvia: Pteriomorpha) Reveal Novel Gene Arrangements. <i>Journal of Shellfish Research</i> , 2018, 37, 1039.	0.3	7
10652	Classification of Small Flat Oysters of <i>Ostrea stentina</i> Species Complex and a New Species <i>Ostrea neostentina</i> sp. nov. (Bivalvia: Ostreidae). <i>Journal of Shellfish Research</i> , 2019, 38, 295.	0.3	11
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10654	Taxonomy and Genetic Diversity of Amphipods Living on <i>Ulva lactuca</i> L. from Gouqi Coast, China1. <i>Pacific Science</i> , 2020, 74, .	0.2	14
10655	Indigenous and introduced species of the <i>Bemisia tabaci</i> complex in sweet potato crops from Argentina. <i>AgriScientia</i> , 2014, 31, 103-107.	0.2	3
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10659	Phylogenetic Study of Dioecious and Parthenogenetic Populations of <i>Canthocamptus staphylinus</i> (Crustacea, Copepoda, Harpacticoida). <i>Bulletin (Southern California Academy of Science)</i> , 2019, 119, 1-10.	0.1	10
10660	Conservation Genetics of the Black Grouse <i>Tetrao tetrix</i> in Poland – Distribution of Genetic Diversity Among the Last Populations. <i>Acta Ornithologica</i> , 2019, 53, 181.	0.1	3
10661	Climate-Driven Range Shifts of the Sharp-Tailed Grouse <i>Tympanuchus phasianellus</i> . <i>Acta Ornithologica</i> , 2020, 54, 213.	0.1	7
10662	Some Tardigrades from Nepal (Asia) with Integrative Description of <i>Macrobotus wandae</i> sp. nov. (Macrobotidae: Hufelandi Group). <i>Annales Zoologici</i> , 2020, 70, 121.	0.1	17
10663	Genetic Diversity of <i>Bacillus thuringiensis</i> from Different Geo-Ecological Regions of Ukraine by Analyzing the 16S rRNA and <i>gyrB</i> Genes and by AP-PCR and saAFLP. <i>Acta Naturae</i> , 2013, 5, 90-100.	1.7	6
10664	Genetic Polymorphisms in <i>VIR</i> Genes among Indian <i>Plasmodium vivax</i> Populations. <i>Korean Journal of Parasitology</i> , 2014, 52, 557-564.	0.5	8
10665	Diversity of <i>vir</i> Genes in <i>Plasmodium vivax</i> from Endemic Regions in the Republic of Korea: an Initial Evaluation. <i>Korean Journal of Parasitology</i> , 2017, 55, 149-158.	0.5	7
10666	Unraveling Haplotype Diversity of the Apical Membrane Antigen-1 Gene in <i>Plasmodium falciparum</i> Populations in Thailand. <i>Korean Journal of Parasitology</i> , 2018, 56, 153-165.	0.5	8

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10669	Impacts of supplementation aquaculture on the genetic diversity of wild Ruditapes decussatus from northern Spain. Aquaculture Environment Interactions, 2015, 6, 241-254.	0.7	23
10670	Genetic homogeneity among geographically distant populations of the blister worm Polydora websteri. Aquaculture Environment Interactions, 2018, 10, 437-446.	0.7	16
10671	New data on Perkinsus mediterraneus in the Balearic Archipelago: locations and affected species. Diseases of Aquatic Organisms, 2014, 112, 69-82.	0.5	4
10672	Mucus: aiding elasmobranch conservation through non-invasive genetic sampling. Endangered Species Research, 2013, 21, 215-222.	1.2	17
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10676	Genetic structure in the blue and red shrimp Aristeus antennatus and the role played by hydrographical and oceanographical barriers. Marine Ecology - Progress Series, 2011, 421, 163-171.	0.9	38
10677	Restricted dispersal of the reef fish Myripristis berndti at the scale of the SW Indian Ocean. Marine Ecology - Progress Series, 2011, 443, 167-180.	0.9	38
10678	Searching for common threads in threadfins: phylogeography of Australian polynemids in space and time. Marine Ecology - Progress Series, 2012, 449, 263-276.	0.9	20
10679	Differential invading potential among cryptic species of a Lessepsian bioinvader, the blotchfin dragonet Callionymus filamentosus. Marine Ecology - Progress Series, 2012, 450, 159-166.	0.9	4
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10684	Genetic structure among spawning aggregations of the gulf coney Hyporthodus acanthistius. Marine Ecology - Progress Series, 2014, 499, 193-201.	0.9	8

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10686	Population genetic structure of <i>Lepidonotothen larseni</i> revisited: cyb and microsatellites suggest limited connectivity in the Southern Ocean. <i>Marine Ecology - Progress Series</i> , 2014, 517, 251-263.	0.9	9
10687	Genetic and migratory evidence for sympatric spawning of tropical Pacific eels from Vanuatu. <i>Marine Ecology - Progress Series</i> , 2015, 521, 171-187.	0.9	33
10688	Lack of adult novel northern lineages of invasive green crab <i>Carcinus maenas</i> along much of the northern US Atlantic coast. <i>Marine Ecology - Progress Series</i> , 2015, 532, 153-159.	0.9	7
10689	Whole mitogenome sequencing refines population structure of the Critically Endangered sawfish <i>Pristis pristis</i> . <i>Marine Ecology - Progress Series</i> , 2015, 533, 237-244.	0.9	35
10690	Phylogeographic perspective on the distribution and dispersal of a marine pathogen, the oyster parasite <i>Bonamia exitiosa</i> . <i>Marine Ecology - Progress Series</i> , 2015, 536, 65-76.	0.9	14
10691	Contrasting population genetic structures in <i>Amphipholis squamata</i> , a complex of brooding, self-reproducing sister species sharing life history traits. <i>Marine Ecology - Progress Series</i> , 2015, 539, 165-177.	0.9	15
10692	When two oceans meet: regional population genetics of an exploited coastal shark, <i>Mustelus mustelus</i> . <i>Marine Ecology - Progress Series</i> , 2016, 544, 183-196.	0.9	16
10693	Population connectivity and phylogeography of the Mediterranean endemic skate <i>Raja polystigma</i> and evidence of its hybridization with the parapatric sibling <i>R. montagui</i> . <i>Marine Ecology - Progress Series</i> , 2016, 554, 99-113.	0.9	28
10694	Candidate gene variation in gilthead sea bream reveals complex spatiotemporal selection patterns between marine and lagoon habitats. <i>Marine Ecology - Progress Series</i> , 2016, 558, 115-127.	0.9	7
10695	Comparative phylogeography to test for predictions of marine larval dispersal in three amphidromous shrimps. <i>Marine Ecology - Progress Series</i> , 2016, 560, 105-120.	0.9	15
10696	Mitochondrial DNA reveals historical maternal lineages and a postglacial expansion of the grey seal in European waters. <i>Marine Ecology - Progress Series</i> , 2017, 566, 217-227.	0.9	3
10697	Population genetics and biophysical modeling inform metapopulation connectivity of the Caribbean king crab <i>Maguimithrax spinosissimus</i> . <i>Marine Ecology - Progress Series</i> , 2019, 610, 83-97.	0.9	16
10698	First Molecular Record of the Pacific Oyster (<i>Crassostrea gigas</i> , Thunberg 1793) in the Marmara Sea, Turkey. <i>Marine Science and Technology Bulletin</i> , 2020, 9, 23-31.	0.2	7
10699	The Small Giant Clam, <i>Tridacna maxima</i> Exhibits Minimal Population Genetic Structure in the Red Sea and Genetic Differentiation From the Gulf of Aden. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	8
10700	Joint Genetic Analyses of Mitochondrial and Y-Chromosome Molecular Markers for a Population from Northwest China. <i>Genes</i> , 2020, 11, 564.	1.0	2
10701	Competitive Displacement between <i>Bemisia tabaci</i> MEAM1 and MED and Evidence for Multiple Invasions of MED. <i>Insects</i> , 2020, 11, 35.	1.0	16
10702	Evolutionary Analysis of GH3 Genes in Six <i>Oryza</i> Species/Subspecies and Their Expression under Salinity Stress in <i>Oryza sativa</i> ssp. <i>japonica</i> . <i>Plants</i> , 2019, 8, 30.	1.6	46

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10704	Genetic variation in native and introduced populations of the red swamp crayfish <i>Procambarus clarkii</i> (Girard, 1852) (Crustacea, Decapoda, Cambaridae) in Mexico and Costa Rica. <i>Aquatic Invasions</i> , 2012, 7, 235-241.	0.6	29
10705	Lack of COI variation for <i>Clavelina oblonga</i> (Tunicata, Ascidiacea) in Brazil: Evidence for its human-mediated transportation?. <i>Aquatic Invasions</i> , 2012, 7, 419-424.	0.6	22
10706	Origins of the invasive red swamp crayfish (<i>Procambarus clarkii</i>) in the Santa Monica Mountains. <i>Aquatic Invasions</i> , 2014, 9, 211-219.	0.6	14
10707	The invasive round goby <i>Neogobius melanostomus</i> and tubenose goby <i>Proterorhinus semilunaris</i> : two introduction routes into Belgium. <i>Aquatic Invasions</i> , 2014, 9, 305-314.	0.6	23
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10825	Morphological and molecular systematic review of <i>Marphysa</i> Quatrefages, 1865 (Annelida:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.9	15
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10840	Pleistocene phylogeography and cryptic diversity of a tiger beetle, <i>Calomera littoralis</i> , in North-Eastern Mediterranean and Pontic regions inferred from mitochondrial COI gene sequences. PeerJ, 2016, 4, e2128.	0.9	11
10841	Stochasticity in space, persistence in time: genetic heterogeneity in harbour populations of the introduced ascidian <i>Styela plicata</i> . PeerJ, 2016, 4, e2158.	0.9	21
10842	Analysis of genotype diversity and evolution of Dengue virus serotype 2 using complete genomes. PeerJ, 2016, 4, e2326.	0.9	45
10843	The adder (<i>Vipera berus</i>) in Southern Altay Mountains: population characteristics, distribution, morphology and phylogenetic position. PeerJ, 2016, 4, e2342.	0.9	4
10844	Extremely low genetic variability within and among locations of the greenfish holothurian <i>Stichopus chloronotus</i> Brandt, 1835 in Okinawa, Japan. PeerJ, 2016, 4, e2410.	0.9	8
10845	The complete chloroplast genome sequence of <i>Gentiana lawrencei</i> var <i>farreri</i> (Gentianaceae) and comparative analysis with its congeneric species. PeerJ, 2016, 4, e2540.	0.9	55
10846	Mitochondrial DNA hyperdiversity and its potential causes in the marine periwinkle <i>Melarhaphe neritoides</i> (Mollusca: Gastropoda). PeerJ, 2016, 4, e2549.	0.9	15
10847	A potential third Manta Ray species near the Yucatán Peninsula? Evidence for a recently diverged and novel genetic <i>Manta</i> group from the Gulf of Mexico. PeerJ, 2016, 4, e2586.	0.9	32
10848	Yangtze River, an insignificant genetic boundary in tufted deer (<i>Elaphodus cephalophus</i>): the evidence from a first population genetics study. PeerJ, 2016, 4, e2654.	0.9	10
10849	Comparative analysis of the complete chloroplast genome sequences in psammophytic <i>Haloxylon</i> species (Amaranthaceae). PeerJ, 2016, 4, e2699.	0.9	76
10850	Neogene paleogeography provides context for understanding the origin and spatial distribution of cryptic diversity in a widespread Balkan freshwater amphipod. PeerJ, 2017, 5, e3016.	0.9	65
10851	The complete chloroplast genome sequence of <i>Morus cathayana</i> and <i>Morus multicaulis</i> , and comparative analysis within genus <i>Morus</i> L. PeerJ, 2017, 5, e3037.	0.9	30
10852	High unexpected genetic diversity of a narrow endemic terrestrial mollusc. PeerJ, 2017, 5, e3069.	0.9	3

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10853	Assembly and comparative analysis of complete mitochondrial genome sequence of an economic plant <i>Salix suchowensis</i> . PeerJ, 2017, 5, e3148.	0.9	55
10854	Mitochondrial diversity in <i>Gonionemus</i> (Trachylina:Hydrozoa) and its implications for understanding the origins of clinging jellyfish in the Northwest Atlantic Ocean. PeerJ, 2017, 5, e3205.	0.9	8
10855	Genome-wide analysis suggests high level of microsynteny and purifying selection affect the evolution of <i>EIN3/EIL</i> family in Rosaceae. PeerJ, 2017, 5, e3400.	0.9	16
10856	The South-American distribution and southernmost record of <i>Biomphalaria peregrina</i> a potential intermediate host of schistosomiasis. PeerJ, 2017, 5, e3401.	0.9	14
10857	Population structure of <i>Bathymodiolus manusensis</i> , a deep-sea hydrothermal vent-dependent mussel from Manus Basin, Papua New Guinea. PeerJ, 2017, 5, e3655.	0.9	10
10858	Characterization of the Polish Primitive Horse (Konik) maternal lines using mitochondrial D-loop sequence variation. PeerJ, 2017, 5, e3714.	0.9	7
10859	Harnessing mtDNA variation to resolve ambiguity in <i>Redfish</i> ™ sold in Europe. PeerJ, 2017, 5, e3746.	0.9	14
10860	Phylogeographic investigation and ecological niche modelling of the endemic frog species <i>Nanorana pleskei</i> revealed multiple refugia in the eastern Tibetan Plateau. PeerJ, 2017, 5, e3770.	0.9	17
10861	Integrative taxonomy of the ornamental <i>peppermint</i> ™ shrimp public market and population genetics of <i>Lysmata bognessi</i> , the most heavily traded species worldwide. PeerJ, 2017, 5, e3786.	0.9	17
10862	The complete chloroplast genome of <i>Cinnamomum camphora</i> and its comparison with related <i>Lauraceae</i> species. PeerJ, 2017, 5, e3820.	0.9	54
10863	Does silvoagropecuary landscape fragmentation affect the genetic diversity of the sigmodontine rodent <i>Oligoryzomys longicaudatus</i> ? PeerJ, 2017, 5, e3842.	0.9	3
10864	The complete chloroplast genome sequence of strawberry (<i>Fragaria</i> — <i>ananassa</i> Duch.) and comparison with related species of Rosaceae. PeerJ, 2017, 5, e3919.	0.9	68
10865	Comparative genomic analysis of the PKS genes in five species and expression analysis in upland cotton. PeerJ, 2017, 5, e3974.	0.9	17
10866	A comparison of chloroplast genome sequences in <i>Aconitum</i> (Ranunculaceae): a traditional herbal medicinal genus. PeerJ, 2017, 5, e4018.	0.9	22
10867	Introgression between ecologically distinct species following increased salinity in the Colorado Delta- Worldwide implications for impacted estuary diversity. PeerJ, 2017, 5, e4056.	0.9	12
10868	Genetic differentiation and phylogeography of Mediterranean-North Eastern Atlantic blue shark (<i>Prionace glauca</i> , L. 1758) using mitochondrial DNA: panmixia or complex stock structure?. PeerJ, 2017, 5, e4112.	0.9	14
10869	Molecular evolution of virulence genes and non-virulence genes in clinical, natural and artificial environmental <i>Legionella pneumophila</i> isolates. PeerJ, 2017, 5, e4114.	0.9	6
10870	Phylogenetic study of Lemnoideae (duckweeds) through complete chloroplast genomes for eight accessions. PeerJ, 2017, 5, e4186.	0.9	13

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10871	Genetic analysis of the Hungarian draft horse population using partial mitochondrial DNA D-loop sequencing. PeerJ, 2018, 6, e4198.	0.9	8
10872	Geographic variation in the advertisement calls of <i>Hyla eximia</i> and its possible explanations. PeerJ, 2014, 2, e420.	0.9	6
10873	Phylogenetic relationships and genetic diversity of the <i>Polypedates leucomystax</i> complex in Thailand. PeerJ, 2018, 6, e4263.	0.9	6
10874	An Indo-Pacific damselfish (<i>Neopomacentrus cyanomos</i>) in the Gulf of Mexico: origin and mode of introduction. PeerJ, 2018, 6, e4328.	0.9	10
10875	Genomic evolution, recombination, and inter-strain diversity of chelonid alphaherpesvirus 5 from Florida and Hawaii green sea turtles with fibropapillomatosis. PeerJ, 2018, 6, e4386.	0.9	23
10876	The little shrimp that could: phylogeography of the circumtropical <i>Stenopus hispidus</i> (Crustacea: Decapoda), reveals divergent Atlantic and Pacific lineages. PeerJ, 2018, 6, e4409.	0.9	11
10877	First endemic freshwater <i>Gammarus</i> from Crete and its evolutionary history—“an integrative taxonomy approach. PeerJ, 2018, 6, e4457.	0.9	14
10878	Phylogeographic structure in three North American tent caterpillar species (Lepidoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 e4479.	0.9	16
10879	Genetic diversity and molecular evolution of <i>Ornithogalum mosaic virus</i> based on the coat protein gene sequence. PeerJ, 2018, 6, e4550.	0.9	11
10880	Genetic divergence and fine scale population structure of the common bottlenose dolphin (<i>Tursiops</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.9	20
10881	Pelagic larval duration, growth rate, and population genetic structure of the tidepool snake moray <i>Uropterygius micropterus</i> around the southern Ryukyu Islands, Taiwan, and the central Philippines. PeerJ, 2018, 6, e4741.	0.9	5
10882	Westwards and northwards dispersal of <i>Triosteum himalayanum</i> (Caprifoliaceae) from the Hengduan Mountains region based on chloroplast DNA phylogeography. PeerJ, 2018, 6, e4748.	0.9	10
10883	Rapid evolution of the <i>Helicobacter pylori</i> AlpA adhesin in a high gastric cancer risk region from Colombia. PeerJ, 2018, 6, e4846.	0.9	3
10884	Some maternal lineages of domestic horses may have origins in East Asia revealed with further evidence of mitochondrial genomes and HVR-1 sequences. PeerJ, 2018, 6, e4896.	0.9	4
10885	In quest of contact: phylogeography of helmeted terrapins (<i>Pelomedusa galeata</i> , <i>P. subrufa</i> sensu) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.9	10
10886	Adaptive genetic variation at three loci in South African vervet monkeys (<i>Chlorocebus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.9	7
10887	Evaluating the utility of the female-specific mitochondrial <i>f-orf</i> gene for population genetic, phylogeographic and systematic studies in freshwater mussels (Bivalvia: Unionida). PeerJ, 2018, 6, e5007.	0.9	7
10888	Mitochondrial diversity of Bulgarian native dogs suggests dual phylogenetic origin. PeerJ, 2018, 6, e5060.	0.9	7

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10889	Asymmetric connectivity of spawning aggregations of a commercially important marine fish using a multidisciplinary approach. PeerJ, 2014, 2, e511.	0.9	30
10890	The genetic status of the Hungarian brown trout populations: exploration of a blind spot on the European map of <i>Salmo trutta</i> studies. PeerJ, 2018, 6, e5152.	0.9	2
10891	Divergence by depth in an oceanic fish. PeerJ, 2014, 2, e525.	0.9	21
10892	Recent genome reduction of <i>Wolbachia</i> in <i>Drosophila recens</i> targets phage WO and narrows candidates for reproductive parasitism. PeerJ, 2014, 2, e529.	0.9	51
10893	Historical connections among river basins and climatic changes explain the biogeographic history of a water rat. PeerJ, 2018, 6, e5333.	0.9	6
10894	Population genetics and migration pathways of the Mediterranean fruit fly <i>Ceratitis capitata</i> inferred with coalescent methods. PeerJ, 2018, 6, e5340.	0.9	6
10895	Deep divergence of Red-crowned Ant Tanager (<i>Habia rubica</i> : Cardinalidae), a multilocus phylogenetic analysis with emphasis in Mesoamerica. PeerJ, 2018, 6, e5496.	0.9	8
10896	Complete paternally inherited mitogenomes of two freshwater mussels <i>Unio pictorum</i> and <i>Sinanodonta woodiana</i> (Bivalvia: Unionidae). PeerJ, 2018, 6, e5573.	0.9	11
10897	Mitogenomics of <i>Perumytilus purpuratus</i> (Bivalvia: Mytilidae) and its implications for doubly uniparental inheritance of mitochondria. PeerJ, 2018, 6, e5593.	0.9	12
10898	Meta-analysis of northeast Atlantic marine taxa shows contrasting phylogeographic patterns following post-LGM expansions. PeerJ, 2018, 6, e5684.	0.9	61
10899	Population structure in the Andaman keelback, <i>Xenochrophis tyleri</i> : geographical distance and oceanic barriers to dispersal influence genetic divergence on the Andaman archipelago. PeerJ, 2018, 6, e5752.	0.9	2
10900	Comparative systematics and phylogeography of <i>Quercus</i> Section <i>Cerris</i> in western Eurasia: inferences from plastid and nuclear DNA variation. PeerJ, 2018, 6, e5793.	0.9	43
10901	Influenced but not determined by historical events: genetic, demographic and morphological differentiation in <i>Heleobia ascotanensis</i> from the Chilean Altiplano. PeerJ, 2018, 6, e5802.	0.9	12
10902	Genome-wide identification and analysis of the <i>CNGC</i> gene family in maize. PeerJ, 2018, 6, e5816.	0.9	20
10903	Genetic evidence supports a distinct lineage of American crocodile (<i>Crocodylus acutus</i>) in the Greater Antilles. PeerJ, 2018, 6, e5836.	0.9	13
10904	First steps towards assessing the evolutionary history and phylogeography of a widely distributed Neotropical grassland bird (Motacillidae: <i>Anthus correndera</i>). PeerJ, 2018, 6, e5886.	0.9	9
10905	Genetic assessment of a bighorn sheep population expansion in the Silver Bell Mountains, Arizona. PeerJ, 2018, 6, e5978.	0.9	2
10906	Complete chloroplast genome sequences of <i>Dioscorea</i> : Characterization, genomic resources, and phylogenetic analyses. PeerJ, 2018, 6, e6032.	0.9	25

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10907	Detection of bacterial endosymbionts in freshwater crustaceans: the applicability of non-degenerate primers to amplify the bacterial 16S rRNA gene. PeerJ, 2018, 6, e6039.	0.9	15
10908	The Plasmodium knowlesi Pk41 surface protein diversity, natural selection, sub population and geographical clustering: a 6-cysteine protein family member. PeerJ, 2018, 6, e6141.	0.9	10
10909	Invasion genetics of the mummichog (<i>Fundulus heteroclitus</i>): recent anthropogenic introduction in Iberia. PeerJ, 2019, 7, e6155.	0.9	4
10910	The origin of exotic pet sugar gliders (<i>Petaurus breviceps</i>) kept in the United States of America. PeerJ, 2019, 7, e6180.	0.9	9
10911	Genetic diversity and its conservation implications of <i>Vitex rotundifolia</i> (Lamiaceae) populations in East Asia. PeerJ, 2019, 7, e6194.	0.9	14
10912	The complete chloroplast genomes of three Betulaceae species: implications for molecular phylogeny and historical biogeography. PeerJ, 2019, 7, e6320.	0.9	26
10913	New insight into the phylogeographic pattern of <i>Liriodendron chinense</i> (Magnoliaceae) revealed by chloroplast DNA: east-west lineage split and genetic mixture within western subtropical China. PeerJ, 2019, 7, e6355.	0.9	11
10914	Characterization of the complete chloroplast genomes of five <i>Populus</i> species from the western Sichuan plateau, southwest China: comparative and phylogenetic analyses. PeerJ, 2019, 7, e6386.	0.9	25
10915	Old wild wolves: ancient DNA survey unveils population dynamics in Late Pleistocene and Holocene Italian remains. PeerJ, 2019, 7, e6424.	0.9	17
10916	Rapid ecological specialization despite constant population sizes. PeerJ, 2019, 7, e6476.	0.9	1
10917	Climate change and conservation in a warm North American desert: effect in shrubby plants. PeerJ, 2019, 7, e6572.	0.9	2
10918	Comparative genomic analysis of the IDD genes in five Rosaceae species and expression analysis in Chinese white pear (<i>Pyrus bretschneideri</i>). PeerJ, 2019, 7, e6628.	0.9	8
10919	Low genetic diversity in captive populations of the critically endangered Blue-crowned Laughingthrush (<i>Garrulax courtoisi</i>) revealed by a panel of novel microsatellites. PeerJ, 2019, 7, e6643.	0.9	4
10920	The biogeography of <i>Elaphe sauromates</i> (Pallas, 1814), with a description of a new rat snake species. PeerJ, 2019, 7, e6944.	0.9	19
10921	Maternal ancestry analyses of red tilapia strains based on D-loop sequences of seven tilapia populations. PeerJ, 2019, 7, e7007.	0.9	16
10922	On the presence of <i>Dipturus nidarosiensis</i> (Storm, 1881) in the Central Mediterranean area. PeerJ, 2019, 7, e7009.	0.9	10
10923	The complete chloroplast genome of <i>Fagus crenata</i> (subgenus <i>Fagus</i>) and comparison with <i>F. engleriana</i> (subgenus <i>Engleriana</i>). PeerJ, 2019, 7, e7026.	0.9	16
10924	Genome-wide analyses of the bHLH gene family reveals structural and functional characteristics in the aquatic plant <i>Nelumbo nucifera</i> . PeerJ, 2019, 7, e7153.	0.9	26

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10925	The impact of one-decade ecological disturbance on genetic changes: a study on the brine shrimp <i>Artemia urmiana</i> from Urmia Lake, Iran. PeerJ, 2019, 7, e7190.	0.9	14
10926	Complete chloroplast genomes of medicinally important <i>Teucrium</i> species and comparative analyses with related species from Lamiaceae. PeerJ, 2019, 7, e7260.	0.9	12
10927	Mitochondrial phylogeny and comparative mitogenomics of closely related pine moth pests (Lepidoptera: <i>Dendrolimus</i>). PeerJ, 2019, 7, e7317.	0.9	8
10928	Conservation of transcriptional elements in the obligate symbiont of the whitefly <i>Bemisia tabaci</i> . PeerJ, 2019, 7, e7477.	0.9	6
10929	Genome-wide identification of growth-regulating factors in moso bamboo (<i>Phyllostachys</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582	0.9	24
10930	Genome-wide identification and characterization of the <i>Hsp70</i> gene family in allopolyploid rapeseed (<i>Brassica napus</i> L.) compared with its diploid progenitors. PeerJ, 2019, 7, e7511.	0.9	8
10931	Comparative analysis of the ribosomal DNA repeat unit (rDNA) of <i>Perna viridis</i> (Linnaeus, 1758) and <i>Perna canaliculus</i> (Gmelin, 1791). PeerJ, 2019, 7, e7644.	0.9	8
10932	Phylogeny and biogeography of the African Bathyergidae: a review of patterns and processes. PeerJ, 2019, 7, e7730.	0.9	22
10933	Multiplexed ISSR genotyping by sequencing distinguishes two precious coral species (Anthozoa:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4	0.9	21
10934	Evaluation of variation within the barcode region of Cytochrome <i>c</i> Oxidase I (COI) for the detection of commercial <i>Callinectes sapidus</i> Rathbun, 1896 (blue crab) products of non-US origin. PeerJ, 2019, 7, e7827.	0.9	17
10935	Identification of an ancestral haplotype in the mitochondrial phylogeny of the ovine haplogroup B. PeerJ, 2019, 7, e7895.	0.9	14
10936	Demographic history and population genetic analysis of <i>Decapterus maruadsi</i> from the northern South China Sea based on mitochondrial control region sequence. PeerJ, 2019, 7, e7953.	0.9	10
10937	Geographic origin and timing of colonization of the Pacific Coast of North America by the rocky shore gastropod <i>Littorina sitkana</i> . PeerJ, 2019, 7, e7987.	0.9	4
10938	Intra-individual heteroplasmy in the <i>Gentiana tongolensis</i> plastid genome (Gentianaceae). PeerJ, 2019, 7, e8025.	0.9	10
10939	Sequencing and analyses on chloroplast genomes of <i>Tetrataenium candicans</i> and two allies give new insights on structural variants, DNA barcoding and phylogeny in Apiaceae subfamily Apioideae. PeerJ, 2019, 7, e8063.	0.9	18
10940	Phylogeography of the rare and endangered lycophyte <i>Isoetes yunguiensis</i> . PeerJ, 2020, 8, e8270.	0.9	5
10941	Evolutionary history of the Cameroon radiation of puddle frogs (Phrynobatrachidae:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 Td (Phrynobatrachidae) Cameroon Volcanic Line. PeerJ, 2020, 8, e8393.	0.9	9
10942	Comparative analysis of chloroplast genomes for five <i>Dicliptera</i> species (Acanthaceae): molecular structure, phylogenetic relationships, and adaptive evolution. PeerJ, 2020, 8, e8450.	0.9	29

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10943	Characterization of the complete mitochondrial genome sequences of three Merulinidae corals and novel insights into the phylogenetics. PeerJ, 2020, 8, e8455.	0.9	7
10944	The complete chloroplast genomes of seventeen <i>Aegilops tauschii</i> : genome comparative analysis and phylogenetic inference. PeerJ, 2020, 8, e8678.	0.9	16
10945	Life-history features and oceanography drive phylogeographic patterns of the chiton <i>Acanthochitona</i> cf. <i>rubrolineata</i> (Lischke, 1873) in the northwestern Pacific. PeerJ, 2020, 8, e8794.	0.9	5
10946	Genome-wide identification of the <i>PEBP</i> genes in pears and the putative role of <i>PbFT</i> in flower bud differentiation. PeerJ, 2020, 8, e8928.	0.9	14
10947	Mitochondrial DNA variation in the Italian Heavy Draught Horse. PeerJ, 2020, 8, e8996.	0.9	5
10948	Comparative analysis of four <i>Zantedeschia</i> chloroplast genomes: expansion and contraction of the IR region, phylogenetic analyses and SSR genetic diversity assessment. PeerJ, 2020, 8, e9132.	0.9	16
10949	Phylogeographic structure and northward range expansion in the barnacle <i>Chthamalus fragilis</i> . PeerJ, 2015, 3, e926.	0.9	11
10950	Comparative analyses of 32 complete plastomes of <i>Tef</i> (<i>Eragrostis tef</i>) accessions from Ethiopia: phylogenetic relationships and mutational hotspots. PeerJ, 2020, 8, e9314.	0.9	11
10951	Genome-wide analysis of the C3H zinc finger family reveals its functions in salt stress responses of <i>Pyrus betulaefolia</i> . PeerJ, 2020, 8, e9328.	0.9	16
10952	Ancient globetrotters' connectivity and putative native ranges of two cosmopolitan biofouling amphipods. PeerJ, 2020, 8, e9613.	0.9	14
10953	DNA barcoding of commercially important reef fishes in Weh Island, Aceh, Indonesia. PeerJ, 2020, 8, e9641.	0.9	19
10954	Trans-species polymorphism at antimicrobial innate immunity cathelicidin genes of Atlantic cod and related species. PeerJ, 2015, 3, e976.	0.9	22
10955	Genome-wide identification and expression analyses of R2R3-MYB transcription factor genes from two Orchid species. PeerJ, 2020, 8, e9781.	0.9	14
10956	Genetic approaches to the conservation of migratory bats: a study of the eastern red bat (<i>Lasiurus</i>)	0.9	18
10957	The highly rearranged mitochondrial genomes of three economically important scale insects and the mitochondrial phylogeny of Coccoidea (Hemiptera: Sternorrhyncha). PeerJ, 2020, 8, e9932.	0.9	10
10958	Phylogeographic analysis and species distribution modelling of the wood frog <i>Batrachyla leptopus</i> (Batrachylidae) reveal interglacial diversification in south western Patagonia. PeerJ, 2020, 8, e9980.	0.9	6
10959	One becomes two: second species of the <i>Euwallacea fornicatus</i> (Coleoptera: Curculionidae:)	0.9	15
10960	Molecular Diversity Analysis of Coat Protein Gene Encoded by Legume Begomoviruses and PCR Assay to Detect Yellow Mosaic Viruses Infecting Soybean in India. British Biotechnology Journal, 2016, 12, 1-10.	0.4	6

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10961	How important was polyploidy in the diversification of herbs in the Chaquean Domain? The case of the <i>Turnera sidoides</i> autopolyploid complex (Passifloraceae: Turneroideae). Botanical Journal of the Linnean Society, 2022, 199, 286-311.	0.8	6
10962	Contemporary adaptive evolution in fragmenting river landscapes: evidence from the native waterflea <i>Ceriodaphnia cornuta</i> . Journal of Plankton Research, 2022, 44, 88-98.	0.8	2
10963	From 13 to 22 in a second stroke: revisiting the European <i>Eumida sanguinea</i> (Phyllodocidae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.0	7
10964	Comparative phylogeography study reveals introgression and incomplete lineage sorting during rapid diversification of <i>Rhodiola</i> . Annals of Botany, 2022, 129, 185-200.	1.4	5
10966	A molecular identification of medicinal Rheum Species cultivated germplasm from the northwest of China using DNA barcoding. Genetic Resources and Crop Evolution, 2022, 69, 997-1008.	0.8	4
10967	An ethylene biosynthesis enzyme controls quantitative variation in maize ear length and kernel yield. Nature Communications, 2021, 12, 5832.	5.8	41
10968	Population genetics of <i>Lepidoglyphus destructor</i> inferred by the analysis of the mitochondrial cytochrome <i>b</i> gene and ribosomal internal transcribed spacer gene sequence. International Journal of Acarology, 2021, 47, 670-676.	0.3	2
10969	Molecular detection and genotype diversity of hemoplasmas in non-hematophagous bats and associated ectoparasites sampled in peri-urban areas from Brazil. Acta Tropica, 2022, 225, 106203.	0.9	12
10970	Developing an efficient DNA barcoding system to differentiate between <i>Lilium</i> species. BMC Plant Biology, 2021, 21, 465.	1.6	5
10971	Canine circovirus and Canine adenovirus type 1 and 2 in dogs with parvoviral enteritis. Veterinary Research Communications, 2022, 46, 223-232.	0.6	9
10972	Phylogenetic relationships of the nematode subfamily Phascolosstrongylinae from macropodid and vombatid marsupials inferred using mitochondrial protein sequence data. Parasites and Vectors, 2021, 14, 523.	1.0	2
10973	Novel Insights Into the Genetic Population Connectivity of Transient Whale Sharks (<i>Rhincodon typus</i>) in Pacific Panama Provide Crucial Data for Conservation Efforts. Frontiers in Marine Science, 2021, 8, .	1.2	7
10974	Following the Trace of HVS II Mitochondrial Region Within the Nine Iranian Ethnic Groups Based on Genetic Population Analysis. Biochemical Genetics, 2021, , 1.	0.8	0
10975	Phenotypic and genetic variability of fungal isolates associated with the Septoria leaf spot disease of lettuce (<i>Lactuca sativa</i>) in Brazil. Journal of Plant Diseases and Protection, 2022, 129, 53-62.	1.6	2
10976	Are ecological communities the seat of endosymbiont horizontal transfer and diversification? A case study with soil arthropod community. Ecology and Evolution, 2021, 11, 14490-14508.	0.8	3
10977	Nucleotide Diversity of the Maize ZmCNR13 Gene and Association With Ear Traits. Frontiers in Genetics, 2021, 12, 773597.	1.1	4
10978	Population genetics of Sambar (<i>Rusa unicolor</i>) from the Western Himalayas: preliminary findings. Molecular Biology Reports, 2022, 49, 811-816.	1.0	4
10979	Genotyping of <i>Taenia hydatigena</i> isolated from Sheep and Goats in KSA Based on Cox1 Gene. Saudi Journal of Biological Sciences, 2021, 29, 1270-1275.	1.8	1

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10981	On the Species Delimitation of the <i>Maddenia</i> Group of <i>Prunus</i> (Rosaceae): Evidence From Plastome and Nuclear Sequences and Morphology. <i>Frontiers in Plant Science</i> , 2021, 12, 743643.	1.7	13
10982	Breed-specific reference sequence optimized mapping accuracy of NGS analyses for pigs. <i>BMC Genomics</i> , 2021, 22, 736.	1.2	0
10983	Genetic structure, diversity and distribution of a threatened lizard affected by widespread habitat fragmentation. <i>Conservation Genetics</i> , 2022, 23, 151-165.	0.8	4
10984	Center of origin and evolutionary history in the high Andean genus <i>Oritrophium</i> (Astereae.) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 Tc</i>	1.1	2
10985	More examples of breakdown the 1:1 partner specificity between figs and fig wasps. , 2021, 62, 15.		5
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11244	<i>Bradyrhizobium altum</i> sp. nov., <i>Bradyrhizobium oropedii</i> sp. nov. and <i>Bradyrhizobium acaciae</i> sp. nov. from South Africa show locally restricted and pantropical nodA phylogeographic patterns. <i>Molecular Phylogenetics and Evolution</i> , 2022, 167, 107338.	1.2	9
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11377	Eight in One: Hidden Diversity of the Bagrid Catfish <i>Tachysurus albomarginatus</i> s.l. (Rendhal, 1928) Widespread in Lowlands of South China. <i>Frontiers in Genetics</i> , 2021, 12, 713793.	1.1	3
11378	Identification and Genetic Characterization of <i>Pseudomonas syringae</i> pv. <i>Â</i> <i>syringae</i> from Sweet Cherry in Turkey. <i>Plant Disease</i> , 2022, 106, 1253-1261.	0.7	2
11379	Genetic diversity and evolutionary analyses of potyviruses infecting narcissus in Iran. <i>Journal of Plant Pathology</i> , 2022, 104, 237-250.	0.6	7
11381	Diversity of <i>Fusarium</i> spp. Associated with Wheat Node and Grain in Representative Sites Across the Western Canadian Prairies. <i>Phytopathology</i> , 2022, 112, 1003-1015.	1.1	4
11382	Strong genetic differentiation demarks populations of <i>Favia</i> across biogeographic regions of the Atlantic Ocean. <i>Coral Reefs</i> , 2022, 41, 523-534.	0.9	3
11383	Rapid Divergence of Key Spermatogenesis Genes in nasuta-Subgroup of <i>Drosophila</i> . <i>Journal of Molecular Evolution</i> , 2022, 90, 2-16.	0.8	0
11384	Molecular phylogenetic analyses based on the complete plastid genomes and nuclear sequences reveal <i>Daphne</i> (Thymelaeaceae) to be non-monophyletic as current circumscription. <i>Plant Diversity</i> , 2022, 44, 279-289.	1.8	10
11385	<i>Paramecium bursaria</i> – A Complex of Five Cryptic Species: Mitochondrial DNA COI Haplotype Variation and Biogeographic Distribution. <i>Diversity</i> , 2021, 13, 589.	0.7	8
11386	Molecular phylogeny and macroevolution of <i>Chaitophorinae</i> aphids (<i>Insecta</i>)	1.7	4
11387	Genome-Wide Identification of the Q-type C2H2 Transcription Factor Family in Alfalfa (<i>Medicago</i>)	1.0	7
11388	Weak population genetic structure of a widely distributed nematode parasite of frogs in the western Palearctic. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 1689.	0.6	2
11389	Two divergent haplogroups of a saccin-like gene in <i>Acropora</i> corals. <i>Scientific Reports</i> , 2021, 11, 23018.	1.6	3
11390	Potassium ion channel gene family provides new insights into powdery mildew responses in <i>Triticum aestivum</i> . <i>Plant Pathology</i> , 2022, 71, 578-593.	1.2	2
11391	Characterization of the complete mitochondrial genome of <i>Myrmus lateralis</i> (Heteroptera,)	0.5	5
11392	Genetic Polymorphism and Natural Selection of Apical Membrane Antigen-1 in <i>Plasmodium falciparum</i> Isolates from Vietnam. <i>Genes</i> , 2021, 12, 1903.	1.0	4
11393	Complete chloroplast genome sequencing support <i>Angelica decursiva</i> is an independent species from <i>Peucedanum praeruptorum</i> . <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 2503-2515.	1.4	5
11394	Biogeographic and demographic history of the Mediterranean snakes <i>Malpolon monspessulanus</i> and <i>Hemorrhois hippocrepsis</i> across the Strait of Gibraltar. <i>Bmc Ecology and Evolution</i> , 2021, 21, 210.	0.7	7
11395	First report of complete mitochondrial genome in the subfamily Alleculinae and mitochondrial genome-based phylogenetics in <i>Tenebrionidae</i> (Coleoptera: Tenebrionoidea). <i>Insect Science</i> , 2022, 29, 1226-1238.	1.5	8

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11396	The Effects of Climate Change on Landscape Connectivity and Genetic Clusters in a Small Subtropical and Warm-Temperate Tree. <i>Frontiers in Plant Science</i> , 2021, 12, 671336.	1.7	7
11397	Will the artificial populations be sustainable? A genetic assessment on <i>Caragana korshinskii</i> afforestation in the semiarid regions of North China. <i>European Journal of Forest Research</i> , 2022, 141, 105-116.	1.1	2
11398	Role of the Andean uplift as an asymmetrical barrier to gene flow in the neotropical leaf-cutting ant <i>Atta cephalotes</i> . <i>Biotropica</i> , 2022, 54, 191-204.	0.8	7
11399	Genome-Wide Identification, Characterization and Expression Analysis of Soybean CHYR Gene Family. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12192.	1.8	9
11400	Natural Variation in OsMKK3 Contributes to Grain Size and Chalkiness in Rice. <i>Frontiers in Plant Science</i> , 2021, 12, 784037.	1.7	12
11401	Subtle East-West Phylogeographic Break of <i>Asteropyrum</i> (Ranunculaceae) in Subtropical China and Adjacent Areas. <i>Diversity</i> , 2021, 13, 627.	0.7	2
11402	Comparative analysis of twelve mitogenomes of Caliscelidae (Hemiptera: Fulgoromorpha) and their phylogenetic implications. <i>PeerJ</i> , 2021, 9, e12465.	0.9	4
11403	Molecular analyses revealed three morphologically similar species of non-native apple snails and their patterns of distribution in freshwater wetlands of Hong Kong. <i>Diversity and Distributions</i> , 2022, 28, 97-111.	1.9	4
11404	Genetic differentiation of <i>Coregonus muksun</i> in natural populations and broodstocks of fish rearing farms in Forvat and Sobsky in relation to the problem of restoring the species population in Western Siberia. <i>IOP Conference Series: Earth and Environmental Science</i> , 2021, 908, 012023.	0.2	0
11405	Swayne's hartebeest in Ethiopia: population estimate, genetic variability and competition with livestock. <i>Oryx</i> , 0, , 1-9.	0.5	1
11406	Molecular identification and genetic diversity of <i>Bartonella</i> spp. in 24 bat species from Thailand. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	6
11407	Diversity of Three Small Type's Giant Clams and Their Associated Endosymbiotic Symbiodiniaceae at Hainan and Xisha Islands, South China Sea. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	1
11408	Evolutionary and phylogenetic analyses of the barcoding region suggest geographical relationships among <i>Blastocystis</i> sp., ST3 in humans. <i>Infection, Genetics and Evolution</i> , 2021, 96, 105151.	1.0	6
11409	Variation in the PRNP gene of Pere David's deer (<i>Elaphurus davidianus</i>) may impact genetic vulnerability to chronic wasting disease. <i>Conservation Genetics</i> , 2022, 23, 313-323.	0.8	2
11410	Fine mapping of a QTL locus (QNFSP07-1) and analysis of candidate genes for four-seeded pods in soybean. <i>Molecular Breeding</i> , 2021, 41, 1.	1.0	3
11411	Specialization on <i>Ficus</i> Supported by Genetic Divergence and Morphometrics in Sympatric Host-Populations of the Camellia Aphid, <i>Aphis aurantii</i> . <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	4
11412	Comparative Phylogeography and Phylogeny of Pennah Croakers (Teleostei: Sciaenidae) in Southeast Asian Waters. <i>Genes</i> , 2021, 12, 1926.	1.0	1
11413	Mitogenomics of modern Mongolic-speaking populations. <i>Molecular Genetics and Genomics</i> , 2021, , 1.	1.0	2

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11414	A comprehensive overview of the genetic diversity in <i>Thylamys elegans</i> (Didelphimorphia: Didelphidae): establishing the phylogeographic determinants. <i>Revista Chilena De Historia Natural</i> , 2021, 94, .	0.5	5
11415	Mito-nuclear discordance in West African mangrove crab species (Decapoda: Brachyura: Sesamidae) suggests uni-directional mitochondrial introgression, despite prolonged evolutionary independence. <i>Marine Biology Research</i> , 0, , 1-10.	0.3	2
11416	Morphological and molecular identification of arrhenotokous strain of <i>Diglyphus wani</i> (Hymenoptera, Eulophidae) found in China as a control agent against agromyzid leafminers. <i>ZooKeys</i> , 2021, 1071, 109-126.	0.5	6
11417	Molecular epidemiology of <i>Paracoccidioides</i> spp. recovered from patients with paracoccidioidomycosis in a teaching hospital from Minas Gerais State of Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009956.	1.3	1
11418	Phylogeographic pattern of a cryptoviviparous mangrove, <i>Aegiceras corniculatum</i> , in the Indo-West Pacific, provides insights for conservation actions. <i>Planta</i> , 2022, 255, 7.	1.6	2
11419	The genetic drivers for the successful invasive potential of a generalist bird, the House crow. <i>Biological Invasions</i> , 0, , 1.	1.2	1
11420	Genetic diversity in a genetically improved line of the Pacific oyster <i>Crassostrea gigas</i> with orange shell based on microsatellites and mtDNA data. <i>Aquaculture</i> , 2022, 549, 737791.	1.7	14
11421	Diversification and secondary contact in the magpieâ€jays (<i>Calocitta</i>) throughout the pacific lowlands of Mesoamerica. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 2371-2386.	0.6	5
11422	Species delimitation and phylogeny of <i>Doto</i> (Nudibranchia: Dotidae) from the Northeast Atlantic, with a discussion on food specialization. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 1754-1774.	0.6	1
11423	Diversity, distribution, and evolutionary history of the most studied African rodents, multimammate mice of the genus <i>Mastomys</i> : An overview after a quarter of century of using DNA sequencing. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 2500-2518.	0.6	7
11424	Population genomics of freeâ€ranging Great Plains whiteâ€tailed and mule deer reflects a long history of interspecific hybridization. <i>Evolutionary Applications</i> , 2022, 15, 111-131.	1.5	10
11425	Complete Chloroplast Genome Sequence of <i>Sonchus brachyotus</i> Helps to Elucidate Evolutionary Relationships with Related Species of Asteraceae. <i>BioMed Research International</i> , 2021, 2021, 1-13.	0.9	13
11428	Evaluation of genetic diversity and origin of song ma village dogs in Vietnam. <i>Biomedical and Biotechnology Research Journal</i> , 2021, 5, 412.	0.3	0
11429	Genetic Diversity and Selection of <i>Plasmodium vivax</i> Apical Membrane Antigen-1 in Chinaâ€Myanmar Border of Yunnan Province, China, 2009â€2016. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 742189.	1.8	3
11430	Comparative genomics and phylogenetic relationships of two endemic and endangered species (<i>Handeliendron bodinieri</i> and <i>Eurycorymbus cavaleriei</i>) of two monotypic genera within Sapindales. <i>BMC Genomics</i> , 2022, 23, 27.	1.2	12
11431	Mitochondrial sequence based characterization and morphometric assessment of <i>Diara buffalo</i> population. <i>Animal Bioscience</i> , 2022, , .	0.8	0
11432	Genome-Wide Identification and Characterization of the RCI2 Gene Family in Allotetraploid <i>Brassica napus</i> Compared with Its Diploid Progenitors. <i>International Journal of Molecular Sciences</i> , 2022, 23, 614.	1.8	5
11433	Perils of brown trout (<i>Salmo</i> spp.) mitigation-driven translocations: a case study from the Vlasina Plateau, Southeast Serbia. <i>Biological Invasions</i> , 2022, 24, 999-1016.	1.2	7

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11434	GhAPC8 regulates leaf blade angle by modulating multiple hormones in cotton (<i>Gossypium hirsutum</i>) Tj ETQq0 0 0,rgBT /Overlock 10 Tf	3.8	6
11435	Diversity of Sodium Transporter HKT1;5 in Genus <i>Oryza</i> . <i>Rice Science</i> , 2022, 29, 31-46.	1.7	3
11436	The impact of prehistoric human dispersals on the presence of tobacco-related oral cancer in Northeast India. <i>Gene</i> , 2022, 813, 146098.	1.0	1
11437	Absence of Concordance between Polyembryony and Apomixis in Maize Confirmed through DNA Sequencing. <i>Ecosistemas Y Recursos Agropecuarios</i> , 2019, 6, .	0.0	1
11438	VariaÃ§Ã£o e divergÃªncia entre Snappers (<i>Lutjaninae</i> â€“ Perciformes) do AtlÃ¢ntico sul ocidental: regiÃ£o controle mitocondrial para diagnose de pressÃ£o pesqueira ou novo Barcode para peixes?. <i>Research, Society and Development</i> , 2020, 9, e977998320.	0.0	4
11439	Population genetic structure of two herds of Aberdeen Angus cattle breed in Colombia. <i>Revista Colombiana De Ciencias Pecuarias</i> , 2021, 34, 278-290.	0.4	1
11440	Genetic characterization of tambaqui stocks from two pisciculture stations in the lower SÃ£o Francisco River. <i>Semina:Ciencias Agrarias</i> , 2020, 41, 3323-3334.	0.1	1
11441	Population genetic structure of diphylobothriid tapeworms (Cestoda: Diphylobothriidea) parasitising fish in the Baikal Rift Zone. <i>Diseases of Aquatic Organisms</i> , 2022, 148, 113-125.	0.5	2
11442	Hydrography rather than lip morphology better explains the evolutionary relationship between <i>Gymnogeophagus labiatus</i> and <i>G. lacustris</i> in Southern Brazil (Cichlidae: Geophagini). <i>Neotropical Ichthyology</i> , 2021, 19, .	0.5	2
11443	The first complete chloroplast genome sequences in Resedaceae: Genome structure and comparative analysis. <i>Science Progress</i> , 2021, 104, 003685042110599.	1.0	6
11444	Molecular phylogeny and systematic of the Schneider's skink <i>Eumeces schneiderii</i> (Daudin, 1802) (Squamata: Scincidae). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 1589-1603.	0.6	1
11445	Assessment the <i>Promachus leoninus</i> Loew 1848 (Diptera: Asilidae) Species, with COI and NADH2 Gene Regions, with New Locality Records in Anatolia. <i>Biological Diversity and Conservation</i> , 0, , .	0.3	0
11446	Phylogeographic pattern, genetic diversity, and evolutionary history of the enigmatic freshwater fish species <i>Aulopyge huegelii</i> (Actinopterygii: Cyprinidae). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 2086-2102.	0.6	3
11447	Allelic diversity at BoLA DRB3 locus and association with predisposition to clinical mastitis in indicus and crossbred cattle. <i>Animal Biotechnology</i> , 2021, , 1-10.	0.7	1
11448	Molecular phylogeography and evolutionary history of the pink rice borer (Lepidoptera: Noctuidae): Implications for refugia identification and pest management. <i>Systematic Entomology</i> , 2022, 47, 371-383.	1.7	5
11449	Identification, Mapping, and Genetic Diversity of Novel Conserved Cross-Species Epitopes of RhopH2 in <i>Plasmodium knowlesi</i> With <i>Plasmodium vivax</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 810398.	1.8	2
11450	Molecular phylogeography reveals multiple Pleistocene divergence events in estuarine crabs from the tropical West Pacific. <i>PLoS ONE</i> , 2022, 17, e0262122.	1.1	1
11451	A Phylogeographical Analysis of the Beetle Pest Species <i>Callosobruchus chinensis</i> (Linnaeus, 1758) in China. <i>Insects</i> , 2022, 13, 145.	1.0	2

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11452	A Mitochondrial Genome Phylogeny of Cleridae (Coleoptera, Cleroidea). <i>Insects</i> , 2022, 13, 118.	1.0	10
11453	Genetic Origins of the Two <i>Canis lupus familiaris</i> (Dog) Freight Dog Populations. <i>Journal of Heredity</i> , 2022, 113, 160-170.	1.0	0
11455	The usefulness of maternally inherited genetic markers for phylogeographic studies in village chicken. <i>Animal Biotechnology</i> , 2023, 34, 863-881.	0.7	2
11456	Comparative analysis of the mitogenomes of two <i>Corydoras</i> (Siluriformes, Loricarioidei) with nine known <i>Corydoras</i> , and a phylogenetic analysis of Loricarioidei. <i>ZooKeys</i> , 2022, 1083, 89-107.	0.5	4
11457	Plastome Phylogenomics of <i>Aucuba</i> (Garryaceae). <i>Frontiers in Genetics</i> , 2022, 13, 753719.	1.1	3
11458	<i>Erianthus</i> germplasm collection in Thailand: genetic structure and phylogenetic aspects of tetraploid and hexaploid accessions. <i>BMC Plant Biology</i> , 2022, 22, 45.	1.6	1
11459	Molecular Prevalence and Phylogenetic Characterization of <i>Blastocystis</i> in Cattle in Kayseri Province, Turkey. <i>Kocatepe Veteriner Dergisi</i> , 0, , .	0.2	0
11460	Sequence Diversity of Tp1 and Tp2 Antigens and Population Genetic Analysis of <i>Theileria parva</i> in Unvaccinated Cattle in Zambia's Chongwe and Chisamba Districts. <i>Pathogens</i> , 2022, 11, 114.	1.2	2
11461	The role of free-flowing tributary rivers in the maintenance of genetic diversity of a migratory fish species living in a river fragmented by dams. <i>Hydrobiologia</i> , 2022, 849, 1221.	1.0	3
11462	Genetic Differentiation among Subspecies of <i>Banksia nivea</i> (Proteaceae) Associated with Expansion and Habitat Specialization. <i>Diversity</i> , 2022, 14, 98.	0.7	6
11463	Coupling molecular and risk analysis to investigate the origin, distribution and potential impact of non-native species: an application to ruffe <i>Gymnocephalus cernua</i> in Turkey. , 2022, 89, 109-121.		7
11464	Phylogeography of ancient and modern brown bears from eastern Eurasia. <i>Biological Journal of the Linnean Society</i> , 2022, 135, 722-733.	0.7	4
11465	Patterns of Genetic Variation in the <i>Eisenia nordenskioldi</i> Complex (Oligochaeta: Lumbricidae) along an Elevation Gradient in Northern China. <i>Diversity</i> , 2022, 14, 35.	0.7	2
11466	A New Species of <i>Diaphus</i> Associated with Seamounts of the Emperor Chain, North-Western Pacific Ocean (Teleostei: Myctophiformes: Myctophidae). <i>Journal of Marine Science and Engineering</i> , 2022, 10, 65.	1.2	7
11467	Molecular Identification and Appraisal of the Genetic Variation of <i>Taenia saginata</i> in Central Regions of Vietnam. <i>Life</i> , 2022, 12, 70.	1.1	4
11468	Transcriptome and Metabolite Insights into Domestication Process of Cultivated Barley in China. <i>Plants</i> , 2022, 11, 209.	1.6	3
11469	Mutational analysis of <i>Aedes aegypti</i> Dicer 2 provides insights into the biogenesis of antiviral exogenous small interfering RNAs. <i>PLoS Pathogens</i> , 2022, 18, e1010202.	2.1	6
11470	Molecular survey and genetic diversity of <i>Bartonella</i> spp. in domestic cats from Paraguay. <i>Infection, Genetics and Evolution</i> , 2022, 97, 105181.	1.0	4

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11471	Assembly and comparative analysis of the first complete mitochondrial genome of <i>Acer truncatum</i> Bunge: a woody oil-tree species producing nervonic acid. <i>BMC Plant Biology</i> , 2022, 22, 29.	1.6	31
11472	DNA Sequence Support for Reclassification of the Endemic Southern Caspian Sea Deepwater Goby as <i>Neogobius bathybius</i> (Formerly <i>Ponticola</i> ; Perciformes: Gobiidae) and Recent Population Expansion of a Continuous Population. <i>Ichthyology and Herpetology</i> , 2022, 110, .	0.3	2
11473	Rapid genetic divergence and mitonuclear discordance in the Taliang knobby newt (<i>Liangshantriton taliangensis</i>; Salamandridae, Caudata) and their driving forces. <i>Zoological Research</i> , 2022, 43, 129-146.	0.9	8
11474	Complete Chloroplast Genome Sequence of <i>Fagus longipetiolata</i> Seemen (Fagaceae): Genome Structure, Adaptive Evolution, and Phylogenetic Relationships. <i>Life</i> , 2022, 12, 92.	1.1	15
11475	Systematics of <i>Mukdenia</i> and <i>Oresitrophe</i> (Saxifragaceae): Insights from genome skimming data. <i>Journal of Systematics and Evolution</i> , 2023, 61, 99-114.	1.6	3
11476	Notes on the taxonomic status and distribution of some <i>Cylindrotomidae</i> (Diptera, Tipuloidea), with emphasis on Japanese species. <i>ZooKeys</i> , 2022, 1083, 13-88.	0.5	1
11477	Origin and Demographic History of Philippine Pigs Inferred from Mitochondrial DNA. <i>Frontiers in Genetics</i> , 2021, 12, 823364.	1.1	4
11478	Genome-wide analysis of VPE family in four <i>Gossypium</i> species and transcriptional expression of VPEs in the upland cotton seedlings under abiotic stresses. <i>Functional and Integrative Genomics</i> , 2022, 22, 179-192.	1.4	14
11479	DNA barcoding and morphological identification of spiny lobsters in South Korean waters: a new record of <i>Panulirus longipes</i> and <i>Panulirus homarus homarus</i>. <i>PeerJ</i> , 2022, 10, e12744.	0.9	2
11480	Systematic Analysis and Functional Characterization of the PLATZ Transcription Factors in Moso Bamboo (<i>Phyllostachys edulis</i>). <i>Journal of Plant Growth Regulation</i> , 2023, 42, 218-236.	2.8	6
11481	Mitochondrial DNA Footprints from Western Eurasia in Modern Mongolia. <i>Frontiers in Genetics</i> , 2021, 12, 819337.	1.1	4
11482	Genetic diversity and selection in Puerto Rican horses. <i>Scientific Reports</i> , 2022, 12, 515.	1.6	4
11484	Genetic Evidence of an Isolation Barrier between Flea Subspecies of <i>Citellophilus tesquorum</i> (Wagner). <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	1.0	1
11485	Genome-wide identification of auxin response factor (ARF) gene family and the miR160-ARF18-mediated response to salt stress in peanut (<i>Arachis hypogaea</i> L.). <i>Genomics</i> , 2022, 114, 171-184.	1.3	30
11486	First insight of genetic diversity, phylogeographic relationships, and population structure of marine sponge <i>Chondrosia reniformis</i> from the eastern and western Mediterranean coasts of Tunisia. <i>Ecology and Evolution</i> , 2022, 12, e8494.	0.8	4
11487	Insights into the geographical origin and phylogeographical patterns of <i>Paradisaea</i> birds-of-paradise. <i>Zoological Journal of the Linnean Society</i> , 2022, 196, 1394-1407.	1.0	1
11488	Genetic evidence indicates the occurrence of the Endangered Kashmir musk deer <i>Moschus cupreus</i> in Uttarakhand, India. <i>Oryx</i> , 2022, 56, 367-372.	0.5	5
11489	Phylogeography and Genetic Structure of Sand Dune Specialist <i>Stilpnolepis centiflora</i> (Asteraceae) in Northwest China Revealed by Molecular Data. <i>Diversity</i> , 2022, 14, 104.	0.7	0

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11490	Genetic diversity and population structure of the long-tailed hamster <i>Cricetulus longicaudatus</i> in Shanxi Province, China. <i>Genes and Genetic Systems</i> , 2022, 96, .	0.2	0
11491	Chloroplast Genome Evolution in Four Montane Zingiberaceae Taxa in China. <i>Frontiers in Plant Science</i> , 2021, 12, 774482.	1.7	16
11494	Insights Into Comparative Analyses and Phylogenomic Implications of <i>Acer</i> (Sapindaceae) Inferred From Complete Chloroplast Genomes. <i>Frontiers in Genetics</i> , 2021, 12, 791628.	1.1	3
11495	DNA Barcoding of Scavenging Amphipod Communities at Active and Inactive Hydrothermal Vents in the Indian Ocean. <i>Frontiers in Marine Science</i> , 2022, 8, .	1.2	5
11496	Insights into genetic variation and demographic history of sharpnose rays: examinations of three species of <i>Telatrygon</i> (Elasmobranchii, Dasyatidae) from the Indo-West Pacific. <i>Integrative Zoology</i> , 2022, 17, 1063-1077.	1.3	2
11497	Evaluation of Bacterial Diversity and Evolutionary Dynamics of Gut <i>Bifidobacterium longum</i> Isolates Obtained from Older Individuals in Hubei Province, China. <i>Microbiology Spectrum</i> , 2022, , e0144221.	1.2	0
11498	Genetic variation in the symbiont partners in the endangered macrolichen <i>Seiophora villosa</i> (Teloschistaceae: Ascomycota). <i>Botanical Journal of the Linnean Society</i> , 2022, 199, 816-829.	0.8	4
11499	Genome-Wide Analysis of KNOX Transcription Factors and Expression Pattern of Dwarf-Related KNOX Genes in Pear. <i>Frontiers in Plant Science</i> , 2022, 13, 806765.	1.7	10
11500	Habitat fragmentation in the Brazilian Atlantic Forest is associated with erosion of frog immunogenetic diversity and increased fungal infections. <i>Immunogenetics</i> , 2022, 74, 431-441.	1.2	8
11501	Balanced Polymorphism at the Pgm-1 Locus of the Pompeii Worm <i>Alvinella pompejana</i> and Its Variant Adaptability Is Only Governed by Two QE Mutations at Linked Sites. <i>Genes</i> , 2022, 13, 206.	1.0	1
11502	Longer mtDNA Fragments Provide a Better Insight into the Genetic Diversity of the Sycamore Lace Bug, <i>Corythucha ciliata</i> (Say, 1832) (Tingidae, Hemiptera), Both in Its Native and Invaded Areas. <i>Insects</i> , 2022, 13, 123.	1.0	1
11503	Otolith Microchemistry and Demographic History Provide New Insight into the Migratory Behavior and Heterogeneous Genetic Divergence of <i>Coilia grayii</i> in the Pearl River. <i>Fishes</i> , 2022, 7, 23.	0.7	2
11504	More opportunities more species: Pleistocene differentiation and northward expansion of an evergreen broad-leaved tree species <i>Machilus thunbergii</i> (Lauraceae) in Southeast China. <i>BMC Plant Biology</i> , 2022, 22, 35.	1.6	4
11505	Spatiotemporal Changes in <i>Plasmodium vivax</i> msp142 Haplotypes in Southern Mexico: From the Control to the Pre-Elimination Phase. <i>Microorganisms</i> , 2022, 10, 186.	1.6	3
11507	Genetic monitoring of the declining European stony sea urchin <i>Paracentrotus lividus</i> from the central Bay of Biscay (Asturias, northwest Spain) and attempts to restore its wild populations. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2022, 32, 309-328.	0.9	3
11508	Pieces in a global puzzle: Population genetics at two whale shark aggregations in the western Indian Ocean. <i>Ecology and Evolution</i> , 2022, 12, e8492.	0.8	4
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11552	SNP discovery and structural insights into OeFAD2 unravelling high oleic/linoleic ratio in olive oil. Computational and Structural Biotechnology Journal, 2022, 20, 1229-1243.	1.9	12
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12321	Forensic Feature Exploration and Comprehensive Genetic Insights Into Yugu Ethnic Minority and Northern Han Population via a Novel NGS-Based Marker Set. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	1

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12323	Genetical, Morphological, Behavioral, and Ecological Traits Support the Existence of Three Brazilian Species of the <i>Anastrepha fraterculus</i> Complex of Cryptic Species. <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	7
12324	Population genetics reveal multiple independent invasions of <i>Spodoptera frugiperda</i> (Lepidoptera: Noctuidae) in China. <i>Bulletin of Entomological Research</i> , 2022, 112, 796-806.	0.5	8
12325	Phylogeny and Biogeographic History of <i>Parnassius</i> Butterflies (Papilionidae: Parnassiinae) Reveal Their Origin and Deep Diversification in West China. <i>Insects</i> , 2022, 13, 406.	1.0	7
12326	Human-mediated ecoevolutionary processes of the herbivorous insect <i>Hyalopterus arundiniformis</i> during the Holocene. <i>Diversity and Distributions</i> , 0, .	1.9	1
12327	Comprehensive Evolutionary Analysis of CPP Genes in <i>Brassica napus</i> L. and Its Two Diploid Progenitors Revealing the Potential Molecular Basis of Allopolyploid Adaptive Advantage Under Salt Stress. <i>Frontiers in Plant Science</i> , 2022, 13, 873071.	1.7	4
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12329	Comparative plastid genome analyses of <i>Rosa</i> : Insights into the phylogeny and gene divergence. <i>Tree Genetics and Genomes</i> , 2022, 18, 1.	0.6	11
12330	Polymorphism of Walleye Pollock <i>Gadus chalcogrammus</i> Mitochondrial DNA Control Region in the Asiatic Part of the Range and its Phylogeographic History. <i>Journal of Ichthyology</i> , 2022, 62, 266-279.	0.2	4
12331	Does <i>Opisthorchis viverrini</i> circulate between humans and domestic cats in an endemic area in Thailand?. <i>Parasitology</i> , 2022, 149, 1334-1338.	0.7	6
12332	<i>Fortunella venosa</i> (Champ. ex Benth.) C. C. Huang and <i>F. hindsii</i> (Champ. ex Benth.) Swingle as Independent Species: Evidence From Morphology and Molecular Systematics and Taxonomic Revision of <i>Fortunella</i> (Rutaceae). <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	4
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12335	Extensive Sympatry and Frequent Hybridization of Ecologically Divergent Aquatic Plants on the Qinghai-Tibetan Plateau. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	2
12336	The transcription factor <i>bZIP68</i> negatively regulates cold tolerance in maize. <i>Plant Cell</i> , 2022, 34, 2833-2851.	3.1	42
12337	Multiomics analysis identifies a <i>CYP9K1</i> haplotype conferring pyrethroid resistance in the malaria vector <i>Anopheles funestus</i> in East Africa. <i>Molecular Ecology</i> , 2022, 31, 3642-3657.	2.0	12
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12341	On the trail of medieval wolves: ancient DNA, CT-based analyses and palaeopathology of a 1000-year-old wolf cranium from the Po Valley (northern Italy). <i>Historical Biology</i> , 2023, 35, 976-987.	0.7	0
12342	Genome-Wide Characterization of the Methyl CpG Binding Domain-Containing Proteins in Watermelon and Functional Analysis of Their Roles in Disease Resistance Through Ectopic Overexpression in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	2
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12345	Genetic diversity and demographic history of the Old World Bollworm, <i>Helicoverpa armigera</i> (Hubner) (Lepidoptera: Noctuidae), in Ethiopia inferred from mitochondrial gene sequences. <i>Ecology and Evolution</i> , 2022, 12, e8907.	0.8	2
12346	Topographic Complexity Facilitates Persistence Compared to Signals of Contraction and Expansion in the Adjacent Subdued Landscape. <i>Frontiers in Conservation Science</i> , 2022, 3, .	0.9	2
12347	Taxonomic delimitation and molecular identification of clusters within the species <i>Zanthoxylum nitidum</i> (Rutaceae) in China. <i>PhytoKeys</i> , 0, 196, 1-20.	0.4	4
12348	Genetic insights into an Apennine population of the Italian red deer. <i>Mammal Research</i> , 2022, 67, 399-406.	0.6	2
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12350	Genome-Wide Identification and Evolution Analysis of the Gibberellin Oxidase Gene Family in Six Gramineae Crops. <i>Genes</i> , 2022, 13, 863.	1.0	9
12351	Molecular confirmation of the hybrid origin of <i>Sparganium longifolium</i> (Typhaceae). <i>Scientific Reports</i> , 2022, 12, 7279.	1.6	2
12352	Morphological and Genetic Divergence in a Gill Monogenean Parasitizing Distant Cichlid Lineages of Lake Tanganyika: <i>Cichlidogyrus nshomboi</i> (Monogenea: Dactylogyridae) from Representatives of Boulengerochromini and Perissodini. <i>Evolutionary Biology</i> , 2022, 49, 221-238.	0.5	5
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12354	The curious case of Charles Darwin's frog, <i>Rana charlesdarwini</i> Das, 1998: Phylogenetic position and generic placement, with taxonomic insights on other minervaryan frogs (Dicroglossidae: Minervarya) in the Andaman and Nicobar Archipelago. <i>Vertebrate Zoology</i> , 0, 72, 169-199.	2.0	1
12355	Fifteen complete chloroplast genomes of <i>Trapa</i> species (Trapaceae): insight into genome structure, comparative analysis and phylogenetic relationships. <i>BMC Plant Biology</i> , 2022, 22, 230.	1.6	11
12356	Mitochondrial composition of and diffusion limiting factors of three social wasp genera <i>Polistes</i> , <i>Ropalidia</i> , and <i>parapolybia</i> (Hymenoptera: Vespidae). <i>Bmc Ecology and Evolution</i> , 2022, 22, 63.	0.7	2
12357	Assessing the genetic consequences of habitat fragmentation on the federally threatened cheat mountain salamander (<i>Plethodon nettingi</i>): a comparative, multi-locus approach. <i>Conservation Genetics</i> , 0, , 1.	0.8	1

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12362	Gene Pool Homogeneity of Western and Eastern Populations of the White-Naped Crane <i>Antigone vipio</i> in Different Flyways. <i>Russian Journal of Genetics</i> , 2022, 58, 566-575.	0.2	4
12363	Species limits and introgression in <i>Pimelodus</i> from the Magdalena-Cauca River basin. <i>Molecular Phylogenetics and Evolution</i> , 2022, 173, 107517.	1.2	3
12364	Phylogeography and evolutionary history of the Panamic Clingfish <i>Gobiesox adustus</i> in the Tropical Eastern Pacific. <i>Molecular Phylogenetics and Evolution</i> , 2022, 173, 107496.	1.2	3
12365	Regional philopatry of scalloped hammerhead sharks (<i>Sphyrna lewini</i>) to nursery areas in the Mexican Pacific. <i>Hydrobiologia</i> , 2022, 849, 3083-3099.	1.0	3
12366	The phylogeographical pattern of the Amur minnow <i>Rhynchocypris lagowskii</i> (Cypriniformes: Cyprinidae). <i>Journal of Herpetology</i> , 2022, 56, 107-115.	0.8	2
12367	The complete chloroplast genome of <i>Persicaria perfoliata</i> and comparative analysis with Four Medicinal Plants of Polygonaceae. <i>Genome</i> , 2022, , .	0.9	0
12368	Exploring phylogenetic relationships within the subgenera of <i>Bambusa</i> based on DNA barcodes and morphological characteristics. <i>Scientific Reports</i> , 2022, 12, 8018.	1.6	3
12369	Invasive Bullfrogs Maintain MHC Polymorphism Including Alleles Associated with Chytrid Fungal Infection. <i>Integrative and Comparative Biology</i> , 2022, 62, 262-274.	0.9	4
12370	Parthenogenesis doubles the rate of amino acid substitution in whiptail mitochondria. <i>Evolution; International Journal of Organic Evolution</i> , 2022, , .	1.1	2
12371	Phylogeny, Evolution, and Transmission Dynamics of Canine and Feline Coronaviruses: A Retro-Pro prospective Study. <i>Frontiers in Microbiology</i> , 2022, 13, 850516.	1.5	1
12372	Chloroplast genomes and nuclear sequences reveal the interspecific relationships of <i>Crataegus bretschnideri</i> C. K. Schneid. and related species in China. <i>Tree Genetics and Genomes</i> , 2022, 18, .	0.6	1
12373	Natural variation MeMYB108 associated with tolerance to stress-induced leaf abscission linked to enhanced protection against reactive oxygen species in cassava. <i>Plant Cell Reports</i> , 2022, 41, 1573-1587.	2.8	4
12374	Divided by the range: evidence for geographic isolation of the highly mobile Emu (<i>Dromaius</i>). <i>Journal of Herpetology</i> , 2022, 56, 107-115.	0.2	1
12375	A population genetic analysis of the Critically Endangered Madagascar big-headed turtle, <i>Erymnochelys madagascariensis</i> across captive and wild populations. <i>Scientific Reports</i> , 2022, 12, .	1.6	1

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12376	Contrasting Patterns of Genetic Diversity and Divergence Between Landlocked and Migratory Populations of Fish <i>Galaxias maculatus</i> , Evaluated Through Mitochondrial DNA Sequencing and Nuclear DNA Microsatellites. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	4
12377	Evolutionary Conservation Genomics Reveals Recent Speciation and Local Adaptation in Threatened Takins. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	7
12379	Unveiling the <i>Mycodrosophila projectans</i> (Diptera, Drosophilidae) species complex: Insights into the evolution of three Neotropical cryptic and syntopic species. <i>PLoS ONE</i> , 2022, 17, e0268657.	1.1	1
12380	Assessing evolutionary history and species boundaries in a polymorphic tropical lizard, the <i>Aspidoscelis lineattissimus</i> species complex (Squamata, Teiidae). <i>Zoologica Scripta</i> , 2022, 51, 533-549.	0.7	0
12381	Phylogenetic, Microbiome, and Diet Characterisation of Wall Lizards in the Columbretes Archipelago (Spain): Clues for Their Conservation. <i>Diversity</i> , 2022, 14, 408.	0.7	1
12382	DNA barcoding and species delimitation of the genus <i>Oxynoemacheilus</i> (Teleostei: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.7	5
12383	DNA barcoding reveals deep divergent molecular units in <i>Pomatomus saltatrix</i> (Perciformes: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Biological Association of the United Kingdom, 0, , 1-13.	0.4	2
12384	Molecular Phylogeography and Intraspecific Divergences in Siberian Wildrye (<i>Elymus sibiricus</i> L.) Wild Populations in China, Inferred From Chloroplast DNA Sequence and cpSSR Markers. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	9
12385	Nucleotide sequence types (ntSTs) of <i>Anaplasma marginale</i> in cattle in Nigeria based on the major surface protein 5 (msp5) gene. <i>Acta Tropica</i> , 2022, 233, 106544.	0.9	2
12386	Pan-European phylogeography of the European roe deer (<i>Capreolus capreolus</i>). <i>Ecology and Evolution</i> , 2022, 12, .	0.8	5
12387	Comprehensive analysis of complete chloroplast genome and phylogenetic aspects of ten <i>Ficus</i> species. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	12
12388	An integrative taxonomic revision and redefinition of <i>Gephyromantis</i> (<i>Laurentomantis</i>) <i>malagasius</i> based on archival DNA analysis reveals four new mantellid frog species from Madagascar. <i>Vertebrate Zoology</i> , 0, 72, 271-309.	2.0	2
12389	Genetic Structure and Demographic History of Yellow Grouper (<i>Epinephelus awoara</i>) from the Coast of Southeastern Mainland China, Inferred by Mitochondrial, Nuclear and Microsatellite DNA Markers. <i>Diversity</i> , 2022, 14, 439.	0.7	1
12390	Beyond Domestic Cats: Environmental Detection of <i>Sporothrix brasiliensis</i> DNA in a Hyperendemic Area of Sporotrichosis in Rio de Janeiro State, Brazil. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 604.	1.5	9
12391	Mitochondrial Genomes Provide New Phylogenetic and Evolutionary Insights into Psilidae (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.0	4
12392	Recombination and darwinian selection as drivers of genetic diversity and evolution of sweet potato leaf curl viruses in Tanzania. <i>Physiological and Molecular Plant Pathology</i> , 2022, 120, 101853.	1.3	4
12393	The chloroplast genomes of <i>Sanicula</i> (Apiaceae): plastome structure, comparative analyses and phylogenetic relationships. <i>Nordic Journal of Botany</i> , 2022, 2022, .	0.2	2
12394	Stepped Geomorphology Shaped the Phylogeographic Structure of a Widespread Tree Species (<i>Toxicodendron verniciflum</i> , Anacardiaceae) in East Asia. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	3

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12395	Genetic diversity of Banat Naked Neck, indigenous chicken breed from Serbia, inferred from mitochondrial DNA D-loop sequence and microsatellite markers. <i>Animal Biotechnology</i> , 0, , 1-10.	0.7	0
12396	Genetic structure of <i>Sclerotinia sclerotiorum</i> populations from sunflower and cabbage in West Azarbaijan province of Iran. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
12397	Genetic Diversity and Phylogenetic Relatedness of <i>Plasmodium ovale curtisi</i> and <i>Plasmodium ovale wallikeri</i> in sub-Saharan Africa. <i>Microorganisms</i> , 2022, 10, 1147.	1.6	1
12398	Morphological and genetic variation of <i>Melolontha</i> spp. from pine stands with different composition and proportion of admixed tree species. <i>European Journal of Forest Research</i> , 2022, 141, 617-628.	1.1	3
12399	First description of the mitogenome and phylogeny: <i>Aedes vexans</i> and <i>Ochlerotatus caspius</i> of the Tribe Aedini (Diptera: Culicidae). <i>Infection, Genetics and Evolution</i> , 2022, 102, 105311.	1.0	3
12411	Diversity of arbuscular mycorrhizal fungi in the rhizosphere of saffron (<i>Crocus sativus</i>) plants along with age of plantation in Taliouine region in Morocco. <i>Acta Biologica Szegediensis</i> , 2022, 2, 199-209.	0.7	1
12412	Haemosporidian parasite diversity and prevalence in the songbird genus <i>Junco</i> across Central and North America. <i>Auk</i> , 2022, 139, .	0.7	3
12413	The c. <i>612A</i> >G mutation of <i>MC4R</i> affects constitutive activity and signaling in domestic goats. <i>Animal Genetics</i> , 0, , .	0.6	0
12414	Molecular Structure and Phylogenetic Analyses of the Complete Chloroplast Genomes of Three Medicinal Plants <i>Conioselinum vaginatum</i> , <i>Ligusticum sinense</i> , and <i>Ligusticum jeholense</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
12415	Cold-adaptive evolution at the reproductive stage in <i>Geng japonica</i> subspecies reveals the role of <i>OsMAPK3</i> and <i>OsLEA9</i> . <i>Plant Journal</i> , 2022, 111, 1032-1051.	2.8	13
12416	An integrative redescription of <i>Echiniscus quadrispinosus quadrispinosus</i> Richters, 1902 (Heterotardigrada, Echiniscidae) from the terra typica in Taunus Mountain Range (Europe; Germany). <i>European Journal of Taxonomy</i> , 0, 823, .	0.6	1
12417	First Comprehensive Analysis of Both Mitochondrial Characteristics and Mitogenome-Based Phylogenetics in the Subfamily Eumeninae (Hymenoptera: Vespidae). <i>Insects</i> , 2022, 13, 529.	1.0	9
12418	Can pollinators track plant expansions? A case study on the genetic structure of a host-dependent pollinating wasp. <i>Ecological Entomology</i> , 2022, 47, 895-905.	1.1	1
12419	Distribution pattern and driving factors of genetic diversity of passerine birds in the Mountains of Southwest China. <i>Avian Research</i> , 2022, 13, 100043.	0.5	2
12420	Geographical distribution and genetic diversity of <i>Plasmodium vivax</i> reticulocyte binding protein 1a correlates with patient antigenicity. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010492.	1.3	2
12421	Plastome characteristics and species identification of Chinese medicinal wintergreens (<i>Gaultheria</i>). <i>Tj ETQq1 1 0.784314 rgBT₄/Overlock</i>	1.8	4
12422	Interannual fluctuations in connectivity among crab populations (<i>Liocarcinus depurator</i>) along the Atlantic-Mediterranean transition. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
12423	Population genetic structure and phenotypic diversity of <i>Aspidodera railletii</i> (Nematoda: <i>Tj ETQq1 1 0.784314 rgBT₄/Overlock 10 Tf 50</i>) Parasites and Vectors, 2022, 15, .	1.0	2

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12424	Exploring the SiCCT Gene Family and Its Role in Heading Date in Foxtail Millet. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
12425	Sequence Characteristics and Phylogenetic Analysis of the <i>Artemisia argyi</i> Chloroplast Genome. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	8
12426	İyüDescription of a new <i>Kurixalus</i> species (Rhacophoridae, Anura) and a northwards range extension of the genus. <i>ZooKeys</i> , 0, 1108, 15-49.	0.5	3
12427	Characterization of the complete mitogenome of the endangered freshwater fish <i>Gobiobotia naktongensis</i> from the Geum River in South Korea: evidence of stream connection with the Paleo-Huanghe. <i>Genes and Genomics</i> , 0, , .	0.5	1
12428	The complete chloroplast genome of critically endangered <i>Chimonobambusa hirtinoda</i> (Poaceae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.6	3
12429	Hidden in plain sight: novel molecular data reveal unexpected genetic diversity among paramphistome parasites (Digenea: Paramphistomoidea) of European water frogs. <i>Parasitology</i> , 2022, 149, 1425-1438.	0.7	4
12430	Comparison of <i>SWEET</i> gene family between maize and foxtail millet through genomic, transcriptomic, and proteomic analyses. <i>Plant Genome</i> , 2022, 15, .	1.6	10
12431	A Non-Canonical MITE in the <i>WOX11</i> Promoter Is Associated with Robust Crown Root development in Rice. <i>Plant and Cell Physiology</i> , 2022, 63, 1052-1062.	1.5	1
12432	Mitochondrial Genome of <i>Strophopteryx fasciata</i> (Plecoptera: Taeniopterygidae), with a Phylogenetic Analysis of Nemouroidea. <i>Genes</i> , 2022, 13, 1116.	1.0	3
12433	Translocation of mitochondrial DNA into the nuclear genome blurs phylogeographic and conservation genetic studies in seabirds. <i>Royal Society Open Science</i> , 2022, 9, .	1.1	8
12434	Invasive <i>Coptodon</i> (Perciformes: Cichlidae) in southwest Turkey: Species identification using sequence data. <i>Su AçırÄ¼nleri Dergisi</i> , 2022, 39, 135-144.	0.1	0
12435	Comparative Analysis of the Complete Chloroplast Genomes of Eight <i>Ficus</i> Species and Insights into the Phylogenetic Relationships of <i>Ficus</i> . <i>Life</i> , 2022, 12, 848.	1.1	2
12436	Genomic analyses show extremely perilous conservation status of African and Asiatic cheetahs (<i>Acinonyx jubatus</i>). <i>Molecular Ecology</i> , 2022, 31, 4208-4223.	2.0	21
12437	Spatial diversity of MHC class II DRB exon2 sequences in North African cape hares (<i>Lepus capensis</i>): positive selection and climatic adaptation signals. <i>Mammalian Biology</i> , 0, , .	0.8	0
12438	Phylogenetic Implication of Large Intergenic Spacers: Insights from a Mitogenomic Comparison of <i>Prosopocoilus</i> Stag Beetles (Coleoptera: Lucanidae). <i>Animals</i> , 2022, 12, 1595.	1.0	5
12439	Contrasting patterns of genetic diversity and lack of population structure in the lesser spotted eagle <i>Clanga pomarina</i> (Aves: Accipitriformes) across its breeding range. <i>Biological Journal of the Linnean Society</i> , 0, , .	0.7	1
12440	High-Throughput Sequencing Discloses the Cucumber Mosaic Virus (CMV) Diversity in Slovakia and Reveals New Hosts of CMV from the Papaveraceae Family. <i>Plants</i> , 2022, 11, 1665.	1.6	5
12441	First Report of Complete Mitochondrial Genome in the Tribes Coomaniellini and Dicercini (Coleoptera: Buprestidae) and Phylogenetic Implications. <i>Genes</i> , 2022, 13, 1074.	1.0	8

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12442	Mitochondrial Lineage Diversity and Phylogeography of <i>Daphnia</i> (Daphnia) (Crustacea: Cladocera) in North-East Russia. <i>Water</i> (Switzerland), 2022, 14, 1946.	1.2	1
12443	Systematic Analysis of NB-ARC Gene Family in Rice and Functional Characterization of GNP12. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
12444	Isolation by distance and past climate resistance shaped the distribution of genealogical lineages of a neotropical lizard. <i>Systematics and Biodiversity</i> , 2022, 20, 1-19.	0.5	0
12445	Genetic diversity of <i>Plasmodium vivax</i> reticulocyte binding protein 2b in global parasite populations. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	2
12446	Comparative Analysis and Phylogenetic Study of the Chloroplast Genome Sequences of Two Korean Endemic <i>Primula</i> Varieties. <i>Diversity</i> , 2022, 14, 458.	0.7	0
12447	Genetic diversity of the two-spotted stink bug <i>Bathycorixa distincta</i> (Pentatomidae) associated with macadamia orchards in South Africa. <i>PLoS ONE</i> , 2022, 17, e0269373.	1.1	4
12448	Comparative mitogenomics elucidates the population genetic structure of <i>Amblyomma testudinarium</i> in Japan and a closely related <i>Amblyomma</i> species in Myanmar. <i>Evolutionary Applications</i> , 2022, 15, 1062-1078.	1.5	8
12449	Comparative Chloroplast Genomics of Seven Endangered <i>Cypripedium</i> Species and Phylogenetic Relationships of Orchidaceae. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
12450	Unraveling the Basis of Neonicotinoid Resistance in Whitefly Species Complex: Role of Endosymbiotic Bacteria and Insecticide Resistance Genes. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	8
12451	Genetic divergence and demography of pudu deer (<i>Pudu puda</i>) in five provinces of southern Chile, analyzed through latitudinal and longitudinal ranges. <i>Neotropical Biology and Conservation</i> , 2022, 17, 117-142.	0.4	0
12452	Network and Evolutionary Analysis Reveals Candidate Genes of Membrane Trafficking Involved in Maize Seed Development and Immune Response. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
12453	Korean Leopard Cat (<i>Prionailurus bengalensis</i>) population with low genetic diversity is distinct from Southeast Asian populations. <i>Global Ecology and Conservation</i> , 2022, 38, e02188.	1.0	1
12454	Comparative plastome analyses and genomic resource development in wild rice (<i>Zizania</i> spp., Poaceae) using genome skimming data. <i>Industrial Crops and Products</i> , 2022, 186, 115244.	2.5	12
12455	Temporal genetic structure of a stock of <i>Prochilodus lineatus</i> (Characiformes: Prochilodontidae) in the Mogi-Guaçu River ecosystem, São Paulo, Brazil. <i>Neotropical Ichthyology</i> , 2022, 20, .	0.5	1
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12457	Genetic polymorphism in the mitochondrial D-loop of Oriental White-backed Vultures (<i>Gyps</i>) Tj ETQq1 1 0.784314 rgBT / Overlock	0.1	0
12458	Identification of confiscated pangolin for conservation purposes through molecular approach. <i>Journal of Threatened Taxa</i> , 2022, 14, 21127-21139.	0.1	1
12459	Phylogeography of Pholidopterini: Revising molecular clock calibration by Mid-Aegean Trench. <i>Insect Systematics and Evolution</i> , 2022, 53, 515-535.	0.2	4

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12461	Phylogeography of a Typical Forest Heliothermic Lizard Reveals the Combined Influence of Rivers and Climate Dynamics on Diversification in Eastern Amazonia. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	0
12462	Phylogeography and Population Genetics Analyses Reveal Evolutionary History of the Desert Resource Plant <i>Lycium ruthenicum</i> (Solanaceae). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
12463	Size Doesn't Matter: Integrative Taxonomy Shows <i>Crepidula adunca</i> and <i>Crepidula norrisiarum</i> Have Overlapping Shell Sizes and Broadly Concordant Distributions. <i>Biological Bulletin</i> , 2022, 242, 222-237.	0.7	0
12464	Comparative chloroplast genomes and phylogenetic analyses of <i>Pinellia</i> . <i>Molecular Biology Reports</i> , 2022, 49, 7873-7885.	1.0	3
12465	Assessment of Genetic Diversity of the Salangid, <i>Neosalanx taihuensis</i> , Based on the Mitochondrial COI Gene in Different Chinese River Basins. <i>Biology</i> , 2022, 11, 968.	1.3	3
12466	Genetic Diversity and Population Genetic Analysis of <i>Plasmodium falciparum</i> Thrombospondin Related Anonymous Protein (TRAP) in Clinical Samples from Saudi Arabia. <i>Genes</i> , 2022, 13, 1149.	1.0	0
12467	Population genetic structure and evolutionary genetics of <i>Anopheles sinensis</i> based on knockdown resistance (<i>kdr</i>) mutations and mtDNA-COII gene in China–Laos, Thailand–Laos, and Cambodia–Laos borders. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	5
12468	Diversity and Molecular Barcoding of Stink Bugs (Hemiptera: Pentatomidae) Associated with <i>Macadamia</i> in South Africa. <i>Insects</i> , 2022, 13, 601.	1.0	2
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12470	Genetic Diversity and Gene Flow Observed in Two Cereal Aphid (Hemiptera: Aphididae) Species and Populations in the Chinese Corn Belt Region. <i>Journal of Entomological Science</i> , 2022, 57, 363-379.	0.2	0
12471	<i>Liobagrus brevispina</i> , a new species of torrent catfish (Siluriformes: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.7	1
12472	Phylogenomic insight into dysploidy, speciation, and plastome evolution of a small Mediterranean genus <i>Reichardia</i> (Cichorieae; Asteraceae). <i>Scientific Reports</i> , 2022, 12, .	1.6	0
12473	Seven snail species hidden in one: Biogeographic diversity in an apparently widespread periwinkle in the Southern Ocean. <i>Journal of Biogeography</i> , 2022, 49, 1521-1534.	1.4	9
12474	Genome-Wide Classification and Evolutionary Analysis Reveal Diverged Patterns of Chalcone Isomerase in Plants. <i>Biomolecules</i> , 2022, 12, 961.	1.8	3
12475	Three Mitochondrial Markers Reveal Genetic Diversity and Structure of Rock Carp (<i>Procypris rabaudi</i>) Endemic to the Upper Yangtze: Implications for Pre-release Genetic Assessment. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1
12476	Identifying cryptic species of <i>Planococcus</i> infesting vineyards to improve control efforts. <i>Journal of Pest Science</i> , 0, , .	1.9	0
12477	Genetic diversity of the endangered Mongolian saiga antelope <i>Saiga tatarica mongolic</i> a (Artiodactyla: Bovidae) provides insights into conservation. <i>Biological Journal of the Linnean Society</i> , 2022, 137, 100-111.	0.7	4

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12479	OsNPF3.1, a member of the NRT1/PTR family, increases nitrogen use efficiency and biomass production in rice. <i>Crop Journal</i> , 2023, 11, 108-118.	2.3	7
12480	Limited phylogeographic and genetic connectivity in <i>Acacia</i> species of low stature in an arid landscape. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	4
12481	Genetic origin and differentiation of ten paddy field-farmed <i>Cyprinus carpio</i> strains in China. <i>Aquaculture</i> , 2022, 561, 738573.	1.7	0
12482	Molecular survey of <i>Cryptoplax japonica</i> (Polyplacophora: Cryptoplacidae) reveals cryptic lineages in the northwestern Pacific. <i>Journal of Molluscan Studies</i> , 2022, 88, .	0.4	0
12483	Phylogeography of walnut pest (Lepidoptera: Gelechioidea) reveals comprehensive influence of geographic barriers and human activities. <i>Journal of Asia-Pacific Entomology</i> , 2022, , 101962.	0.4	1
12484	The Palearctic blackfly <i>Simulium equinum</i> (Diptera: Simuliidae) as a biting pest of captive nyala antelopes (<i>Tragelaphus angasii</i>). <i>Zoo Biology</i> , 0, , .	0.5	2
12485	Mitochondrial Genomes of two <i>Lycosa</i> spiders (Araneae, Lycosidae): Genome Description and Phylogenetic Implications. <i>Diversity</i> , 2022, 14, 538.	0.7	6
12486	Comparative Genomic and Phylogenetic Analysis of Chloroplast Genomes of Hawthorn (<i>Crataegus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	2
12487	Genetic structure, population diversity and ancestry of Nicobari fowl based on mtDNA complete D-loop sequences. <i>Journal of Genetics</i> , 2022, 101, .	0.4	0
12488	Habitat connectivity, gene flow, and population genetic structure in a Neotropical understory insectivore, the Rufous-and-white Wren. <i>Auk</i> , 0, , .	0.7	1
12489	Family-level phylogeny of infraorder Systellognatha (Insecta: Plecoptera) inferred from mitochondrial genomes. <i>Zoologica Scripta</i> , 2022, 51, 589-602.	0.7	2
12490	Population Genetic Differentiation and Structure of <i>Maruca vitrata</i> (Lepidoptera: Crambidae) in India. <i>Diversity</i> , 2022, 14, 546.	0.7	2
12491	Phylogenetics and evolution of wheat streak mosaic virus: Its global origin and the source of the Australian epidemic. <i>Plant Pathology</i> , 2022, 71, 1660-1673.	1.2	5
12492	A tale about vipers' tails: phylogeography of black-tailed rattlesnakes. <i>Herpetozoa</i> , 0, 35, 141-153.	1.0	1
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12494	Genetic Variation and Population Structure of the Old World Bollworm <i>Helicoverpa armigera</i> (Hübner, 1808) (Lepidoptera: Noctuidae) in Ethiopia. <i>Environmental Entomology</i> , 0, , .	0.7	0
12495	Vast Gene Flow among the Spanish Populations of the Pest <i>Bactrocera oleae</i> (Diptera, Tephritidae), Phylogeography of a Metapopulation to Be Controlled and Its Mediterranean Genetic Context. <i>Insects</i> , 2022, 13, 642.	1.0	2

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12497	Anthropogenic influences on genetic diversity and differentiation of the clearhead icefish (<i>Protosalanx hyalocranium</i>), as revealed by mitochondrial and microsatellite DNA markers. <i>Regional Studies in Marine Science</i> , 2022, 55, 102547.	0.4	1
12498	Species identification of two <i>Loliginidae</i> cryptic species in China Seas with morphological and molecular methods. <i>Regional Studies in Marine Science</i> , 2022, 55, 102549.	0.4	0
12499	Mitochondrial DNA cytochrome-b assisted DNA barcoding for the exploration of spatio-genetic variation among the population of <i>Labeo rohita</i> from different parts of India. <i>Ecological Genetics and Genomics</i> , 2022, 24, 100131.	0.3	0
12500	Ceriodaphnia (Cladocera: Daphniidae) in China: Lineage diversity, phylogeography and possible interspecific hybridization. <i>Molecular Phylogenetics and Evolution</i> , 2022, 175, 107586.	1.2	5
12501	Comparative Analysis of the Complete Chloroplast Genomes in <i>Allium</i> Section <i>Bromatorrhiza</i> Species (<i>Amaryllidaceae</i>): Phylogenetic Relationship and Adaptive Evolution. <i>Genes</i> , 2022, 13, 1279.	1.0	5
12502	Genetic diversity and population dynamic of <i>Ziziphus jujuba</i> var. <i>spinosa</i> (Bunge) Hu ex H. F. Chow in Central China. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	2
12503	Molecular characterization of <i>Echinococcus granulosus sensu lato</i> genotypes in dromedary camels from extreme Sahara of Algeria based on analysis of <i>nad2</i> and <i>nad5</i> genetic markers. <i>Acta Tropica</i> , 2022, 234, 106616.	0.9	3
12504	Marbled crayfish <i>Procambarus virginalis</i> invades a nature reserve: how to stop further introductions?. , 2022, 89, 888-901.		3
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12506	Consideration of genetic variation and evolutionary history in future conservation of Indian one-horned rhinoceros (<i>Rhinoceros unicornis</i>). <i>Bmc Ecology and Evolution</i> , 2022, 22, .	0.7	0
12507	Phylogeography of <i>Kisaura</i> Ross (Trichoptera: Philopotamidae) of the Japanese Archipelago and the character displacement evolution observed in a secondary contact area between genetically differentiated intra-specific lineages. <i>Zoological Journal of the Linnean Society</i> , 0, , .	1.0	1
12508	Molecular Identification of the G-Protein Genes and Their Expression Profiles in Response to Nitrogen Deprivation in <i>Brassica napus</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 8151.	1.8	5
12509	Complete mitogenomes of Turkish tree squirrels, <i>Sciurus anomalus</i> and <i>S. vulgaris</i> , (<i>Sciuridae</i>): Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	1.0	2
12510	DNA Barcoding and Species Delimitation for Dogfish Sharks Belonging to the <i>Squalus</i> Genus (<i>Squaliformes: Squalidae</i>). <i>Diversity</i> , 2022, 14, 544.	0.7	5
12511	A Study about the Piggery Sector Sustainability, Pig Breed Diversity and Its Ecological Implications in Urban Districts of Uttarakhand. , 0, , .		0
12512	Genetic Diversity and Identification of MC1R SNPs Association with Colors in Iraqi Local Ducks. <i>IOP Conference Series: Earth and Environmental Science</i> , 2022, 1060, 012066.	0.2	1
12513	Genomic analysis of arginine vasopressin gene in riverine buffalo reveals its potential association with silent estrus behavior. <i>Molecular Biology Reports</i> , 0, , .	1.0	1

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12514	Introgression at the emerging secondary contact zone of magpie <i>Pica pica</i> subspecies (Aves: Corvidae): integrating data on nuclear and mitochondrial markers, vocalizations, and field observations. <i>Organisms Diversity and Evolution</i> , 0, , .	0.7	1
12515	Complete chloroplast genomes and phylogeny in three <i>Euterpe</i> palms (<i>E. edulis</i> , <i>E. oleracea</i> and <i>E.</i>) <i>Tj ETQq1 1 0.784314 rgBT₁ /Overlock</i>	1.1	2
12516	Genetic diversity of medically important scorpions of the genus <i>Centruroides</i> (Buthidae) from Panama including two endemic species. <i>Journal of Genetics</i> , 2022, 101, .	0.4	0
12517	Contrasting mtDNA and microsatellite data of great reed warbler <i>Acrocephalus arundinaceus</i> breeding populations on a small geographic scale. <i>Biologia Futura</i> , 0, , .	0.6	0
12518	Phylogeographic Structuring of the Kuroshio-Type Prawn <i>Macrobrachium japonicum</i> (Decapoda:) <i>Tj ETQq0 0 0 rgBT₁ /Overlock 10 Tf 50 5</i>	0.7	2
12519	Prevalence of Mutations in the <i>Pfdhfr</i> , <i>Pfdhps</i> , and <i>Pfmdr1</i> Genes of Malarial Parasites Isolated from Symptomatic Patients in Dogondoutchi, Niger. <i>Tropical Medicine and Infectious Disease</i> , 2022, 7, 155.	0.9	4
12520	Guiding marine protected area network design with comparative phylogeography and population genomics: An exemplary case from the Southern Ocean. <i>Diversity and Distributions</i> , 2022, 28, 1891-1907.	1.9	1
12521	Phylogeography supports lineage divergence for an endemic rattlesnake (<i>Crotalus ravus</i>) of the Neotropical montane forest in the Trans-Mexican Volcanic Belt. <i>Biological Journal of the Linnean Society</i> , 2022, 137, 496-512.	0.7	3
12522	Diversification rates in Tardigrada indicate a decreasing tempo of lineage splitting regardless of reproductive mode. <i>Organisms Diversity and Evolution</i> , 0, , .	0.7	1
12523	Community Characteristics and Genetic Diversity of Macrobenthos in Haima Cold Seep. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
12524	Extensive sharing of chloroplast haplotypes among East Asian <i>Cerris</i> oaks: The imprints of shared ancestral polymorphism and introgression. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	7
12525	Abundance of Pteroviruses within Tasmanian Pea Crops and Surrounding Weeds, and the Genetic Diversity of TuYV Isolates Found. <i>Viruses</i> , 2022, 14, 1690.	1.5	4
12526	First Report of Two <i>Jaculus</i> Rodents as Potential Reservoir Hosts of <i>Leishmania</i> Parasites in Tunisia. <i>Microorganisms</i> , 2022, 10, 1502.	1.6	1
12527	Multiplex Polymerase Chain Reaction Method with Species-specific Primers for Differentiation of Two Closely Related Fish Species, <i>Beryx splendens</i> and <i>B. mollis</i> ; (Actinopterygii: Beryciformes). <i>Japan Agricultural Research Quarterly</i> , 2022, 56, 283-294.	0.1	0
12528	Population genetics and genetic variation of <i>Ctenocephalides felis</i> and <i>Pulex irritans</i> in China by analysis of nuclear and mitochondrial genes. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	2
12529	Türkiye <i>Podarcis siculus siculus</i> (Rafinesque-Schmaltz, 1810) Populasyonları ve Kenini Ortaya Çıkarmak İçin Türleri Belirlenmesi. <i>Uluslararası Tarım Ve Yaban Hayat Bilimleri Dergisi</i> 2022, 8, 1 340-348.		1
12530	Genetic Diversity and Population Structure of <i>Spirobolus bungii</i> as Revealed by Mitochondrial DNA Sequences. <i>Insects</i> , 2022, 13, 729.	1.0	2
12531	The encounter of distinct <i>Morimus asper</i> (Coleoptera: Cerambycidae) phylogeographic lineages on the Balkan Peninsula: conservation implications. <i>Journal of Insect Conservation</i> , 2022, 26, 773-792.	0.8	1

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12533	Temporal genetic variation of the Chinese longsnout catfish (<i>Leiocassis longirostris</i>) in the upper Yangtze River with resource decline. <i>Environmental Biology of Fishes</i> , 2022, 105, 1139-1151.	0.4	1
12534	Molecular Characterization of Animal <i>Fasciola</i> Spp. Isolates from Lorestan Province, Western Iran. <i>Iranian Journal of Public Health</i> , 0, , .	0.3	1
12535	Molecular diversity, haplotype distribution and genetic variation flow of <i>Bipolaris sorokiniana</i> fungus causing spot blotch disease in different wheat-growing zones. <i>Journal of Applied Genetics</i> , 2022, 63, 793-803.	1.0	4
12536	Phylogeography of <i>Lanius senator</i> in its breeding range: conflicts between alpha taxonomy, subspecies distribution and genetics. , 2022, 89, 941-956.		1
12537	Nucleotide polymorphisms of the maize <i>ZmFWL7</i> gene and their association with ear-related traits. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
12538	A widespread commensal loses its identity: suggested taxonomic revision for <i>Indotyphlops braminus</i> (Scoleophidia: Typhlopidae) based on molecular data. <i>Organisms Diversity and Evolution</i> , 2023, 23, 169-183.	0.7	1
12539	Genetic diversity and population structure of Tongcheng pigs in China using whole-genome SNP chip. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	7
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12541	Dispersal Routes of <i>Cercospora zeina</i> Causing Maize Gray Leaf Spot in China. <i>Journal of Integrative Agriculture</i> , 2022, , .	1.7	0
12542	Demographic history and population genetic structure of <i>Anisakis pegreffii</i> in the cutlassfish <i>Trichiurus japonicus</i> along the coast of mainland China and Taiwan. <i>Parasitology Research</i> , 2022, 121, 2803-2816.	0.6	3
12543	Intraspecific hybridisation of an invasive lizard on Lord Howe Island. <i>Australian Journal of Zoology</i> , 2022, 69, 184-196.	0.6	0
12544	Genetic Diversity, Population Structure, and Conservation Units of <i>Castanopsis sclerophylla</i> (Fagaceae). <i>Forests</i> , 2022, 13, 1239.	0.9	1
12545	Genetic Diversity and Population Structure of Head Blight Disease Causing Fungus <i>Fusarium graminearum</i> in Northern Wheat Belt of India. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 820.	1.5	3
12546	Genome-wide identification, structural analysis and expression profiles of short internodes related sequence gene family in quinoa. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
12547	Comparative analysis of mitochondrial genomes among the family Peltoperlidae (Plecoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.1	1
12548	The role of ecological and geographical drivers of lineage diversification in the Squirrel cuckoo <i>Piaya cayana</i> in Mexico: a mitochondrial DNA perspective. <i>Journal of Ornithology</i> , 2023, 164, 37-53.	0.5	2
12549	Genetic differentiation in wild <i>Kappaphycus</i> Doty and <i>Eucheuma</i> J. Agardh (Solieriaceae, Rhodophyta) from East Malaysia reveals high inter- and intraspecific diversity with strong biogeographic signal. <i>Journal of Applied Phycology</i> , 2022, 34, 2719-2733.	1.5	3

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12550	New taxonomic framework for Arthrodermataceae: a comprehensive analysis based on their phylogenetic reconstruction, divergence time estimation, phylogenetic split network, and phylogeography. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 1319-1333.	0.7	4
12551	DNA Barcoding of Prunus Species Collection Conserved in the National Gene Bank of Egypt. <i>Molecular Biotechnology</i> , 0, , .	1.3	3
12552	Loliginid paralarvae from the Southeastern Gulf of Mexico: Abundance, distribution, and genetic structure. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
12554	Complete chloroplast genomes and comparative analyses of <i>Hippeastrum milady</i> [™] , <i>Hippeastrum albertii</i> and <i>Hippeastrum reticulatum</i> (Amaryllidaceae). <i>PLoS ONE</i> , 2022, 17, e0271335.	1.1	0
12555	Sequencing and comparative analysis of chloroplast genomes of three medicinal plants: <i>Gentiana manshurica</i> , <i>G. scabra</i> and <i>G. triflora</i> . <i>Physiology and Molecular Biology of Plants</i> , 0, , .	1.4	3
12556	Genome Organization and Comparative Evolutionary Mitochondriomics of Brown Planthopper, <i>Nilaparvata lugens</i> Biotype 4 Using Next Generation Sequencing (NGS). <i>Life</i> , 2022, 12, 1289.	1.1	0
12557	Genetic diversity and molecular evolution of sugarcane mosaic virus, comparing whole genome and coat protein sequence phylogenies. <i>Archives of Virology</i> , 2022, 167, 2239-2247.	0.9	3
12558	Plastome structure of 8 <i>Calanthe</i> s.l. species (Orchidaceae): comparative genomics, phylogenetic analysis. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	7
12559	Genetic diversity of DGAT1 gene linked to milk production in cattle populations of Ethiopia. <i>BMC Genomic Data</i> , 2022, 23, .	0.7	3
12560	A 50-year-old redescription: molecular and morphometric characterization of <i>Hepatozoon carinicauda</i> PessÃ'a and Cavalheiro, 1969 in the brown-banded water snake <i>Helicops angulatus</i> (Linnaeus, 1758). <i>Parasitology</i> , 2022, 149, 1468-1478.	0.7	1
12561	Sequence Polymorphisms in <i>Vibrio cholerae</i> HapR Affect Biofilm Formation under Aerobic and Anaerobic Conditions. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	3
12562	Genetic Structure of a Native Neotropical Fish Species: New Insights about a South American Bioindicator. <i>Archives of Environmental Contamination and Toxicology</i> , 0, , .	2.1	1
12563	Whole mitogenomes of Turkish white-toothed shrews, genus <i>Crociodura</i> (Eulipotyphla: Soricidae), with new insights into the phylogenetic positions of <i>Crociodura leucodon</i> and the <i>Crociodura suaveolens</i> group. <i>Organisms Diversity and Evolution</i> , 2023, 23, 221-241.	0.7	2
12564	Identification and genetic diversity analysis of <i>Rickettsia</i> in <i>Dermacentor nuttalli</i> within inner Mongolia, China. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	6
12565	Phylogenetic Analysis of Mitochondrial Genome of Tabanidae (Diptera: Tabanidae) Reveals the Present Status of Tabanidae Classification. <i>Insects</i> , 2022, 13, 695.	1.0	3
12566	First Report of <i>Candidatus Mycoplasma haematomacacae</i> [™] in Laboratory-Kept Rhesus Monkeys (<i>Macaca</i>) Tj ETQq1 1 0,784314 0,6	0.6	0
12567	Population genetic structure of <i>Neoschongastia gallinarum</i> in South China based on mitochondrial DNA markers. <i>Parasitology Research</i> , 2022, 121, 2793-2802.	0.6	5
12568	Evolution of the odorant-binding protein gene family in <i>Drosophila</i> . <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	4

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12571	Morphological Identification and Phylogenetic Analysis of Laelapin Mite Species (<i>Acari: Mesostigmata:</i>) Tj ETQq1 1 0,784314 6gBT /Over	0.5	0
12572	Unveiling new perspective of phylogeography, genetic diversity, and population dynamics of Southeast Asian and Pacific chickens. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
12573	Across the Gobi Desert: impact of landscape features on the biogeography and phylogeographically-structured release calls of the Mongolian Toad, <i>Strauchbufo raddei</i> in East Asia. <i>Evolutionary Ecology</i> , 2022, 36, 1007-1043.	0.5	1
12574	Genetic Diversity and Population Structure of <i>Cylindrocarpon</i> -like Fungi Infecting Ginseng Roots in Northeast China. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 814.	1.5	0
12575	DNA barcoding reveals long-term speciation processes in subspecies of the <i>Melipona</i> (<i>Michmelia</i>) <i>seminigra</i> complex (<i>Hymenoptera: Apidae</i>). <i>European Journal of Entomology</i> , 0, 119, 309-317.	1.2	0
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12580	Genetic variability of mass-selected and wild populations of Iwagaki oyster (<i>Crassostrea nippona</i>) revealed by microsatellites and mitochondrial COI sequences. <i>Aquaculture</i> , 2022, 561, 738737.	1.7	4
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12584	Comparative chloroplast genome analysis of <i>Ficus</i> (<i>Moraceae</i>): Insight into adaptive evolution and mutational hotspot regions. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	16
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12592	Sequence analysis of exon 1 and intron 1 of growth hormone gene in six chicken genotypes raised in tropical environment. <i>Biotechnology in Animal Husbandry</i> , 2022, 38, 41-54.	0.5	0
12593	The entire chloroplast genome sequence of <i>Asparagus cochinchinensis</i> and genetic comparison to <i>Asparagus</i> species. <i>Open Life Sciences</i> , 2022, 17, 893-906.	0.6	3
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12595	FARKLI SU KAYNAKLARINDAN Å°ZOLE EDÅ°LEN ACANTHAMOEBA TÅœRLERÅ°NÅ°N MOLEKÅœLER PREVALANSI VE GENOTÅ°PLERÅ°NÅ°N BELÅ°RLENMESÅ°. <i>Saglik Bilimleri Dergisi</i> , 0, , .	0.1	0
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12599	Historical persistence and isolation by distance of. <i>Australian Journal of Botany</i> , 2022, 70, 358-371.	0.3	1
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12606	Genomic analyses reveal natural selection on reproduction related genes between two closely related <i>Populus</i> (<i>Salicaceae</i>) species. <i>Journal of Systematics and Evolution</i> , 2023, 61, 852-867.	1.6	0
12607	Evolution of the <i>Ace-1</i> and <i>Gste2</i> Mutations and Their Potential Impact on the Use of Carbamate and Organophosphates in IRS for Controlling <i>Anopheles gambiae</i> s.l., the Major Malaria Mosquito in Senegal. <i>Pathogens</i> , 2022, 11, 1021.	1.2	1

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12611	Elucidation of the population structure and genetic diversity of <i>Bipolaris oryzae</i> associated with rice brown spot disease using SSR markers. <i>3 Biotech</i> , 2022, 12, .	1.1	1
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12623	Molecular Studies of Relationships and Identifications Among Insects of the Subfamily Panchaetothripinae (Thysanoptera, Thripidae). <i>Journal of Insect Science</i> , 2022, 22, .	0.6	1
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12637	Mitochondrial Genetic Diversity of <i>Bemisia tabaci</i> (Gennadius) (Hemiptera: Aleyrodidae) Associated with Cassava in Lao PDR. <i>Insects</i> , 2022, 13, 861.	1.0	4
12638	Diversity and Distribution of Whiteflies Colonizing Cassava in Eastern Democratic Republic of Congo. <i>Insects</i> , 2022, 13, 849.	1.0	0
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12650	Using genetic tools to inform conservation of fragmented populations of Asian elephants (<i>Elephas maximus</i>). <i>Conservation Genetics</i> , 2022, 23, 1061-1070.	1.3	0
12651	Genetic Differentiation and Molecular Phylogenetics of North African Catfish from Three Distinct Waterbodies. <i>Ribarstvo, Croatian Journal of Fisheries</i> , 2022, 80, 123-132.	0.2	0
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12662	Complete chloroplast genome sequencing and comparative analysis of threatened dragon trees <i>Dracaena serrulata</i> and <i>Dracaena cinnabari</i> . <i>Scientific Reports</i> , 2022, 12, .	1.6	2
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12665	STUDIES OF MORPHOLOGICAL AND GENETIC VARIABILITY OF <i>HERICIUM ERINACEUS</i> FROM THE NORTHWEST AREA OF THE SIERRA MADRE OCCIDENTAL, DURANGO, MEXICO. <i>Southwestern Naturalist</i> , 2022, 66, .	0.1	0
12667	Classification of 17 species <i>Aegilops</i> using DNA barcoding and SNPs, reveals gene flow among <i>Aegilops biuncialis</i> , <i>Aegilops juvenalis</i> , and <i>Aegilops columnaris</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
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12682	Molecular phylogeny and taxonomy of the genus <i>Nectogale</i> (Mammalia: Eulipotyphla:). <i>Journal of Systematics and Evolution</i> , 2022, 10, 1-10.	0.8	1
12683	Genetic variation in the spotted seal (<i>Phoca largha</i> Pallas, 1811) from the Rimsky-Korsakov Archipelago (Peter the Great Bay, western sea of Japan) as inferred from mitochondrial DNA control region sequences. <i>Zoologischer Anzeiger</i> , 2022, 301, 174-178.	0.4	1
12684	Genetic diversity in the transmission-blocking vaccine candidate <i>Plasmodium vivax</i> gametocyte protein Pvs230 from the China-Myanmar border area and central Myanmar. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	1
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12686	Phylogeography of the striped field mouse (<i>Apodemus agrarius</i> Pallas, 1771) in light of new data from central part of Northern Eurasia. <i>PLoS ONE</i> , 2022, 17, e0276466.	1.1	3
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12691	High Genetic Diversity and Gene Flow Detected in Populations of <i>Bombus morio</i> from South Brazil. <i>Neotropical Entomology</i> , 2022, 51, 809-820.	0.5	2
12692	DNA Barcoding and Species Classification of <i>Morchella</i> . <i>Genes</i> , 2022, 13, 1806.	1.0	4
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12701	Natural selection drives the evolution of mitogenomes in <i>Acrossocheilus</i> . <i>PLoS ONE</i> , 2022, 17, e0276056.	1.1	6
12702	Genetic structure of <i>Enyalius capetinga</i> (Squamata, Leiosauridae) in Central Cerrado and transitional areas between the Cerrado and the Atlantic forest, with updated geographic distribution. <i>Genetica</i> , 0, , .	0.5	0
12703	A molecular perspective on the systematics and distribution of <i>Loxopholis</i> lizards in South and Central America, with advances on the biogeography of the tribe Ecleopodini (Gymnophthalmidae: Tj ETQq1 1 0.784314 rgBT /Overlock 10 T)	0.7	0
12704	Introduced, Mixed, and Peripheral: Conservation of Mitochondrial-DNA Lineages in the Wild Boar (<i>Sus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.7	0
12705	Phylogeography reveals a panmictic population of the Chilean nylon shrimp along its exploitation range in the southeast Pacific Ocean. <i>Organisms Diversity and Evolution</i> , 0, , .	0.7	0
12706	Natural variation and domestication selection of <i>ZmSULTR3;4</i> is associated with maize lateral root length in response to salt stress. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
12707	Genetic Diversity and Population Genetic Structure Analysis of <i>Plasmodium knowlesi</i> Thrombospondin-Related Apical Merozoite Protein (TRAMP) in Clinical Samples. <i>Genes</i> , 2022, 13, 1944.	1.0	2

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12709	Pangenome-wide analysis of cyclic nucleotide-gated channel (CNGC) gene family in citrus Spp. Revealed their intraspecies diversity and potential roles in abiotic stress tolerance. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	9
12710	Genetic Diversity of Circumsporozoite Surface Protein of <i>Plasmodium vivax</i> from the Central Highlands, Vietnam. <i>Pathogens</i> , 2022, 11, 1158.	1.2	2
12712	Mitochondrial diversity and phylogenetic structure of Yellowcheek (<i>Elopichthys bambusa</i>) in the Yangtze River. <i>Journal of Applied Ichthyology</i> , 2022, 38, 596-603.	0.3	3
12713	Cross-watershed distribution pattern challenging the elimination of <i>Oncomelania hupensis</i> , the intermediate host of <i>Schistosoma japonicum</i> , in Sichuan province, China. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	3
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12716	Comparative Genomic Analysis Uncovers the Chloroplast Genome Variation and Phylogenetic Relationships of <i>Camellia</i> Species. <i>Biomolecules</i> , 2022, 12, 1474.	1.8	1
12717	Complete chloroplast genomes of <i>Sorbus sensu stricto</i> (Rosaceae): comparative analyses and phylogenetic relationships. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	11
12718	Molecular population genetic analysis of <i>Eriocheir japonica</i> inhabiting Andeok Valley. <i>Journal of Asia-Pacific Biodiversity</i> , 2022, , .	0.2	0
12719	Genetic population structure of the critically endangered stellate sturgeon (<i>Acipenser</i>) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 34</i> . <i>Marine and Freshwater Ecosystems</i> , 2022, 32, 1926-1939.	0.9	1
12721	Pre- and post-pollination barriers between two exotic and five native <i>Sagittaria</i> species: Implications for species conservation. <i>Plant Diversity</i> , 2023, 45, 456-468.	1.8	1
12722	The first records of <i>Niphargus hrabei</i> and <i>N. potamophilus</i> in Ukraine and Bulgaria significantly enlarge the ranges of these species. , 2022, 89, 1191-1200.		1
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12724	Genetic analysis of a 66-kDa protein-encoding gene of <i>Angiostrongylus cantonensis</i> and <i>Angiostrongylus malaysiensis</i> . <i>Parasitology</i> , 2023, 150, 98-114.	0.7	2
12725	Prevalence of H6Y mutation in β -tubulin causing thiophanate-methyl resistant in <i>Monilinia fructicola</i> from Fujian, China. <i>Pesticide Biochemistry and Physiology</i> , 2022, 188, 105262.	1.6	3
12726	Transcriptomes of Different Tissues for Expression Characteristics Analysis of MYB gene Family in Kenaf (<i>Hibiscus cannabinus</i> L.). <i>Tropical Plant Biology</i> , 0, , .	1.0	2
12727	Analysis of Homologous Regions of Small RNAs MIR397 and MIR408 Reveals the Conservation of Microsynteny among Rice Crop-Wild Relatives. <i>Cells</i> , 2022, 11, 3461.	1.8	7

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12729	Polymorphism of mtDNA gene Cyt b of walleye pollock, <i>Gadus chalcogrammus</i> (Gadidae), in the Chukchi Sea, western Bering Sea, and Sea of Okhotsk. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2022, , 105216.	0.6	1
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12731	Landscape genetics across the Andes mountains: Environmental variation drives genetic divergence in the leaf-cutting ant <i>Atta cephalotes</i> . <i>Molecular Ecology</i> , 2023, 32, 95-109.	2.0	4
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12737	Polymorphism of mtDNA gene Cyt b of the Chukchi Sea polar cod, <i>Boreogadus saida</i> (Gadidae.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 0,6 1	0.6	1
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12739	Comparative analysis of genetic diversity and structure among four shell color strains of the Pacific oyster <i>Crassostrea gigas</i> based on the mitochondrial COI gene and microsatellites. <i>Aquaculture</i> , 2023, 563, 738990.	1.7	6
12740	Genome-wide analysis of the CSN genes in land plants and their expression under various abiotic stress and phytohormone conditions in rice. <i>Gene</i> , 2023, 850, 146905.	1.0	2
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12748	Genetic variation of the small yellow croaker (<i>Larimichthys polyactis</i>) inferred from mitochondrial DNA provides novel insight into the fluctuation of resources. <i>Acta Oceanologica Sinica</i> , 2022, 41, 88-95.	0.4	1
12749	Eastern king prawn <i>Penaeus plebejus</i> stock enhancement—Genetic evidence that hatchery bred prawns have survived in the wild after release. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
12750	Behavioural and phylogeographic observations on <i>Epipomponia nawai</i> (Dyer, 1904): an East Asian moth (Lepidoptera; Epipyropidae) whose larvae are ectoparasitic on cicadas (Hemiptera; Cicadidae; Sonatini). <i>Journal of Asia-Pacific Entomology</i> , 2022, , 102007.	0.4	0
12751	A New Species of <i>Lycodapus</i> from the Emperor Seamount Chain, Northwestern Pacific Ocean (Teleostei: Zoarcidae). <i>Diversity</i> , 2022, 14, 972.	0.7	2
12752	Morphological, Ecological, and Genetic Variation of the Whitefish <i>Coregonus lavaretus sensu lato</i> from the Upper and Middle Stream of the Lena River. <i>Russian Journal of Genetics</i> , 2022, 58, 1334-1351.	0.2	1
12753	Multilocus evidence provides insight into the demographic history and asymmetrical gene flow between <i>Ostrinia furnacalis</i> and <i>Ostrinia nubilalis</i> (Lepidoptera: Crambidae) in the Yili area, Xinjiang, China. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	1
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12757	Molecular Structure and Phylogenetic Analyses of the Plastomes of Eight <i>Sorbus</i> Sensu Stricto Species. <i>Biomolecules</i> , 2022, 12, 1648.	1.8	2
12758	Conservation of evolutionary patterns and processes in the Maloti minnow, <i>Pseudobarbus quathlambae</i> (Cyprinidae, Smiliogastrini), a narrow-range stream fish imperiled by water transfer scheme developments in the Lesotho Highlands. <i>Hydrobiologia</i> , 0, , .	1.0	0
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12761	Mitochondrial DNA variation of the caracal (<i>Caracal caracal</i>) in Iran and range-wide phylogeographic comparisons. <i>Mammalian Biology</i> , 0, , .	0.8	0
12762	Weed Hosts Represent an Important Reservoir of Turnip Yellow Virus and a Possible Source of Virus Introduction into Oilseed Rape Crop. <i>Viruses</i> , 2022, 14, 2511.	1.5	5
12763	Genome-wide SNPs reveal novel patterns of spatial genetic structure in <i>Aedes albopictus</i> (Diptera) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	1.3	1
12764	Stramonita Genus Exhibits a New Uncovered Species: A Cryptic Species Collected from Accra, Ghana (Eastern Atlantic Ocean). <i>Thalassas</i> , 0, , .	0.1	0

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12767	Low Genetic Polymorphism in the Immunogenic Sequences of <i>Rhipicephalus microplus</i> Clade C. <i>Vaccines</i> , 2022, 10, 1909.	2.1	4
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12775	Genetic Relationships and Signatures of Adaptation to the Climatic Conditions in Populations of <i>Apis cerana</i> Based on the Polymorphism of the Gene <i>Vitellogenin</i> . <i>Insects</i> , 2022, 13, 1053.	1.0	0
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12780	Distribution and Identification of <i>Ulva aragoensis</i> (Ulvaceae, Chlorophyta), a Constituent Species of Green Tides in the Southern Yellow Sea, Based on Molecular Data. <i>Journal of Marine Science and Engineering</i> , 2022, 10, 1767.	1.2	2
12782	Geographic factors and climatic fluctuation drive the genetic structure and demographic history of <i>Cycas taiwaniana</i> (Cycadaceae), an endemic endangered species to Hainan Island in China. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	4
12783	Structural characterization of four <i>Rhododendron</i> spp. chloroplast genomes and comparative analyses with other azaleas. <i>Biocell</i> , 2023, 47, 657-668.	0.4	1
12784	Cryptic species complex or an incomplete speciation? Phylogeographic analysis reveals an intricate Pleistocene history of <i>Priapulius caudatus</i> Lamarck, 1816. <i>Zoologischer Anzeiger</i> , 2023, 302, 113-130.	0.4	3

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12786	Genetic diversity and population structure of the crescent perch <i>Terapon jarbua</i> (Centrarchiformes: Tj ETQq1 1 0.784314 rgBT /Over	0.4	1
12787	Characterization of the chloroplast genome and phylogenetic analysis of <i>Ceratopteris pteridoides</i> (Pteridaceae). <i>Gene Reports</i> , 2023, 30, 101716.	0.4	0
12788	Molecular characterization of <i>Ehrlichia canis</i> and <i>Babesia vogeli</i> reveals multiple genogroups associated with clinical traits in dogs from urban areas of Colombia. <i>Ticks and Tick-borne Diseases</i> , 2023, 14, 102111.	1.1	1
12789	Sex-biased, but not plumage color-based, prevalence of haemosporidian parasites in free-range chickens. <i>Parasitology International</i> , 2023, 93, 102722.	0.6	0
12790	Genetic diversity study of three Indian major carps from four riverine ecosystems. <i>Aquatic Ecosystem Health and Management</i> , 2022, 25, 15-24.	0.3	0
12791	<i>Cynips quercus</i> in the Western Palearctic: the role of Anatolia between Asia and Europe. <i>Acta Mathematica Spalatensis</i> , 0, , .	0.1	0
12792	Multi-Locus Sequencing Reveals Putative Novel Anaplasmataceae Agents, <i>â€ˆ</i> Candidatus <i>Ehrlichia dumleri</i> â€™ and <i>Anaplasma</i> sp., in Ring-Tailed Coatis (Carnivora: <i>Nasua nasua</i>) from Urban Forested Fragments at Midwestern Brazil. <i>Microorganisms</i> , 2022, 10, 2379.	1.6	5
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12795	Phylogeographic Diversity Analysis of <i>Bipolaris sorokiniana</i> (Sacc.) Shoemaker Causing Spot Blotch Disease in Wheat and Barley. <i>Genes</i> , 2022, 13, 2206.	1.0	5
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12800	Substantial genetic mixing among sexual and androgenetic lineages within the clam genus <i>Corbicula</i> . , 0, 2, .		5
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12805	The phylogeography of some soil-feeding termites shaped by the Andes. <i>Organisms Diversity and Evolution</i> , 0, , .	0.7	1
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12816	Genetic analysis reveals the putative native range and widespread double clonal reproduction in the invasive longhorn crazy ant. <i>Molecular Ecology</i> , 2023, 32, 1020-1033.	2.0	5
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12823	African-specific polymorphisms in <i>Plasmodium falciparum</i> serine repeat antigen 5 in Uganda and Burkina Faso clinical samples do not interfere with antibody response to BK-SE36 vaccination. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	2
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12827	Extensive reorganization of the chloroplast genome of <i>Corydalis platycarpa</i> : A comparative analysis of their organization and evolution with other <i>Corydalis</i> plastomes. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
12828	Characterization of Two New <i>Apodemus</i> Mitogenomes (Rodentia: Muridae) and Mitochondrial Phylogeny of Muridae. <i>Diversity</i> , 2022, 14, 1089.	0.7	2
12829	Molecular characterization of <i>Hyalomma dromedarii</i> and evaluation of acaricidal potential of herbal methanolic extracts against <i>H. dromedarii</i> larvae in comparison to synthetic acaricides. <i>Experimental and Applied Acarology</i> , 2023, 89, 141-156.	0.7	0
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12831	Genome-wide survey of catalase genes in <i>Brassica rapa</i> , <i>Brassica oleracea</i> , and <i>Brassica napus</i> : identification, characterization, molecular evolution, and expression profiling of BnCATs in response to salt and cadmium stress. <i>Protoplasma</i> , 2023, 260, 899-917.	1.0	4
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12833	Population genetic structure and evolutionary demographic patterns of <i>Phrynoderma karaavali</i> , an edible frog species of Kerala, India. <i>Journal of Genetics</i> , 2023, 102, .	0.4	2
12834	Population structure of mud flounder <i>Paralichthys orbignyanus</i> from the south-western Atlantic Ocean. <i>Journal of Fish Biology</i> , 2023, 102, 455-464.	0.7	0
12835	Diversity of <i>PsSym29</i> and <i>PsNRLK1</i> genes in the VIR germplasm collection of pea (<i>Pisum sativum</i> L.). <i>Ecological Genetics</i> , 2022, 20, 271-278.	0.1	1
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12837	Comparative analysis of the mitochondrial genome of <i>Dermacentor steini</i> from different regions in China. <i>Parasitology</i> , 2023, 150, 195-205.	0.7	4
12838	Morphological Characteristics and Comparative Chloroplast Genome Analyses between Red and White Flower Phenotypes of <i>Pyracantha fortuneana</i> (Maxim.) Li (Rosaceae), with Implications for Taxonomy and Phylogeny. <i>Genes</i> , 2022, 13, 2404.	1.0	3

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12841	Dynamics of Genetic Diversity Among Indian Sugarcane Bacilliform Virus Species and Implications of Associated Recombination Events in the Virus. <i>Sugar Tech</i> , 2023, 25, 705-716.	0.9	2
12842	Diversity of interstitial nemertean of the genus <i>Ototyphlonemertes</i> (Nemertea: Monostilifera) Tj ETQq1 1 0.784314 rgBT /Overlock 10 genus. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	0
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12849	Comprehensive identification and expression analyses of the SnRK gene family in <i>Casuarina equisetifolia</i> in response to salt stress. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	1
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12851	Genetic Diversity Relationship in Azakheli Buffalo Inferred from mtDNA and MC1R Sequences Comparison. <i>BioMed Research International</i> , 2022, 2022, 1-8.	0.9	1
12852	Vectorial capacity and TEP1 genotypes of <i>Anopheles gambiae</i> sensu lato mosquitoes on the Kenyan coast. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	0
12853	Isolation and endemism in the subterranean aquatic snails of the genus <i>Belgrandiella</i> A. J. Wagner, 1928 (Caenogastropoda: Truncatelloidea: Hydrobiidae). <i>Hydrobiologia</i> , 2023, 850, 4089-4113.	1.0	4
12854	Comparative phylogenetic analysis of oolong tea (Phoenix Dancong tea) using complete chloroplast genome sequences. <i>Heliyon</i> , 2022, 8, e12557.	1.4	4
12855	Genetic Polymorphism and Phylogenetics of <i>Aedes aegypti</i> from Sudan Based on ND4 Mitochondrial Gene Variations. <i>Insects</i> , 2022, 13, 1144.	1.0	3
12857	Linking integrative taxonomy and ecology: Diversity and population structure of two platyhelminth parasites (Digenea: Lepidapedidae) of sympatric deep-sea fishes in the Western Mediterranean. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2023, 192, 103948.	0.6	1

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12859	High Coverage Mitogenomes and Y-Chromosomal Typing Reveal Ancient Lineages in the Modern-Day Székely Population in Romania. <i>Genes</i> , 2023, 14, 133.	1.0	3
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12886	Comparative mitogenomics and phylogenetic analyses of the genus <i>Menida</i> (Hemiptera, Heteroptera). <i>Tj ETQq1 1 0.784314 rgBT / Dv</i>	0.5	1
12887	Comprehensive analysis of complete chloroplast genome sequence of <i>Plantago asiatica</i> L. (Plantaginaceae). <i>Plant Signaling and Behavior</i> , 2023, 18, .	1.2	2
12888	Insights into the divergent evolution of the oceanic squid <i>Sthenoteuthis oualaniensis</i> (Cephalopoda: Ommastrephidae) from the Indian Ocean. <i>Integrative Zoology</i> , 2023, 18, 924-948.	1.3	4
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12896	New perspectives for fascioliasis in Upper Egypt's new endemic region: Sociodemographic characteristics and phylogenetic analysis of <i>Fasciola</i> in humans, animals, and lymnaeid vectors. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0011000.	1.3	1
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12903	Morphological and Genetic Differentiation of <i>Loliolus</i> (<i>Nipponoligo</i>) <i>beka</i> (Cephalopoda:). Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 0.7	0.7	0
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12910	Helminth Community Structure of Tits <i>Cyanistes caeruleus</i> and <i>Parus major</i> (Paridae) during Their Autumn Migration on the Southern Baltic Coast. Animals, 2023, 13, 421.	1.0	1
12911	<i>Meloidogyne graminicola</i> Population Structure in China Suggests a South-to-North Expansion. Plant Disease, 2023, 107, 2070-2080.	0.7	1
12912	Comparisons of genetic population structures of copepods <i>Pseudocalanus</i> spp. in the Okhotsk Sea: the first record of <i>P. acuspis</i> in coastal waters off Japan. Marine Biodiversity, 2023, 53, .	0.3	0
12913	Complete chloroplast genomes provide insights into evolution and phylogeny of <i>Zingiber</i> (<i>Zingiberaceae</i>). BMC Genomics, 2023, 24, .	1.2	11
12914	A historic religious sanctuary may have preserved ancestral genetics of Japanese sika deer (<i>Cervus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T 0.8	0.8	3
12915	Spatial and phylogenetic structure of Alpine stonefly assemblages across seven habitats using DNA-species. Oecologia, 2023, 201, 513-524.	0.9	1

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12918	Phylogeographical analysis and phylogenetic inference based on the cytochrome <i>b</i> gene in the genus <i>Caiman</i> (Crocodylia: Alligatoridae) in Central and South America. Biological Journal of the Linnean Society, 2023, 138, 289-303.	0.7	2
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12920	Local characteristics of molecular epidemiology of <i>Acinetobacter baumannii</i> in Jilin province (northeast China). BMC Microbiology, 2023, 23, .	1.3	0
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12922	Phylogenetic analyses reveal bat communities in Northwestern Mexico harbor a high diversity of novel cryptic ectoparasite species. Ecology and Evolution, 2023, 13, .	0.8	1
12923	Traditional taxonomy underestimates the number of species of <i>Bokermannohyla</i> (Amphibia: Tj ETQq1 1 0.784314 rgBT /Overlock 0.5 Biodiversity, 2023, 21, .	0.5	0
12924	Phylogeographic investigation of the bladder grasshopper <i>Bullacris unicolor</i> (Orthoptera) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 42	0.6	0
12925	Morphological and molecular characterization of <i>Hysterothylacium</i> spp. parasitizing <i>Pomatomus saltatrix</i> and <i>Pagrus pagrus</i> of the State of São Paulo, Brazil. Anais Da Academia Brasileira De Ciencias, 2023, 95, .	0.3	0
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12931	Genetic diversity, phylogenetic and phylogeographic analyses of <i>Oncideres impluviata</i> (Germar, 1823) (Coleoptera: Cerambycidae) in Rio Grande do Sul state, Brazil. Revista Brasileira De Entomologia, 2023, 67, .	0.1	0
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12936	Genome-Wide Identification, Characterization and Expression Profiling of Potato (<i>Solanum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj 50 422 T	1.0	0
12937	Chloroplast DNA reveals genetic population structure in <i>Sinomenium acutum</i> in subtropical China. <i>Chinese Herbal Medicines</i> , 2023, , .	1.2	0
12938	<scp>DNA</scp> barcoding of Chinese snakes reveals hidden diversity and conservation needs. <i>Molecular Ecology Resources</i> , 2023, 23, 1124-1141.	2.2	2
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12942	Molecular phylogenetics and diversity of the Himalayan shrew (<i>Soriculus nigrescens</i> Gray, 1842) (<i>Eulipotyphla</i> , <i>Soricidae</i>) in Southwest China. <i>Zootaxa</i> , 2023, 5263, 061-078.	0.2	2
12943	Restricted connectivity for cobia <scp> <i>Rachycentron canadum</i> </scp> (Perciformes:) Tj ETQq0 0 0 rgBT /Overlock 10 Tj 50 422 T	0.9	0
12944	Molecular identification and genetic diversity of equine ocular setariasis in Thailand based on the COI, 12S rDNA, and ITS1 regions. <i>Infection, Genetics and Evolution</i> , 2023, 110, 105425.	1.0	1
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12949	Heterosis and genetic diversity of intraspecific hybrids crosses between two selected lines of the Pacific oyster <i>Crassostrea gigas</i> . <i>Aquaculture</i> , 2023, 569, 739369.	1.7	2
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12956	Signatures of purifying selection and site-specific positive selection on the mitochondrial DNA of dromedary camels (<i>Camelus dromedarius</i>). <i>Mitochondrion</i> , 2023, 69, 36-42.	1.6	2

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12958	Haplotypes of <i>Dirofilaria repens</i> from Poland and selected countries of Central, North-Eastern Europe and the Middle East: An evaluation on the relation between the genetic diversity and the geographic distribution of the fast-spreading parasite. <i>Veterinary Parasitology</i> , 2023, 315, 109882.	0.7	8
12959	Mass migration, population genetics and historical population expansion in the Neotropical butterfly <i>Kricogonia lyside</i> (Lepidoptera: Pieridae). <i>Biological Journal of the Linnean Society</i> , 0, , .	0.7	0
12960	Characterization of the Plastid Genome of the Vulnerable Endemic <i>Indosasa lipoensis</i> and Phylogenetic Analysis. <i>Diversity</i> , 2023, 15, 197.	0.7	3
12961	Phylogeography and genetic diversity of the <i>Scapholeberis kingii</i> species complex (Cladocera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582	1.2	0
12962	Genetic diversity of <i>Contraecaecum rudolphii</i> sp. A (Nematoda: Anisakidae) parasitizing the European Shag <i>Phalacrocorax aristotelis desmarestii</i> from the Spanish Mediterranean coast. <i>Frontiers in Veterinary Science</i> , 0, 10, .	0.9	2
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12965	Mitochondrial diversity and genetic structure of common carp (<i>Cyprinus carpio</i>) in Pearl River and Nanduijiang River. <i>Journal of Fish Biology</i> , 2023, 102, 1109-1120.	0.7	1
12966	Evolution of the WRKY66 Gene Family and Its Mutations Generated by the CRISPR/Cas9 System Increase the Sensitivity to Salt Stress in <i>Arabidopsis</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 3071.	1.8	5
12967	Characterization of the Complete Mitochondrial Genome of a Flea Beetle <i>Luperomorpha xanthodera</i> (Coleoptera: Chrysomelidae: Galerucinae) and Phylogenetic Analysis. <i>Genes</i> , 2023, 14, 414.	1.0	1
12968	Integrative description of <i>Macrobotus kosmali</i> sp. nov. (<i>hufelandi</i> group) from the Island of Madeira (Portugal). , 2023, 90, 126-138.		0
12969	Large-scale genetic surveys for main extant population of wild giant panda (<i>Ailuropoda</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 267 738-749.	1.5	2
12970	Highly divergent regions in the complete plastome sequences of <i>Aquilaria</i> are suitable for DNA barcoding applications including identifying species origin of agarwood products. <i>3 Biotech</i> , 2023, 13, .	1.1	1
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12973	The Impact of Variation in the Toll-like Receptor 3 Gene on Epizootic Hemorrhagic Disease in Illinois Wild White-Tailed Deer (<i>Odocoileus virginianus</i>). <i>Genes</i> , 2023, 14, 426.	1.0	1
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13064	A review of the subgenus <i>Parapisa</i> of <i>Apisa</i> (Lepidoptera: Erebiidae: Arctiinae) with description of a remarkable species from Cameroonian Highlands. <i>Arthropod Systematics and Phylogeny</i> , 0, 81, 371-394.	5.5	0
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