

# Arlequin suite ver 3.5: a new series of programs to perform population genetics analyses under Linux and Windows

Molecular Ecology Resources

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Marine Turtle Newsletter. Canadian Field-Naturalist, 2007, 121, 117.	0.0	3
2	Microsatellite loci for the okapi ( <i>Okapia johnstoni</i> ). Conservation Genetics Resources, 2010, 2, 337-339.	0.4	4
3	Microsatellite markers for the proboscis monkey ( <i>Nasalis larvatus</i> ). Conservation Genetics Resources, 2010, 2, 159-163.	0.4	9
4	Genetic diversity and structure of blue whales ( <i>Balaenoptera musculus</i> ) in Australian feeding aggregations. Conservation Genetics, 2010, 11, 2437-2441.	0.8	25
5	ABCtoolbox: a versatile toolkit for approximate Bayesian computations. BMC Bioinformatics, 2010, 11, 116.	1.2	309
6	Population genetic structure of <i>Cichla pleiozona</i> (Perciformes: Cichlidae) in the Upper Madera basin (Bolivian Amazon): Sex-biased dispersal?. Molecular Phylogenetics and Evolution, 2010, 57, 1334-1340.	1.2	11
7	Distinguishing between population bottleneck and population subdivision by a Bayesian model choice procedure. Molecular Ecology, 2010, 19, 4648-4660.	2.0	110
8	Larval settlement preference maximizes genetic mixing in an inbreeding population of a simultaneous hermaphrodite ( <i>Bugula stolonifera</i> , Bryozoa). Molecular Ecology, 2010, 19, 5511-5520.	2.0	11
9	Population differentiation in the swordtail characin ( <i>Corynopoma riisei</i> ): a role for sensory drive?. Journal of Evolutionary Biology, 2010, 23, 1907-1918.	0.8	12
10	Molecular analysis of <i>Acanthemblemaria macrospilus</i> (Teleostei: Chaenopsidae) with description of a new species from the Gulf of California, Mexico. Zootaxa, 2010, 2525, .	0.2	10
11	Analysis of Microsatellite DNA Markers Reveals no Genetic Differentiation between Wild and Hatchery Populations of Pacific Threadfin in Hawaii. International Journal of Biological Sciences, 2010, 6, 827-833.	2.6	16
12	Long-Range Comparison between Genes and Languages Based on Syntactic Distances. Human Heredity, 2010, 70, 245-254.	0.4	20
13	Identification of Local- and Habitat-Dependent Selection: Scanning Functionally Important Genes in Nine-Spined Sticklebacks ( <i>Pungitius pungitius</i> ). Molecular Biology and Evolution, 2010, 27, 2775-2789.	3.5	49
14	Genetic variation in avocado stem weevils <i>Copturus aguacatae</i> (Coleoptera: Curculionidae) in Mexico. Mitochondrial DNA, 2010, 21, 38-43.	0.6	8
15	SPLATCHE2: a spatially explicit simulation framework for complex demography, genetic admixture and recombination. Bioinformatics, 2010, 26, 2993-2994.	1.8	113
16	Parallel adaptive evolution of Atlantic cod on both sides of the Atlantic Ocean in response to temperature. Proceedings of the Royal Society B: Biological Sciences, 2010, 277, 3725-3734.	1.2	206
17	Assessing Genetic Diversity of Canada Thistle ( <i>Cirsium arvense</i> ) in North America with Microsatellites. Weed Science, 2010, 58, 387-394.	0.8	15
18	Genetic Variation of <i>Anastrepha suspensa</i> (Diptera: Tephritidae) in Florida and the Caribbean Using Microsatellite DNA Markers. Journal of Economic Entomology, 2010, 103, 2214-2222.	0.8	13

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19	Influence of Host Phylogeographic Patterns and Incomplete Lineage Sorting on Within-Species Genetic Variability in <i>Wigglesworthia</i> Species, Obligate Symbionts of Tsetse Flies. <i>Applied and Environmental Microbiology</i> , 2011, 77, 8400-8408.	1.4	11
20	Microsatellite Variation in <i>Helicoverpa zea</i> (Boddie) Populations in the Southern United States. <i>Southwestern Entomologist</i> , 2011, 36, 271-286.	0.1	16
21	Fine-scale population genetic structure of the yellow perch <i>Perca flavescens</i> in Lake Erie. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2011, 68, 1435-1453.	0.7	36
22	Microsatellite population structure of Newfoundland black bears ( <i>Ursus americanus hamiltoni</i> ). <i>Canadian Journal of Zoology</i> , 2011, 89, 831-839.	0.4	4
23	Spawning Habitat and Geography Influence Population Structure and Juvenile Migration Timing of Sockeye Salmon in the Wood River Lakes, Alaska. <i>Transactions of the American Fisheries Society</i> , 2011, 140, 763-782.	0.6	44
24	Application of a method for estimating effective population size and admixture using diagnostic single nucleotide polymorphisms (SNPs): implications for conservation of threatened Paiute cutthroat trout ( <i>Oncorhynchus clarkii seleniris</i> ) in Silver King Creek, California. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2011, 68, 1369-1386.	0.7	8
25	A High Incidence of Selection on Physiologically Important Genes in the Three-Spined Stickleback, <i>Gasterosteus aculeatus</i> . <i>Molecular Biology and Evolution</i> , 2011, 28, 181-193.	3.5	90
26	Connectivity dominates larval replenishment in a coastal reef fish metapopulation. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 2954-2961.	1.2	114
27	The Y-STR Genetic Diversity of an Idaho Basque Population, with Comparison to European Basques and US Caucasians. <i>Human Biology</i> , 2011, 83, 685-694.	0.4	1
28	On the amphi-Atlantic <i>Siphonaria pectinata</i> (Linnaeus, 1758) (Gastropoda: Heterobranchia:) Tj ETQq1 1 0.784314 9.4 / Overlock 10 TF 13	0.4	1
29	Genetic polymorphism of the new PowerPlex® ESI 17 system in a Tibetan population from Dharamsala (India). <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e461-e462.	0.1	1
30	Hierarchical analysis of 15 Y-chromosome SNPs and demographic history of Afro-derived isolated communities in Alagoas, Brazil. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e172-e173.	0.1	1
31	Genetic characterization of Somali and Iraqi populations using a set of 33 X-chromosome Indels. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e137-e138.	0.1	4
32	Identification of a functional transposon insertion in the maize domestication gene <i>tb1</i> . <i>Nature Genetics</i> , 2011, 43, 1160-1163.	9.4	639
33	Gene Flow and Hybridization between Numerically Imbalanced Populations of Two Duck Species in the Falkland Islands. <i>PLoS ONE</i> , 2011, 6, e23173.	1.1	24
34	Single Nucleotide Polymorphisms (SNPs) under Diversifying Selection Provide Increased Accuracy and Precision in Mixed Stock Analyses of Sockeye Salmon from the Copper River, Alaska. <i>Transactions of the American Fisheries Society</i> , 2011, 140, 865-881.	0.6	70
35	Coastal pollution limits pelagic larval dispersal. <i>Nature Communications</i> , 2011, 2, 226.	5.8	56
36	Biodiversity in Date Palm: Molecular Markers as Indicators. , 2011, , 371-406.		4

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37	Characterization of <i>Fasciola</i> spp. in Myanmar on the basis of spermatogenesis status and nuclear and mitochondrial DNA markers. <i>Parasitology International</i> , 2011, 60, 474-479.	0.6	39
38	Study of DXS9895 and DXS7130: Population data from North of Portugal. <i>Journal of Clinical Forensic and Legal Medicine</i> , 2011, 18, 21-22.	0.5	6
39	Genomic scans detect signatures of selection along a salinity gradient in populations of the intertidal seaweed <i>Fucus serratus</i> on a 12km scale. <i>Marine Genomics</i> , 2011, 4, 41-49.	0.4	28
40	Paternal Genetic History of the Basque Population of Spain. <i>Human Biology</i> , 2011, 83, 455-475.	0.4	12
41	Development and characterization of 35 single nucleotide polymorphism markers for the brown alga <i>Fucus vesiculosus</i> . <i>European Journal of Phycology</i> , 2011, 46, 342-351.	0.9	4
42	Complex evolutionary history of the Mexican stoneroller <i>Camptostoma ornatum</i> Girard, 1856 (Actinopterygii: Cyprinidae). <i>BMC Evolutionary Biology</i> , 2011, 11, 153.	3.2	17
43	Genetic continuity across a deeply divergent linguistic contact zone in North Maluku, Indonesia. <i>BMC Genetics</i> , 2011, 12, 100.	2.7	5
44	Dispersal of <i>Mycobacterium tuberculosis</i> via the Canadian fur trade. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6526-6531.	3.3	56
45	Preliminary results of mitochondrial DNA sequence variation in Jujuy population (Argentina). <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e7-e8.	0.1	1
46	Study of 25 X-chromosome Single Nucleotide Polymorphisms in African and Asian populations. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e139-e140.	0.1	1
47	Discordant Phylogeographic and Biogeographic Breaks in California Halibut. <i>Bulletin (Southern)</i> Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 34	0.1	2
48	Geographical Distributions of Mitochondrial DNA Lineages Reflect Ancient Directions of River Flow: A Case Study of the Japanese Freshwater Shrimp <i>Neocaridina denticulata denticulata</i> (Decapoda:) Tj ETQq1 103784314 rgBT /Overlock 10 Tf 50 34	0.1	2
49	Population genetic structure of reared and wild gilthead sea bream ( <i>Sparus aurata</i> ) in the Adriatic Sea inferred with microsatellite loci. <i>Aquaculture</i> , 2011, 318, 309-315.	1.7	43
50	Conservation genetics of evolutionary lineages of the endangered mountain yellow-legged frog, <i>Rana muscosa</i> (Amphibia: Ranidae), in southern California. <i>Biological Conservation</i> , 2011, 144, 2031-2040.	1.9	24
51	Relative effects of road mortality and decreased connectivity on population genetic diversity. <i>Biological Conservation</i> , 2011, 144, 3143-3148.	1.9	169
52	Systematics and redescription of the European meiofaunal slug <i>Microhedyle glandulifera</i> (Kowalevsky, 1901) (Heterobranchia: Acochlidia): evidence from molecules and morphology. <i>Journal of Molluscan Studies</i> , 2011, 77, 388-400.	0.4	12
53	Molecular systematics of the Middle American genus <i>Hypopachus</i> (Anura: Microhylidae). <i>Molecular Phylogenetics and Evolution</i> , 2011, 61, 265-277.	1.2	13
54	A molecular phylogeny of the Sierra-Finches ( <i>Phrygilus</i> , Passeriformes): Extreme polyphyly in a group of Andean specialists. <i>Molecular Phylogenetics and Evolution</i> , 2011, 61, 521-533.	1.2	27

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55	Genetic consequences of interglacial isolation in a steppe bird. <i>Molecular Phylogenetics and Evolution</i> , 2011, 61, 671-676.	1.2	23
56	Genetic structure of <i>Brachidontes puniceus</i> populations in Cape Verde archipelago shows signature of expansion during the last glacial maximum. <i>Journal of Molluscan Studies</i> , 2011, 77, 175-181.	0.4	15
57	Climate-driven local adaptation of ecophysiology and phenology in balsam poplar, <i>Populus balsamifera</i> L. (Salicaceae). <i>American Journal of Botany</i> , 2011, 98, 99-108.	0.8	103
58	Assessing population structure: $F_{ST}$ and related measures. <i>Molecular Ecology Resources</i> , 2011, 11, 5-18.	2.2	967
59	Application of SNPs for population genetics of nonmodel organisms: new opportunities and challenges. <i>Molecular Ecology Resources</i> , 2011, 11, 123-136.	2.2	391
60	Single nucleotide polymorphisms across a species' range: implications for conservation studies of Pacific salmon. <i>Molecular Ecology Resources</i> , 2011, 11, 195-217.	2.2	54
61	Comparison of $F_{ST}$ outlier tests for SNP loci under selection. <i>Molecular Ecology Resources</i> , 2011, 11, 184-194.	2.2	448
62	The GHEP-EMPOP collaboration on mtDNA population data: A new resource for forensic casework. <i>Forensic Science International: Genetics</i> , 2011, 5, 146-151.	1.6	41
63	Origin and distribution of autopolyploids via apomixis in the alpine species <i>Ranunculus kuepferi</i> (Ranunculaceae). <i>Taxon</i> , 2011, 60, 355-364.	0.4	45
64	High genetic differentiation of <i>Aegla longirostri</i> (Crustacea, Decapoda, Anomura) populations in southern Brazil revealed by multi-loci microsatellite analysis. <i>Genetics and Molecular Research</i> , 2011, 10, 4133-4146.	0.3	12
65	Genetic diversity of worldwide Jerusalem artichoke ( <i>Helianthus tuberosus</i> ) germplasm as revealed by RAPD markers. <i>Genetics and Molecular Research</i> , 2011, 10, 4012-4025.	0.3	9
66	Does <i>Primula intricata</i> Gren. et Godr. Merit Species Rank? A Taxonomic Revision Based on nrDNA, cpDNA and AFLP Data. <i>Notulae Botanicae Horti Agrobotanici Cluj-Napoca</i> , 2011, 39, 24.	0.5	1
67	Genetic characterization of the northwestern Pacific population of a deep-sea demersal fish, <i>Bothrocara hollandi</i> . <i>Plankton and Benthos Research</i> , 2011, 6, 108-114.	0.2	13
68	Spatial Geographic Mosaic in an Aquatic Predator-Prey Network. <i>PLoS ONE</i> , 2011, 6, e22472.	1.1	19
69	Geographic Variation in Advertisement Calls in a Tree Frog Species: Gene Flow and Selection Hypotheses. <i>PLoS ONE</i> , 2011, 6, e23297.	1.1	49
70	Molecular and Phenotypic Evidence of a New Species of Genus <i>Esox</i> (Esocidae, Esociformes.) <i>Tj ETQq1 1 0.784314</i> <i>rgBT /Overlock 10 TF</i>	1.1	45
71	Sequential Fragmentation of Pleistocene Forests in an East Africa Biodiversity Hotspot: Chameleons as a Model to Track Forest History. <i>PLoS ONE</i> , 2011, 6, e26606.	1.1	29
72	Comparative Phylogeography in a Specific and Obligate Pollination Antagonism. <i>PLoS ONE</i> , 2011, 6, e28662.	1.1	23

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91	Genome-wide association analysis of clinical vs. nonclinical origin provides insights into <i>Saccharomyces cerevisiae</i> pathogenesis. <i>Molecular Ecology</i> , 2011, 20, 4085-4097.	2.0	46
92	Recent long-distance transgene flow into wild populations conforms to historical patterns of gene flow in cotton ( <i>Gossypium hirsutum</i> ) at its centre of origin. <i>Molecular Ecology</i> , 2011, 20, 4182-4194.	2.0	69
93	A multi-gene approach reveals a complex evolutionary history in the <i>Cyanistes</i> species group. <i>Molecular Ecology</i> , 2011, 20, 4123-4139.	2.0	37
94	Population genomics of wild and laboratory zebrafish ( <i>Danio rerio</i> ). <i>Molecular Ecology</i> , 2011, 20, 4259-4276.	2.0	79
95	Climate-driven genetic divergence of limpets with different life histories across a southeast African marine biogeographic disjunction: different processes, same outcome. <i>Molecular Ecology</i> , 2011, 20, 5025-5041.	2.0	39
96	Drift and selection influence geographic variation at immune loci of prairie-chickens. <i>Molecular Ecology</i> , 2011, 20, 4695-4706.	2.0	30
97	Self-sustaining populations, population sinks or aggregates of strays: chum ( <i>Oncorhynchus keta</i> ) and Chinook salmon ( <i>Oncorhynchus tshawytscha</i> ) in the Wood River system, Alaska. <i>Molecular Ecology</i> , 2011, 20, 4925-4937.	2.0	8
98	Asymmetric introgression between the M and S forms of the malaria vector, <i>Anopheles gambiae</i> , maintains divergence despite extensive hybridization. <i>Molecular Ecology</i> , 2011, 20, 4983-4994.	2.0	70
99	Genetic evidence for multiple events of hybridization between wolves and domestic dogs in the Iberian Peninsula. <i>Molecular Ecology</i> , 2011, 20, 5154-5166.	2.0	118
100	Phylogeographic analyses of the southern leopard frog: the impact of geography and climate on the distribution of genetic lineages vs. subspecies. <i>Molecular Ecology</i> , 2011, 20, 5295-5312.	2.0	20
101	Phylogeographic consequences of different introduction histories of invasive Australian <i>Acacia</i> species and <i>Paraserianthes lophantha</i> (Fabaceae) in South Africa. <i>Diversity and Distributions</i> , 2011, 17, 861-871.	1.9	79
102	Genetic diversity and structure in two spotted hyena populations reflects social organization and male dispersal. <i>Journal of Zoology</i> , 2011, 285, 281-291.	0.8	16
103	A review of ecological models for brown trout: towards a new demogenetic model. <i>Ecology of Freshwater Fish</i> , 2011, 20, 167-198.	0.7	33
104	“SAME SAME BUT DIFFERENT” REPLICATED ECOLOGICAL SPECIATION AT WHITE SANDS. <i>Evolution; International Journal of Organic Evolution</i> , 2011, 65, 946-960.	1.1	106
105	GENE GENEALOGIES REVEAL DIFFERENTIATION AT SEX PHEROMONE OLFACTORY RECEPTOR LOCI IN PHEROMONE STRAINS OF THE EUROPEAN CORN BORER, <i>OSTRINIA NUBILALIS</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2011, 65, 1583-1593.	1.1	20
106	Geographic variation in oviposition preference for male and female host plants in a geometrid moth: implications for evolution of host choice. <i>Entomologia Experimentalis Et Applicata</i> , 2011, 141, 178-184.	0.7	5
107	Evolutionary history of the Karoo bush rat, <i>Myotomys unisulcatus</i> (Rodentia: Muridae): discordance between morphology and genetics. <i>Biological Journal of the Linnean Society</i> , 2011, 102, 510-526.	0.7	28
108	A cryptic contact zone between divergent mitochondrial DNA lineages in southwestern North America supports past introgressive hybridization in the yellow-rumped warbler complex (Aves:). <i>Tj ETQq1 1 0.784304 rgBT / Overlock 10</i>	0.4	10

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109	Genetic diversity of wild populations of the grey short-tailed opossum, <i>Monodelphis domestica</i> (Didelphimorphia: Didelphidae), in Brazilian landscapes. Biological Journal of the Linnean Society, 2011, 104, 251-263.	0.7	24
110	Effect of oceanographic barriers and overfishing on the population genetic structure of the European spiny lobster ( <i>Palinurus elephas</i> ). Biological Journal of the Linnean Society, 2011, 104, 407-418.	0.7	30
111	Population structure and dispersal in a patchy landscape: nuclear and mitochondrial markers reveal area effects in the spider <i>Theridion californicum</i> (Araneae: Theridiidae). Biological Journal of the Linnean Society, 2011, 104, 600-620.	0.7	13
112	Haplotype phasing: existing methods and new developments. Nature Reviews Genetics, 2011, 12, 703-714.	7.7	537
113	Temporal change in genetic integrity suggests loss of local adaptation in a wild Atlantic salmon ( <i>Salmo salar</i> ) population following introgression by farmed escapees. Heredity, 2011, 106, 500-510.	1.2	119
114	Species delimitation and biogeography of two fir species ( <i>Abies</i> ) in central China: cytoplasmic DNA variation. Heredity, 2011, 107, 362-370.	1.2	30
115	Microsatellites and <i>Alu</i> elements from the human MHC in Valencia (Spain): analysis of genetic relationships and linkage disequilibrium. International Journal of Immunogenetics, 2011, 38, 483-491.	0.8	8
116	Complex genetic patterns in the mangrove wood-borer <i>Sphaeroma terebrans</i> Bate, 1866 (Isopoda). Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 100	0.7	10
117	Comparative phylogeography and connectivity of sibling species of the marine copepod <i>Clausocalanus</i> (Calanoida). Journal of Experimental Marine Biology and Ecology, 2011, 404, 108-115.	0.7	45
118	Genetic variation of 15 autosomal microsatellite loci in a Nayarit population (Mexico). Legal Medicine, 2011, 13, 323-327.	0.6	3
119	Deep mitochondrial divergence within a <i>Heliconius</i> butterfly species is not explained by cryptic speciation or endosymbiotic bacteria. BMC Evolutionary Biology, 2011, 11, 358.	3.2	23
120	Southeast Asian diversity: first insights into the complex mtDNA structure of Laos. BMC Evolutionary Biology, 2011, 11, 49.	3.2	35
121	Evolution and connectivity in the world-wide migration system of the mallard: Inferences from mitochondrial DNA. BMC Genetics, 2011, 12, 99.	2.7	39
122	Risk variants in BMP4 promoters for nonsyndromic cleft lip/palate in a Chilean population. BMC Medical Genetics, 2011, 12, 163.	2.1	23
123	Multiple origins of European populations of the giant liver fluke <i>Fascioloides magna</i> (Trematoda). Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 100	1.3	52
124	Relation of HLA-A, -B, -DRB1 Alleles and Haplotypes in Patients with Acute Leukemia: A Case Control Study. Archives of Medical Research, 2011, 42, 305-310.	1.5	12
125	Postglacial recolonization of eastern Blacknose Dace, <i>Rhinichthys atratulus</i> (Teleostei). Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 100	0.8	10
126	Comprehensive study of mtDNA among Southwest Asian dogs contradicts independent domestication of wolf, but implies dog-wolf hybridization. Ecology and Evolution, 2011, 1, 373-385.	0.8	59



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127	Range-wide genetic population structure of common pochard ( <i>Aythya ferina</i> ): a potentially important vector of highly pathogenic avian influenza viruses. <i>Ecology and Evolution</i> , 2011, 1, 529-545.	0.8	18
128	Discovery of <i>Pseudocalanus moultoni</i> (Frost, 1989) in Northeast Atlantic waters based on mitochondrial COI sequence variation. <i>Journal of Plankton Research</i> , 2011, 33, 1487-1495.	0.8	22
129	Evolutionary dynamics of cycle length in pearl millet: the role of farmer's practices and gene flow. <i>Genetica</i> , 2011, 139, 1367-1380.	0.5	16
130	FMR1 Linked haplotype analysis in a mentally retarded male population. <i>Open Medicine (Poland)</i> , 2011, 6, 750-757.	0.6	1
131	Analysis of meristic and mitochondrial DNA variation in <i>Syngnathus abaster</i> (Teleostea: Syngnathidae) from two western Mediterranean lagoons. <i>Biologia (Poland)</i> , 2011, 66, 1140-1147.	0.8	7
132	Diversity in genetic structure and chemotype composition of <i>Fusarium graminearum sensu stricto</i> populations causing wheat head blight in individual fields in Germany. <i>European Journal of Plant Pathology</i> , 2011, 131, 39-48.	0.8	57
133	<i>Salamandra salamandra</i> (Amphibia: Caudata: Salamandridae) in Portugal: not all black and yellow. <i>Genetica</i> , 2011, 139, 1095-1105.	0.5	6
134	Genetic structure of traditional varieties of bitter manioc in three soils in Central Amazonia. <i>Genetica</i> , 2011, 139, 1259-1271.	0.5	17
135	Patterns of spatial genetic structuring in the endangered limpet <i>Patella ferruginea</i> : implications for the conservation of a Mediterranean endemic. <i>Genetica</i> , 2011, 139, 1293-1308.	0.5	29
136	Polyploid origin, genetic diversity and population structure in the tetraploid sea lavender <i>Limonium narbonense</i> Miller (Plumbaginaceae) from eastern Spain. <i>Genetica</i> , 2011, 139, 1309-1322.	0.5	29
137	Phylogeography, genetic structure, and gene flow in the endemic freshwater shrimp <i>Palaemonetes suttkusi</i> from Cuatro Ci�negas, Mexico. <i>Conservation Genetics</i> , 2011, 12, 557-567.	0.8	19
138	Genetic structure in remnant populations of an endangered cyprinodontid fish, <i>Orestias ascotanensis</i> , endemic to the Ascot�n salt pan of the Altiplano. <i>Conservation Genetics</i> , 2011, 12, 1639-1643.	0.8	27
139	Genetic analysis of the endemic island loggerhead shrike, <i>Lanius ludovicianus anthonyi</i> . <i>Conservation Genetics</i> , 2011, 12, 1485-1493.	0.8	17
140	Nucleotide diversity and linkage disequilibrium in <i>Populus nigra</i> cinnamyl alcohol dehydrogenase (CAD4) gene. <i>Tree Genetics and Genomes</i> , 2011, 7, 1011-1023.	0.6	138
141	A Large Population Genetic Study of 15 Autosomal Short Tandem Repeat Loci for Establishment of Korean DNA Profile Database. <i>Molecules and Cells</i> , 2011, 32, 15-20.	1.0	42
142	Does spatial genetic structure increase with altitude? An answer from <i>Picea abies</i> in Tyrol, Austria. <i>Plant Systematics and Evolution</i> , 2011, 292, 133-141.	0.3	20
143	Genetic structure in peripheral Western European populations of the endangered species <i>Cochlearia pyrenaica</i> (Brassicaceae). <i>Plant Systematics and Evolution</i> , 2011, 297, 75-85.	0.3	15
144	Low connectivity and declining genetic variability along a depth gradient in <i>Corallium rubrum</i> populations. <i>Coral Reefs</i> , 2011, 30, 991-1003.	0.9	75

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145	Population structure and marker-trait association analysis of the US peanut ( <i>Arachis hypogaea</i> L.) mini-core collection. <i>Theoretical and Applied Genetics</i> , 2011, 123, 1307-1317.	1.8	128
146	Discordance in Variation of the ITS Region and the Mitochondrial COI Gene in the Subterranean Amphipod <i>Crangonyx islandicus</i> . <i>Journal of Molecular Evolution</i> , 2011, 73, 34-44.	0.8	9
147	Evolutionary genetics of MHC class II beta genes in the brown hare, <i>Lepus europaeus</i> . <i>Immunogenetics</i> , 2011, 63, 743-751.	1.2	16
148	HaploSearch: A tool for haplotype-sequence two-way transformation. <i>Mitochondrion</i> , 2011, 11, 366-367.	1.6	24
149	Reductive divergence of enterobacterial repetitive intergenic consensus sequences among Gammaproteobacteria genomes. <i>Journal of Microbiology</i> , 2011, 49, 35-45.	1.3	1
150	Genetic differentiation of wild and hatchery Oujiang color common carp: potential application to the identification of escapees. <i>Fisheries Science</i> , 2011, 77, 591-597.	0.7	5
151	Microsatellites reveal widespread predominance of an invasive over an indigenous <i>Bemisia tabaci</i> in Venezuela. <i>Phytoparasitica</i> , 2011, 39, 419-428.	0.6	13
152	First microsatellite panel for the Wood Tiger Moth ( <i>Parasemia plantaginis</i> ). <i>Conservation Genetics Resources</i> , 2011, 3, 197-199.	0.4	4
153	Characterization of thirteen new polymorphic microsatellite markers from the honeycomb grouper <i>Epinephelus merra</i> . <i>Conservation Genetics Resources</i> , 2011, 3, 629-631.	0.4	4
154	Microsatellite DNA markers for mating systems analysis in the Leishan moustache toad ( <i>Vibrissaphora</i> ) Tj ETQq1 1 0.784314 4gBT /Over 0.4	0.4	4
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306	Genetic divergence among three morphs of <i>Acentrogobius pflaumii</i> (Gobiidae) around Japan and their identification using multiplex haplotype-specific PCR of mitochondrial DNA. <i>Ichthyological Research</i> , 2012, 59, 216-222.	0.5	7

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365	Genetic diversity, population structure, and movements of mountain lions ( <i>Puma concolor</i> ) in Texas. <i>Journal of Mammalogy</i> , 2012, 93, 989-1000.	0.6	21
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405	General lack of phylogeographic structure in two sympatric, forest obligate squirrels ( <i>Sciurus</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 0 0	0.6	13
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560	Morphological differentiation in a common garden experiment among native and non-native specimens of the invasive weed yellow starthistle ( <i>Centaurea solstitialis</i> ). <i>Biological Invasions</i> , 2012, 14, 1459-1467.	1.2	34
561	Patterns of genetic variation of a Lessepsian parasite. <i>Biological Invasions</i> , 2012, 14, 1725-1736.	1.2	7
562	Global and endemic Asian lineages of the emerging pathogenic fungus <i>Batrachochytrium dendrobatidis</i> widely infect amphibians in China. <i>Diversity and Distributions</i> , 2012, 18, 307-318.	1.9	65
563	Regional divergence and mosaic spatial distribution of two closely related damselfly species ( <i>Enallagma hageni</i> and <i>Enallagma ebrium</i> ). <i>Journal of Evolutionary Biology</i> , 2012, 25, 196-209.	0.8	9
564	Phylogeography of <i>Acesta</i> clams from submarine seamounts and escarpments along the western margin of North America. <i>Marine Ecology</i> , 2012, 33, 75-87.	0.4	13
565	Heterozygosity predicts clutch and egg size but not plasticity in a house sparrow population with no evidence of inbreeding. <i>Molecular Ecology</i> , 2012, 21, 406-420.	2.0	38
566	Extensive gene flow over Europe and possible speciation over Eurasia in the ectomycorrhizal basidiomycete <i>Laccaria amethystina</i> complex. <i>Molecular Ecology</i> , 2012, 21, 281-299.	2.0	62
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568	Phylogeography at large spatial scales: incongruent patterns of population structure and demography of Pan-American butterflies associated with weedy habitats. <i>Journal of Biogeography</i> , 2012, 39, 382-396.	1.4	5
569	Genetic structure of a native cyprinid in a reservoir-altered stream network. <i>Freshwater Biology</i> , 2012, 57, 155-165.	1.2	19
570	Computer simulations: tools for population and evolutionary genetics. <i>Nature Reviews Genetics</i> , 2012, 13, 110-122.	7.7	221
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572	Strong population genetic structure and its management implications in the mud carp <i>Cirrhinus molitorella</i> , an indigenous freshwater species subject to an aquaculture and culture-based fishery. <i>Journal of Fish Biology</i> , 2012, 80, 651-668.	0.7	10
573	CONTRASTING PATTERNS OF DIVERSITY AND POPULATION DIFFERENTIATION AT THE INNATE IMMUNITY GENE TOLL-LIKE RECEPTOR 2 (TLR2) IN TWO SYMPATRIC RODENT SPECIES. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 720-731.	1.1	40
574	A specific mix of generalists: bacterial symbionts in Mediterranean <i>Ircinia</i> spp.. <i>FEMS Microbiology Ecology</i> , 2012, 79, 619-637.	1.3	75
575	Population differentiation, bottleneck and selection of Eurasian perch ( <i>Perca fluviatilis</i> L.) at the Asian edge of its natural range. <i>Biochemical Systematics and Ecology</i> , 2012, 40, 6-12.	0.6	7
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578	Population structuring and historical demography of a common clam worm <i>Perinereis aibuhitensis</i> near the coasts of Shandong Peninsula. <i>Biochemical Systematics and Ecology</i> , 2012, 44, 70-78.	0.6	11
579	Virulence factors and genetic variability of <i>Staphylococcus aureus</i> strains isolated from raw sheep's milk cheese. <i>International Journal of Food Microbiology</i> , 2012, 153, 53-57.	2.1	41
580	Geological habitat template overrides late Quaternary climate change as a determinant of range dynamics and phylogeography in some habitat specialist water beetles. <i>Journal of Biogeography</i> , 2012, 39, 970-983.	1.4	12
581	The role of seed dispersal, pollination and historical effects on genetic patterns of an insular plant that has lost its only seed disperser. <i>Journal of Biogeography</i> , 2012, 39, 1996-2006.	1.4	35
582	Genetically diverse but with surprisingly little geographical structure: the complex history of the widespread herb <i>Carex nigra</i> (Cyperaceae). <i>Journal of Biogeography</i> , 2012, 39, 2279-2291.	1.4	50
583	Gene flow among wild and domesticated almond species: insights from chloroplast and nuclear markers. <i>Evolutionary Applications</i> , 2012, 5, 317-329.	1.5	65
584	Demographic history of an elusive carnivore: using museums to inform management. <i>Evolutionary Applications</i> , 2012, 5, 619-628.	1.5	8
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586	<i>De novo</i> characterization of the <i>Timema cristinae</i> transcriptome facilitates marker discovery and inference of genetic divergence. <i>Molecular Ecology Resources</i> , 2012, 12, 549-561.	2.2	14
587	Demographic History of <i>Shorea curtisii</i> (Dipterocarpaceae) Inferred from Chloroplast DNA Sequence Variations. <i>Biotropica</i> , 2012, 44, 577-585.	0.8	22
588	LOCAL SELECTION UNDERLIES THE GEOGRAPHIC DISTRIBUTION OF SEX-RATIO DRIVE IN DROSOPHILA NEOTESTACEA. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 973-984.	1.1	26
589	LOW RATES OF BINDIN CODON EVOLUTION IN LECITHOTROPHIC HELIOCIDARIS SEA URCHINS. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 1709-1721.	1.1	7
590	COLONIZATION HISTORY AND POPULATION GENETICS OF THE COLOR-POLYMORPHIC HAWAIIAN HAPPY-FACE SPIDER THERIDION GRALLATOR (ARANEAE, THERIDIIDAE). <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 2815-2833.	1.1	22
591	TESTING THE LINK BETWEEN POPULATION GENETIC DIFFERENTIATION AND CLADE DIVERSIFICATION IN COSTA RICAN ORCHIDS. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 3035-3052.	1.1	29
592	The influence of habitat fragmentation on genetic diversity of a rare bird species that commonly faces environmental fluctuations. <i>Journal of Avian Biology</i> , 2012, 43, 168-176.	0.6	18
593	North-south population subdivision of <i>Juniperus seravschanica</i> in Kyrgyzstan revealed through novel plastid DNA markers. <i>Journal of Systematics and Evolution</i> , 2012, 50, 411-421.	1.6	1
594	Geographic variation of chloroplast DNA in <i>Platycarya strobilacea</i> (Juglandaceae). <i>Journal of Systematics and Evolution</i> , 2012, 50, 374-385.	1.6	31

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596	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
597	Genetic variability of <i>Echinococcus granulosus sensu stricto</i> in Europe inferred by mitochondrial DNA sequences. <i>Infection, Genetics and Evolution</i> , 2012, 12, 377-383.	1.0	115
598	Ascariasis in people and pigs: New inferences from DNA analysis of worm populations. <i>Infection, Genetics and Evolution</i> , 2012, 12, 227-235.	1.0	57
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601	Genetic and phenotypic diversity and random association of DNA markers of isolates of the fungal plant pathogen <i>Sclerotinia sclerotiorum</i> from soil on a fine geographic scale. <i>Soil Biology and Biochemistry</i> , 2012, 55, 28-36.	4.2	25
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603	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
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605	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
606	Climate and refugial origin influence the mitochondrial lineage distribution of weasels ( <i>Mustela</i> ). <i>Journal of Biogeography</i> , 2012, 39, 107-114.	0.7	33
607	Phylogeography of European sea bass in the north-east Atlantic: a correction and reanalysis of the mitochondrial DNA data from Coscia & Mariani (2011). <i>Biological Journal of the Linnean Society</i> , 2012, 106, 455-458.	0.7	5
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609	Extensive local-scale gene flow and long-term population stability in the intertidal mollusc <i>Katharina tunicata</i> (Mollusca: Polyplacophora). <i>Biological Journal of the Linnean Society</i> , 2012, 106, 589-597.	0.7	7
610	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
611	Phylogeography of two cryptic species of African desert jerboas (Dipodidae: <i>Jaculus</i> ). <i>Biological Journal of the Linnean Society</i> , 2012, 107, 27-38.	0.7	30
612	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

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614	Population genetics of the hazel hen <i>Bonasa bonasia</i> in Poland assessed with non-invasive samples. <i>Open Life Sciences</i> , 2012, 7, 759-775.	0.6	6
615	Hybridization between <i>Cottus gobio</i> and <i>Cottus poecilopus</i> in the Odra River drainage basin (Czech) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i>	0.8	1
616	Causes and consequences of living in closed societies: lessons from a long-term socio-genetic study on Bechstein's bats. <i>Molecular Ecology</i> , 2012, 21, 633-646.	2.0	61
617	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
618	Parallel phylogeographic structure in ecologically similar sympatric sister taxa. <i>Molecular Ecology</i> , 2012, 21, 987-1004.	2.0	54
619	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
620	Evidence for selection at cytokine loci in a natural population of field voles ( <i>Microtus</i> ) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i>	2.0	44
621	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
622	Microsatellite genotyping reveals end-Pleistocene decline in mammoth autosomal genetic variation. <i>Molecular Ecology</i> , 2012, 21, 3391-3402.	2.0	36
623	Recent population decline and selection shape diversity of taxol-related genes. <i>Molecular Ecology</i> , 2012, 21, 3006-3021.	2.0	24
624	Heavily male-biased long-distance dispersal of orangutans (genus: <i>Pongo</i> ), as revealed by Y-chromosomal and mitochondrial genetic markers. <i>Molecular Ecology</i> , 2012, 21, 3173-3186.	2.0	110
625	Population genetic structure and long-distance dispersal among seabird populations: Implications for colony persistence. <i>Molecular Ecology</i> , 2012, 21, 2863-2876.	2.0	46
626	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
627	The trouble with isolation by distance. <i>Molecular Ecology</i> , 2012, 21, 2839-2846.	2.0	525
628	Dynamics of introgressive hybridization assessed by SNP population genomics of coding genes in stocked brook charr ( <i>Salvelinus fontinalis</i> ). <i>Molecular Ecology</i> , 2012, 21, 2877-2895.	2.0	77
629	Neither philopatric nor panmictic: microsatellite and mtDNA evidence suggests lack of natal homing but limits to dispersal in Pacific lamprey. <i>Molecular Ecology</i> , 2012, 21, 2916-2930.	2.0	80
630	Cultivation shapes genetic novelty in a globally important invader. <i>Molecular Ecology</i> , 2012, 21, 3187-3199.	2.0	34

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632	Behavioural vs. molecular sources of conflict between nuclear and mitochondrial DNA: the role of male-biased dispersal in a Holarctic sea duck. <i>Molecular Ecology</i> , 2012, 21, 3562-3575.	2.0	40
633	Lack of genetic differentiation between monarch butterflies with divergent migration destinations. <i>Molecular Ecology</i> , 2012, 21, 3433-3444.	2.0	85
634	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
635	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
636	Phylogeography of Asian wild rice, <i>Oryza rufipogon</i> : a genome-wide view. <i>Molecular Ecology</i> , 2012, 21, 4593-4604.	2.0	79
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638	Effects of vicariant barriers, habitat stability, population isolation and environmental features on species divergence in the south-western Australian coastal reptile community. <i>Molecular Ecology</i> , 2012, 21, 3809-3822.	2.0	34
639	Environmental selection on transcriptome-derived SNPs in a high gene flow marine fish, the Atlantic herring ( <i>Clupea harengus</i> ). <i>Molecular Ecology</i> , 2012, 21, 3686-3703.	2.0	205
640	Spatially explicit models of dynamic histories: examination of the genetic consequences of Pleistocene glaciation and recent climate change on the American Pika. <i>Molecular Ecology</i> , 2012, 21, 3757-3775.	2.0	65
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642	Defining spatial and temporal patterns of phylogeographic structure in Madagascar's iguanid lizards (genus <i>Oplurus</i> ). <i>Molecular Ecology</i> , 2012, 21, 3839-3851.	2.0	14
643	Broad-scale adaptive genetic variation in alpine plants is driven by temperature and precipitation. <i>Molecular Ecology</i> , 2012, 21, 3729-3738.	2.0	161
644	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
645	Mitochondrial genomes reveal the global phylogeography and dispersal routes of the migratory locust. <i>Molecular Ecology</i> , 2012, 21, 4344-4358.	2.0	171
646	Migration distance rather than migration rate explains genetic diversity in human patrilocal groups. <i>Molecular Ecology</i> , 2012, 21, 4958-4969.	2.0	29
647	Population structure, mitochondrial polyphyly and the repeated loss of human biting ability in anopheline mosquitoes from the southwest Pacific. <i>Molecular Ecology</i> , 2012, 21, 4327-4343.	2.0	22
648	Disentangling invasion processes in a dynamic shipping-boating network. <i>Molecular Ecology</i> , 2012, 21, 4227-4241.	2.0	35

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649	Allotetraploid <i>Mimulus sookensis</i> are highly interfertile despite independent origins. <i>Molecular Ecology</i> , 2012, 21, 5280-5298.	2.0	23
650	Haplotype frequencies based on eight polymorphic sites at the 3' untranslated region of the <i>HLA-G</i> gene in individuals from two different geographical regions of Brazil. <i>Tissue Antigens</i> , 2012, 79, 272-278.	1.0	31
651	Genetic characterization of healthy and sebaceous adenitis affected Standard Poodles from the United States and the United Kingdom. <i>Tissue Antigens</i> , 2012, 80, 46-57.	1.0	17
652	Machine learning identifies specific habitats associated with genetic connectivity in <i>Hyla squirella</i> . <i>Journal of Evolutionary Biology</i> , 2012, 25, 1039-1052.	0.8	23
653	A simulation study on the performance of differentiation-based methods to detect selected loci using linked neutral markers. <i>Journal of Evolutionary Biology</i> , 2012, 25, 1364-1376.	0.8	53
654	Contrasting patterns of selection acting on MHC class I and class II DRB genes in the Alpine marmot ( <i>Marmota marmota</i> ). <i>Journal of Evolutionary Biology</i> , 2012, 25, 1686-1693.	0.8	14
655	Morphological and genetic distinctiveness of metallicolous and non-metallicolous populations of <i>Armeria maritima</i> s.l. (Plumbaginaceae) in Poland. <i>Plant Biology</i> , 2012, 14, 586-595.	1.8	27
656	Dispersal ability in codling moth: mark-release-recapture experiments and kinship analysis. <i>Agricultural and Forest Entomology</i> , 2012, 14, 399-407.	0.7	26
657	Molecular systematics of the <i>Navanax aenigmaticus</i> species complex (Mollusca, Cephalaspidea): coming full circle. <i>Zoologica Scripta</i> , 2012, 41, 374-385.	0.7	35
658	Effect of random sample size on the accuracy of nucleotide diversity estimation. <i>Russian Journal of Genetics</i> , 2012, 48, 746-750.	0.2	1
659	Phylogeography of red deer ( <i>Cervus elaphus</i> ): Analysis of MtDNA cytochrome b polymorphism. <i>Biology Bulletin</i> , 2012, 39, 323-330.	0.1	13
660	Interdisciplinary approach to the demography of Jamaica. <i>BMC Evolutionary Biology</i> , 2012, 12, 24.	3.2	26
661	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
662	Evolutionary forces shaping genomic islands of population differentiation in humans. <i>BMC Genomics</i> , 2012, 13, 107.	1.2	51
663	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> . <i>American Journal of Physical Anthropology</i> , 2012, 147, 1-10.	2.1	28
664	The population genetics of quechuas, the largest native south american group: Autosomal sequences, SNPs, and microsatellites evidence high level of diversity. <i>American Journal of Physical Anthropology</i> , 2012, 147, 443-451.	2.1	11
665	Mitochondrial cytochrome b sequences resolve the taxonomy of field mice ( <i>Apodemus</i> ) in the western Balkan refugium. <i>Acta Theriologica</i> , 2012, 57, 1-7.	1.1	12
666	The Caucasian corticioid fungi: level of endemism, similarity, and possible contribution to European fungal diversity. <i>Fungal Diversity</i> , 2012, 52, 35-48.	4.7	8



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668	Population genetics of the nurse shark ( <i>Ginglymostoma cirratum</i> ) in the western Atlantic. <i>Marine Biology</i> , 2012, 159, 489-498.	0.7	50
669	Association of CISH -292A/T genetic variant with hepatitis B virus infection. <i>Immunogenetics</i> , 2012, 64, 261-265.	1.2	14
670	Genetic population assignment reveals a long-distance incursion to an island by a stoat ( <i>Mustela</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	1.2	23
671	Remaining genetic diversity in Brazilian Merganser ( <i>Mergus octosetaceus</i> ). <i>Conservation Genetics</i> , 2012, 13, 293-298.	0.8	8
672	Genetic evidence for recent range fragmentation and severely restricted dispersal in the critically endangered Sierra Madre Sparrow, <i>Xenospiza baileyi</i> . <i>Conservation Genetics</i> , 2012, 13, 283-291.	0.8	11
673	Phylogeography of an endangered Western North American springsnail. <i>Conservation Genetics</i> , 2012, 13, 299-305.	0.8	8
674	The role of barriers and gradients in differentiation processes of pyrgulinid microgastropods of Lake Ohrid. <i>Hydrobiologia</i> , 2012, 682, 61-73.	1.0	30
675	A study of genetic variations, population size, and population dynamics of the catadromous Japanese eel <i>Anguilla japonica</i> (Pisces) in northern Taiwan. <i>Hydrobiologia</i> , 2012, 683, 203-216.	1.0	7
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677	Polymorphisms of beta-lactoglobulin promoter region in three Sicilian goat breeds. <i>Molecular Biology Reports</i> , 2012, 39, 3203-3210.	1.0	10
678	A method for the analysis of 32 X chromosome insertion deletion polymorphisms in a single PCR. <i>International Journal of Legal Medicine</i> , 2012, 126, 97-105.	1.2	45
679	Analysis of 12 X-STRs in Greenlanders, Danes and Somalis using Argus X-12. <i>International Journal of Legal Medicine</i> , 2012, 126, 121-128.	1.2	70
680	Loss of small glaciers will diminish beta diversity in Pyrenean streams at two levels of biological organization. <i>Global Ecology and Biogeography</i> , 2013, 22, 40-51.	2.7	76
681	Novel SNP development and analysis at a NADP <sup>+</sup> -specific IDH enzyme gene in a four species mixed oak forest. <i>Plant Biology</i> , 2013, 15, 126-137.	1.8	9
682	The gene flow and mode of reproduction of <i>Dothistroma septosporum</i> in the Czech Republic. <i>Plant Pathology</i> , 2013, 62, 59-68.	1.2	15
683	Assessing the genetic diversity of castor bean from Chiapas, MÃ©xico using SSR and AFLP markers. <i>Industrial Crops and Products</i> , 2013, 41, 134-143.	2.5	23
684	Worldwide genetic relationships of pigs as inferred from X chromosome <sup>sc</sup> SNP <sub>s</sub> . <i>Animal Genetics</i> , 2013, 44, 130-138.	0.6	9

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685	Tracing glacial refugia of <i>Triturus</i> newts based on mitochondrial DNA phylogeography and species distribution modeling. <i>Frontiers in Zoology</i> , 2013, 10, 13.	0.9	89
686	Dissecting the genetic structure of Korean population using genome-wide SNP arrays. <i>Genes and Genomics</i> , 2013, 35, 355-363.	0.5	11
687	Inference of human continental origin and admixture proportions using a highly discriminative ancestry informative 41-SNP panel. <i>Investigative Genetics</i> , 2013, 4, 13.	3.3	93
688	The number of markers and samples needed for detecting bottlenecks under realistic scenarios, with and without recovery: a simulation-based study. <i>Molecular Ecology</i> , 2013, 22, 3444-3450.	2.0	64
689	Genetic diversity and maternal origin of Bangladeshi chicken. <i>Molecular Biology Reports</i> , 2013, 40, 4123-4128.	1.0	20
690	Continental-scale assessment of genetic diversity and population structure in quaking aspen ( <i>Picea canadensis</i> ). <i>Journal of Biogeography</i> , 2013, 40, 1780-1791.	1.4	66
691	Are local extinctions and recolonizations continuing at the colder limits of marine fish distributions? <i>Halobatrachus didactylus</i> (Bloch & Schneider, 1801), a possible candidate. <i>Marine Biology</i> , 2013, 160, 2461-2467.	0.7	10
692	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
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969	Conservation and management of peripheral populations: Spatial and temporal influences on the genetic structure of wood frog ( <i>Rana sylvatica</i> ) populations. <i>Biological Conservation</i> , 2013, 158, 351-358.	1.9	41
970	Mature male parr contribution to the effective size of an anadromous <i>A</i> tlantic salmon ( <i>Salmo salar</i> ) population over 30 years. <i>Molecular Ecology</i> , 2013, 22, 2394-2407.	2.0	43
971	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
972	Single population and common natal origin for Adriatic Scomber scombrus stocks: evidence from an integrated approach. <i>ICES Journal of Marine Science</i> , 2013, 70, 387-398.	1.2	32
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975	Genomics, bears, fruit. <i>Nature Genetics</i> , 2013, 45, 1-1.	9.4	95
976	Genetic structure in urban and rural populations of <i>Apodemus agrarius</i> in Poland. <i>Mammalian Biology</i> , 2013, 78, 171-177.	0.8	26
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982	Genomic scan for single nucleotide polymorphisms reveals patterns of divergence and gene flow between ecologically divergent species. <i>Molecular Ecology</i> , 2013, 22, 842-855.	2.0	110
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984	Y-chromosome variation in Tajiks and Iranians. <i>Annals of Human Biology</i> , 2013, 40, 48-54.	0.4	6
985	Extreme genetic depauperation and differentiation of both populations and species in Eurasian feather grasses ( <i>Stipa</i> ). <i>Plant Systematics and Evolution</i> , 2013, 299, 259-269.	0.3	33
986	Positive natural selection of TRIB2, a novel gene that influences visceral fat accumulation, in East Asia. <i>Human Genetics</i> , 2013, 132, 201-217.	1.8	19
987	Whole-genome analysis with SNPs from BOPA1 shows clearly defined groupings of Western Mediterranean, Ethiopian, and Fertile Crescent barleys. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 251-264.	0.8	15
988	Nothing but a trace left? Autochthony and conservation status of Northern Adriatic <i>Salmo trutta</i> inferred from PCR multiplexing, mtDNA control region sequencing and microsatellite analysis. <i>Hydrobiologia</i> , 2013, 702, 201-213.	1.0	26
989	Conservation genetics of endangered leaf-beetle <i>Cheilotoma musciformis</i> populations in Poland. <i>Journal of Insect Conservation</i> , 2013, 17, 67-77.	0.8	16
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994	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
995	Postglacial recolonization history of the European crabapple ( <i>Malus sylvestris</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 101 2249-2263.	2.0	86
996	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
997	Multilocus sequence typing of <i>Enterocytozoon bieneusi</i> : Lack of geographic segregation and existence of genetically isolated sub-populations. <i>Infection, Genetics and Evolution</i> , 2013, 14, 111-119.	1.0	49
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999	Analysis of 15 autosomal STR loci in the population of the State of Acre, Brazilian Amazonia. <i>Forensic Science International: Genetics Supplement Series</i> , 2013, 4, e11-e12.	0.1	0
1000	Population data of 12 X-chromosomal STR loci in Chinese Han samples from Hebei Province. <i>Forensic Science International: Genetics</i> , 2013, 7, e43-e44.	1.6	8
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1007	Toll like receptor 2 and 4 polymorphisms in malaria endemic populations of India. <i>Human Immunology</i> , 2013, 74, 223-229.	1.2	10
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1011	Geographic Genetic Structure in Two Laticaudine Sea Kraits, <i>Laticauda laticaudata</i> and <i>Laticauda semifasciata</i> (Serpentes: Elapidae), in the Ryukyu-Taiwan Region as Inferred from Mitochondrial Cytochrome b Sequences. <i>Zoological Science</i> , 2013, 30, 633-641.	0.3	9
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1013	Lack of host specificity of <i>Colletotrichum</i> spp. isolates associated with anthracnose symptoms on mango in Brazil. <i>Plant Pathology</i> , 2013, 62, 1038-1047.	1.2	19
1014	Mitochondrial Haplotypes Indicate Parapatric-like Phylogeographic Structure in Blue-Spotted Maskray ( <i>Neotrygon kuhlii</i> ) from the Coral Triangle Region. <i>Journal of Heredity</i> , 2013, 104, 725-733.	1.0	20
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1016	Genotyping of two populations of Southern Baltic Sea trout <i>Salmo trutta m. trutta</i> using an Atlantic salmon derived SNP-array. <i>Marine Genomics</i> , 2013, 9, 25-32.	0.4	26
1017	A first molecular investigation of monumental olive trees in Apulia region. <i>Scientia Horticulturae</i> , 2013, 162, 204-212.	1.7	30
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1021	Population genetic analyses of 15 STR loci from seven forensically-relevant populations residing in the state of Kuwait. <i>Forensic Science International: Genetics</i> , 2013, 7, e106-e107.	1.6	9
1022	Genetic diversity of the endangered Chinese endemic herb <i>Dayaoshania cotinifolia</i> (Gesneriaceae) revealed by simple sequence repeat (SSR) markers. <i>Biochemical Systematics and Ecology</i> , 2013, 48, 51-57.	0.6	3
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1024	Genetic diversity, population structure, and demographic history of exploited sea urchin populations ( <i>Tripneustes gratilla</i> ) in the Philippines. <i>Journal of Experimental Marine Biology and Ecology</i> , 2013, 449, 284-293.	0.7	14
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1026	Population genetics of 17 Y-STR loci in Chinese Manchu population from Liaoning Province, Northeast China. <i>Forensic Science International: Genetics</i> , 2013, 7, e84-e85.	1.6	48
1027	HLA-G haplotype structure shows good conservation between different populations and good correlation with high, normal and low soluble HLA-G expression. <i>Human Immunology</i> , 2013, 74, 203-206.	1.2	51

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1042	Social and genetic population structure of free-ranging cheetah in Botswana: implications for conservation. European Journal of Wildlife Research, 2013, 59, 281-285.	0.7	7
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1044	Genetic variation and reproductive mode in two epiphytic lichens of conservation concern: a transatlantic study of <i>Evernia divaricata</i> and <i>Usnea longissima</i> . Botany, 2013, 91, 69-81.	0.5	13
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1047	River islands, refugia and genetic structuring in the endemic brown frog <i>Rana kukunoris</i> ( <i>Anura</i> : <i>Ranidae</i> ) of the <i>Qinghai-Tibetan Plateau</i> . <i>Molecular Ecology</i> , 2013, 22, 130-142.	2.0	36
1048	Genomic conflict drives patterns of <i>X-linked</i> population structure in <i>Drosophila neotestacea</i> . <i>Molecular Ecology</i> , 2013, 22, 157-169.	2.0	10
1049	A question of time: the land snail <i>Murella muralis</i> ( <i>Gastropoda</i> : <i>Trochomorphidae</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 22, 170-186.	2.0	21
1050	Footprints of selection in wild populations of <i>Bicyclus anynana</i> along a latitudinal cline. <i>Molecular Ecology</i> , 2013, 22, 341-353.	2.0	13
1051	The evolution of north-east Atlantic gadfly petrels using statistical phylogeography. <i>Molecular Ecology</i> , 2013, 22, 495-507.	2.0	19
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1053	Genotypic composition and the relationship between genotypic composition and geographical proximity of the cyanobacterium <i>Microcystis aeruginosa</i> in western Japan. <i>Canadian Journal of Microbiology</i> , 2013, 59, 266-272.	0.8	2
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1059	PHYLOGEOGRAPHIC STRUCTURE AND OUTBREEDING DEPRESSION REVEAL EARLY STAGES OF REPRODUCTIVE ISOLATION IN THE NEOTROPICAL ORCHID <i>EPIDENDRUM DENTICULATUM</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 2024-2039.	1.1	49
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1062	Does the Reproductive Strategy Affect the Transmission and Genetic Diversity of Bionts in Cyanolichens? A Case Study Using Two Closely Related Species. <i>Microbial Ecology</i> , 2013, 65, 517-530.	1.4	37
1063	Using population genetic methods to identify the origin of an invasive population and to diagnose cryptic subspecies of <i>Telchin licus</i> ( <i>Lepidoptera</i> : <i>Castniidae</i> ). <i>Bulletin of Entomological Research</i> , 2013, 103, 89-97.	0.5	15

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1066	Mitochondrial Cytochrome b Phylogeny and Historical Biogeography of the Tohoku Salamander, <i>Hynobius Lichenatus</i> (Amphibia, Caudata). <i>Zoological Science</i> , 2013, 30, 167-173.	0.3	18
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1074	Human loci involved in drug biotransformation: worldwide genetic variation, population structure, and pharmacogenetic implications. <i>Human Genetics</i> , 2013, 132, 563-577.	1.8	16
1075	Genetic relationships between <i>M. t. H. alla</i> and <i>M. mongolian</i> populations of <i>Hipparchia autonoe</i> ( <i>Lepidoptera</i> ): Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 297 Td	0.4	8
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1085	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
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1087	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
1088	Neolithic mitochondrial haplogroup H genomes and the genetic origins of Europeans. <i>Nature Communications</i> , 2013, 4, 1764.	5.8	180
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1091	Microsatellite Data Analysis for Population Genetics. <i>Methods in Molecular Biology</i> , 2013, 1006, 271-295.	0.4	36
1092	<i>Cucumber mosaic virus</i> populations in Tunisian pepper crops are mainly composed of virus reassortants with resistance-breaking properties. <i>Plant Pathology</i> , 2013, 62, 1415-1428.	1.2	20
1093	Microevolution in time and space: <i>SNP</i> analysis of historical <i>DNA</i> reveals dynamic signatures of selection in <i>Atlantic cod</i> . <i>Molecular Ecology</i> , 2013, 22, 2424-2440.	2.0	86
1095	Eco-evolutionary dynamics in response to selection on life-history. <i>Ecology Letters</i> , 2013, 16, 754-763.	3.0	63
1096	Fingerprinting and genetic diversity of <i>Olea europaea</i> L. ssp. <i>europaea</i> accessions from the cultivar <i>Galega</i> using RAPD markers. <i>Scientia Horticulturae</i> , 2013, 156, 24-28.	1.7	9
1097	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
1098	LANDSCAPE GENOMICS IN ATLANTIC SALMON ( <i>SALMO SALAR</i> ): SEARCHING FOR GENE-ENVIRONMENT INTERACTIONS DRIVING LOCAL ADAPTATION. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 3469-3487.	1.1	106
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1100	Genetic evidence of TAP1 gene variant as a susceptibility factor in Indian leprosy patients. <i>Human Immunology</i> , 2013, 74, 803-807.	1.2	18

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1103	Long-term panmixia in a cosmopolitan <sc>P</sc>acific coral reef fish and a nebulous genetic boundary with its broadly sympatric sister species. Journal of Evolutionary Biology, 2013, 26, 783-799.	0.8	15
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1105	Genetic structure of a Japanese brown frog (<i>Rana japonica</i>) population implies severe restriction of gene flow caused by recent urbanization in a<i>satoyama</i>landscape. Mitochondrial DNA, 2013, 24, 697-704.	0.6	8
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1110	Quaternary refugia in southwestern Iran: insights from two sympatric moth species (Insecta,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 347 To	0.7	39
1111	Complex evolutionary history of the pallid dottedâ€œblue butterfly (Lycaenidae: <i>Euphilotes</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 347 To 2059-2070.	1.4	2
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1115	Analysis of genetic ancestry in the admixed Brazilian population from Rio de Janeiro using 46 autosomal ancestry-informative indel markers. Annals of Human Biology, 2013, 40, 94-98.	0.4	55
1116	Historical demography and genetic differentiation inferred from the mitochondrial DNA of the silky shark (Carcharhinus falciformis) in the Pacific Ocean. Fisheries Research, 2013, 147, 36-46.	0.9	24
1117	Phylogenetic and biogeographical relationships of the<i>Sander</i>pikeperches (Percidae:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 To 2013, 110, 156-179.	0.7	32
1118	Whole-genome sequencing of giant pandas provides insights into demographic history and local adaptation. Nature Genetics, 2013, 45, 67-71.	9.4	303

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1126	Multilocus phylogeny and Bayesian estimates of species boundaries reveal hidden evolutionary relationships and cryptic diversity in Southeast Asian monitor lizards. <i>Molecular Ecology</i> , 2013, 22, 3495-3510.	2.0	40
1127	Genetic variability, population size and reproduction potential in <i>Ligularia sibirica</i> (L.) populations in Estonia. <i>Conservation Genetics</i> , 2013, 14, 661-669.	0.8	24
1128	The population structure and recent colonization history of Oregon threespine stickleback determined using restriction-site associated DNA sequencing. <i>Molecular Ecology</i> , 2013, 22, 2864-2883.	2.0	119
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1131	Population genomics of Pacific lamprey: adaptive variation in a highly dispersive species. <i>Molecular Ecology</i> , 2013, 22, 2898-2916.	2.0	166
1132	A skeletonless sponge of Caribbean mangroves: invasive or undescribed?. <i>Invertebrate Biology</i> , 2013, 132, 81-94.	0.3	4
1133	Differentiation within and between river basins of <i>Podostemum irgangii</i> (Podostemaceae), a rapid-water macrophyte of southern Brazil. <i>Aquatic Botany</i> , 2013, 107, 33-38.	0.8	5
1134	Quaternary range and demographic expansion of <i>Laelaspis darwini</i> ( <i>Laelaspis</i> family) in the Monte Desert of Central Argentina using Bayesian phylogeography and ecological niche modelling. <i>Molecular Ecology</i> , 2013, 22, 4038-4054.	2.0	33
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1136	Phylogeography of the sand dollar genus <i>Mellita</i> : Cryptic speciation along the coasts of the Americas. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 1033-1042.	1.2	25

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1144	Temporal genetic structure and relatedness in the Tufted Duck <i>Aythya fuligula</i> suggests limited kin association in winter. <i>Ibis</i> , 2013, 155, 499-507.	1.0	7
1145	High resolution mapping of Y haplogroup G in Tyrol (Austria). <i>Forensic Science International: Genetics</i> , 2013, 7, 529-536.	1.6	9
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1153	INTEGRATIVE TESTING OF HOW ENVIRONMENTS FROM THE PAST TO THE PRESENT SHAPE GENETIC STRUCTURE ACROSS LANDSCAPES. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 3386-3402.	1.1	110
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1156	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
1157	No evidence for nuclear introgression despite complete mt<scp>DNA</scp> replacement in the <scp>C</scp>arpathian newt (<i><scp>L</scp>issotriton montandoni</i>). <i>Molecular Ecology</i> , 2013, 22, 1884-1903.	2.0	96
1158	Fine-scale population genetic structure in <i>Artemia urmiana</i> (GÃ¼nther, 1890) based on mtDNA sequences and ISSR genomic fingerprinting. <i>Organisms Diversity and Evolution</i> , 2013, 13, 531-543.	0.7	22
1159	<scp>DNA</scp> barcoding reveals cryptic diversity in the peanut worm <i>Sipunculus nudus</i>. <i>Molecular Ecology Resources</i> , 2013, 13, 596-606.	2.2	25
1160	Paternal origins of Chinese cattle. <i>Animal Genetics</i> , 2013, 44, 446-449.	0.6	46
1161	Population genetics of 17 Y-STR markers in West Libya (Tripoli region). <i>Forensic Science International: Genetics</i> , 2013, 7, e59-e61.	1.6	12
1162	Conservation Genetics of <i>Gambusia krumholzi</i> (Teleostei: Poeciliidae) with Assessment of the Species Status of <i>G. clarkhubbsi</i> and Hybridization with <i>G. speciosa</i>. <i>Copeia</i> , 2013, 2013, 72-79.	1.4	7
1163	Assessing the genetic impact of massive restocking on wild mallard. <i>Animal Conservation</i> , 2013, 16, 295-305.	1.5	24
1164	An emerging infectious pathogen endangers an ancient lineage of common carp by acting synergistically with conspecific exotic strains. <i>Animal Conservation</i> , 2013, 16, 324-330.	1.5	13
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1168	A measure of genetic diversity of goldenseal ( <i>Hydrastis canadensis</i> L.) by RAPD analysis. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 1201-1207.	0.8	0
1169	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
1170	SNP-revealed genetic diversity in wild emmer wheat correlates with ecological factors. <i>BMC Evolutionary Biology</i> , 2013, 13, 169.	3.2	36
1171	Phylogeography of the Rickettâ€™s big-footed bat, <i>Myotis pilosus</i> (Chiroptera: Vespertilionidae): a novel pattern of genetic structure of bats in China. <i>BMC Evolutionary Biology</i> , 2013, 13, 241.	3.2	8
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1174	Human introductions create opportunities for intra-specific hybridization in an alien lizard. <i>Biological Invasions</i> , 2013, 15, 1101-1112.	1.2	22
1175	Landscape heterogeneity and local adaptation define the spatial genetic structure of Pacific salmon in a pristine environment. <i>Conservation Genetics</i> , 2013, 14, 483-498.	0.8	22
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1185	Semi-natural river system maintains functional connectivity and gene flow of the critically endangered gravel grasshopper ( <i>Chorthippus pullus</i> ). <i>Biological Conservation</i> , 2013, 158, 88-97.	1.9	6
1186	Genetic characterization of an X-STR decaplex on the population of Pichincha (Ecuador). <i>Forensic Science International: Genetics Supplement Series</i> , 2013, 4, e144-e145.	0.1	4
1187	Evaluation of the PowerPlex Fusion System in a sample from East Timor. <i>Forensic Science International: Genetics Supplement Series</i> , 2013, 4, e105-e106.	0.1	6
1188	Development and multiplexing of microsatellite loci for the near threatened freshwater mussel <i>Potomida littoralis</i> (Cuvier, 1798) using 454 sequencing. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2013, 23, 619-623.	0.9	10
1189	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
1190	Discordant Genetic Diversity and Geographic Patterns Between <i>Crassicutis cichlasomae</i> (Digenea: Tj ETQq1 1 0.784314 rgBT /Overlode Middle-America. <i>Journal of Parasitology</i> , 2013, 99, 978-988.	0.3	14

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1192	Phylogeographic history and taxonomy of some afro-alpine grasses assessed based on AFLPs and morphometry: <i>Deschampsia cespitosa</i> , <i>D. angusta</i> and <i>Koeleria capensis</i> . Alpine Botany, 2013, 123, 107-122.	1.1	22
1193	Neutral and quantitative genetic differentiation among <i>Trollius europaeus</i> populations within a fragmented landscape. Alpine Botany, 2013, 123, 55-63.	1.1	1
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1198	Population structure and landscape genetics of two endangered frog species of genus <i>Odorrana</i> : different scenarios on two islands. Heredity, 2013, 110, 46-56.	1.2	22
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1205	Invasion genetics of vendace ( <i>Coregonus albula</i> ) in the <i>L. nari</i> <i>P. asvik</i> watercourse: revealing the origin and expansion pattern of a rapid colonization event. Ecology and Evolution, 2013, 3, 1400-1412.	0.8	24
1206	Intragenomic sequence variation at the ITS1-ITS2 region and at the 18S and 28S nuclear ribosomal DNA genes of the New Zealand mud snail, <i>Potamopyrgus antipodarum</i> (Hydrobiidae: Mollusca). Journal of Molluscan Studies, 2013, 79, 205-217.	0.4	11
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1208	Origins of Shared Genetic Variation in African Cichlids. Molecular Biology and Evolution, 2013, 30, 906-917.	3.5	86
1209	The Population Genomics of Repeated Evolution in the Blind Cavefish <i>Astyanax mexicanus</i> . Molecular Biology and Evolution, 2013, 30, 2383-2400.	3.5	87

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1215	Genetic Population Structure of US Atlantic Coastal Striped Bass ( <i>Morone saxatilis</i> ). <i>Journal of Heredity</i> , 2013, 104, 510-520.	1.0	17
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1324	Positive correlation between variants of lipid metabolism-related genes and coronary heart disease. <i>Molecular Medicine Reports</i> , 2013, 8, 260-266.	1.1	6
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1337	Isolation and characterisation of microsatellite loci in the bush stone-curlew ( <i>Burhinus grallarius</i> ), a declining Australian bird. <i>Australian Journal of Zoology</i> , 2013, 61, 421.	0.6	0
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1355	Population Data for 17 Y-STRs in Samples from Southeastern Anatolia Region of Turkey. <i>International Journal of Human Genetics</i> , 2013, 13, 105-111.	0.1	8
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1366	ITS1 Copy Number Varies among <i>Batrachochytrium dendrobatidis</i> Strains: Implications for qPCR Estimates of Infection Intensity from Field-Collected Amphibian Skin Swabs. <i>PLoS ONE</i> , 2013, 8, e59499.	1.1	96
1367	Integrative Phylogeography of <i>Calotriton</i> Newts (Amphibia, Salamandridae), with Special Remarks on the Conservation of the Endangered Montseny Brook Newt ( <i>Calotriton arnoldi</i> ). <i>PLoS ONE</i> , 2013, 8, e62542.	1.1	18
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1369	Analysis of Population Substructure in Two Sympatric Populations of Gran Chaco, Argentina. <i>PLoS ONE</i> , 2013, 8, e64054.	1.1	22
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1422	Population Structure, Linkage Disequilibrium and Selective Loci in Natural Populations of <i>Prunus davidiana</i> . <i>Journal of Agricultural Science</i> , 2013, 5, .	0.1	1
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1439	Adaptive Genetic Divergence along Narrow Environmental Gradients in Four Stream Insects. <i>PLoS ONE</i> , 2014, 9, e93055.	1.1	29
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1479	Short Communication Cross-species transferability of eastern white pine ( <i>Pinus strobus</i> ) nuclear microsatellite markers to five Mexican white pines. <i>Genetics and Molecular Research</i> , 2014, 13, 7571-7576.	0.3	15



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1633	Cross-species outlier detection reveals different evolutionary pressures between sister species. <i>New Phytologist</i> , 2014, 204, 215-229.	3.5	31
1634	Lack of association between winter coat colour and genetic population structure in the Japanese hare, <i>Lepus brachyurus</i> (Lagomorpha: Leporidae). <i>Biological Journal of the Linnean Society</i> , 2014, 111, 761-776.	0.7	10
1635	Is isolation by adaptation driving genetic divergence among proximate Dolly Varden char populations?. <i>Ecology and Evolution</i> , 2014, 4, 2515-2532.	0.8	23
1636	Genetic and morphometric divergence in threespine stickleback in the Chignik catchment, Alaska. <i>Ecology and Evolution</i> , 2014, 4, 144-156.	0.8	14
1637	Fin whale MDH &#1 and MPI allozyme variation is not reflected in the corresponding DNA sequences. <i>Ecology and Evolution</i> , 2014, 4, 1787-1803.	0.8	5
1638	Time-series analysis reveals genetic responses to intensive management of razorback sucker (<i>Xyrauchen texanus</i>). <i>Evolutionary Applications</i> , 2014, 7, 339-354.	1.5	21
1639	Low genetic diversity and high inbreeding of the endangered yews in Central Himalaya: implications for conservation of their highly fragmented populations. <i>Diversity and Distributions</i> , 2014, 20, 1270-1284.	1.9	27
1640	Clock Gene Evolution: Seasonal Timing, Phylogenetic Signal, or Functional Constraint?. <i>Journal of Heredity</i> , 2014, 105, 407-415.	1.0	5
1641	Recipient of the 2013 <i>Molecular Ecology</i> Prize: Laurent Excoffier. <i>Molecular Ecology</i> , 2014, 23, 16-19.	2.0	0
1642	Environmental versus geographical determinants of genetic structure in two subalpine conifers. <i>New Phytologist</i> , 2014, 201, 180-192.	3.5	52
1643	Early Holocene chicken domestication in northern China. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17564-17569.	3.3	181

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1646	Influence of Host Shift on Genetic Differentiation of the Oriental Fruit Fly, <i>Bactrocera dorsalis</i> . Journal of Integrative Agriculture, 2014, 13, 2701-2708.	1.7	2
1647	Population divergences despite long pelagic larval stages: lessons from crocodile icefishes ( <i>Channichthyidae</i> ). Molecular Ecology, 2014, 23, 284-299.	2.0	21
1648	Selective pressures on MHC class II genes in the guppy ( <i>Poecilia reticulata</i> ). Tj ETQq0 0 0 rgBT /Overlock Biology, 2014, 27, 2347-2359.	0.8	55
1649	Tumor necrosis factor haplotype diversity in Mestizo and Native populations of Mexico. Tissue Antigens, 2014, 83, 247-259.	1.0	5
1650	Male lineage strata of Brazilian population disclosed by the simultaneous analysis of STRs and SNPs. Forensic Science International: Genetics, 2014, 13, 264-268.	1.6	14
1651	Development of MHC-Linked Microsatellite Markers in the Domestic Cat and Their Use to Evaluate MHC Diversity in Domestic Cats, Cheetahs, and Gir Lions. Journal of Heredity, 2014, 105, 493-505.	1.0	10
1652	Spatiotemporal changes in the genetic diversity of harmful algal blooms caused by the toxic dinoflagellate <i>Alexandrium minutum</i> . Molecular Ecology, 2014, 23, 549-560.	2.0	74
1653	Identifying geographic hot spots of reassortment in a multipartite plant virus. Evolutionary Applications, 2014, 7, 569-579.	1.5	7
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1656	Increased genetic divergence between two closely related fir species in areas of range overlap. Ecology and Evolution, 2014, 4, 1019-1029.	0.8	12
1657	Mitochondrial DNA variation and phylogenetic relationships among five tuna species based on sequencing of D-loop region. Mitochondrial DNA, 2016, 27, 1-5.	0.6	7
1658	Influence of Forest Road Culverts and Waterfalls on the Fine-Scale Distribution of Brook Trout Genetic Diversity in a Boreal Watershed. Transactions of the American Fisheries Society, 2014, 143, 1577-1591.	0.6	57
1659	Population genetic structure of <i>Microdochium majus</i> and <i>Microdochium nivale</i> associated with Fusarium head blight of wheat in Hokkaido, Japan. European Journal of Plant Pathology, 2014, 140, 787-795.	0.8	7
1660	Lack of mitochondrial DNA structure in <i>Bos taurus</i> donkey is consistent with a quick spread of the species after domestication. Animal Genetics, 2014, 45, 144-147.	0.6	17
1661	High genetic diversity in a small population: the case of Chilean blue whales. Ecology and Evolution, 2014, 4, 1398-1412.	0.8	29

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1662	Maternal Genetic Heritage of Southeastern Europe Reveals a New Croatian Isolate and a Novel, Local Sub-Branching in the X2 Haplogroup. <i>Annals of Human Genetics</i> , 2014, 78, 178-194.	0.3	11
1663	Predicting 5-fluorouracil toxicity: DPD genotype and 5,6-dihydrouracil:uracil ratio. <i>Pharmacogenomics</i> , 2014, 15, 1653-1666.	0.6	55
1664	Phylogenetic relationships and genetic diversity of <i>Nemesis</i> Risso, 1826 species found on different elasmobranch host species off the KwaZulu-Natal coast, South Africa. <i>African Journal of Marine Science</i> , 2014, 36, 163-173.	0.4	8
1665	Genetic Structure and Diversity of Japanese Chum Salmon Populations Inferred from Single-Nucleotide Polymorphism Markers. <i>Transactions of the American Fisheries Society</i> , 2014, 143, 1231-1246.	0.6	13
1666	Genetic History of Walleyes Spawning in Lake Erie's Cattaraugus Creek: a Comparison of Pre- and Poststocking. <i>Transactions of the American Fisheries Society</i> , 2014, 143, 1295-1307.	0.6	9
1667	Population structure in the tropical peatmoss, <i>Sphagnum tumidulum</i> Besch. (Sphagnaceae). <i>Bryologist</i> , 2014, 117, 329.	0.1	3
1668	Evidence for a new introduction of the pitch canker fungus <i> Fusarium circinatum</i> in South Africa. <i>Plant Pathology</i> , 2014, 63, 530-538.	1.2	23
1669	WFS1 mutations in hearing-impaired children. <i>International Journal of Audiology</i> , 2014, 53, 446-451.	0.9	9
1670	NO to obsolete definitions: YES to blanks. <i>Tissue Antigens</i> , 2014, 83, 119-120.	1.0	9
1671	Measuring connectivity of invasive stoat populations to inform conservation management. <i>Wildlife Research</i> , 2014, 41, 395.	0.7	4
1672	Mitochondrial Control Region Variability in <i>Mytilus galloprovincialis</i> Populations from the Central-Eastern Mediterranean Sea. <i>International Journal of Molecular Sciences</i> , 2014, 15, 11614-11625.	1.8	10
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1675	Multilocus Microsatellite Genotyping Array for Investigation of Genetic Epidemiology of <i>Pneumocystis jirovecii</i> . <i>Journal of Clinical Microbiology</i> , 2014, 52, 1391-1399.	1.8	26
1676	Ecology and Genetic Structure of Zoonotic <i>Anisakis</i> spp. from Adriatic Commercial Fish Species. <i>Applied and Environmental Microbiology</i> , 2014, 80, 1281-1290.	1.4	71
1677	Genetic architectures of ADME genes in five Eurasian admixed populations and implications for drug safety and efficacy. <i>Journal of Medical Genetics</i> , 2014, 51, 614-622.	1.5	22
1678	Analyses of age and population genetic structure of the broadbanded thornyhead <i>Sebastolobus macrochir</i> in North Japan suggest its broad dispersion and migration before settlement. <i>Journal of Oceanography</i> , 2014, 70, 457-462.	0.7	4
1679	Population at the edge: increased divergence but not inbreeding towards northern range limit in <i>Acer campestre</i> . <i>Tree Genetics and Genomes</i> , 2014, 10, 1739-1753.	0.6	13

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1681	The role of the urals in the genetic diversity of the European moose subspecies ( <i>Alces alces alces</i> ). <i>Biology Bulletin</i> , 2014, 41, 522-528.	0.1	4
1682	A population genetic window into the past and future of the walleye <i>Sander vitreus</i> : relation to historic walleye and the extinct "blue pike" <i>S. v. glaucus</i> . <i>BMC Evolutionary Biology</i> , 2014, 14, 133.	3.2	17
1683	Targeted approach to identify genetic loci associated with evolved dioxin tolerance in Atlantic Killifish ( <i>Fundulus heteroclitus</i> ). <i>BMC Evolutionary Biology</i> , 2014, 14, 7.	3.2	30
1684	Genetic structuring of remnant forest patches in an endangered medicinal tree in North-western Ethiopia. <i>BMC Genetics</i> , 2014, 15, 31.	2.7	5
1685	Causes and consequences of fine-scale population structure in a critically endangered freshwater seal. <i>BMC Ecology</i> , 2014, 14, 22.	3.0	27
1686	Thermal niche evolution and geographical range expansion in a species complex of western Mediterranean diving beetles. <i>BMC Evolutionary Biology</i> , 2014, 14, 187.	3.2	27
1687	Mitochondrial sequences reveal a clear separation between Angolan and South African giraffe along a cryptic rift valley. <i>BMC Evolutionary Biology</i> , 2014, 14, 219.	3.2	31
1688	Taming the wild: resolving the gene pools of non-model <i>Arabidopsis</i> lineages. <i>BMC Evolutionary Biology</i> , 2014, 14, 224.	3.2	61
1689	Mitogenomics of the Speartooth Shark challenges ten years of control region sequencing. <i>BMC Evolutionary Biology</i> , 2014, 14, 232.	3.2	39
1690	Population structure of a microparasite infecting <i>Daphnia</i> : spatio-temporal dynamics. <i>BMC Evolutionary Biology</i> , 2014, 14, 247.	3.2	4
1691	Molecular evaluation of orphan Afghan common wheat ( <i>Triticum aestivum</i> L.) landraces collected by Dr. Kihara using single nucleotide polymorphic markers. <i>BMC Plant Biology</i> , 2014, 14, 320.	1.6	25
1692	Genetic variation in the mitochondrial 16S ribosomal RNA gene of <i>Ixodes scapularis</i> (Acari: Ixodidae). <i>Parasites and Vectors</i> , 2014, 7, 530.	1.0	12
1693	No reduction in genetic diversity of Swiss stone pine ( <i>Pinus cembra</i> L.) in Tatra Mountains despite high fragmentation and small population size. <i>Conservation Genetics</i> , 2014, 15, 1433-1445.	0.8	25
1694	Genetic diversity of Albanian goat breeds revealed by mtDNA sequence variation. <i>Biotechnology and Biotechnological Equipment</i> , 2014, 28, 77-81.	0.5	3
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1696	CYP3A5*3 and POR*28 Genetic Variants Influence the Required Dose of Tacrolimus in Heart Transplant Recipients. <i>Therapeutic Drug Monitoring</i> , 2014, 36, 710-715.	1.0	32
1697	Genetic diversity and insecticide resistance during the growing season in the green peach aphid (Hemiptera: Aphididae) on primary and secondary hosts: a farm-scale study in Central Chile. <i>Bulletin of Entomological Research</i> , 2014, 104, 182-194.	0.5	15



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1699	Genomic Analyses of Three Malaria Vectors Reveals Extensive Shared Polymorphism but Contrasting Population Histories. Molecular Biology and Evolution, 2014, 31, 889-902.	3.5	39
1700	Estimating exotic gene flow into native pine stands: zygotic vs. gametic components. Molecular Ecology, 2014, 23, 5435-5447.	2.0	17
1701	Connectivity in the slender Sargassum shrimp ( <i>Latreutes fucorum</i> ): implications for a Sargasso Sea protected area. Journal of Plankton Research, 2014, 36, 1408-1412.	0.8	7
1702	Evolutionary relationships within Triops (Branchiopoda: Notostraca) using complete mitochondrial genomes. Journal of Crustacean Biology, 2014, 34, 795-800.	0.3	7
1703	Population Genetic Structure and Demographic History of <i>Atrina pectinata</i> Based on Mitochondrial DNA and Microsatellite Markers. PLoS ONE, 2014, 9, e95436.	1.1	41
1704	First records and range extensions for two <i>Acesta</i> clam species (Bivalvia: Limidae) in the Gulf of California, Mexico. Marine Biodiversity Records, 2014, 7, .	1.2	2
1705	Did common disjunct populations of freshwater fishes in northern Australia form from the same biogeographic events?. Freshwater Science, 2014, 33, 263-272.	0.9	8
1706	Noninvasive genetic sampling allows estimation of capercaillie numbers and population structure in the Bohemian Forest. European Journal of Wildlife Research, 2014, 60, 789-801.	0.7	22
1707	Detection and Genetic Diversity of a Heliothine Invader (Lepidoptera: Noctuidae) From North and Northeast of Brazil. Journal of Economic Entomology, 2014, 107, 970-980.	0.8	56
1708	Juvenile green turtles on the northern edge of their range: mtDNA evidence of long-distance westward dispersals in the northern Pacific Ocean. Endangered Species Research, 2014, 24, 171-179.	1.2	22
1709	Genetic Structure and Colonization History of the Fruit Fly <i>Bactrocera tau</i> (Diptera: Tj ETQq1 1 0.784314 rgBT /Ovello	0.8	23
1710	Phylogeography of the Chinese Beard Eel, <i>Cirrhimuraena chinensis</i> Kaup, Inferred from Mitochondrial DNA: A Range Expansion after the Last Glacial Maximum. International Journal of Molecular Sciences, 2014, 15, 13564-13577.	1.8	9
1711	Landscape genetics in mammals. Mammalia, 2014, 78, .	0.3	17
1712	Variable-number tandem repeats genotyping used to aid and inform management strategies for a bovine Johne's disease incursion in tropical and subtropical Australia. Journal of Veterinary Diagnostic Investigation, 2014, 26, 651-657.	0.5	13
1713	A Call for Tiger Management Using "Reserves" of Genetic Diversity. Journal of Heredity, 2014, 105, 295-302.	1.0	12
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1715	Microsatellite markers for <i>Bokermannohyla</i> species (Anura, Hylidae) from the Brazilian Cerrado and Atlantic Forest domains. Amphibia - Reptilia, 2014, 35, 355-360.	0.1	11

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1718	Adaptations to Climate-Mediated Selective Pressures in Sheep. Molecular Biology and Evolution, 2014, 31, 3324-3343.	3.5	149
1719	Comparative evaluation of potential indicators and temporal sampling protocols for monitoring genetic erosion. Evolutionary Applications, 2014, 7, 984-998.	1.5	102
1720	The effect of multi-year vs single-year stocking on lake sturgeon ( <i>Acipenser fulvescens</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582	0.3	7
1721	The socio-genetics of a complex society: female gelada relatedness patterns mirror association patterns in a multilevel society. Molecular Ecology, 2014, 23, 6179-6191.	2.0	35
1722	Genetic diversity and adaptive variations under static and dynamic management: a case of rice landraces from parts of Odisha in India. Plant Genetic Resources: Characterisation and Utilisation, 2014, 12, 170-177.	0.4	1
1723	Ecological and genetic differentiation in <i>Persea boninensis</i> (Lauraceae) endemic to the Bonin (Ogasawara) Islands. Plant Species Biology, 2014, 29, 16-24.	0.6	6
1724	The origins of Chinese domestic cattle as revealed by ancient DNA analysis. Journal of Archaeological Science, 2014, 41, 423-434.	1.2	61
1725	Genetic diversity and population structure of Indian <i>Isoetes dixitei</i> Shende based on amplified fragment length polymorphisms and intron sequences of LEAFY. Aquatic Botany, 2014, 113, 1-7.	0.8	4
1726	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
1727	Multi-locus DNA sequence variation in a complex of four leaf beetle species with parapatric distributions: Mitochondrial and nuclear introgressions reveal recent hybridization. Molecular Phylogenetics and Evolution, 2014, 78, 14-24.	1.2	12
1728	Molecular variability and genetic relationship and structure of Iranian <i>Prunus</i> rootstocks revealed by SSR and AFLP markers. Scientia Horticulturae, 2014, 172, 258-264.	1.7	12
1729	Comparative performance between "next generation" multiplex systems and the new European Standard Set of STR markers in the Portuguese Population. Forensic Science International: Genetics, 2014, 8, 137-142.	1.6	2
1730	Autosomal SNPs study of a population sample from North of Portugal and a sample of immigrants from the Eastern Europe living in Portugal. Legal Medicine, 2014, 16, 118-120.	0.6	5
1731	Genetic diversity and structure of an endemic and critically endangered stream river salamander (Caudata: Ambystoma leorae) in Mexico. Conservation Genetics, 2014, 15, 49-59.	0.8	23
1732	Evolutionary systematics of the Australian <i>Eocyclus</i> fauna (Crustacea: Branchiopoda:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107	0.6	27
1733	Phylogeographic analysis and genetic cluster recognition for the conservation of Ural Owls ( <i>Strix</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 11	0.5	11

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1734	Distribution patterns and introduction pathways of the cosmopolitan brown alga <i>Colpomenia peregrina</i> using mt <i>cox3</i> and <i>atp6</i> sequences. <i>Journal of Applied Phycology</i> , 2014, 26, 491-504.	1.5	15
1735	New microsatellite loci for the threatened eastern hog-nosed snake ( <i>Heterodon platirhinos</i> ) in Ontario, Canada. <i>Conservation Genetics Resources</i> , 2014, 6, 69-71.	0.4	1
1736	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
1737	Phylogenetics of a recent radiation in the mallards and allies ( <i>Aves</i> : <i>Anas</i> ): Inferences from a genomic transect and the multispecies coalescent. <i>Molecular Phylogenetics and Evolution</i> , 2014, 70, 402-411.	1.2	51
1738	Tracing the origin of US brown marmorated stink bugs, <i>Halyomorpha halys</i> . <i>Biological Invasions</i> , 2014, 16, 153-166.	1.2	90
1739	High cryptic diversity and persistent lineage segregation in endemic <i>Romecytheridea</i> (Crustacea). <i>Tj ETQq1 1 0.784314 rgBT /Overlook</i>	1.0	25
1740	Two sympatric lineages of the Raven <i>Corvus corax jordansi</i> coexist on the Eastern Canary Islands. <i>Journal of Ornithology</i> , 2014, 155, 243-251.	0.5	2
1741	Molecular evidence for further overlooked species within the <i>Gammarus fossarum</i> complex (Crustacea: Amphipoda). <i>Hydrobiologia</i> , 2014, 721, 165-184.	1.0	86
1742	Limited gene flow in <i>Uca minax</i> (LeConte 1855) along a tidally influenced river system. <i>Open Life Sciences</i> , 2014, 9, 28-36.	0.6	4
1743	From species divergence to population structure: A multimer approach on the most basal lineage of Salamandridae, the spectacled salamanders (genus <i>Salamandrina</i> ) from Italy. <i>Molecular Phylogenetics and Evolution</i> , 2014, 70, 1-12.	1.2	11
1744	Genetic diversity, population structure and differentiation of rice species from Niger and their potential for rice genetic resources conservation and enhancement. <i>Genetic Resources and Crop Evolution</i> , 2014, 61, 199-213.	0.8	16
1745	Identification of mango ( <i>Mangifera indica</i> L.) landraces from Eastern and Central Kenya using a morphological and molecular approach. <i>Genetic Resources and Crop Evolution</i> , 2014, 61, 7-22.	0.8	25
1746	Molecular evidence for co-occurring cryptic lineages within the <i>Sepioteuthis</i> cf. <i>lessoniana</i> species complex in the Indian and Indo-West Pacific Oceans. <i>Hydrobiologia</i> , 2014, 725, 165-188.	1.0	38
1747	Population genetics of Blanding's turtle ( <i>Emys blandingii</i> ) in the midwestern United States. <i>Conservation Genetics</i> , 2014, 15, 61-73.	0.8	14
1748	Fine-scale sampling reveals distinct isolation by distance patterns in chum salmon ( <i>Oncorhynchus</i> ). <i>Tj ETQq0 0 0 rgBT /Overlook 10 Tf 50</i>	0.8	16
1749	Evidence of population bottleneck in <i>Astragalus michauxii</i> (Fabaceae), a narrow endemic of the southeastern United States. <i>Conservation Genetics</i> , 2014, 15, 153-164.	0.8	14
1750	Cryptic genetic subdivision in the San Benito evening primrose ( <i>Camissonia benitensis</i> ). <i>Conservation Genetics</i> , 2014, 15, 165-175.	0.8	7
1751	Isolation and characterization of twenty-eight polymorphic microsatellite markers in <i>Odontobutis potamophila</i> and cross-amplification in other Gobioidae. <i>Conservation Genetics Resources</i> , 2014, 6, 601-604.	0.4	4

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1752	The genetic structure of <i>Arabidopsis thaliana</i> in the south-western Mediterranean range reveals a shared history between North Africa and southern Europe. <i>BMC Plant Biology</i> , 2014, 14, 17.	1.6	53
1753	Evidence of at least two evolutionary lineages in <i>Melipona subnitida</i> (Apidae, Meliponini) suggested by mtDNA variability and geometric morphometrics of forewings. <i>Die Naturwissenschaften</i> , 2014, 101, 17-24.	0.6	38
1754	Modern maize varieties going local in the semi-arid zone in Tanzania. <i>BMC Evolutionary Biology</i> , 2014, 14, 1.	3.2	251
1755	Demography of the upward-shifting temperate woody species of the <i>Rhododendron pseudochrysanthum</i> complex and ecologically relevant adaptive divergence in its trailing edge populations. <i>Tree Genetics and Genomes</i> , 2014, 10, 111-126.	0.6	21
1756	Autosomal STR loci for improving the kinship discrimination power for missing children and forensic application. <i>Genes and Genomics</i> , 2014, 36, 355-363.	0.5	3
1757	Limited genetic structure among broad-scale regions for two commercially harvested, tropical deep-water snappers in New Caledonia. <i>Fisheries Science</i> , 2014, 80, 13-19.	0.7	11
1758	Molecular detection of intra-population structure in a threatened potoroid, <i>Potorous tridactylus</i> : conservation management and sampling implications. <i>Conservation Genetics</i> , 2014, 15, 547-560.	0.8	10
1759	Fine-scale phylogeographic contact zone in Austrian brown trout <i>Salmo trutta</i> reveals multiple waves of post-glacial colonization and a pre-dominance of natural versus anthropogenic admixture. <i>Conservation Genetics</i> , 2014, 15, 561-572.	0.8	41
1760	Optimization of 14 microsatellite loci in a Mediterranean demosponge subjected to population decimation, <i>Ircinia fasciculata</i> . <i>Conservation Genetics Resources</i> , 2014, 6, 301-303.	0.4	4
1761	Development and characterization of 15 polymorphic microsatellite markers for North Pacific albatrosses using paired-end Illumina shotgun sequencing. <i>Conservation Genetics Resources</i> , 2014, 6, 491-493.	0.4	0
1762	Haplotype diversity of 23 Y-chromosomal STRs in a population sample from the Federal District (Brazil) – a territory that arose from nothing. <i>International Journal of Legal Medicine</i> , 2014, 128, 945-947.	1.2	5
1763	Recent expansion led to the lack of genetic structure of <i>Sargassum aquifolium</i> populations in Southeast Asia. <i>Marine Biology</i> , 2014, 161, 785-795.	0.7	17
1764	Multiple cryptic refugia of forest grass <i>Bromus benekenii</i> in Europe as revealed by ISSR fingerprinting and species distribution modelling. <i>Plant Systematics and Evolution</i> , 2014, 300, 1437-1452.	0.3	10
1765	Haptoglobin (HP) and Haptoglobin-related protein (HPR) copy number variation, natural selection, and trypanosomiasis. <i>Human Genetics</i> , 2014, 133, 69-83.	1.8	72
1766	Interspecific hybridization contributes to high genetic diversity and apparent effective population size in an endemic population of mottled ducks ( <i>Anas fulvigula maculosa</i> ). <i>Conservation Genetics</i> , 2014, 15, 509-520.	0.8	26
1767	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
1768	Still a one species genus? Strong genetic diversification in the world's largest living odonate, the Neotropical damselfly <i>Megaloprepus caerulatus</i> . <i>Conservation Genetics</i> , 2014, 15, 469-481.	0.8	19
1769	Limited genetic diversity in the critically endangered Mexican howler monkey ( <i>Alouatta palliata</i> ) Tj ETQq1 1 0.784314 rgBT /Qyerlock 10	0.7	19

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1770	Mitochondrial DNA sequence variation in whiting <i>Merlangius merlangus</i> in the North East Atlantic. <i>Environmental Biology of Fishes</i> , 2014, 97, 103-110.	0.4	2
1771	Development of 17 novel microsatellite markers for the longnose sucker ( <i>Catostomus catostomus</i> ) and successful cross-specific amplification of 14 previously developed markers from congeneric species. <i>Conservation Genetics Resources</i> , 2014, 6, 329-332.	0.4	5
1772	Microsatellite markers unravel the population genetic structure of the Azorean Leontodon: implications in conservation. <i>Plant Systematics and Evolution</i> , 2014, 300, 987-1001.	0.3	11
1773	Development of 27 trinucleotide microsatellite markers for <i>Saccharina japonica</i> using next generation sequencing technology. <i>Conservation Genetics Resources</i> , 2014, 6, 341-344.	0.4	18
1774	Genetic Diversity and Population Structure of Seedling Populations of <i>Pyrus pashia</i> . <i>Plant Molecular Biology Reporter</i> , 2014, 32, 644-651.	1.0	13
1775	Brown and Polar Bear Y Chromosomes Reveal Extensive Male-Biased Gene Flow within Brother Lineages. <i>Molecular Biology and Evolution</i> , 2014, 31, 1353-1363.	3.5	90
1776	Evolutionary history of the Maltese wall lizard <i>Podarcis filfolensis</i> : insights on the “Expansion”-“Contraction” model of Pleistocene biogeography. <i>Molecular Ecology</i> , 2014, 23, 1167-1187.	2.0	50
1777	Conservation assessment of an extremely restricted bromeliad highlights the need for population-based conservation on granitic inselbergs of the Brazilian Atlantic Forest. <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2014, 209, 250-259.	0.6	14
1778	Testing the competition-colonization trade-off with a 32-year study of a saxicolous lichen community. <i>Ecology</i> , 2014, 95, 306-315.	1.5	11
1779	Competition-driven speciation in cichlid fish. <i>Nature Communications</i> , 2014, 5, 3412.	5.8	49
1780	Phylogeography of the Dark Fruit-Eating Bat <i>Artibeus obscurus</i> in the Brazilian Amazon. <i>Journal of Heredity</i> , 2014, 105, 48-59.	1.0	7
1781	Demographic history of a recent invasion of house mice on the isolated island of <i>Gough</i> . <i>Molecular Ecology</i> , 2014, 23, 1923-1939.	2.0	50
1782	Structure and dynamics of hybrid zones at different stages of speciation in the common vole ( <i>Microtus arvalis</i> ). <i>Molecular Ecology</i> , 2014, 23, 673-687.	2.0	52
1783	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
1784	Comparative phylogeography in marginal seas of the northwestern Pacific. <i>Molecular Ecology</i> , 2014, 23, 534-548.	2.0	149
1785	Looking to the past and the future: were the Madeira River rapids a geographical barrier to the boto ( <i>Cetacea: Iniidae</i> )?. <i>Conservation Genetics</i> , 2014, 15, 619.	0.8	37
1786	Intraspecific lineages of the lizard <i>Phrynocephalus putjati</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
1787	Phylogeography and population history of <i>Leopardus guigna</i> , the smallest American felid. <i>Conservation Genetics</i> , 2014, 15, 631-653.	0.8	31

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1788	Poecilogony in <i>Polydora hoplura</i> (Polychaeta: Spionidae) from commercially important molluscs in South Africa. <i>Marine Biology</i> , 2014, 161, 887-898.	0.7	23
1789	Evolutionary origins and genetic variation of the Seychelles treefrog, <i>Tachycnemis seychellensis</i> (Duméril and Bibron, 1841) (Amphibia: Anura: Hyperoliidae). <i>Molecular Phylogenetics and Evolution</i> , 2014, 75, 194-201.	1.2	13
1790	Late <i>Miocene</i> lineage divergence and ecological differentiation of rare endemic <i>Juniperus blancoi</i> : clues for the diversification of <i>North American</i> conifers. <i>New Phytologist</i> , 2014, 203, 335-347.	3.5	23
1791	Phylogeography and demographic history of two widespread Indo-Pacific mudskippers (Gobiidae: <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i>	1.2	18
1792	On the origin of the <i>North Norwegian</i> lemming. <i>Molecular Ecology</i> , 2014, 23, 2060-2071.	2.0	37
1793	Postglacial expansion and not human influence best explains the population structure in the endangered kea ( <i>Nestor notabilis</i> ). <i>Molecular Ecology</i> , 2014, 23, 2193-2209.	2.0	32
1794	Correlation between pelagic larval duration and realised dispersal: long-distance genetic connectivity between northern New Zealand and the Kermadec Islands archipelago. <i>Marine Biology</i> , 2014, 161, 297-312.	0.7	16
1795	Genetic structure of green turtle ( <i>Chelonia mydas</i> ) peripheral populations nesting in the northwestern Pacific rookeries: evidence for northern refugia and postglacial colonization. <i>Marine Biology</i> , 2014, 161, 495-507.	0.7	31
1796	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
1797	Does temporal and spatial segregation explain the complex population structure of humpback whales on the coast of West Africa?. <i>Marine Biology</i> , 2014, 161, 805-819.	0.7	19
1798	Afro-Eurasia and the Americas present barriers to gene flow for the cosmopolitan neustonic nudibranch <i>Glaucus atlanticus</i> . <i>Marine Biology</i> , 2014, 161, 899-910.	0.7	24
1799	Phylogeographical analysis of <i>Ligia oceanica</i> (Crustacea: Isopoda) reveals two deeply divergent mitochondrial lineages. <i>Biological Journal of the Linnean Society</i> , 2014, 112, 16-30.	0.7	17
1800	Genetic structure of disjunct Argentinean populations of the subtropical tree <i>Anadenanthera colubrina</i> var. <i>cebil</i> (Fabaceae). <i>Plant Systematics and Evolution</i> , 2014, 300, 1693-1705.	0.3	12
1801	Evaluation of genetic parameters of 22 autosomal STR loci (PowerPlex® Fusion System) in a population sample from Northern Italy. <i>International Journal of Legal Medicine</i> , 2014, 128, 281-283.	1.2	21
1802	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
1803	Dispersal in the inquiline social parasite ant <i>Plagiolepis xene</i> . <i>Insectes Sociaux</i> , 2014, 61, 197-202.	0.7	4
1804	Mitochondrial DNA phylogeography of <i>Semisulcospira libertina</i> (Gastropoda: Cerithioidea: <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 Td</i>	1.0	18
1805	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



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1806	Diversity and population structure of <i>Plasmodium falciparum</i> in Thailand based on the spatial and temporal haplotype patterns of the C-terminal 19-kDa domain of merozoite surface protein-1. <i>Malaria Journal</i> , 2014, 13, 54.	0.8	12
1807	Genetic structure of a phytophagous mite species affected by crop practices: the case of <i>Tetranychus urticae</i> in clementine mandarins. <i>Experimental and Applied Acarology</i> , 2014, 62, 477-498.	0.7	18
1808	Genetic diversity and linkage disequilibrium analysis in elite sugar beet breeding lines and wild beet accessions. <i>Theoretical and Applied Genetics</i> , 2014, 127, 559-571.	1.8	18
1809	The effect of host social system on parasite population genetic structure: comparative population genetics of two ectoparasitic mites and their bat hosts. <i>BMC Evolutionary Biology</i> , 2014, 14, 18.	3.2	29
1810	Complex genetic structure of a euryhaline marine fish in temporarily open/closed estuaries from the wider Gulf of Aden. <i>Marine Biology</i> , 2014, 161, 1113-1126.	0.7	14
1811	Lack of sex-biased dispersal promotes fine-scale genetic structure in alpine ungulates. <i>Conservation Genetics</i> , 2014, 15, 837-851.	0.8	16
1812	Evaluating hybridization as a potential facilitator of successful cogongrass ( <i>Imperata cylindrica</i> ) invasion in Florida, USA. <i>Biological Invasions</i> , 2014, 16, 2147-2161.	1.2	8
1813	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
1814	Mitochondrial DNA Diversity of Honey Bees ( <i>Apis mellifera</i> ) from Unmanaged Colonies and Swarms in the United States. <i>Biochemical Genetics</i> , 2014, 52, 245-257.	0.8	13
1815	Development and characterization of 24 microsatellite markers in a eublepharid gecko, <i>Goniurosaurus kuroiwae</i> . <i>Conservation Genetics Resources</i> , 2014, 6, 247-249.	0.4	2
1816	Large-scale mitochondrial DNA analysis in Southeast Asia reveals evolutionary effects of cultural isolation in the multi-ethnic population of Myanmar. <i>BMC Evolutionary Biology</i> , 2014, 14, 17.	3.2	56
1817	The Influence of Social Systems on Patterns of Mitochondrial DNA Variation in Baboons. <i>International Journal of Primatology</i> , 2014, 35, 210-225.	0.9	35
1818	Range-wide comparisons of northern leatherside chub populations reveal historical and contemporary patterns of genetic variation. <i>Conservation Genetics</i> , 2014, 15, 757-770.	0.8	9
1819	Isolation and characterization of 14 microsatellite markers in <i>Macrodasyntes hirsutum</i> (Hymenoptera: Torymidae). <i>Applied Entomology and Zoology</i> , 2014, 49, 197-200.	0.6	0
1820	Tests of multiple molecular markers for the identification of Great Spotted and Syrian Woodpeckers and their hybrids. <i>Journal of Ornithology</i> , 2014, 155, 591-600.	0.5	15
1821	Human maternal heritage in Andalusia (Spain): its composition reveals high internal complexity and distinctive influences of mtDNA haplogroups U6 and L in the western and eastern side of region. <i>BMC Genetics</i> , 2014, 15, 11.	2.7	20
1822	Temporal genetic structure in a poecilogonous polychaete: the interplay of developmental mode and environmental stochasticity. <i>BMC Evolutionary Biology</i> , 2014, 14, 12.	3.2	17
1823	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

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1824	Caves as microrefugia: Pleistocene phylogeography of the troglomorphic North American scorpion <i>Pseudouroctonus reddeni</i> . <i>BMC Evolutionary Biology</i> , 2014, 14, 9.	3.2	38
1825	Genome-scale analysis of demographic history and adaptive selection. <i>Protein and Cell</i> , 2014, 5, 99-112.	4.8	10
1826	New data on the phylogeography and genetic diversity of the brown bear <i>Ursus arctos</i> Linnaeus, 1758 of Northeastern Eurasia (mtDNA control region polymorphism analysis). <i>Biology Bulletin</i> , 2014, 41, 38-46.	0.1	8
1827	Genetic diversity and population structure in the US Upland cotton ( <i>Gossypium hirsutum</i> L.). <i>Theoretical and Applied Genetics</i> , 2014, 127, 283-295.	1.8	151
1828	The population biology of mitigation: impacts of habitat creation on an endangered plant species. <i>Conservation Genetics</i> , 2014, 15, 679-695.	0.8	9
1829	Conservation genetic assessment of the critically endangered Julimes pupfish, <i>Cyprinodon julimes</i> . <i>Conservation Genetics</i> , 2014, 15, 483-488.	0.8	15
1830	Genetic differentiation and spatial structure of <i>Geosmithia morbida</i> , the causal agent of thousand cankers disease in black walnut ( <i>Juglans nigra</i> ). <i>Current Genetics</i> , 2014, 60, 75-87.	0.8	21
1831	Population structure and conservation genetic assessment of the endangered Pugnose Shiner, <i>Notropis anogenus</i> . <i>Conservation Genetics</i> , 2014, 15, 343-353.	0.8	13
1832	Isolation, characterization and genotyping of single nucleotide polymorphisms in the non-model tree species <i>Frangula alnus</i> (Rhamnaceae). <i>Conservation Genetics Resources</i> , 2014, 6, 267-269.	0.4	9
1833	Archival genetic analysis suggests recent immigration has altered a population of Chinook salmon in an unsupplemented wilderness area. <i>Conservation Genetics</i> , 2014, 15, 387-403.	0.8	7
1834	Characterisation of novel microsatellite markers for the surf clams <i>Paphies subtriangulata</i> and <i>P. australis</i> (Bivalvia: Mesodesmatidae). <i>Conservation Genetics Resources</i> , 2014, 6, 315-317.	0.4	0
1835	A preliminary study for identification of candidate AFLP markers under artificial selection for shell color in pearl oyster <i>Pinctada fucata</i> . <i>Gene</i> , 2014, 542, 8-15.	1.0	18
1836	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
1837	<sc>spads</sc> 1.0: a toolbox to perform spatial analyses on <sc>DNA</sc> sequence data sets. <i>Molecular Ecology Resources</i> , 2014, 14, 647-651.	2.2	91
1838	Low effective population sizes and limited connectivity in xerothermic beetles: implications for the conservation of an endangered habitat. <i>Animal Conservation</i> , 2014, 17, 454-466.	1.5	7
1839	Untangling the <i>Spurilla neapolitana</i> (Delle Chiaje, 1841) species complex: a review of the genus <i>Spurilla</i> Bergh, 1864 (Mollusca: Nudibranchia: Aeolidiidae). <i>Zoological Journal of the Linnean Society</i> , 2014, 170, 132-154.	1.0	41
1840	Remarkably low genetic diversity and strong population structure in common bottlenose dolphins ( <i>Tursiops truncatus</i> ) from coastal waters of the Southwestern Atlantic Ocean. <i>Conservation Genetics</i> , 2014, 15, 879.	0.8	51
1841	Rapid genetic adaptation precedes the spread of an exotic plant species. <i>Molecular Ecology</i> , 2014, 23, 2157-2164.	2.0	111

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1842	Evaluation of large-scale genetic structure in complex demographic and historical scenarios: The mitochondrial DNA and Y-chromosome pools of the Iberian Atlantic façade. <i>American Journal of Physical Anthropology</i> , 2014, 153, 617-626.	2.1	0
1843	Species boundaries in <i>Philaethria</i> butterflies: an integrative taxonomic analysis based on genitalia ultrastructure, wing geometric morphometrics, DNA sequences, and amplified fragment length polymorphisms. <i>Zoological Journal of the Linnean Society</i> , 2014, 170, 690-709.	1.0	11
1844	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
1845	Genetic and phenotypic divergence in an island bird: isolation by distance, by colonization or by adaptation?. <i>Molecular Ecology</i> , 2014, 23, 1028-1039.	2.0	89
1846	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
1847	Limited phylogeographic structure for five bathyal ophiuroids at continental scales. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2014, 84, 18-28.	0.6	30
1848	Brazilian quilombos: A repository of Amerindian alleles. <i>American Journal of Human Biology</i> , 2014, 26, 142-150.	0.8	6
1849	Shifting ranges of two tree weta species ( <i>Hemideina</i> spp.): competitive exclusion and changing climate. <i>Journal of Biogeography</i> , 2014, 41, 524-535.	1.4	42
1850	Local adaptation with high gene flow: temperature parameters drive adaptation to altitude in the common frog ( <i>Rana temporaria</i> ). <i>Molecular Ecology</i> , 2014, 23, 561-574.	2.0	66
1851	Revisiting comparisons of genetic diversity in stable and declining species: assessing genome-wide polymorphism in North American bumble bees using RAD sequencing. <i>Molecular Ecology</i> , 2014, 23, 788-801.	2.0	88
1852	THE INTERPLAY BETWEEN LOCAL ECOLOGY, DIVERGENT SELECTION, AND GENETIC DRIFT IN POPULATION DIVERGENCE OF A SEXUALLY ANTAGONISTIC FEMALE TRAIT. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 1934-1946.	1.1	22
1853	Recovery of wolverines in the Western United States: Recent extirpation and recolonization or range retraction and expansion?. <i>Journal of Wildlife Management</i> , 2014, 78, 325-334.	0.7	15
1854	Polish population data on 15 autosomal STRs of AmpFISTR NGM PCR kit. <i>Forensic Science International: Genetics</i> , 2014, 9, 142-149.	1.6	6
1855	Climate rather than geography separates two European honeybee subspecies. <i>Molecular Ecology</i> , 2014, 23, 2353-2361.	2.0	29
1856	Population genetics of 17 Y-STR markers in Turkish Cypriots from Cyprus. <i>Forensic Science International: Genetics</i> , 2014, 10, e1-e3.	1.6	14
1857	Mitochondrial phylogeography of the European wild boar: the effect of climate on genetic diversity and spatial lineage sorting across Europe. <i>Journal of Biogeography</i> , 2014, 41, 987-998.	1.4	56
1858	High rates of hybridisation reveal fragile reproductive barriers between endangered Australian sea snakes. <i>Biological Conservation</i> , 2014, 171, 200-208.	1.9	20
1859	Population genetics of <i>Formica aquilonia</i> wood ants in Scotland: the effects of long-term forest fragmentation and recent reforestation. <i>Conservation Genetics</i> , 2014, 15, 853-868.	0.8	11

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1860	Combining microsatellites and geometric morphometrics for the study of redbfish ( <i>Sebastes</i> spp.) population structure in the Northwest Atlantic. <i>Fisheries Research</i> , 2014, 154, 102-119.	0.9	20
1861	Chloroplast DNA-based genetic diversity and phylogeography of <i>Pyrus betulaefolia</i> (Rosaceae) in Northern China. <i>Tree Genetics and Genomes</i> , 2014, 10, 739-749.	0.6	30
1862	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
1863	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
1864	Neutral and selective processes shape MHC gene diversity and expression in stocked brook charr populations ( <i>Salvelinus fontinalis</i> ). <i>Molecular Ecology</i> , 2014, 23, 1730-1748.	2.0	21
1865	Local and regional founder effects in lake zooplankton persist after thousands of years despite high dispersal potential. <i>Molecular Ecology</i> , 2014, 23, 1014-1027.	2.0	55
1866	Allele frequencies of the five new European Standard Set (ESS) STRs and 15 established STRs in a Turkish population. <i>Forensic Science International: Genetics</i> , 2014, 9, e26.	1.6	13
1867	Genetic structure of pike ( <i>Esox lucius</i> ) reveals a complex and previously unrecognized colonization history of <i>Ireland</i> . <i>Journal of Biogeography</i> , 2014, 41, 548-560.	1.4	22
1868	Historical and non-invasive samples: a study case of genotyping errors in newly isolated microsatellites for the lesser anteater ( <i>Tamandua tetradactyla</i> L., Pilosa). <i>Molecular Ecology Resources</i> , 2014, 14, 531-540.	2.2	5
1869	Microsatellite and mitochondrial markers reveal strong gene flow barriers for <i>Anopheles farauti</i> in the Solomon Archipelago: implications for malaria vector control. <i>International Journal for Parasitology</i> , 2014, 44, 225-233.	1.3	14
1870	A new multiplex SNP genotyping assay for detecting hybridization and introgression between the <i>M</i> and <i>S</i> molecular forms of <i>Anopheles gambiae</i> . <i>Molecular Ecology Resources</i> , 2014, 14, 297-305.	2.2	26
1871	Maternal History of Oceania from Complete mtDNA Genomes: Contrasting Ancient Diversity with Recent Homogenization Due to the Austronesian Expansion. <i>American Journal of Human Genetics</i> , 2014, 94, 721-733.	2.6	64
1872	Evidence from recently deglaciated mountain ranges that <i>Baetis alpinus</i> (Ephemeroptera) could lose significant genetic diversity as alpine glaciers disappear. <i>Freshwater Science</i> , 2014, 33, 207-216.	0.9	35
1873	Genetic population structure of European anchovy in the Mediterranean Sea and the Northeast Atlantic Ocean using sequence analysis of the mitochondrial DNA control region. <i>ICES Journal of Marine Science</i> , 2014, 71, 391-397.	1.2	27
1874	Is variable connectivity among populations of a continental gobiid fish driven by local adaptation or passive dispersal?. <i>Freshwater Biology</i> , 2014, 59, 1672-1686.	1.2	23
1875	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
1876	Polymorphic microsatellite loci for a neotropical leaf-litter frog ( <i>Craugastor bransfordii</i> ) characterized through Illumina sequencing. <i>Conservation Genetics Resources</i> , 2014, 6, 697-698.	0.4	2
1877	At the Edge of a Species Boundary: A New and Relatively Young Species of <i>Leptopelis</i> (Anura:) Tj ETQq1 1 0.784314 rgBT /Overlock 100. 100.	0.2	18

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1878	Validation of microsatellite multiplexes for parentage analysis and species discrimination in two hybridizing species of coral reef fish ( <i>Plectropomus</i> spp.), <i>Serranidae</i> . Ecology and Evolution, 2014, 4, 2046-2057.	0.8	26
1879	Isolation and characterization of microsatellite loci in Darwin's fox ( <i>Lycalopex fulvipes</i> ) and cross-amplification in other canid species. Conservation Genetics Resources, 2014, 6, 759-761.	0.4	0
1880	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
1881	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
1882	Genetic restoration of a threatened population of greater prairie-chickens. Biological Conservation, 2014, 174, 12-19.	1.9	25
1883	Does the <i>Platanthera dilatata</i> (Orchidaceae) complex contain cryptic species or continuously variable populations?. Plant Systematics and Evolution, 2014, 300, 1465-1476.	0.3	6
1884	Shifts in the abundance and community structure of soil ammonia oxidizers in a wet sclerophyll forest under long-term prescribed burning. Science of the Total Environment, 2014, 470-471, 578-586.	3.9	25
1885	Genetic Structure of Little Brown Bats ( <i>Myotis lucifugus</i> ) Corresponds with Spread of White-Nose Syndrome among Hibernacula. Journal of Heredity, 2014, 105, 354-364.	1.0	34
1886	Allele frequencies for 26 STR loci in a population of Tuscany (Central Italy). International Journal of Legal Medicine, 2014, 128, 455-456.	1.2	2
1887	Locals, resettlers, and pilgrims: A genetic portrait of three pre-Columbian Andean populations. American Journal of Physical Anthropology, 2014, 154, 402-412.	2.1	12
1888	Predicting HLA alleles from high-resolution SNP data in three Southeast Asian populations. Human Molecular Genetics, 2014, 23, 4443-4451.	1.4	80
1889	Phylogeography of <i>Peromyscus schmidlyi</i> : an endemic of the Sierra Madre Occidental, Mexico. Journal of Mammalogy, 2014, 95, 254-268.	0.6	8
1890	Molecular data indicate the presence of a novel species of <i>Centropomus</i> (Centropomidae) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262	1.2	19
1891	Development of genetic structure in a heterogeneous landscape over a short time frame: the reintroduced Asiatic wild ass. Conservation Genetics, 2014, 15, 1231-1242.	0.8	13
1892	Genetic structure of populations of whale sharks among ocean basins and evidence for their historic rise and recent decline. Molecular Ecology, 2014, 23, 2590-2601.	2.0	89
1893	Recent speciation and secondary contact in endemic ants. Molecular Ecology, 2014, 23, 2529-2542.	2.0	14
1894	Floral divergence in closely related <i>Leucospermum tottum</i> (Proteaceae) varieties pollinated by birds and long-proboscid flies. Evolutionary Ecology, 2014, 28, 849-868.	0.5	10
1895	Demographic processes shaping genetic variation of the solitary phase of the desert locust. Molecular Ecology, 2014, 23, 1749-1763.	2.0	24

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1896	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
1897	Mitochondrial nuclear discord in six congeneric lineages of <i>Holarctic</i> ducks (genus <i>Tj</i> ). <i>ETQq1</i> 1 0.784314 <i>rgBT</i> / <i>Overlock</i> 10 Tf 507	2.0	32
1898	Divergent population structure and climate associations of a chromosomal inversion polymorphism across the <i>Mimulus guttatus</i> species complex. <i>Molecular Ecology</i> , 2014, 23, 2844-2860.	2.0	60
1899	PARALLEL EVOLUTION OF LOCAL ADAPTATION AND REPRODUCTIVE ISOLATION IN THE FACE OF GENE FLOW. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 935-949.	1.1	165
1900	Phylogeography of noble crayfish ( <i>Astacus astacus</i> ) reveals multiple refugia. <i>Freshwater Biology</i> , 2014, 59, 761-776.	1.2	44
1901	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
1902	Genetic Variation and Population Structure in the Endangered Hermann's Tortoise: The Roles of Geography and Human-Mediated Processes. <i>Journal of Heredity</i> , 2014, 105, 70-81.	1.0	18
1903	Quantifying morphological and genetic variation of sympatric populations to guide conservation of endangered, microendemic springsnails. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2014, 24, 536-545.	0.9	14
1904	SNP discovery in wild and domesticated populations of blue catfish, <i>Ictalurus furcatus</i> , using genotyping-by-sequencing and subsequent SNP validation. <i>Molecular Ecology Resources</i> , 2014, 14, 1261-1270.	2.2	28
1905	Treatment-resistant schizophrenia and DAT and SERT polymorphisms. <i>Gene</i> , 2014, 543, 125-132.	1.0	33
1906	Evidence for adaptive divergence of thermal responses among <i>Bemisia tabaci</i> populations from tropical <i>Colombia</i> following a recent invasion. <i>Journal of Evolutionary Biology</i> , 2014, 27, 1160-1171.	0.8	14
1907	Phylogenetic characterisation of <i>Taenia</i> tapeworms in spotted hyenas and reconsideration of the 'Out of Africa' hypothesis of <i>Taenia</i> in humans. <i>International Journal for Parasitology</i> , 2014, 44, 533-541.	1.3	32
1908	Phylogeography and Pleistocene refugia of the Little Owl <i>Athene noctua</i> inferred from mtDNA sequence data. <i>Ibis</i> , 2014, 156, 639-657.	1.0	24
1909	Differentiation between sediment and hypolimnion methanogen communities in humic lakes. <i>Environmental Microbiology</i> , 2014, 16, 1411-1423.	1.8	21
1910	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
1911	Allelic frequencies and statistical data from 30 INDEL loci in Uruguayan population. <i>Forensic Science International: Genetics</i> , 2014, 9, e27-e29.	1.6	34
1912	New insights into the genetic structure of <i>Araucaria araucana</i> forests based on molecular and historic evidences. <i>Tree Genetics and Genomes</i> , 2014, 10, 839-851.	0.6	20
1913	Genetic diversity of the pan-European freshwater mussel <i>Anodonta anatina</i> (Bivalvia: Unionoida) based on CO1: new phylogenetic insights and implications for conservation. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2014, 24, 561-574.	0.9	55



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1914	Patterns of cyto-nuclear linkage disequilibrium in <i>Silene latifolia</i> : genomic heterogeneity and temporal stability. <i>Heredity</i> , 2014, 112, 99-104.	1.2	19
1915	A first assessment of genetic variability in the Eurasian Stone-curlew <i>Burhinus oedicnemus</i> . <i>Ibis</i> , 2014, 156, 687-692.	1.0	7
1916	Selection from parasites favours immunogenetic diversity but not divergence among locally adapted host populations. <i>Journal of Evolutionary Biology</i> , 2014, 27, 960-974.	0.8	32
1917	Faunal record identifies Bering isthmus conditions as constraint to end-Pleistocene migration to the New World. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20132167.	1.2	78
1918	Nucleotide diversity and linkage disequilibrium at 58 stress response and phenology candidate genes in a European beech ( <i>Fagus sylvatica</i> L.) population from southeastern France. <i>Tree Genetics and Genomes</i> , 2014, 10, 15-26.	0.6	36
1919	Prolactin Receptor Gene Diversity in Azara's Owl Monkeys ( <i>Aotus azarai</i> ) and Humans ( <i>Homo sapiens</i> ) Suggests a Non-Neutral Evolutionary History among Primates. <i>International Journal of Primatology</i> , 2014, 35, 129-155.	0.9	5
1920	Inbreeding and strong population subdivision in an endangered salamander. <i>Conservation Genetics</i> , 2014, 15, 137-151.	0.8	20
1921	Population genetics of insertion-deletion polymorphisms in South Koreans using Investigator DIPlex kit. <i>Forensic Science International: Genetics</i> , 2014, 8, 80-83.	1.6	42
1922	Conserving marine biodiversity: insights from life-history trait candidate genes in Atlantic cod ( <i>Gadus</i> )	0.8	29
1923	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
1924	Genetic consequences of habitat fragmentation during a range expansion. <i>Heredity</i> , 2014, 112, 291-299.	1.2	128
1925	Highly differentiated populations of the narrow endemic and endangered species <i>Primula cicutariifolia</i> in China, revealed by ISSR and SSR. <i>Biochemical Systematics and Ecology</i> , 2014, 53, 59-68.	0.6	12
1926	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
1927	Haplotype diversity and evolutionary history of the Lr34 locus of wheat. <i>Molecular Breeding</i> , 2014, 33, 639-655.	1.0	13
1928	Phylogeography-Based Delimitation of Subspecies Boundaries in the Common Pheasant ( <i>Phasianus</i> )	0.8	11
1929	Phylogeographic and population genetic analyses reveal Pleistocene isolation followed by high gene flow in a wide ranging, but endangered, freshwater mussel. <i>Heredity</i> , 2014, 112, 282-290.	1.2	47
1930	Phylogeography and genetic structure of two Patagonian shag species (Aves: Phalacrocoracidae). <i>Molecular Phylogenetics and Evolution</i> , 2014, 72, 42-53.	1.2	23
1931	Molecular insights into the purple-flowered ancestor of garden petunias. <i>American Journal of Botany</i> , 2014, 101, 119-127.	0.8	24

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1932	Habitat fragmentation and the genetic structure of the Amazonian palm <i>Mauritia flexuosa</i> L.f. (Arecaceae) on the island of Trinidad. <i>Conservation Genetics</i> , 2014, 15, 355-362.	0.8	9
1933	Nuclear and plastid markers reveal the persistence of genetic identity: A new perspective on the evolutionary history of <i>Petunia exserta</i> . <i>Molecular Phylogenetics and Evolution</i> , 2014, 70, 504-512.	1.2	42
1934	Molecular Epidemiology of Ascariasis: A Global Perspective on the Transmission Dynamics of <i>Ascaris</i> in People and Pigs. <i>Journal of Infectious Diseases</i> , 2014, 210, 932-941.	1.9	109
1935	Effect of founding events on coat colour polymorphism of <i>Apodemus speciosus</i> (Rodentia): Tj ETQq1 1 0.784314 rgBT /Overl	0.7	10
1936	Genomic regions repeatedly involved in divergence among plantâ€specialized pea aphid biotypes. <i>Journal of Evolutionary Biology</i> , 2014, 27, 2013-2020.	0.8	25
1937	Multilocus Analysis Using Putative Fungal Effectors to Describe a Population of <i>Fusarium oxysporum</i> from Sugar Beet. <i>Phytopathology</i> , 2014, 104, 886-896.	1.1	35
1938	Genotyping by sequencing resolves shallow population structure to inform conservation of Chinook salmon ( <i>Oncorhynchus tshawytscha</i> ). <i>Evolutionary Applications</i> , 2014, 7, 355-369.	1.5	178
1939	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
1940	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
1941	Genetic diversity and ecological niche modelling of the restricted <i>Recordia reitzii</i> (Verbenaceae) from southern Brazilian Atlantic forest. <i>Botanical Journal of the Linnean Society</i> , 2014, 176, 332-348.	0.8	22
1942	Deep phylogeographical structure and parallel host range evolution in the leaf beetle <i>Agelasa nigriceps</i> . <i>Molecular Ecology</i> , 2014, 23, 421-434.	2.0	5
1943	Conservation genomics of anadromous Atlantic salmon across its North American range: outlier loci identify the same patterns of population structure as neutral loci. <i>Molecular Ecology</i> , 2014, 23, 5680-5697.	2.0	115
1944	Human pharmacogenomic variation of antihypertensive drugs: from population genetics to personalized medicine. <i>Pharmacogenomics</i> , 2014, 15, 157-167.	0.6	14
1945	Multiple paternity is a shared reproductive strategy in the live-bearing surfperches (Embiotocidae) that may be associated with female fitness. <i>Ecology and Evolution</i> , 2014, 4, 2316-2329.	0.8	11
1946	Loss of genetic integrity in wild lake trout populations following stocking: insights from an exhaustive study of 72 lakes from Quebec, Canada. <i>Evolutionary Applications</i> , 2014, 7, 625-644.	1.5	75
1947	MHC class II diversity of koala ( <i>Phascolarctos cinereus</i> ) populations across their range. <i>Heredity</i> , 2014, 113, 287-296.	1.2	30
1948	Conservation and Management of Polytypic Species: The Little Striped Whiptail Complex ( <i>Aspidoscelis inornata</i> ) as a Case Study. <i>Copeia</i> , 2014, 2014, 519-529.	1.4	13
1949	Spatial genetic features of eastern oysters ( <i>Crassostrea virginica</i> Gmelin) in the Gulf of Mexico: northward movement of a secondary contact zone. <i>Ecology and Evolution</i> , 2014, 4, 1671-1685.	0.8	18

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1950	Panmixia defines the genetic diversity of a unique arthropodâ€dispersed fungus specific to <i>Protea</i> flowers. <i>Ecology and Evolution</i> , 2014, 4, 3444-3455.	0.8	17
1951	Comparison of population genetic estimates amongst wild, <i>F</i> 1 and <i>F</i> 2 cultured abalone ( <i>Haliotis midae</i> ). <i>Animal Genetics</i> , 2014, 45, 456-459.	0.6	19
1952	Signature of post-glacial expansion and genetic structure at the northern range limit of the speckled wood butterfly. <i>Biological Journal of the Linnean Society</i> , 2014, 113, 136-148.	0.7	16
1953	Demographic histories and genetic diversities of <i>Fennoscandian</i> marine and landlocked ringed seal subspecies. <i>Ecology and Evolution</i> , 2014, 4, 3420-3434.	0.8	24
1954	Isolation and characterization of eight microsatellite loci in the brook lamprey <i>Lampetra planeri</i> (Petromyzontiformes) using 454 sequence data. <i>Journal of Fish Biology</i> , 2014, 85, 960-964.	0.7	3
1955	Phylogeographic evidence for two mesic refugia in a biodiversity hotspot. <i>Heredity</i> , 2014, 113, 454-463.	1.2	29
1956	Association analysis of polymorphisms in caprine KISS1 gene with reproductive traits. <i>Animal Reproduction Science</i> , 2014, 151, 71-77.	0.5	21
1957	<i>Ficus insipida</i> subsp. <i>insipida</i> (Moraceae) reveals the role of ecology in the phylogeography of widespread Neotropical rain forest tree species. <i>Journal of Biogeography</i> , 2014, 41, 1697-1709.	1.4	25
1958	Population structure, population history and <i>DNA</i> barcoding of fruit fly <i>Bactrocera latifrons</i> ( <i>B. endel</i> ) ( <i>Diptera</i> ) Tj ETQq0 0 0 rgBT /Overlock 10.3 f 50 417 Td ( <i>B. latifrons</i> )	1.3	17
1959	New genetic variants in the <i>CCR5</i> gene and the distribution of known polymorphisms in <i>Omani</i> population. <i>International Journal of Immunogenetics</i> , 2014, 41, 20-28.	0.8	4
1960	New host and lineage diversity of avian haemosporidia in the northern Andes. <i>Evolutionary Applications</i> , 2014, 7, 799-811.	1.5	53
1961	Population genetic structure of the Australian caddisfly <i>Lectrides varians</i> Mosely (Trichoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10.3 f 50 417 Td ( <i>Lectrides varians</i> ) Conservation, 2014, 18, 1037-1046.	0.8	8
1962	Differing impact of a major biogeographic barrier on genetic structure in two large kangaroos from the monsoon tropics of Northern Australia. <i>Ecology and Evolution</i> , 2014, 4, 554-567.	0.8	25
1963	Population Genetic Structure of Spotted Eagle Rays, <i>Aetobatus narinari</i> , off Sarasota, Florida and the Southeastern United States. <i>Copeia</i> , 2014, 2014, 503-512.	1.4	11
1964	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
1965	Can novel genetic analyses help to identify lowâ€dispersal marine invasive species?. <i>Ecology and Evolution</i> , 2014, 4, 2848-2866.	0.8	19
1966	Population differentiation of zander ( <i>Sander lucioperca</i> ) across native and newly colonized ranges suggests increasing admixture in the course of an invasion. <i>Evolutionary Applications</i> , 2014, 7, 555-568.	1.5	22
1967	Outlier <i>SNP</i> markers reveal fineâ€scale genetic structuring across <i>European</i> hake populations ( <i>Merluccius merluccius</i> ). <i>Molecular Ecology</i> , 2014, 23, 118-135.	2.0	171

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1968	Novel Y-chromosome polymorphisms in Chinese domestic yak. <i>Animal Genetics</i> , 2014, 45, 449-452.	0.6	10
1969	Making the cryptic visible “ resolving the species complex of <i>Aphodius fimetarius</i> ( <i>Linnæus</i> ) and <i>Aphodius pedellus</i> (de <i>Géer</i> ) ( <i>Coleoptera: Scarabaeidae</i> ) by three complementary methods. <i>Systematic Entomology</i> , 2014, 39, 531-547.	1.7	24
1970	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
1971	Genetic population structure of the Pacific bluefin tuna <i>Thunnus orientalis</i> and the yellowfin tuna <i>Thunnus albacares</i> in the North Pacific Ocean. <i>Fisheries Science</i> , 2014, 80, 1193-1204.	0.7	14
1972	Evolution of an Experimental Population of <i>Phytophthora capsici</i> in the Field. <i>Phytopathology</i> , 2014, 104, 1107-1117.	1.1	14
1973	Phylogeographic pattern and glacial refugia of a rocky shore species with limited dispersal capability: the case of Montagu’s blenny ( <i>Coryphoblennius galerita</i> , <i>Blenniidae</i> ). <i>Marine Biology</i> , 2014, 161, 2509-2520.	0.7	13
1974	Colombia’s racial crucible: Y chromosome evidence from six admixed communities in the Department of Bolivar. <i>Annals of Human Biology</i> , 2014, 41, 453-459.	0.4	28
1975	Forensic STR loci reveal common genetic ancestry of the Thai-Malay Muslims and Thai Buddhists in the deep Southern region of Thailand. <i>Journal of Human Genetics</i> , 2014, 59, 675-681.	1.1	13
1976	Immunoglobulin genes in Andalusia (Spain). Genetic diversity in the Mediterranean space. <i>Comptes Rendus - Biologies</i> , 2014, 337, 646-656.	0.1	9
1977	Cryptic speciation along a bathymetric gradient. <i>Biological Journal of the Linnean Society</i> , 2014, 113, 897-913.	0.7	22
1978	A Look into Genetic Diversity of Enset ( <i>Ensete ventricosum</i> (Welw.) Cheesman) Using Transferable Microsatellite Sequences of Banana in Ethiopia. <i>Journal of Crop Improvement</i> , 2014, 28, 159-183.	0.9	17
1979	Genetic connectivity between trans-oceanic populations of <i>Capreolia implexa</i> (Gelidiales, Rhodophyta) in cool temperate waters of Australasia and Chile. <i>Aquatic Botany</i> , 2014, 119, 73-79.	0.8	29
1980	Birds are islands for parasites. <i>Biology Letters</i> , 2014, 10, 20140255.	1.0	33
1981	Genetic variation among western populations of the Horned Lark ( <i>Eremophila alpestris</i> ) indicates recent colonization of the Channel Islands off southern California, mainland-bound dispersal, and postglacial range shifts. <i>Auk</i> , 2014, 131, 162-174.	0.7	18
1982	Microsatellite Primer Development for Post Oak, <i>Quercus stellata</i> (Fagaceae). <i>Applications in Plant Sciences</i> , 2014, 2, 1400070.	0.8	9
1983	Morphological and Genetic Variation Between the Japanese Populations of the Amphidromous Snail <i>Stenomelania crenulata</i> (Cerithioidea: Thiaridae). <i>Zoological Science</i> , 2014, 31, 593.	0.3	6
1984	Population Structure of Florida Scrub Lizards ( <i>Sceloporus woodi</i> ) in an Anthropogenically Fragmented Forest. <i>Herpetologica</i> , 2014, 70, 266-278.	0.2	8
1985	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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1986	Phylogeography of the Scaled Quail in the American Southwest. Western North American Naturalist, 2014, 74, 18-32.	0.2	8
1987	First Records of the Night Smelt, <i>Spirinchus starksi</i> , in the Salish Sea, Washington. Northwestern Naturalist, 2014, 95, 40-43.	0.5	0
1988	Characterization and Conservation Concerns of Green Turtles ( <i>Chelonia mydas</i> ) Nesting in Hong Kong, China. Pacific Science, 2014, 68, 231-243.	0.2	18
1989	Microsatellite primers in <i>Agave utahensis</i> (Asparagaceae), a keystone species in the Mojave Desert and Colorado Plateau. Applications in Plant Sciences, 2014, 2, 1400047.	0.8	18
1990	It's not what it looks like: molecular data fails to substantiate morphological differences in two sea hares (Mollusca, Heterobranchia, Aplysiidae) from southern Brazil. Helgoland Marine Research, 2014, 68, 523-530.	1.3	7
1991	Wetlands explain most in the genetic divergence pattern of <i>Oncomelania hupensis</i> . Infection, Genetics and Evolution, 2014, 27, 436-444.	1.0	9
1992	Human genetics of the Kula Ring: Y-chromosome and mitochondrial DNA variation in the Massim of Papua New Guinea. European Journal of Human Genetics, 2014, 22, 1393-1403.	1.4	16
1993	Genetic diversity, population structure and phenotypic variation in European <i>Salix viminalis</i> L. (Salicaceae). Tree Genetics and Genomes, 2014, 10, 1595-1610.	0.6	44
1994	Population Genetics of Arctic Grayling Distributed Across Large, Unobstructed River Systems. Transactions of the American Fisheries Society, 2014, 143, 802-816.	0.6	5
1995	Molecular and morphological systematics of neustonic nudibranchs (Mollusca : Gastropoda : Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 174.	0.5	55
1996	Hybridisation between native <i>Oreochromis</i> species and introduced Nile tilapia <i>O. niloticus</i> in the Kafue River, Zambia. African Journal of Aquatic Science, 2014, 39, 23-34.	0.5	64
1997	The landscape genetics of syntopic topminnows ( <i>Fundulus notatus</i> and <i>F. olivaceus</i> ) in a riverine contact zone. Ecology of Freshwater Fish, 2014, 23, 572-580.	0.7	6
1998	Y-chromosome analysis in a Northwest Iberian population: Unraveling the impact of Northern African lineages. American Journal of Human Biology, 2014, 26, 740-746.	0.8	1
1999	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. Journal of Phycology, 2014, 50, 885-896.	1.0	16
2000	High sequence variation and low population differentiation of mitochondrial control regions of wild Large yellow croaker in South China Sea. Biochemical Systematics and Ecology, 2014, 56, 151-157.	0.6	5
2001	Mitochondrial DNA diversity of Anatolian indigenous domestic goats. Journal of Animal Breeding and Genetics, 2014, 131, 487-495.	0.8	5
2002	Understanding the formation of Mediterranean-African-Asian disjunctions: evidence for Miocene climate-driven vicariance and recent long-distance dispersal in the Tertiary relict <i>Smilax aspera</i> (Smilacaceae). New Phytologist, 2014, 204, 243-255.	3.5	47
2003	ORIGIN OF <i>DERMACENTOR ALBIPICTUS</i> (ACARI: IXODIDAE) ON ELK IN THE YUKON, CANADA. Journal of Wildlife Diseases, 2014, 50, 544-551.	0.3	15

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2004	Isolation and characterization of 16 highly polymorphic tetranucleotide microsatellite DNA markers in <i>Paa spinosa</i> . <i>Biochemical Systematics and Ecology</i> , 2014, 57, 257-261.	0.6	1
2005	Migration history and stock structure of two putatively diadromous teleost fishes, as determined by genetic and otolith chemistry analyses. <i>Freshwater Science</i> , 2014, 33, 193-206.	0.9	23
2006	Phylogeographic Patterns Among the Subspecies of <i>Notophthalmus viridescens</i> (Eastern Newt) in South Carolina. <i>Southeastern Naturalist</i> , 2014, 13, 444-455.	0.2	1
2007	Hybridization effects and genetic diversity of the common and black tufted marmoset ( <i>Callithrix jacchus</i> ) and ( <i>Callithrix penicillata</i> ) mitochondrial control region. <i>American Journal of Physical Anthropology</i> , 2014, 155, 522-536.	2.1	33
2008	Cytosuclear discordance and the species status of <i>Myotis myotis</i> and <i>Myotis blythii</i> ( <i>Chiroptera</i> ). <i>Zoologica Scripta</i> , 2014, 43, 549-561.	0.7	31
2009	Molecular phylogeography and intraspecific divergence of <i>Spiraea alpina</i> (Rosaceae) distributed in the Qinghai-Tibetan Plateau and adjacent regions inferred from nrDNA. <i>Biochemical Systematics and Ecology</i> , 2014, 57, 278-286.	0.6	13
2010	History of Oilseed Rape Cropping and Geographic Origin Affect the Genetic Structure of <i>Plasmodiophora brassicae</i> Populations. <i>Phytopathology</i> , 2014, 104, 532-538.	1.1	23
2011	Microsatellite Variability Among Black Skimmer ( <i>Rynchops niger intercedens</i> ) Populations in Southern South America. <i>Waterbirds</i> , 2014, 37, 175-182.	0.2	4
2012	Comparative phylogeography of codistributed aquatic insects in western North America: insights into dispersal and regional patterns of genetic structure. <i>Freshwater Biology</i> , 2014, 59, 2051-2063.	1.2	9
2013	Human influence on the dispersal and genetic structure of French <i>Globodera tabacum</i> populations. <i>Infection, Genetics and Evolution</i> , 2014, 27, 309-317.	1.0	23
2014	Species- and sex-specific connectivity effects of habitat fragmentation in a suite of woodland birds. <i>Ecology</i> , 2014, 95, 1556-1568.	1.5	63
2015	From refugia to rookeries: Phylogeography of Atlantic green turtles. <i>Journal of Experimental Marine Biology and Ecology</i> , 2014, 461, 306-316.	0.7	39
2016	DNA barcoding and phylogeographic analysis of <i>Nipponacmea</i> limpets (Gastropoda: Lottiidae) in China. <i>Journal of Molluscan Studies</i> , 2014, 80, 420-429.	0.4	16
2017	Comparative rangewide phylogeography of four endemic Taiwanese bat species. <i>Molecular Ecology</i> , 2014, 23, 3566-3586.	2.0	20
2018	Contrasting Population Histories of the Deep-Sea Demersal Fish, <i>Lycodes matsubara</i> , in the Sea of Japan and the Sea of Okhotsk. <i>Zoological Science</i> , 2014, 31, 375.	0.3	18
2019	Y chromosome haplotype diversity of domestic sheep ( <i>Ovis aries</i> ) in northern Eurasia. <i>Animal Genetics</i> , 2014, 45, 903-907.	0.6	15
2020	Epigenetic variation reflects dynamic habitat conditions in a rare floodplain herb. <i>Molecular Ecology</i> , 2014, 23, 3523-3537.	2.0	113
2021	Phylogeography of <i>Cephalotaxus oliveri</i> (Cephalotaxaceae) in relation to habitat heterogeneity, physical barriers and the uplift of the Yungui Plateau. <i>Molecular Phylogenetics and Evolution</i> , 2014, 80, 205-216.	1.2	21



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2022	Limited genetic structure and diversity in the water rail ( <i>Rallus aquaticus</i> ) L., 1758 (Aves: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 496-500.	0.6	3
2023	<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
2024	Phylogeographical Analysis of a Cold-Temperate Freshwater Fish, the Amur Sleeper ( <i>Percottus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 496-500.	0.3	16
2025	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
2026	Brazil nuts are subject to infection with B and G aflatoxin-producing fungus, <i>Aspergillus pseudonomius</i> . <i>International Journal of Food Microbiology</i> , 2014, 186, 14-21.	2.1	25
2027	Genomics of the divergence continuum in an African plant biodiversity hotspot, I: drivers of population divergence in <i>Restio capensis</i> (Restionaceae). <i>Molecular Ecology</i> , 2014, 23, 4373-4386.	2.0	45
2028	Little fox on the prairie: genetic structure and diversity throughout the distribution of a grassland carnivore in the United States. <i>Conservation Genetics</i> , 2014, 15, 1503-1514.	0.8	8
2029	Transoceanic genetic similarities of kelp-associated sea slug populations: long-distance dispersal via rafting?. <i>Journal of Biogeography</i> , 2014, 41, 2357-2370.	1.4	56
2030	Morphometric and genetic divergence in island and mainland populations of <i>Anolis nebulosus</i> (Squamata: Polychrotidae) from Jalisco (Mexico): an instance of insular gigantism. <i>Italian Journal of Zoology</i> , 2014, 81, 204-214.	0.6	11
2031	Reinforcement generates reproductive isolation between neighbouring conspecific populations of spadefoot toads. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140949.	1.2	42
2032	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
2033	Genetic Structure and Cryptic Genealogy of the Bonin Flying Fox ( <i>Pteropus pselaphon</i> ) Revealed by Mitochondrial DNA and Microsatellite Markers. <i>Acta Chiropterologica</i> , 2014, 16, 15-26.	0.2	4
2034	Population data of 12 X-chromosome STR loci in Yanbian Korean samples from China. <i>Forensic Science International: Genetics</i> , 2014, 13, 143-144.	1.6	13
2035	Population genetic structure in the endemic cyprinid fish <i>Microphysogobio alticorpus</i> in Taiwan: Evidence for a new phylogeographical area. <i>Biochemical Systematics and Ecology</i> , 2014, 57, 108-116.	0.6	7
2036	Population data of 17 Y-STR loci in Nanyang Han population from Henan Province, Central China. <i>Forensic Science International: Genetics</i> , 2014, 13, 145-146.	1.6	17
2037	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
2038	Rapid radiation and hybridization contribute to weak differentiation and hinder phylogenetic inferences in the New World Mallard complex ( <i>Anasspp.</i> ). <i>Auk</i> , 2014, 131, 524-538.	0.7	30
2039	Recruitment and recovery of pink abalone ( <i>Haliotis corrugata</i> ) in a historically overexploited kelp forest: Are local populations self-sustaining?. <i>Journal of Experimental Marine Biology and Ecology</i> , 2014, 460, 184-192.	0.7	9

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2041	Footprints of divergent selection in natural populations of <i>Castanopsis fargesii</i> (Fagaceae). <i>Heredity</i> , 2014, 113, 533-541.	1.2	23
2042	High morphological diversity in remote island populations of the peat moss <i>Sphagnum palustre</i> : glacial refugium, adaptive radiation or just plasticity?. <i>Bryologist</i> , 2014, 117, 95.	0.1	16
2043	Dispersal potential and population genetic structure in the marine intertidal of the eastern North Pacific. <i>Ecological Monographs</i> , 2014, 84, 435-456.	2.4	59
2044	Forensic population data for 20 STR loci in Argentina. <i>Forensic Science International: Genetics</i> , 2014, 13, e20-e21.	1.6	12
2045	Contrasting genetic structure of the Eurasian otter ( <i>Lutra lutra</i> ) across a latitudinal divide. <i>Journal of Mammalogy</i> , 2014, 95, 814-823.	0.6	10
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2049	So, you want to use next-generation sequencing in marine systems? Insight from the Pan-Pacific Advanced Studies Institute. <i>Bulletin of Marine Science</i> , 2014, 90, 79-122.	0.4	53
2050	Prolonged isolation and persistence of a common endemic on granite outcrops in both mesic and semi-arid environments in south-western Australia. <i>Journal of Biogeography</i> , 2014, 41, 2032-2044.	1.4	43
2051	Contemporary population structure and post-glacial genetic demography in a migratory marine species, the blacknose shark, <i>Carcharhinus acronotus</i> . <i>Molecular Ecology</i> , 2014, 23, 5480-5495.	2.0	49
2052	The history of the North African mitochondrial DNA haplogroup U6 gene flow into the African, Eurasian and American continents. <i>BMC Evolutionary Biology</i> , 2014, 14, 109.	3.2	41
2053	Evidence of weak genetic structure and recent gene flow between <i>Bactrocera dorsalis</i> s.s. and <i>B. papayae</i> , across Southern Thailand and West Malaysia, supporting a single target pest for SIT applications. <i>BMC Genetics</i> , 2014, 15, 70.	2.7	14
2054	Genetic diversity and population structure of <i>Plasmodium vivax</i> in Central China. <i>Malaria Journal</i> , 2014, 13, 262.	0.8	22
2055	Circulation of four <i>Anaplasma phagocytophilum</i> ecotypes in Europe. <i>Parasites and Vectors</i> , 2014, 7, 365.	1.0	207
2056	Genetic fragmentation in India's third longest river system, the Narmada. <i>SpringerPlus</i> , 2014, 3, 385.	1.2	7
2057	Nuclear and chloroplast diversity and phenotypic distribution of rice ( <i>Oryza sativa</i> L.) germplasm from the democratic people's republic of Korea (DPRK; North Korea). <i>Rice</i> , 2014, 7, 7.	1.7	14

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2060	Cryptic Diversity in Common Mustached Bats<i>Pteronotus</i>cf.<i>parnellii</i>(Mormoopidae) in French Guiana and Brazilian Amapa. Acta Chiropterologica, 2014, 16, 1-13.	0.2	37
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2068	Multigenerational outbreeding effects in Chinook salmon ( <i>Oncorhynchus tshawytscha</i> ). Genetica, 2014, 142, 281-293.	0.5	10
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2071	Isolation and characterization of microsatellite markers for <i>Forsythia suspensa</i> (Thunb.) Vahl (Oleaceae) using 454 sequencing technology. Biochemical Systematics and Ecology, 2014, 57, 328-331.	0.6	6
2072	The Population History of Endogenous Retroviruses in Mule Deer ( <i>Odocoileus hemionus</i> ). Journal of Heredity, 2014, 105, 173-187.	1.0	13
2073	Seascape continuity plays an important role in determining patterns of spatial genetic structure in a coral reef fish. Molecular Ecology, 2014, 23, 2902-2913.	2.0	34
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2077	Molecular characterization of <i>Sarcocystis</i> species from Polish roe deer based on ssu rRNA and <i>cox1</i> sequence analysis. <i>Parasitology Research</i> , 2014, 113, 3029-3039.	0.6	20
2078	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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2081	Genetic characterization and structure of the endemic Colombian silvery brown bare-face tamarin, <i>Saguinus leucopus</i> (Callitrichinae, Cebidae, Primates). <i>Primates</i> , 2014, 55, 415-435.	0.7	10
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2090	Assessment of genetic diversity among sorghum landraces and their wild/weedy relatives in western Kenya using simple sequence repeat (SSR) markers. <i>Conservation Genetics</i> , 2014, 15, 1269-1280.	0.8	3
2091	Cryptic structure and niche divergence within threatened Galápagos giant tortoises from southern Isabela Island. <i>Conservation Genetics</i> , 2014, 15, 1357-1369.	0.8	16
2092	Multiple colonizations of Lake Biwa by <i>Sarcocheilichthys</i> fishes and their population history. <i>Environmental Biology of Fishes</i> , 2014, 97, 741-755.	0.4	19
2093	Progression of molecular and phenotypic diversification in resynthesized <i>Brassica juncea</i> (L) gene pool with determinate inflorescence. <i>Euphytica</i> , 2014, 199, 325-338.	0.6	12

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2095	Genetic divergence and evidence for sympatric host-races in the highly polyphagous brown tail moth, <i>Euproctis chrysorrhoea</i> (Lepidoptera: Erebididae). <i>Evolutionary Ecology</i> , 2014, 28, 829-848.	0.5	11
2096	Wild cyclic voles maintain high neutral and MHC diversity without strong evidence for parasite-mediated selection. <i>Evolutionary Ecology</i> , 2014, 28, 957-975.	0.5	15
2097	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
2098	Patterns of simple sequence repeats in cultivated blueberries ( <i>Vaccinium</i> section <i>Cyanococcus</i> spp.) and their use in revealing genetic diversity and population structure. <i>Molecular Breeding</i> , 2014, 34, 675-689.	1.0	84
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2102	Microsatellite analysis supports clonal propagation and reduced divergence of <i>Trypanosoma vivax</i> from asymptomatic to fatally infected livestock in South America compared to West Africa. <i>Parasites and Vectors</i> , 2014, 7, 210.	1.0	27
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2105	The history of sturgeon in the Baltic Sea. <i>Journal of Biogeography</i> , 2014, 41, 1590-1602.	1.4	22
2106	Genetic analysis of 17 Y-chromosomal STR loci of Chinese Tujia ethnic group residing in Youyang Region of Southern China. <i>Legal Medicine</i> , 2014, 16, 173-175.	0.6	14
2107	Genetic analysis of Anatolian apples ( <i>Malus</i> sp.) by simple sequence repeats. <i>Journal of Systematics and Evolution</i> , 2014, 52, 580-588.	1.6	9
2108	Genetic analysis of Anatolian pear germplasm by simple sequence repeats. <i>Annals of Applied Biology</i> , 2014, 164, 441-452.	1.3	13
2109	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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2111	Landscape genomics and a common garden trial reveal adaptive differentiation to temperature across Europe in the tree species <i>Alnus glutinosa</i> . <i>Molecular Ecology</i> , 2014, 23, 4709-4721.	2.0	124

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2113	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
2114	Diversification in the <i>Scleranthus</i> <i>Americanus</i> <i>Pampas</i> : the genetic and morphological variation of the widespread <i>Pentunia axillaris</i> complex ( <i>Solanaceae</i> ). <i>Molecular Ecology</i> , 2014, 23, 374-389.	2.0	54
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2118	Fine-scale spatial genetic structure of common and declining bumble bees across an agricultural landscape. <i>Molecular Ecology</i> , 2014, 23, 3384-3395.	2.0	41
2119	Phylogeography of the Gambel's Quail ( <i>Callipepla gambelii</i> ) of western North America. <i>Wilson Journal of Ornithology</i> , 2014, 126, 218.	0.1	5
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2121	Genetic assignment tests reveal dispersal of white-tailed deer: implications for chronic wasting disease. <i>Journal of Mammalogy</i> , 2014, 95, 646-654.	0.6	13
2122	When physical oceanography meets population genetics: The case study of the genetic/evolutionary discontinuity in the endangered goliath grouper ( <i>Epinephelus itajara</i> ; Perciformes: Epinephelidae) with comments on the conservation of the species. <i>Biochemical Systematics and Ecology</i> , 2014, 56, 255-266.	0.6	11
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2124	Timing for success: expression phenotype and local adaptation related to latitude in the boreal forest tree, <i>Populus balsamifera</i> . <i>Tree Genetics and Genomes</i> , 2014, 10, 911-922.	0.6	7
2125	High genetic similarity between Polish and North European Scots pine ( <i>Pinus sylvestris</i> L.) populations at nuclear gene loci. <i>Tree Genetics and Genomes</i> , 2014, 10, 1015-1025.	0.6	17
2126	A unifying study of phenotypic and molecular genetic variability in natural populations of <i>Anadenanthera colubrina</i> var. <i>cebil</i> from Yungas and Paranaense biogeographic provinces in Argentina. <i>Journal of Genetics</i> , 2014, 93, 123-132.	0.4	9
2127	Development of 16 microsatellite loci for the endangered sandhill dunnart ( <i>Sminthopsis</i> ) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i>	0.4	2
2128	Characterization of 15 novel microsatellite loci for <i>Cypripedium calceolus</i> (Orchidaceae) using MiSeq sequencing. <i>Conservation Genetics Resources</i> , 2014, 6, 527-529.	0.4	9
2129	Mining microsatellites for <i>Gray's beaked whale</i> from second-generation sequencing data. <i>Conservation Genetics Resources</i> , 2014, 6, 657-659.	0.4	2



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2131	Validation of microsatellite multiplexes for parentage analysis in a coral reef fish ( <i>Lutjanus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 662	0.4	2
2132	Development and characterization of 36 novel microsatellite markers for lake chub ( <i>Couesius</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662	0.4	4
2133	Mitochondrial evidence for genetic diversity and low phylogeographic differentiation in the Marsh Warbler <i>Acrocephalus palustris</i> (Aves: Acrocephalidae). <i>Organisms Diversity and Evolution</i> , 2014, 14, 409-417.	0.7	7
2134	Mitochondrial DNA haplogroups and homogeneity in the Korean population. <i>Genes and Genomics</i> , 2014, 36, 583-590.	0.5	12
2135	Microsatellite multiplex assay for the analysis of Atlantic sturgeon populations. <i>Journal of Applied Genetics</i> , 2014, 55, 505-510.	1.0	8
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2137	Isolation and characterization of 15 polymorphic microsatellite markers for the fig-pollinating wasp, <i>Blastophaga nipponica</i> (Hymenoptera: Agaonidae). <i>Applied Entomology and Zoology</i> , 2014, 49, 487-491.	0.6	4
2138	The influence of habitat structure on genetic differentiation in red fox populations in north-eastern Poland. <i>Acta Theriologica</i> , 2014, 59, 367-376.	1.1	23
2139	Genetic and morphological variety in Lepidoptera: Evidence from monomorphic <i>Panolis flammea</i> L. and polymorphic <i>Archips podana</i> Scop.. <i>Russian Journal of Genetics</i> , 2014, 50, 613-620.	0.2	0
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2141	Population structure of guppies in north-eastern Venezuela, the area of putative incipient speciation. <i>BMC Evolutionary Biology</i> , 2014, 14, 28.	3.2	7
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2143	Density drives polyandry and relatedness influences paternal success in the Pacific gooseneck barnacle, <i>Pollicipes elegans</i> . <i>BMC Evolutionary Biology</i> , 2014, 14, 81.	3.2	24
2144	Genetic species identification and population structure of <i>Halophila</i> (Hydrocharitaceae) from the Western Pacific to the Eastern Indian Ocean. <i>BMC Evolutionary Biology</i> , 2014, 14, 92.	3.2	52
2145	Development and characterization of 16 polymorphic microsatellite markers from Taiwan cow-tail fir, <i>Keteleeria davidiana</i> var. <i>formosana</i> (Pinaceae) and cross-species amplification in other <i>Keteleeria</i> taxa. <i>BMC Research Notes</i> , 2014, 7, 255.	0.6	6
2146	Sympatric Asian felid phylogeography reveals a major Indochinese-Sundaic divergence. <i>Molecular Ecology</i> , 2014, 23, 2072-2092.	2.0	56
2147	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

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2149	Whole-genome sequence variation, population structure and demographic history of the Dutch population. Nature Genetics, 2014, 46, 818-825.	9.4	641
2150	Landscape structure and climatic variation determine Atlantic salmon genetic connectivity in the Northwest Atlantic. Canadian Journal of Fisheries and Aquatic Sciences, 2014, 71, 246-258.	0.7	37
2151	Spatial structure in European moose (<i>Alces alces</i>): genetic data reveal a complex population history. Journal of Biogeography, 2014, 41, 2173-2184.	1.4	34
2152	Phylogeographical structure within <i>Boa constrictor imperator</i> across the lowlands and mountains of Central America and Mexico. Journal of Biogeography, 2014, 41, 2371-2384.	1.4	34
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2312	Phylogenetic relationships of <i>Petunia patagonica</i> (Solanaceae) revealed by molecular and biogeographical evidence. <i>Phytotaxa</i> , 2015, 222, 17.	0.1	11
2313	Demographic response of cutlassfish ( <i>Trichiurus japonicus</i> and <i>T. nanhaiensis</i> ) to fluctuating palaeo-climate and regional oceanographic conditions in the China seas. <i>Scientific Reports</i> , 2014, 4, 6380.	1.6	26
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2557	Molecular Proxies for Climate Maladaptation in a Long-Lived Tree ( <i>Pinus pinaster</i> Aiton.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 1.25 78	1.25	78
2558	Population genetic analysis of insertion-deletion polymorphisms in a Brazilian population using the Investigator DIPplex kit. <i>Forensic Science International: Genetics</i> , 2015, 19, 10-14.	1.6	18
2559	Migration and Gene Flow Among Domestic Populations of the Chagas Insect Vector <i>Triatoma dimidiata</i> (Hemiptera: Reduviidae) Detected by Microsatellite Loci. <i>Journal of Medical Entomology</i> , 2015, 52, 419-428.	0.9	32
2560	Severely depleted genetic diversity and population structure of a large predatory marine fish (Lates) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 0.8 10	0.8	10
2561	Population connectivity of endangered Ozark big-eared bats ( <i>Corynorhinus townsendii ingens</i> ). <i>Journal of Mammalogy</i> , 2015, 96, 522-530.	0.6	6
2562	A study of genetic polymorphisms in mitochondrial DNA hypervariable regions I and II of the five major ethnic groups and Vedda population in Sri Lanka. <i>Legal Medicine</i> , 2015, 17, 539-546.	0.6	8
2563	p53 gene discriminates two ecologically divergent sister species of pine voles. <i>Heredity</i> , 2015, 115, 444-451.	1.2	3
2564	Linkage disequilibrium with HLA-DRB1-DQB1 haplotypes explains the association of TNF-308G>A variant with type 1 diabetes in a Brazilian cohort. <i>Gene</i> , 2015, 568, 50-54.	1.0	6
2565	The population genomic signature of environmental selection in the widespread insect-pollinated tree species <i>Frangula alnus</i> at different geographical scales. <i>Heredity</i> , 2015, 115, 415-425.	1.2	19



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2566	Mitochondrial DNA Structure of <i>Pyganodon grandis</i> (Bivalvia: Unionidae) from the Lake Erie Watershed and Selected Locations in its Northern Distribution. <i>American Malacological Bulletin</i> , 2015, 33, 34-42.	0.2	4
2567	Molecular phylogenetic analysis of <i>Fasciola</i> flukes from eastern India. <i>Parasitology International</i> , 2015, 64, 334-338.	0.6	34
2568	Population genetic structure and genetic diversity of the threatened White Mountain arctic butterfly ( <i>Oeneis melissa semidea</i> ). <i>Conservation Genetics</i> , 2015, 16, 1253-1264.	0.8	10
2569	Limited genetic differentiation among chinstrap penguin ( <i>Pygoscelis antarctica</i> ) colonies in the Scotia Arc and Western Antarctic Peninsula. <i>Polar Biology</i> , 2015, 38, 1493-1502.	0.5	18
2570	Phylogeny and Evolution of Multiple Common Carp ( <i>Cyprinus carpio</i> L.) Populations Clarified by Phylogenetic Analysis Based on Complete Mitochondrial Genomes. <i>Marine Biotechnology</i> , 2015, 17, 565-575.	1.1	22
2571	Genetic variation of 17 STR loci in Dai population in mainland China. <i>Forensic Science International: Genetics</i> , 2015, 19, 37-38.	1.6	9
2572	The perplexing population genetic structure of <i>Bellamyia purificata</i> (Gastropoda: Viviparidae): low genetic differentiation despite low dispersal ability. <i>Journal of Molluscan Studies</i> , 2015, 81, 466-475.	0.4	14
2573	Evolutionary history and adaptive significance of the polymorphic Pan I in migratory and stationary populations of Atlantic cod ( <i>Gadus morhua</i> ). <i>Marine Genomics</i> , 2015, 22, 45-54.	0.4	10
2574	Genome-wide genetic diversity of rove beetle populations along a metal pollution gradient. <i>Ecotoxicology and Environmental Safety</i> , 2015, 119, 98-105.	2.9	19
2575	Toward the genetic origins of a potentially non-native population of threespine stickleback ( <i>Gasterosteus aculeatus</i> ) in Alberta. <i>Conservation Genetics</i> , 2015, 16, 859-873.	0.8	3
2576	Genetic Diversity of Loquat [ <i>Eriobotrya japonica</i> (Thunb.) Lindl.] Native to Guizhou Province (China) and Its Potential in the Genetic Improvement of Domesticated Cultivars. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 952-961.	1.0	9
2577	Lack of genetic structure and evidence for long-distance dispersal in ash ( <i>Fraxinus excelsior</i> ) populations under threat from an emergent fungal pathogen: implications for restorative planting. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	18
2578	The illegal exploitation of hog badgers ( <i>Arctonyx collaris</i> ) in China: genetic evidence exposes regional population impacts. <i>Conservation Genetics Resources</i> , 2015, 7, 697-704.	0.4	7
2579	Self-Assessment of Color Categories and Its Relationship with HLA Profiling in Brazilian Bone Marrow Donors. <i>Biology of Blood and Marrow Transplantation</i> , 2015, 21, 1140-1144.	2.0	13
2580	Forensic and population genetic analyses of Danes, Greenlanders and Somalis typed with the Yfiler Â® Plus PCR amplification kit. <i>Forensic Science International: Genetics</i> , 2015, 16, 232-236.	1.6	48
2581	Within-island speciation with an exceptional case of distinct separation between two sibling lizard species divided by a narrow stream. <i>Molecular Phylogenetics and Evolution</i> , 2015, 90, 164-175.	1.2	18
2582	Evidence of polygamy in the socially monogamous Amazonian fish <i>Arapaima gigas</i> (Schinz, 1822) (Osteoglossiformes, Arapaimidae). <i>Neotropical Ichthyology</i> , 2015, 13, 195-204.	0.5	22
2583	Restitution and genetic differentiation of salmon populations in the southern Baltic genotyped with the Atlantic salmon 7K SNP array. <i>Genetics Selection Evolution</i> , 2015, 47, 39.	1.2	12

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2584	Genomic variation in tomato, from wild ancestors to contemporary breeding accessions. BMC Genomics, 2015, 16, 257.	1.2	190
2585	Population structure of <i>Hirundichthys oxycephalus</i> in the northwestern Pacific inferred from mitochondrial cytochrome oxidase I gene. Zoological Studies, 2015, 54, e19.	0.3	2
2586	Inter-basin dispersal through irrigation canals explains low genetic structure in <i>Diplomystes cf. chilensis</i> , an endangered freshwater catfish from Central Chile. Limnologica, 2015, 53, 10-16.	0.7	14
2587	Paternity in eastern grey kangaroos: moderate skew despite strong sexual dimorphism. Behavioral Ecology, 2015, 26, 1147-1155.	1.0	12
2588	Phylogeography of <i>Nanorana parkeri</i> (Anura: Ranidae) and multiple refugia on the Tibetan Plateau revealed by mitochondrial and nuclear DNA. Scientific Reports, 2015, 5, 9857.	1.6	26
2589	Statistical and population genetics issues of two Hungarian datasets from the aspect of DNA evidence interpretation. Forensic Science International: Genetics, 2015, 19, 18-21.	1.6	1
2590	Estimation of genetic divergence based on mitochondrial DNA variation for an invasive alien species, <i>Metcalfa pruinosa</i> (Say), in Korea. Journal of Asia-Pacific Entomology, 2015, 18, 447-451.	0.4	4
2591	Allele frequencies of 23 autosomal short tandem repeat loci in the Philippine population. Legal Medicine, 2015, 17, 295-297.	0.6	17
2592	Genetic Population Structure of Black Drum in U.S. Waters. North American Journal of Fisheries Management, 2015, 35, 464-477.	0.5	6
2593	A lack of association between the IKZF2 rs12619285 polymorphism and coronary heart disease. Experimental and Therapeutic Medicine, 2015, 9, 1309-1313.	0.8	5
2594	Phylogeography and Population Structure of the Imperiled Redtail Splitfin (Goodeidae: <i>Xenotoca</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.4	12
2595	On the population genetic portrait of kaluga, <i>Acipenser dauricus georgi</i> , 1775: Analysis of sequence variation in the mitochondrial dna control region. Russian Journal of Genetics, 2015, 51, 877-885.	0.2	3
2596	Population Genetic Structure of Southern Flounder Inferred from Multilocus DNA Profiles. Marine and Coastal Fisheries, 2015, 7, 220-232.	0.6	7
2597	Molecular tracing of confiscated pangolin scales for conservation and illegal trade monitoring in Southeast Asia. Global Ecology and Conservation, 2015, 4, 414-422.	1.0	71
2598	Another functional frame-shift polymorphism of <i>DEFB126</i> (rs11467497) associated with male infertility. Journal of Cellular and Molecular Medicine, 2015, 19, 1077-1084.	1.6	12
2599	A practical guide to environmental association analysis in landscape genomics. Molecular Ecology, 2015, 24, 4348-4370.	2.0	584
2600	Isolation over 35 years in a heated biotest basin causes selection on MHC class II genes in the European perch ( <i>Perca fluviatilis</i> L.). Ecology and Evolution, 2015, 5, 1440-1455.	0.8	18
2601	Human mining activity across the ages determines the genetic structure of modern brown trout ( <i>Salmo trutta</i> L.) populations. Evolutionary Applications, 2015, 8, 573-585.	1.5	46

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2602	Postglacial range shift and demographic expansion of the marine intertidal snail <i>Batillaria attramentaria</i> . <i>Ecology and Evolution</i> , 2015, 5, 419-435.	0.8	18
2603	Comparative genetic diversity in a sample of pony breeds from the U.K. and North America: a case study in the conservation of global genetic resources. <i>Ecology and Evolution</i> , 2015, 5, 3507-3522.	0.8	6
2604	Queen execution increases relatedness among workers of the invasive Argentine ant, <i>Linepithema humile</i> . <i>Ecology and Evolution</i> , 2015, 5, 4098-4107.	0.8	8
2605	Genetic Variation and Structure in Contrasting Geographic Distributions: Widespread Versus Restricted Black-Tailed Prairie Dogs (Subgenus <i>Cynomys</i> ). <i>Journal of Heredity</i> , 2015, 106, 478-490.	1.0	12
2606	Patterns of Genetic Diversity in the Globally Invasive Species Wild Parsnip ( <i>Pastinaca sativa</i> ). <i>Invasive Plant Science and Management</i> , 2015, 8, 415-429.	0.5	5
2607	Low levels of hybridization between sympatric Arctic char ( <i>Salvelinus</i> ) highlights their genetic distinctiveness and ecological segregation. <i>Ecology and Evolution</i> , 2015, 5, 3031-3045.	0.8	22
2608	Population genetic structure and approximate Bayesian computation analyses reveal the southern origin and northward dispersal of the oriental fruit moth <i>Graepholitha molesta</i> (Lepidoptera: Tortricidae) in its native range. <i>Molecular Ecology</i> , 2015, 24, 4094-4111.	2.0	53
2609	Drift, not selection, shapes toll-like receptor variation among oceanic island populations. <i>Molecular Ecology</i> , 2015, 24, 5852-5863.	2.0	44
2610	Effects of landscape matrix on population connectivity of an arboreal mammal, <i>Petaurus breviceps</i> . <i>Ecology and Evolution</i> , 2015, 5, 3939-3953.	0.8	14
2611	Population-level consequences of complementary sex determination in a solitary parasitoid. <i>BMC Evolutionary Biology</i> , 2015, 15, 98.	3.2	15
2612	Phylogeography of the sand dune ant <i>Mycetophylax simplex</i> along the Brazilian Atlantic Forest coast: remarkably low mtDNA diversity and shallow population structure. <i>BMC Evolutionary Biology</i> , 2015, 15, 106.	3.2	22
2613	The genetic prehistory of domesticated cattle from their origin to the spread across Europe. <i>BMC Genetics</i> , 2015, 16, 54.	2.7	100
2614	Genetic diversity of male and female Chinese bayberry ( <i>Myrica rubra</i> ) populations and identification of sex-associated markers. <i>BMC Genomics</i> , 2015, 16, 394.	1.2	31
2615	RAD-QTL Mapping Reveals Both Genome-Level Parallelism and Different Genetic Architecture Underlying the Evolution of Body Shape in Lake Whitefish ( <i>Coregonus clupeaformis</i> ) Species Pairs. <i>Genes, Genomes, Genetics</i> , 2015, 5, 1481-1491.	0.8	62
2616	Genetic isolation of Korean populations of <i>Apodemus peninsulae</i> (Rodentia: Muridae) from their neighboring populations. <i>Genes and Genomics</i> , 2015, 37, 999-1005.	0.5	0
2617	DNA Taxonomy of <i>Paranemertes</i> (Nemertea: Hoplonemertea) with Spirally Fluted Stylets. <i>Zoological Science</i> , 2015, 32, 571-578.	0.3	10
2618	A holistic picture of Austronesian migrations revealed by phylogeography of Pacific paper mulberry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13537-13542.	3.3	68
2619	Reduced Genetic Diversity and Increased Dispersal in Guigna ( <i>Leopardus guigna</i> ) in Chilean Fragmented Landscapes. <i>Journal of Heredity</i> , 2015, 106, 522-536.	1.0	24

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2620	Large-scale population genetics of the mountain ant <i>Proformica longiseta</i> (Hymenoptera: Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	0.7	13
2621	Temporal stability of parasite distribution and genetic variability values of <i>Contracaecum osculatum</i> sp. D and <i>C. osculatum</i> sp. E (Nematoda: Anisakidae) from fish of the Ross Sea (Antarctica). <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2015, 4, 356-367.	0.6	19
2622	Microsatellite DNA analysis of Pacific hake <i>Merluccius productus</i> population structure in the Salish Sea. <i>ICES Journal of Marine Science</i> , 2015, 72, 2720-2731.	1.2	11
2623	Analysis of HLA-B15 and HLA-B27 in spondyloarthritis with peripheral and axial clinical patterns. <i>BMJ Open</i> , 2015, 5, e009092-e009092.	0.8	26
2624	Deeper Mitochondrial Sequencing Reveals Cryptic Diversity and Structure in Brazilian Green Turtle Rookeries. <i>Chelonian Conservation and Biology</i> , 2015, 14, 167.	0.1	25
2625	Deciphering Hatchery Stock Influences on Wild Populations of Vermont Lake Trout. <i>Transactions of the American Fisheries Society</i> , 2015, 144, 124-139.	0.6	6
2626	Genetic provenance and best practice woodland management: a case study in native alder ( <i>Alnus</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	0.6	11
2627	Copy number variation and genetic diversity of MHC Class IIb alleles in an alien population of <i>Xenopus laevis</i> . <i>Immunogenetics</i> , 2015, 67, 591-603.	1.2	20
2628	Spatial Genetic and Body-Size Trends in Atlantic Canada <i>Canis latrans</i> (Coyote) Populations. <i>Northeastern Naturalist</i> , 2015, 22, 598-612.	0.1	4
2629	<i>Fusarium circinatum</i> isolates from northern Spain are commonly infected by three distinct mitoviruses. <i>Archives of Virology</i> , 2015, 160, 2093-2098.	0.9	12
2630	Phylogeography and limited distribution of the endangered freshwater crayfish, <i>Euastacus urospinosus</i> . <i>Australian Journal of Zoology</i> , 2015, 63, 236.	0.6	2
2631	Phenotypic plasticity accounts for most of the variation in leaf manganese concentrations in <i>Phytolacca americana</i> growing in manganese-contaminated environments. <i>Plant and Soil</i> , 2015, 396, 215-227.	1.8	21
2632	Microsatellite DNA variation of oval squid <i>Sepioteuthis</i> sp. 2 reveals a single fishery stock on the coastline of mainland Japan. <i>Fisheries Science</i> , 2015, 81, 839-847.	0.7	4
2633	Microsatellite variation and rare alleles in a bottlenecked Hawaiian Islands endemic: implications for reintroductions. <i>Endangered Species Research</i> , 2015, 28, 117-122.	1.2	3
2634	Genetic diversity and population structure of endangered <i>Aquilaria malaccensis</i> revealed potential for future conservation. <i>Journal of Genetics</i> , 2015, 94, 697-704.	0.4	7
2635	Genetic data support independent glacial refugia and open ocean barriers to dispersal for the Southern Ocean sea spider <i>Austropallene cornigera</i> (M��bius, 1902). <i>Journal of Crustacean Biology</i> , 2015, 35, 480-490.	0.3	49
2636	Genetic diversity and demographic history of the terrestrial hermit crabs <i>Birgus latro</i> and <i>Coenobita brevis</i> in the North-Western Pacific Region. <i>Journal of Crustacean Biology</i> , 2015, 35, 793-803.	0.3	17
2637	Genetic polymorphisms of 22 autosomal STR loci in Chinese Han population. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e45-e47.	0.1	12

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2638	Association of HLA and cytokine gene polymorphisms with idiopathic pulmonary fibrosis. Kaohsiung Journal of Medical Sciences, 2015, 31, 613-620.	0.8	19
2639	Genetic differentiation of Pacific smelt <i>Osmerus mordax dentex</i> inferred from the data of mitochondrial DNA analysis. Russian Journal of Genetics, 2015, 51, 1221-1232.	0.2	10
2640	Population genetics of the invasive giant hogweed ( <i>Heracleum</i> sp.) in a northern European region. Plant Ecology, 2015, 216, 1155-1162.	0.7	6
2641	First Remarks on Genetic Variation of the Little Known Leaf Miner <i>Angelabella tecomae</i> Vargas & Parra (Gracillariidae) in the Atacama Desert of Northern Chile. Journal of the Lepidopterists' Society, 2015, 69, 192-196.	0.0	7
2642	ATPase 8/6 gene based genetic diversity assessment of snakehead murrel, <i>Channa striata</i> (Perciformes), Tj ETQq0 0.0 rgBT /Overlock 10	0.2	3
2643	Genetic diversity and population connectivity of the Asian green mussel <i>Perna viridis</i> in South China Sea, inferred from mitochondria DNA markers. Biochemical Systematics and Ecology, 2015, 61, 470-476.	0.6	14
2644	Genetic and morphological evidence for introgression between three species of willows. BMC Evolutionary Biology, 2015, 15, 193.	3.2	29
2645	Estimating the molecular evolutionary rates of mitochondrial genes referring to Quaternary ice age events with inferred population expansions and dispersals in Japanese <i>Apodemus</i> . BMC Evolutionary Biology, 2015, 15, 187.	3.2	43
2646	Deeply divergent sympatric mitochondrial lineages of the earthworm <i>Lumbricus rubellus</i> are not reproductively isolated. BMC Evolutionary Biology, 2015, 15, 217.	3.2	50
2647	Computer simulation of human leukocyte antigen genes supports two main routes of colonization by human populations in East Asia. BMC Evolutionary Biology, 2015, 15, 240.	3.2	19
2648	Phylogeographic data revealed shallow genetic structure in the kelp <i>Saccharina japonica</i> (Laminariales, Phaeophyta). BMC Evolutionary Biology, 2015, 15, 237.	3.2	24
2649	Climate oscillations, glacial refugia, and dispersal ability: factors influencing the genetic structure of the least salmonfly, <i>Pteronarcella badia</i> (Plecoptera), in Western North America. BMC Evolutionary Biology, 2015, 15, 279.	3.2	21
2650	Development and characterization of new polymorphic microsatellite loci for <i>Trionyx triunguis</i> (Testudines: Trionychidae) in the Mediterranean Basin. Amphibia - Reptilia, 2015, 36, 318-324.	0.1	2
2651	Genetic structure and differentiation of the fire salamander <i>Salamandra salamandra</i> at the northern margin of its range in the Carpathians. Amphibia - Reptilia, 2015, 36, 301-311.	0.1	7
2652	Genetic diversity of <i>Narcissus tortifolius</i> , an endangered endemic species from Southeastern Spain. Plant Biosystems, 2015, , 1-9.	0.8	3
2653	Population data for 15 autosomal STR loci in the Dong ethnic minority from Guizhou Province, Southwest China. Forensic Science International: Genetics, 2015, 16, 237-238.	1.6	35
2654	Defining Genetic, Taxonomic, and Geographic Boundaries Among Species of the <i>Psorophora confinnis</i> (Diptera: Culicidae) Complex in North and South America. Journal of Medical Entomology, 2015, 52, 907-917.	0.9	2
2655	Genetic diversity of <i>Trichomonas vaginalis</i> clinical isolates from Henan province in central China. Pathogens and Global Health, 2015, 109, 242-246.	1.0	17

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2656	<i>Fistularia commersonii</i> (Teleostea: Fistulariidae): walking through the Lessepsian paradox of mitochondrial DNA. Italian Journal of Zoology, 2015, 82, 499-512.	0.6	8
2657	Cytogenetic and Molecular Evidence of Additional Cryptic Diversity in High Elevation Black fly <i>Simulium feuerborni</i> (Diptera: Simuliidae) Populations in Southeast Asia. Journal of Medical Entomology, 2015, 52, 829-836.	0.9	16
2658	Spatial genetic structure of the crested auklet ( <i>Aethia cristatella</i> Pallas, 1769) colony based on the mitochondrial dna control region and microsatellite loci. Russian Journal of Genetics, 2015, 51, 898-907.	0.2	2
2659	Ancient woodlands in the limelight: delineation and genetic structure of ancient woodland species <i>Tilia cordata</i> and <i>Tilia platyphyllos</i> (Tiliaceae) in the UK. Tree Genetics and Genomes, 2015, 11, 1.	0.6	21
2660	Comparative phylogeography of endemic Azorean arthropods. BMC Evolutionary Biology, 2015, 15, 250.	3.2	6
2661	Variation in NAT2 acetylation phenotypes is associated with differences in food-producing subsistence modes and ecoregions in Africa. BMC Evolutionary Biology, 2015, 15, 263.	3.2	33
2662	HLA-frequencies of Austrian umbilical cord blood samples. Human Immunology, 2015, 76, 863-867.	1.2	1
2663	Genetic Stock Structure of <i>Terapon jarbua</i> in Taiwanese Waters. Marine and Coastal Fisheries, 2015, 7, 464-473.	0.6	20
2664	Ontogenetic habitat shifts of green turtles ( <i>Chelonia mydas</i> ) suggested by the size modality in foraging aggregations along the coasts of the western Japanese main islands. Journal of Experimental Marine Biology and Ecology, 2015, 463, 181-188.	0.7	15
2665	Mechanistic insights into landscape genetic structure of two tropical amphibians using field-derived resistance surfaces. Molecular Ecology, 2015, 24, 580-595.	2.0	28
2666	A reversal of fortunes: climate change "winners" and "losers" in Antarctic Peninsula penguins. Scientific Reports, 2014, 4, 5024.	1.6	82
2667	Biogeography of the smooth snake ( <i>Coronella austriaca</i> ): origin and conservation of the northernmost population. Biological Journal of the Linnean Society, 2015, 114, 426-435.	0.7	6
2668	Population genetics for 23 Y-STR loci in Tibetan in China and confirmation of DYS448 null allele. Forensic Science International: Genetics, 2015, 16, e7-e10.	1.6	37
2669	Analysis of 36 Y-STR marker units including a concordance study among 2085 Dutch males. Forensic Science International: Genetics, 2015, 14, 174-181.	1.6	29
2670	Emerging and endemic types of Ostreid herpesvirus 1 were detected in bivalves in China. Journal of Invertebrate Pathology, 2015, 124, 98-106.	1.5	65
2671	Genetic evidence for spatial structuring in a continuous African elephant ( <i>Loxodonta africana</i> ) population. Conservation Genetics, 2015, 16, 613-623.	0.8	4
2672	From north to south and back: the role of the Balkans and other southern peninsulas in the recolonization of Europe by wild boar. Journal of Biogeography, 2015, 42, 716-728.	1.4	20
2673	Development and characterisation of nine polymorphic microsatellite markers for <i>Tephrosia calophylla</i> Bedd. (Fabaceae). Saudi Journal of Biological Sciences, 2015, 22, 164-167.	1.8	0



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2675	Adaptive genetic variation in the smoke tree ( <i>Cotinus coggygria</i> Scop.) is driven by precipitation. <i>Biochemical Systematics and Ecology</i> , 2015, 59, 63-69.	0.6	10
2676	Evolutionary systematics of the Australian Cyzicidae (Crustacea, Branchiopoda, Spinicaudata) with the description of a new genus. <i>Zoological Journal of the Linnean Society</i> , 2015, 173, 271-295.	1.0	24
2677	Association of four CpG-SNPs in the vascular-related genes with coronary heart disease. <i>Biomedicine and Pharmacotherapy</i> , 2015, 70, 80-83.	2.5	11
2678	Body size distribution demonstrates flexible habitat shift of green turtle ( <i>Chelonia mydas</i> ). <i>Global Ecology and Conservation</i> , 2015, 3, 115-120.	1.0	12
2679	Genetic structure, admixture and invasion success in a Holarctic defoliator, the gypsy moth ( <i>Lymantria dispar</i> , Lepidoptera: Erebiidae). <i>Molecular Ecology</i> , 2015, 24, 1275-1291.	2.0	47
2680	Comparative multilocus phylogeography of two Palaearctic spruce bark beetles: influence of contrasting ecological strategies on genetic variation. <i>Molecular Ecology</i> , 2015, 24, 1292-1310.	2.0	34
2681	Genetic isolation by distance reveals restricted dispersal across a range of life histories: implications for biodiversity conservation planning across highly variable marine environments. <i>Diversity and Distributions</i> , 2015, 21, 698-710.	1.9	67
2682	Molecular analyses confirm genetically distinct populations of two indigenous estuarine fish species in an isolated coastal lake: implications for the management of introduced ichthyofauna. <i>Conservation Genetics</i> , 2015, 16, 801-809.	0.8	6
2683	Genetic variation of the East Balkan Swine ( <i>Sus scrofa</i> ) in Bulgaria, revealed by mitochondrial DNA and Y chromosomal DNA. <i>Animal Genetics</i> , 2015, 46, 209-212.	0.6	5
2684	Genetic Diversity and Structure of Brazilian Populations of <i>Diatraea saccharalis</i> (Lepidoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342	0.8	19
2685	PPAR $\beta$ and IL-6 $\alpha^{174G>C}$ gene variants in Croatian patients with ischemic stroke. <i>Gene</i> , 2015, 560, 200-204.	1.0	9
2686	Microsatellite Analysis of the Population Genetic Structure of <i>Anolis carolinensis</i> Introduced to the Ogasawara Islands. <i>Zoological Science</i> , 2015, 32, 47-52.	0.3	5
2687	Temporal Population Genetic Structure of Yellow Perch Spawning Groups in the Lower Great Lakes. <i>Transactions of the American Fisheries Society</i> , 2015, 144, 211-226.	0.6	7
2688	Significant genetic differentiation between the Yellow Sea and East China Sea populations of cocktail shrimp <i>Trachypenaeus curvirostris</i> revealed by the mitochondrial DNA COI gene. <i>Biochemical Systematics and Ecology</i> , 2015, 59, 78-84.	0.6	25
2689	DNA barcoding of sunn pest adult parasitoids using cytochrome c oxidase subunit I (COI). <i>Biochemical Systematics and Ecology</i> , 2015, 59, 70-77.	0.6	9
2690	Genetic diversity of <i>Allium munzii</i> (Amaryllidaceae), a rare southern California species and implication for its conservation. <i>Biochemical Systematics and Ecology</i> , 2015, 59, 91-99.	0.6	9
2691	Genetic diversity and structure of Manila clam ( <i>Ruditapes philippinarum</i> ) populations from Liaodong peninsula revealed by SSR markers. <i>Biochemical Systematics and Ecology</i> , 2015, 59, 116-125.	0.6	19

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2693	Genetic diversity and population structure of the ark shell <i>Scapharca broughtonii</i> along the coast of China based on microsatellites. <i>Biochemical Systematics and Ecology</i> , 2015, 58, 235-241.	0.6	12
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2700	Y-chromosome diversity in Catalan surname samples: insights into surname origin and frequency. <i>European Journal of Human Genetics</i> , 2015, 23, 1549-1557.	1.4	42
2701	Admixture and genetic relationships of Mexican Mestizos regarding Latin American and Caribbean populations based on 13 CODIS-STRs. <i>HOMO- Journal of Comparative Human Biology</i> , 2015, 66, 44-59.	0.3	46
2702	Exploitation of the non-Saccharomyces yeast <i>Starmerella bacillaris</i> (synonym <i>Candida zemplinina</i> ) in wine fermentation: Physiological and molecular characterizations. <i>International Journal of Food Microbiology</i> , 2015, 199, 33-40.	2.1	118
2703	Disentangling the controversial identity of the halfbeak stock ( <i>Hemiramphus brasiliensis</i> and <i>H. balao</i> ) from northeastern Brazil using multilocus DNA markers. <i>Reviews in Fish Biology and Fisheries</i> , 2015, 25, 379-394.	2.4	0
2704	Ancient onset of geographical divergence, interpopulation genetic exchange, and natural selection on the <i>Mcl1r</i> coat-colour gene in the house mouse ( <i>Mus musculus</i> ). <i>Biological Journal of the Linnean Society</i> , 2015, 114, 778-794.	0.7	16
2705	Taking the discovery approach in integrative taxonomy: decrypting a complex of narrow-endemic Alpine harvestmen (Opiliones: Phalangidae: <i>Megabunus</i> ). <i>Molecular Ecology</i> , 2015, 24, 863-889.	2.0	19
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2707	Interpreting negative results with taxonomic and conservation implications: Another look at the distinctness of coastal California Gnatcatchers. <i>Auk</i> , 2015, 132, 380-388.	0.7	26
2708	Effects of population size and isolation on the genetic structure of the East African mountain white-eye <i>Zosterops poliogaster</i> (Aves). <i>Biological Journal of the Linnean Society</i> , 2015, 114, 828-836.	0.7	10
2709	Genetic insights into the hybrid origin of <i>Abies</i> <i>— borisii-regis</i> Mattf.. <i>Plant Systematics and Evolution</i> , 2015, 301, 749-759.	0.3	19

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2712	Phylogeographical patterns in <i>Coenosia attenuata</i> (Diptera: Muscidae): a widespread predator of insect species associated with greenhouse crops. <i>Biological Journal of the Linnean Society</i> , 2015, 114, 308-326.	0.7	12
2713	Assessing the phylogeographic history of the montane caddisfly <i>Tremma gallicum</i> using mitochondrial and restriction-associated DNA (RAD) markers. <i>Ecology and Evolution</i> , 2015, 5, 648-662.	0.8	25
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2721	Results for five sets of forensic genetic markers studied in a Greek population sample. <i>Forensic Science International: Genetics</i> , 2015, 16, 132-137.	1.6	21
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2724	Living between rapids: genetic structure and hybridization in botos (Cetacea: Iniidae: <i>Iniia</i> spp.) of the Madeira River, Brazil. <i>Biological Journal of the Linnean Society</i> , 2015, 114, 764-777.	0.7	40
2725	Native California soils are selective reservoirs for multidrug-resistant bacteria. <i>Environmental Microbiology Reports</i> , 2015, 7, 442-449.	1.0	11
2726	Differences in gene flow in a twofold secondary contact zone of pond turtles in southern Italy (Testudines: Emydidae: <i>Emys orbicularis galloitalica</i> , <i>E. A. hellenica</i> , <i>E. A. trinacris</i> ). <i>Zoologica Scripta</i> , 2015, 44, 233-249.	0.7	44
2727	Preliminary assessment of the prototype Yfiler <sup>®</sup> Plus kit in a population study of Northern Italian males. <i>International Journal of Legal Medicine</i> , 2015, 129, 729-730.	1.2	24

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2729	Differences in speciation progress in feather mites (Analgidae) inhabiting the same host: the case of <i>Zachvatkinia</i> and <i>Alloptes</i> living on arctic and long-tailed skuas. <i>Experimental and Applied Acarology</i> , 2015, 65, 163-179.	0.7	27
2730	The influence of life history and climate driven diversification on the mtDNA phylogeographic structures of two southern African <i>Mastomys</i> species (Rodentia: Muridae: Murinae). <i>Biological Journal of the Linnean Society</i> , 2015, 114, 58-68.	0.7	10
2731	Delimitation of cryptic species inside <i>Claviceps purpurea</i> . <i>Fungal Biology</i> , 2015, 119, 7-26.	1.1	42
2732	New Multilocus Variable-Number Tandem-Repeat Analysis Tool for Surveillance and Local Epidemiology of Bacterial Leaf Blight and Bacterial Leaf Streak of Rice Caused by <i>Xanthomonas oryzae</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 688-698.	1.4	69
2733	Geographical barriers and climate influence demographic history in narrowleaf cottonwoods. <i>Heredity</i> , 2015, 114, 387-396.	1.2	27
2734	Population structure and gene flow in the endangered southern brown bandicoot ( <i>Isodon obesulus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.8	20
2735	Genetic evidence for ecological divergence in kokanee salmon. <i>Molecular Ecology</i> , 2015, 24, 798-811.	2.0	57
2736	Investigator HDplex markers: allele frequencies and mutational events in a North Italian population. <i>International Journal of Legal Medicine</i> , 2015, 129, 731-733.	1.2	7
2737	The past, present and future of a lizard: The phylogeography and extinction risk of <i>Sceloporus serrifer</i> (Squamata: Phrynosomatidae) under a global warming scenario. <i>Zoologischer Anzeiger</i> , 2015, 254, 86-98.	0.4	12
2738	Analysis of nuclear microsatellites reveals limited differentiation between Colchic and Hyrcanian populations of the wind-pollinated relict tree <i>Zelkova carpinifolia</i> (Ulmaceae). <i>American Journal of Botany</i> , 2015, 102, 119-128.	0.8	21
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2741	Extensive genome-wide autozygosity in the population isolates of Daghestan. <i>European Journal of Human Genetics</i> , 2015, 23, 1405-1412.	1.4	21
2742	Establishing the evolutionary compatibility of potential sources of colonizers for overfished stocks: a population genomics approach. <i>Molecular Ecology</i> , 2015, 24, 564-579.	2.0	16
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2744	CYP2B6 Gene Single-Nucleotide Polymorphisms in an Italian Population Sample and Relationship with Nicotine Dependence. <i>Genetic Testing and Molecular Biomarkers</i> , 2015, 19, 103-107.	0.3	6
2745	Recent worldwide expansion of <i>Nosema ceranae</i> (Microsporidia) in <i>Apis mellifera</i> populations inferred from multilocus patterns of genetic variation. <i>Infection, Genetics and Evolution</i> , 2015, 31, 87-94.	1.0	36

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2748	Population data for 22 autosomal STR loci from Estonia. <i>International Journal of Legal Medicine</i> , 2015, 129, 1219-1220.	1.2	18
2749	Approximate Bayesian Computation Reveals the Crucial Role of Oceanic Islands for the Assembly of Continental Biodiversity. <i>Systematic Biology</i> , 2015, 64, 579-589.	2.7	63
2750	Reassessing the evolutionary history of ass-like equids: Insights from patterns of genetic variation in contemporary extant populations. <i>Molecular Phylogenetics and Evolution</i> , 2015, 85, 88-96.	1.2	18
2751	How do gap dynamics and colonization of a human disturbed area affect genetic diversity and structure of a pioneer tropical tree species?. <i>Forest Ecology and Management</i> , 2015, 344, 38-52.	1.4	13
2752	Molecular assessment of translocation and management of an endangered subspecies of white-tailed deer ( <i>Odocoileus virginianus</i> ). <i>Conservation Genetics</i> , 2015, 16, 635-647.	0.8	17
2753	Local Genetic Differentiation and Diversity of the Oita Salamander ( <i>Hynobius dunni</i> ) in Kyushu Revealed by Mitochondrial and Microsatellite DNA Analyses. <i>Current Herpetology</i> , 2015, 34, 1-11.	0.5	5
2754	Genetic diversity in shea tree ( <i>Vitellaria paradoxa</i> subspecies <i>nilotica</i> ) ethno-varieties in Uganda assessed with microsatellite markers. <i>Forests Trees and Livelihoods</i> , 2015, 24, 163-175.	0.5	17
2755	Development and characterization of microsatellite loci in <i>Opisthopappus taihangensis</i> (Compositae), a rare herb endemic to China. <i>Conservation Genetics Resources</i> , 2015, 7, 269-271.	0.4	2
2756	Mutations in the two ribosomal RNA genes in mitochondrial DNA among Finnish children with hearing impairment. <i>BMC Medical Genetics</i> , 2015, 16, 3.	2.1	9
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2758	A novel genetic variant database for Korean native cattle (Hanwoo): HanwooGDB. <i>Genes and Genomics</i> , 2015, 37, 15-22.	0.5	3
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2761	Population structure and sequence divergence in the mitochondrial DNA control region of gizzard shad <i>Konosirus punctatus</i> in Korea and Japan. <i>Ichthyological Research</i> , 2015, 62, 379-385.	0.5	16
2762	Single-nucleotide polymorphism identification and genotyping in <i>Camelina sativa</i> . <i>Molecular Breeding</i> , 2015, 35, 35.	1.0	36
2763	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

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2765	Genetic structure of Florida green turtle rookeries as indicated by mitochondrial DNA control region sequences. <i>Conservation Genetics</i> , 2015, 16, 673-685.	0.8	31
2766	A new set of pure microsatellite loci in the common octopus <i>Octopus vulgaris</i> Cuvier, 1797 for multiplex PCR assay and their cross-amplification in <i>O. maya</i> Voss & Solís Ramírez, 1966. <i>Conservation Genetics Resources</i> , 2015, 7, 299-301.	0.4	5
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2768	Contrasting population genetic structure among freshwater-resident and anadromous lampreys: the role of demographic history, differential dispersal and anthropogenic barriers to movement. <i>Molecular Ecology</i> , 2015, 24, 1188-1204.	2.0	52
2769	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
2770	Inferring and outlining past population declines with linked microsatellites: a case study in two spruce species. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	4
2771	Patterns of spatial genetic variation in <i>Patella ulyssiponensis</i> : insights from the western Mediterranean marine ecoregion. <i>Hydrobiologia</i> , 2015, 755, 39-55.	1.0	14
2772	Urban development explains reduced genetic diversity in a narrow range endemic freshwater fish. <i>Conservation Genetics</i> , 2015, 16, 625-634.	0.8	8
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2776	Eleven new polymorphic microsatellite markers for the Red-billed chough ( <i>Pyrrhocorax</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 Td (py	0.4	4
2777	Population genetic structure of the red fox ( <i>Vulpes vulpes</i> ) in the UK. <i>Mammal Research</i> , 2015, 60, 9-19.	0.6	21
2778	Toll-like receptor diversity in 10 threatened bird species: relationship with microsatellite heterozygosity. <i>Conservation Genetics</i> , 2015, 16, 595-611.	0.8	42
2779	MHC class II variation in a rare and ecological specialist mouse lemur reveals lower allelic richness and contrasting selection patterns compared to a generalist and widespread sympatric congener. <i>Immunogenetics</i> , 2015, 67, 229-245.	1.2	17
2780	Ghosts of glaciers and the disjunct distribution of a threatened California moth ( <i>Euproserpinus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 1	1.9	6
2781	Too much of a good thing: sea ice extent may have forced emperor penguins into refugia during the last glacial maximum. <i>Global Change Biology</i> , 2015, 21, 2215-2226.	4.2	32



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2783	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
2784	Development and characterization of microsatellite loci from <i>Metcalfa pruinosa</i> (Hemiptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662 7	0.6	0
2785	Genetic differentiation in the ice-dependent fish <i>Pleuragramma antarctica</i> along the Antarctic Peninsula. <i>Journal of Biogeography</i> , 2015, 42, 1103-1113.	1.4	16
2786	Association of positively selected eIF3a polymorphisms with toxicity of platinum-based chemotherapy in NSCLC patients. <i>Acta Pharmacologica Sinica</i> , 2015, 36, 375-384.	2.8	21
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2788	Genomic and phenotypic differentiation among <i>Methanosarcina mazei</i> populations from Columbia River sediment. <i>ISME Journal</i> , 2015, 9, 2191-2205.	4.4	42
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2790	Genetic structure and diversity in natural populations of three predominantly self-pollinating wild <i>Lactuca</i> species in Israel. <i>Genetic Resources and Crop Evolution</i> , 2015, 62, 991-1008.	0.8	13
2791	Microsatellite Markers for <i>Heracleum persicum</i> (Apiaceae) and Allied Taxa: Application of Next-Generation Sequencing to Develop Genetic Resources for Invasive Species Management. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1381-1390.	1.0	16
2792	Development and characterization of novel microsatellite markers for <i>Arion</i> slug species. <i>Conservation Genetics Resources</i> , 2015, 7, 501-503.	0.4	5
2793	<i>Tortella rigens</i> (Bryophyta, Pottiaceae): relationships, regional variation, and conservation aspects. <i>Plant Systematics and Evolution</i> , 2015, 301, 1361-1375.	0.3	15
2794	Genetic moderation of interpersonal psychotherapy efficacy for low-income mothers with major depressive disorder: Implications for differential susceptibility. <i>Development and Psychopathology</i> , 2015, 27, 19-35.	1.4	22
2795	Parallels between two geographically and ecologically disparate cave invasions by the same species, <i>A-sellus aquaticus</i> ( <i>I-sopoda</i> , <i>C-rustacea</i> ). <i>Journal of Evolutionary Biology</i> , 2015, 28, 864-875.	0.8	57
2796	Traces of forgotten historical events in mountain communities in <i>C-entral I-taly</i> : A genetic insight. <i>American Journal of Human Biology</i> , 2015, 27, 508-519.	0.8	9
2797	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
2798	Local population genetic structure of the montane caddisfly <i>D-rusus discolor</i> is driven by overland dispersal and spatial scaling. <i>Freshwater Biology</i> , 2015, 60, 209-221.	1.2	34
2799	Genetic diversity and structure of <i>Jatropha curcas</i> L. in its centre of origin. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2015, 13, 9-17.	0.4	21

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2801	Genetic diversity of different indigenous chicken ecotypes using highly polymorphic MHC-linked and non-MHC microsatellite markers. <i>Animal Genetic Resources = Ressources Genetiques Animales = Recursos Geneticos Animales</i> , 2015, 56, 1-7.	0.2	17
2802	Contrasting Transmission Dynamics of Co-endemic <i>Plasmodium vivax</i> and <i>P. falciparum</i> : Implications for Malaria Control and Elimination. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003739.	1.3	63
2803	Identification of spawning sites of the tiger puffer <i>Takifugu rubripes</i> in Nanao Bay, Japan, using DNA analysis. <i>Fisheries Science</i> , 2015, 81, 485-494.	0.7	10
2804	Genetic temporal dynamics in restored wetlands: A case of a predominantly clonal species, <i>Berula erecta</i> (Huds.) Coville. <i>Aquatic Botany</i> , 2015, 126, 7-15.	0.8	1
2805	Genetic Diversity and Population Structure of <i>Trypanosoma brucei</i> in Uganda: Implications for the Epidemiology of Sleeping Sickness and Nagana. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003353.	1.3	25
2806	Neutral and Adaptive Drivers of Microgeographic Genetic Divergence within Continuous Populations: The Case of the Neotropical Tree <i>Eperua falcata</i> (Aubl.). <i>PLoS ONE</i> , 2015, 10, e0121394.	1.1	53
2807	High molecular diversity in the true service tree ( <i>Sorbus domestica</i> ) despite rareness: data from Europe with special reference to the Austrian occurrence. <i>Annals of Botany</i> , 2015, 115, 1105-1115.	1.4	22
2808	Systematics of North Pacific sand lances of the genus <i>Ammodytes</i> based on molecular and morphological evidence, with the description of a new species from Japan. <i>Fishery Bulletin</i> , 2015, 113, 129-156.	0.1	44
2809	The admixture zone of <i>Betula humilis</i> Schrk. phylogenetic lineages follows the eastern central European suture zone. <i>Plant Ecology and Diversity</i> , 2015, 8, 323-329.	1.0	4
2810	Population genetic structure at the northern range limit of the threatened eastern hog-nosed snake ( <i>Heterodon platirhinos</i> ). <i>Conservation Genetics</i> , 2015, 16, 1265-1276.	0.8	2
2811	Population genetics of Himalayan balsam ( <i>Impatiens glandulifera</i> ): comparison of native and introduced populations. <i>Plant Ecology and Diversity</i> , 2015, 8, 317-321.	1.0	24
2812	Genotypic characterization of ten microsatellite loci in two Brazilian free range (Caipira) chicken lines. <i>Ciencia Rural</i> , 2015, 45, 877-883.	0.3	3
2813	Genetic diversity in aspen and its relation to arthropod abundance. <i>Frontiers in Plant Science</i> , 2015, 5, 806.	1.7	9
2814	Analysis of the genetic diversity of <i>Eucalyptus cladocalyx</i> (sugar gum) using ISSR markers. <i>Acta Scientiarum - Agronomy</i> , 2015, 37, 133.	0.6	8
2815	A Comparison of Genetic Diversity and Phenotypic Plasticity among European Beech ( <i>Fagus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock Manipulation. <i>International Journal of Plant Sciences</i> , 2015, 176, 232-244.	0.6	32
2816	Genetic Variability in Island Populations of Two Rodent Species: Bank Vole ( <i>Myodes glareolus</i> ) and Yellow-Necked Mouse ( <i>Apodemus flavicollis</i> ). <i>Annales Zoologici Fennici</i> , 2015, 52, 145-159.	0.2	7
2817	Genetic Differentiation in Native and Introduced Populations of <i>Cryptolaemus montrouzieri</i> (Coleoptera: Coccinellidae) and Its Implications for Biological Control Programs. <i>Journal of Economic Entomology</i> , 2015, 108, 2458-2464.	0.8	7

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2818	Low contemporary effective population size detected in the Critically Endangered giant sea bass, <i>Stereolepis gigas</i> , due to fisheries overexploitation. <i>Fisheries Research</i> , 2015, 172, 71-78.	0.9	10
2819	Density of river otters ( <i>Lontra canadensis</i> ) in relation to energy development in the Green River Basin, Wyoming. <i>Science of the Total Environment</i> , 2015, 532, 780-790.	3.9	17
2820	Genetic diversity and structure of the Lesvos sheep breed. <i>Small Ruminant Research</i> , 2015, 130, 54-59.	0.6	11
2821	Isolation and characterization of 19 novel microsatellite loci in <i>Rhododendron aureum</i> and <i>Rhododendron brachycarpum</i> (Ericaceae). <i>Biochemical Systematics and Ecology</i> , 2015, 61, 520-523.	0.6	5
2822	Pelagic early life stages promote connectivity in the demersal labrid <i>Choerodon rubescens</i> . <i>Journal of Experimental Marine Biology and Ecology</i> , 2015, 472, 142-150.	0.7	9
2823	Study of the influence of genes related to muscle oxidative processes on beef color. <i>Meat Science</i> , 2015, 108, 17-20.	2.7	5
2824	Characterisation of the relationship between <i>Spirometra erinaceieuropaei</i> and <i>Diphyllbothrium</i> species using complete <i>cytb</i> and <i>cox1</i> genes. <i>Infection, Genetics and Evolution</i> , 2015, 35, 1-8.	1.0	25
2825	Population data for 15 autosomal STR loci from Latvia. <i>International Journal of Legal Medicine</i> , 2015, 129, 739-740.	1.2	4
2826	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
2827	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
2828	Human seroprevalence against <i>Borrelia burgdorferi</i> sensu lato in two comparable regions of the eastern Alps is not correlated to vector infection rates. <i>Ticks and Tick-borne Diseases</i> , 2015, 6, 221-227.	1.1	14
2829	60,000 years of interactions between Central and Eastern Africa documented by major African mitochondrial haplogroup L2. <i>Scientific Reports</i> , 2015, 5, 12526.	1.6	33
2830	Population Genetic Structure in Hyacinth Macaws ( <i>Anodorhynchus hyacinthinus</i> ) and Identification of the Probable Origin of Confiscated Individuals. <i>Journal of Heredity</i> , 2015, 106, 491-502.	1.0	32
2831	Estimating sex-specific abundance in fawning areas of a high-density Columbian black-tailed deer population using fecal DNA. <i>Journal of Wildlife Management</i> , 2015, 79, 39-49.	0.7	34
2832	Differential gene flow patterns for two commercially exploited shark species, tope ( <i>Galeorhinus</i> ) and bonnethead ( <i>Sphyrna tiburo</i> ). <i>Fisheries Research</i> , 2015, 172, 190-196.	0.9	13
2833	STR-based genetic structure of the Berber population of Bejaia (Northern Algeria) and its relationships to various ethnic groups. <i>Gene</i> , 2015, 574, 140-148.	1.0	11
2834	Genetic structure of leopard shark ( <i>Triakis semifasciata</i> ) populations along the Pacific coast of North America. <i>Journal of Experimental Marine Biology and Ecology</i> , 2015, 472, 151-157.	0.7	14
2835	Broad-scale genetic patterns of New Zealand abalone, <i>Haliotis iris</i> , across a distribution spanning 13° latitude and major oceanic water masses. <i>Genetica</i> , 2015, 143, 487-500.	0.5	9

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2837	Z chromosome divergence, polymorphism and relative effective population size in a genus of lekking birds. <i>Heredity</i> , 2015, 115, 452-459.	1.2	28
2838	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
2839	DXS998 and DXS548-FRAXAC1 represents a novel informative haplotype at the FMR1 locus in the Iranian population. <i>Gene</i> , 2015, 570, 180-184.	1.0	2
2840	Genetic population study of Y-chromosome markers in Benin and Ivory Coast ethnic groups. <i>Forensic Science International: Genetics</i> , 2015, 19, 232-237.	1.6	7
2841	Deep genetic divergence between austral populations of the red alga <i>Gigartina skottsbergii</i> reveals a cryptic species endemic to the Antarctic continent. <i>Polar Biology</i> , 2015, 38, 2021-2034.	0.5	28
2842	Population structure of red snapper ( <i>Lutjanus campechanus</i> ) in U.S. waters of the western Atlantic Ocean and the northeastern Gulf of Mexico. <i>Fisheries Research</i> , 2015, 172, 17-25.	0.9	11
2843	Haplotype differences for copy number variants in the 22q11.23 region among human populations: a pigmentation-based model for selective pressure. <i>European Journal of Human Genetics</i> , 2015, 23, 116-123.	1.4	10
2844	Characterisation of microsatellite markers for fig-pollinating wasps in the <i>Pleistodontes imperialis</i> species complex. <i>Australian Journal of Zoology</i> , 2015, 63, 122.	0.6	2
2845	Genetic analysis of Dolly Varden ( <i>Salvelinus malma</i> ) across its North American range: evidence for a contact zone in southcentral Alaska. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2015, 72, 1048-1057.	0.7	20
2846	Isolation and Characterisation of Eight Microsatellite Markers of the Thorn-Tailed Rayadito ( <i>Aphrastura spinicauda</i> ). <i>Ardeola</i> , 2015, 62, 179-183.	0.4	9
2847	Genetic and ecological data reveal species boundaries between viviparous and oviparous lizard lineages. <i>Heredity</i> , 2015, 115, 517-526.	1.2	32
2848	Molecular and Morphological Evidence for <i>Rana kunyuensis</i> as a Junior Synonym of <i>Rana coreana</i> (Anura: Ranidae). <i>Journal of Herpetology</i> , 2015, 49, 302.	0.2	11
2849	Stochastic effects associated with resting egg banks lead to genetically differentiated active populations in large branchiopods from temporary water bodies. <i>Hydrobiologia</i> , 2015, 760, 239-253.	1.0	8
2850	Genetic diversity and structure in two protected <i>Posidonia oceanica</i> meadows. <i>Marine Environmental Research</i> , 2015, 109, 124-131.	1.1	16
2851	Could MicroRNA polymorphisms influence warfarin dosing? A pharmacogenetics study on mir133 genes. <i>Thrombosis Research</i> , 2015, 136, 367-370.	0.8	20
2852	The Tanaka Line shaped the phylogeographic pattern of the cotton tree ( <i>Bombax ceiba</i> ) in southwest China. <i>Biochemical Systematics and Ecology</i> , 2015, 60, 150-157.	0.6	15
2853	Structure of genetic diversity in marginal populations of black poplar ( <i>Populus nigra</i> L.). <i>Biochemical Systematics and Ecology</i> , 2015, 61, 297-302.	0.6	12

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2855	Genetic heterogeneity and local adaptation of Asian seabass across Indonesian Archipelago revealed with gene-associated SNP markers. <i>Fisheries Research</i> , 2015, 170, 205-211.	0.9	6
2856	Genetic diversity of high-elevation populations of an endangered medicinal plant. <i>AoB PLANTS</i> , 2015, 7, .	1.2	15
2857	Genetic structure of the common shrew <i>Sorex araneus</i> L. 1758 (Mammalia, Lipotyphla) in continuous and fragmented areas. <i>Russian Journal of Genetics</i> , 2015, 51, 607-618.	0.2	8
2858	Population genetics of the speckled peacock bass ( <i>Cichla temensis</i> ), South America's most important inland sport fishery. <i>Conservation Genetics</i> , 2015, 16, 1345-1357.	0.8	18
2859	Impact of DEFB1 gene regulatory polymorphisms on hBD-1 salivary concentration. <i>Archives of Oral Biology</i> , 2015, 60, 1054-1058.	0.8	20
2860	Autophagy and inflammatory bowel disease: Association between variants of the autophagy-related IRGM gene and susceptibility to Crohn's disease. <i>Digestive and Liver Disease</i> , 2015, 47, 744-750.	0.4	35
2861	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
2862	Genetic Analysis of the <i>Aspergillus flavus</i> Vegetative Compatibility Group to Which a Biological Control Agent That Limits Aflatoxin Contamination in U.S. Crops Belongs. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5889-5899.	1.4	41
2863	Links between Genetic Groups, Indole Alkaloid Profiles and Ecology within the Grass-Parasitic <i>Claviceps purpurea</i> Species Complex. <i>Toxins</i> , 2015, 7, 1431-1456.	1.5	28
2864	Genetic analysis of 17 Y-STR loci in Han, Dong, Miao and Tujia populations from Hunan province, central-southern China. <i>Forensic Science International: Genetics</i> , 2015, 19, 250-251.	1.6	15
2865	Genetic analysis of 17 Y-STR loci in Han population from Gansu province, northwestern China. <i>Forensic Science International: Genetics</i> , 2015, 19, 134-135.	1.6	7
2866	HLA-E coding and 3' untranslated region variability determined by next-generation sequencing in two West-African population samples. <i>Human Immunology</i> , 2015, 76, 945-953.	1.2	33
2867	Population data of 15 short tandem repeat loci in 1084 individuals from six Han and four ethnic populations in China. <i>Forensic Science International: Genetics</i> , 2015, 19, 146-147.	1.6	7
2868	The subspecies of Antarctic Terns ( <i>Sterna vittata</i> ) wintering on the South African coast: evidence from morphology, genetics and stable isotopes. <i>Emu</i> , 2015, 115, 223-236.	0.2	3
2869	Mitogenomic Meta-Analysis Identifies Two Phases of Migration in the History of Eastern Eurasian Sheep. <i>Molecular Biology and Evolution</i> , 2015, 32, 2515-2533.	3.5	122
2870	Characterization and distribution of mating-type genes of the turfgrass pathogen <i>Sclerotinia homoeocarpa</i> on a global scale. <i>Fungal Genetics and Biology</i> , 2015, 81, 25-40.	0.9	15
2871	Genetic variability within and among populations of an invasive, exotic orchid. <i>AoB PLANTS</i> , 2015, 7, plv077.	1.2	28

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2873	Significant genetic structure despite high vagility revealed through mitochondrial phylogeography of an Australian freshwater turtle ( <i>Chelodina longicollis</i> ). <i>Marine and Freshwater Research</i> , 2015, 66, 1045.	0.7	3
2874	Phylogeography of the arid-adapted Malagasy bullfrog, <i>Laliostoma labrosum</i> , influenced by past connectivity and habitat stability. <i>Molecular Phylogenetics and Evolution</i> , 2015, 92, 11-24.	1.2	12
2875	Defining management units for cetaceans by combining genetics, morphology, acoustics and satellite tracking. <i>Global Ecology and Conservation</i> , 2015, 3, 839-850.	1.0	52
2876	Geographic patterns of genetic variation in three genomes of North American diploid strawberries with special reference to <i>Fragaria vesca</i> subsp. <i>bracteata</i> . <i>Botany</i> , 2015, 93, 573-588.	0.5	3
2877	Genetic distinctiveness of red foxes in the Intermountain West as revealed through expanded mitochondrial sequencing. <i>Journal of Mammalogy</i> , 2015, 96, 297-307.	0.6	12
2878	Developing a common bean core collection suitable for association mapping studies. <i>Genetics and Molecular Biology</i> , 2015, 38, 67-78.	0.6	29
2879	Molecular DNA identity of the mouflon of Cyprus ( <i>Ovis orientalis ophion</i> , Bovidae): Near Eastern origin and divergence from Western Mediterranean conspecific populations. <i>Systematics and Biodiversity</i> , 2015, 13, 472-483.	0.5	26
2880	Isolation and Characterization of Polymorphic Microsatellite Markers from the Malaria Vector <i>Anopheles fluviatilis</i> Species T (Diptera: Culicidae). <i>Journal of Medical Entomology</i> , 2015, 52, 408-412.	0.9	2
2881	Global Survey of Variation in a Human Olfactory Receptor Gene Reveals Signatures of Non-Neutral Evolution. <i>Chemical Senses</i> , 2015, 40, 481-488.	1.1	31
2882	Population Structure of the Chagas Disease Vector <i>Triatoma infestans</i> in an Urban Environment. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003425.	1.3	19
2883	Introduced Pacific oysters <i>Crassostrea gigas</i> in South Africa: demographic change, genetic diversity and body condition. <i>African Journal of Marine Science</i> , 2015, 37, 89-98.	0.4	8
2884	Parallel Domestication of the <i>Heading Date 1</i> Gene in Cereals. <i>Molecular Biology and Evolution</i> , 2015, 32, 2726-2737.	3.5	54
2885	Effect of oceanic straits on gene flow in the recently endangered little brown bat ( <i>Myotis</i> Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf). <i>Journal of Zoology</i> , 2015, 93, 427-437.	0.4	7
2886	Toward a genome-wide approach for detecting hybrids: informative SNPs to detect introgression between domestic cats and European wildcats ( <i>Felis silvestris</i> ). <i>Heredity</i> , 2015, 115, 195-205.	1.2	51
2887	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
2888	Does population genetic structure support present management regulations of the northern shrimp ( <i>Pandalus borealis</i> ) in Skagerrak and the North Sea?. <i>ICES Journal of Marine Science</i> , 2015, 72, 863-871.	1.2	19
2889	A Pharmacogenetics Study in Mozambican Patients Treated with Nevirapine: Full Resequencing of TRAF3IP2 Gene Shows a Novel Association with SJS/TEN Susceptibility. <i>International Journal of Molecular Sciences</i> , 2015, 16, 5830-5838.	1.8	7



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2890	A lack of association between the CRP rs2794520 polymorphism and coronary artery disease. Biomedical Reports, 2015, 3, 110-114.	0.9	1
2891	Contrasting signals of genetic diversity and historical demography between two recently diverged marine and estuarine fish species. Marine Ecology - Progress Series, 2015, 526, 157-167.	0.9	8
2892	Continental-scale analysis reveals deep diversification within the polytypic Red-crowned Ant Tanager ( <i>Habia rubica</i> , Cardinalidae). Molecular Phylogenetics and Evolution, 2015, 89, 182-193.	1.2	19
2893	Population structure enhances perspectives on regional management of the western Indian Ocean green turtle. Conservation Genetics, 2015, 16, 1069-1083.	0.8	18
2894	Does size matter? Comparative population genetics of two butterflies with different wingspans. Organisms Diversity and Evolution, 2015, 15, 567-575.	0.7	0
2895	Integration of Random Forest with population-based outlier analyses provides insight on the genomic basis and evolution of run timing in Chinook salmon ( <i>Oncorhynchus tshawytscha</i> ). Molecular Ecology, 2015, 24, 2729-2746.	2.0	76
2896	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. Journal of Experimental Marine Biology and Ecology, 2015, 468, 97-104.	0.7	14
2897	Genetic diversity in <i>Monoporeia affinis</i> at polluted and reference sites of the Baltic Bothnian Bay. Marine Pollution Bulletin, 2015, 93, 245-249.	2.3	8
2898	Genetic structure in Mongolian gazelles based on mitochondrial and microsatellite markers. Mammalian Biology, 2015, 80, 303-311.	0.8	7
2899	Population and forensic genetic analyses of mitochondrial DNA control region variation from six major provinces in the Korean population. Forensic Science International: Genetics, 2015, 17, 99-103.	1.6	10
2900	Genotypic diversity of apomictic microspecies of the <i>Taraxacum scanicum</i> group ( <i>Taraxacum</i> sect.) Tj ETQq0 0 0 rgBT./Overlock 10 Tf 50	0.3	16
2901	Genetic and linguistic correlation of the Kra��Dai-speaking groups in Thailand. Journal of Human Genetics, 2015, 60, 371-380.	1.1	18
2902	Evidence of rapid change in genetic structure and diversity during range expansion in a recovering large terrestrial carnivore. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20150092.	1.2	36
2903	Population data for 15 autosomal STR loci in the Bouyei ethnic minority from Guizhou Province, Southwest China. Forensic Science International: Genetics, 2015, 17, 108-109.	1.6	31
2904	Identification, development, and application of 12 polymorphic EST-SSR markers for an endemic Chinese walnut ( <i>Juglans cathayensis</i> L.) using next-generation sequencing technology. Biochemical Systematics and Ecology, 2015, 60, 74-80.	0.6	45
2905	A blurring of life-history lines: Immune function, molt and reproduction in a highly stable environment. General and Comparative Endocrinology, 2015, 213, 65-73.	0.8	11
2906	<i>Pomphorhynchus laevis</i> (Acanthocephala) from the Sava River basin: New insights into strain formation, mtDNA-like sequences and dynamics of infection. Parasitology International, 2015, 64, 243-250.	0.6	17
2907	Population and forensic data for three sets of forensic genetic markers in four ethnic groups from Iran: Persians, Lurs, Kurds and Azeris. Forensic Science International: Genetics, 2015, 17, 43-46.	1.6	16

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2908	Mitogenome revealed multiple postdomestication genetic mixtures of <i>W</i> est <i>A</i> frican sheep. <i>Journal of Animal Breeding and Genetics</i> , 2015, 132, 399-405.	0.8	10
2909	Temporal and Spatial Genetic Variability Among Tarnished Plant Bug (Hemiptera: Miridae) Populations in a Small Geographic Area. <i>Annals of the Entomological Society of America</i> , 2015, 108, 181-192.	1.3	10
2910	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
2911	Palm diversification in two geologically contrasting regions of western Amazonia. <i>Journal of Biogeography</i> , 2015, 42, 1503-1513.	1.4	16
2912	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
2913	Molecular blood group typing in Banjar, Jawa, Mandailing and Kelantan Malays in Peninsular Malaysia. <i>Transfusion and Apheresis Science</i> , 2015, 53, 69-73.	0.5	6
2914	Red foxes ( <i>Vulpes vulpes</i> ) at their expanding front in the Canadian Arctic have indigenous maternal ancestry. <i>Polar Biology</i> , 2015, 38, 913-917.	0.5	11
2915	Population genetic data for 17 autosomal STR markers in the Hani population from China. <i>International Journal of Legal Medicine</i> , 2015, 129, 995-996.	1.2	15
2916	A genome-wide AFLP replacement in a hybrid population derived from two closely related <i>Viola</i> species from contrasting habitats. <i>Plant Systematics and Evolution</i> , 2015, 301, 1073-1084.	0.3	3
2917	Demographic histories of two deep-sea eelpouts, <i>Lycodes japonicus</i> and <i>Lycodes ocellatus</i> : paleoenvironmental implications of the western North Pacific deep waters. <i>Ichthyological Research</i> , 2015, 62, 363-367.	0.5	10
2918	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
2919	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
2920	Protecting the breeders: research informs legislative change in a marine turtle fishery. <i>Biodiversity and Conservation</i> , 2015, 24, 1775-1796.	1.2	14
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2922	Fragmentation genetics of the grassland butterfly <i>Polyommatus coridon</i> : Stable genetic diversity or extinction debt?. <i>Conservation Genetics</i> , 2015, 16, 549-558.	0.8	15
2924	The phylogeographic history of the threatened <i>Diana fritillary</i> , <i>Speyeria diana</i> (Lepidoptera: Tj ETQq1 1 0.784314 rgBT /Overl 10 TTS	0.8	9
2925	Conservation genetics of a desert fish species: the Lahontan tui chub ( <i>Siphateles bicolor</i> ssp.). <i>Conservation Genetics</i> , 2015, 16, 743-758.	0.8	3
2926	Low MHC variation in isolated island populations of the Natterjack toad ( <i>Bufo calamita</i> ). <i>Conservation Genetics</i> , 2015, 16, 1007-1010.	0.8	10

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2927	Genetic differentiation in the endangered myrmecophilous butterfly <i>Niphandia fusca</i> : a comparison of natural and secondary habitats. <i>Conservation Genetics</i> , 2015, 16, 979-986.	0.8	3
2928	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
2929	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
2930	New insights into connectivity patterns of mesophotic red coral ( <i>Corallium rubrum</i> ) populations. <i>Hydrobiologia</i> , 2015, 759, 63-73.	1.0	13
2931	Disparate past demographic histories of three small Scombridae (Actinopterygii) species in Tunisian waters. <i>Hydrobiologia</i> , 2015, 758, 19-30.	1.0	4
2932	Genetic Analyses Suggest Male Philopatry and Territoriality in Savanna-Woodland Chimpanzees ( <i>Pan</i> ) Tj ETQq1 1 0.784314 rgBT /Ove 377-397.	0.9	8
2933	Nucleotide diversity estimates of tomatillo ( <i>Physalis philadelphica</i> ) accessions including nine new inbred lines. <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	11
2934	An Operational SNP Panel Integrated to SSR Marker for the Assessment of Genetic Diversity and Population Structure of the Common Bean. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1697-1711.	1.0	20
2935	Development of a 9-locus X-STR multiplex PCR system for genetic analysis of three ethnic populations in China. <i>Journal of Huazhong University of Science and Technology [Medical Sciences]</i> , 2015, 35, 183-187.	1.0	3
2936	Molecular characterization of rainbow trout, <i>Oncorhynchus mykiss</i> (Walbaum, 1792) stocks in India. <i>Journal of Genetics</i> , 2015, 94, 13-18.	0.4	9
2937	Burial condition is the most important factor for mtDNA PCR amplification success in Palaeolithic equid remains from the Alpine foreland. <i>Archaeological and Anthropological Sciences</i> , 2015, 7, 505-515.	0.7	20
2938	Development and characterisation of 20 novel microsatellite markers for the little blue penguin ( <i>Eudyptula minor</i> ) using next-generation sequencing. <i>Conservation Genetics Resources</i> , 2015, 7, 143-145.	0.4	3
2939	Isolation and characterization of 23 microsatellite loci in the stingless bee <i>Melipona subnitida</i> using next-generation sequencing. <i>Conservation Genetics Resources</i> , 2015, 7, 239-241.	0.4	4
2940	Microsatellite primers for the red-crowned parakeet ( <i>Cyanoramphus novaezelandiae</i> ). <i>Conservation Genetics Resources</i> , 2015, 7, 419-421.	0.4	1
2941	Development and characterization of nine novel microsatellite markers for the milkfish <i>Chanos chanos</i> . <i>Conservation Genetics Resources</i> , 2015, 7, 451-453.	0.4	5
2942	Identification and characterization of 12 tetranucleotide microsatellite markers in the white-spotted char <i>Salvelinus leucomaenis</i> . <i>Conservation Genetics Resources</i> , 2015, 7, 497-499.	0.4	1
2943	Phylogenetic analysis of two haploid markers of 500-years-old human remains found in a central region of Korea. <i>Genes and Genomics</i> , 2015, 37, 33-43.	0.5	2
2944	Genetic analysis of four European huchen ( <i>Hucho hucho</i> Linnaeus, 1758) broodstocks from Poland, Germany, Slovakia, and Ukraine: implication for conservation. <i>Journal of Applied Genetics</i> , 2015, 56, 469-480.	1.0	12

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2945	Genetic diversity of the endemic honeybee: <i>Apis mellifera unicolor</i> (Hymenoptera: Apidae) in Madagascar. <i>Apidologie</i> , 2015, 46, 735-747.	0.9	10
2946	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
2947	Mitochondrial diversity of <i>Lakonian</i> people from the <i>A</i> laskan <i>N</i> orth <i>S</i> lope provides evidence for the origins of the Paleo- and Neo- <i>E</i> skimo peoples. <i>American Journal of Physical Anthropology</i> , 2015, 157, 603-614.	2.1	23
2948	Long-distance dispersal and recolonization of a fire-destroyed niche by a mite-associated fungus. <i>Fungal Biology</i> , 2015, 119, 245-256.	1.1	17
2949	Charrs of the genus <i>Salvelinus</i> from Nachikinskoe Lake (Kamchatka Peninsula) and their position in the phylogenetic system of the <i>S. alpinus</i> - <i>S. malma</i> complex. <i>Journal of Ichthyology</i> , 2015, 55, 97-104.	0.2	7
2950	The population genetics of wild chimpanzees in Cameroon and Nigeria suggests a positive role for selection in the evolution of chimpanzee subspecies. <i>BMC Evolutionary Biology</i> , 2015, 15, 3.	3.2	25
2951	Eurasian house mouse ( <i>Mus musculus</i> L.) differentiation at microsatellite loci identifies the Iranian plateau as a phylogeographic hotspot. <i>BMC Evolutionary Biology</i> , 2015, 15, 26.	3.2	59
2952	Genetic differentiation and phylogeography of partially sympatric species complex <i>Rhizophora mucronata</i> Lam. and <i>R. stylosa</i> Griff. using SSR markers. <i>BMC Evolutionary Biology</i> , 2015, 15, 57.	3.2	49
2953	Species distribution and introgressive hybridization of two <i>Avicennia</i> species from the Western Hemisphere unveiled by phylogeographic patterns. <i>BMC Evolutionary Biology</i> , 2015, 15, 61.	3.2	23
2954	Fine-scale genetic analysis of the exploited Nile monitor ( <i>Varanus niloticus</i> ) in Sahelian Africa. <i>BMC Genetics</i> , 2015, 16, 32.	2.7	11
2955	Mitochondrial DNA and the Y chromosome suggest the settlement of Madagascar by Indonesian sea nomad populations. <i>BMC Genomics</i> , 2015, 16, 191.	1.2	61
2956	Molecular markers for analyses of intraspecific genetic diversity in the Asian Tiger mosquito, <i>Aedes albopictus</i> . <i>Parasites and Vectors</i> , 2015, 8, 188.	1.0	65
2957	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
2958	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
2959	Deconstructing intercontinental invasion pathway hypotheses of the Mediterranean fruit fly ( <i>Ceratitis capitata</i> ) using a Bayesian inference approach: are port interceptions and quarantine protocols successfully preventing new invasions?. <i>Diversity and Distributions</i> , 2015, 21, 813-825.	1.9	37
2960	Genetic relationships and ecological divergence in <i>Salix</i> species and populations in Taiwan. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	74
2961	Kinship, inbreeding and fine-scale spatial structure influence gut microbiota in a hindgut-fermenting tortoise. <i>Molecular Ecology</i> , 2015, 24, 2521-2536.	2.0	96
2962	A novel set of microsatellite markers for the European Grapevine Moth <i>Lobesia botrana</i> isolated using next-generation sequencing and their utility for genetic characterization of populations from Europe and the Middle East. <i>Bulletin of Entomological Research</i> , 2015, 105, 408-416.	0.5	6

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2965	Comparative phylogeography of co-distributed <i>Phrygilus</i> species (Aves, Thraupidae) from the Central Andes. Molecular Phylogenetics and Evolution, 2015, 90, 150-163.	1.2	9
2966	Female natal philopatry and gene flow between divergent clades of pallid bats ( <i>Antrozous pallidus</i> ). Journal of Mammalogy, 2015, 96, 531-540.	0.6	13
2967	Phylogeographic Analyses of American Black Bears ( <i>Ursus americanus</i> ) Suggest Four Glacial Refugia and Complex Patterns of Postglacial Admixture. Molecular Biology and Evolution, 2015, 32, 2338-2350.	3.5	90
2968	Using ABC and microsatellite data to detect multiple introductions of invasive species from a single source. Heredity, 2015, 115, 262-272.	1.2	20
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2970	Impact of glaciations on genetic diversity of pelagic mollusks: Antarctic <i>Limacina antarctica</i> and Arctic <i>Limacina helicina</i> . Marine Ecology - Progress Series, 2015, 525, 143-152.	0.9	19
2971	Genetic variability and biogeography of the widespread red alga <i>Hypnea flexicaulis</i> (Gigartinales, Rhodophyta) based on <i>rbcL</i> and <i>cox1</i> sequences. Botanica Marina, 2015, 58, 167-174.	0.6	6
2972	Sexual selection protects against extinction. Nature, 2015, 522, 470-473.	13.7	162
2973	Molecular evidence supports coastal dispersal among estuaries for two benthic marine worm (Nephtyidae) species in southeastern Australia. Marine Biology, 2015, 162, 1319-1327.	0.7	7
2974	Wetland Conservation in the Gulf of Mexico: The Example of the Salt Marsh Morning Glory, <i>Ipomoea sagittata</i> . Wetlands, 2015, 35, 709-721.	0.7	8
2975	Application of microsatellite markers as potential tools for traceability of Girgentana goat breed dairy products. Food Research International, 2015, 74, 115-122.	2.9	33
2976	Genetic variability and population structure of <i>Bergenia ciliata</i> (Saxifragaceae) in the Western Himalaya inferred from DAMD and ISSR markers. Biochemical Systematics and Ecology, 2015, 60, 165-170.	0.6	12
2977	Coevolutionary patterns and diversification of avian malaria parasites in African sunbirds (Family) <i>Troglodytes</i> . PLoS ONE, 2015, 10, e0142101.	0.7	42
2978	Genetically distinct populations of northern shrimp, <i>Pandalus borealis</i> , in the North Atlantic: adaptation to different temperatures as an isolation factor. Molecular Ecology, 2015, 24, 1742-1757.	2.0	58
2979	Y-chromosomal variation of local goat breeds of Turkey close to the domestication centre. Journal of Animal Breeding and Genetics, 2015, 132, 449-453.	0.8	16
2980	Genetic divergence and phylogeography of the alpine plant taxon <i>Onobrychis transsilvanica</i> (Fabaceae). Botany, 2015, 93, 257-266.	0.5	5

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2982	Pollen dispersal and breeding structure in a hawkmoth-pollinated Pampa grasslands species <i>Petunia axillaris</i> (Solanaceae). <i>Annals of Botany</i> , 2015, 115, 939-948.	1.4	37
2983	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
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2988	Moroccan study of HLA (-A, -B, -C, -DR, -DQ) polymorphism in 647 unrelated controls: Updating data. <i>Molecular and Cellular Probes</i> , 2015, 29, 197-207.	0.9	16
2989	Short-term genetic consequences of habitat loss and fragmentation for the neotropical palm <i>Oenocarpus bataua</i> . <i>Heredity</i> , 2015, 115, 389-395.	1.2	31
2990	Diversity of MHC <i>DQB</i> and <i>DRB</i> Genes in the Endangered Australian Sea Lion ( <i>Neophoca</i> ) Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf	1.0	25
2991	Past and present drivers of population structure in a small coastal fish, the European long snouted seahorse <i>Hippocampus guttulatus</i> . <i>Conservation Genetics</i> , 2015, 16, 1139-1153.	0.8	21
2992	The Crested Auklet, <i>Aethia cristatella</i> (Alcidae, Charadriiformes), does not vary geographically in genetics, morphology or vocalizations. <i>Marine Biology</i> , 2015, 162, 1329-1342.	0.7	10
2993	Optimization and validation of a multiplex assay for microsatellite loci analysis in the field cricket, <i>Gryllus campestris</i> (Orthoptera: Gryllidae). <i>Journal of Asia-Pacific Entomology</i> , 2015, 18, 421-424.	0.4	2
2994	High genetic diversity in the harvestman <i>Geraeocormobius sylvorum</i> (Arachnida, Opiliones.) Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf	0.6	7
2995	Population differentiation determined from putative neutral and divergent adaptive genetic markers in <i>Eulachon</i> ( <i>Thaleichthys pacificus</i> , Osmeridae), an anadromous Pacific smelt. <i>Molecular Ecology Resources</i> , 2015, 15, 1421-1434.	2.2	56
2996	Replicate altitudinal clines reveal that evolutionary flexibility underlies adaptation to drought stress in annual <i>Mimulus guttatus</i> . <i>New Phytologist</i> , 2015, 206, 152-165.	3.5	132
2997	Estimating the temporal and spatial extent of gene flow among sympatric lizard populations (genus) Tj ETQq0 0 0 rgBT / Overlock 10 Tf	2.0	16
2998	Convergence of Y Chromosome STR Haplotypes from Different SNP Haplogroups Compromises Accuracy of Haplogroup Prediction. <i>Journal of Genetics and Genomics</i> , 2015, 42, 403-407.	1.7	24



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3000	Tracing the genetic origin of Europe's first farmers reveals insights into their social organization. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20150339.	1.2	127
3001	Susceptibility of amphibians to chytridiomycosis is associated with MHC class II conformation. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20143127.	1.2	114
3002	Analysis of sailfish ( <i>Istiophorus platypterus</i> ) population structure in the North Pacific Ocean. <i>Fisheries Research</i> , 2015, 166, 33-38.	0.9	12
3003	Genetic admixture supports an ancient hybrid origin of the endangered <i>Hawaiian duck</i> . <i>Journal of Evolutionary Biology</i> , 2015, 28, 1005-1015.	0.8	31
3004	Population genetics of freeze tolerance among natural populations of <i>Populus balsamifera</i> across the growing season. <i>New Phytologist</i> , 2015, 207, 710-722.	3.5	22
3005	Post-fragmentation population structure in a cooperative breeding Afrotropical cloud forest bird: emergence of a source-sink population network. <i>Molecular Ecology</i> , 2015, 24, 1172-1187.	2.0	15
3006	Polymorphisms at 17 Y-STR loci in Botswana populations. <i>Forensic Science International: Genetics</i> , 2015, 17, 47-52.	1.6	4
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3008	Completion of a worldwide reference panel of samples for an ancestry informative Indel assay. <i>Forensic Science International: Genetics</i> , 2015, 17, 75-80.	1.6	30
3009	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
3010	Rethinking refugia: Tree topology, divergence dates, and demographic history trace the distribution of the endangered Plymouth gentian ( <i>Sabatia kennedyana</i> ) from the Pleistocene glaciation to present day. <i>American Journal of Botany</i> , 2015, 102, 609-620.	0.8	5
3011	Population genetic structure of serotine bats ( <i>Eptesicus serotinus</i> ) across Europe and implications for the potential spread of bat rabies (European bat lyssavirus EBLV-1). <i>Heredity</i> , 2015, 115, 83-92.	1.2	18
3012	Multiple host-shifts by the emerging honeybee parasite, <i>Varroa jacobsoni</i> . <i>Molecular Ecology</i> , 2015, 24, 2379-2391.	2.0	63
3013	Genetic population structure of the commercially most important demersal fish in the Southwest Atlantic: The whitemouth croaker ( <i>Micropogonias furnieri</i> ). <i>Fisheries Research</i> , 2015, 167, 333-337.	0.9	15
3014	Phylogeography of <i>Ophryotrocha labronica</i> (Polychaeta, Dorvilleidae) along the Italian coasts. <i>Marine Ecology</i> , 2015, 36, 1088-1097.	0.4	6
3015	Hybridization and asymmetric introgression across a narrow zone of contact between <i>Neotoma fuscipes</i> and <i>N. macrotis</i> (Rodentia: Cricetidae). <i>Biological Journal of the Linnean Society</i> , 2015, 115, 162-172.	0.7	33
3016	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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3018	Differences in population connectivity of a benthic marine invertebrate <i>Evechinus chloroticus</i> (Echinodermata: Echinoidea) across large and small spatial scales. <i>Conservation Genetics</i> , 2015, 16, 965-978.	0.8	16
3019	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
3020	Mitochondrial DNA sequence variation, demographic history, and population structure of Amur sturgeon <i>Acipenser schrenckii</i> Brandt, 1869. <i>Russian Journal of Genetics</i> , 2015, 51, 169-184.	0.2	9
3021	Highly discriminatory capacity of the PowerPlex Â® Y23 System for the study of isolated populations. <i>Forensic Science International: Genetics</i> , 2015, 17, 104-107.	1.6	21
3022	Effects of Forest Fragmentation on Genetic Diversity of the Critically Endangered Primate, the Pied Tamarin ( <i>Saguinus bicolor</i> ): Implications for Conservation. <i>Journal of Heredity</i> , 2015, 106, 512-521.	1.0	30
3023	Conservation Genetics of the Scalloped Hammerhead Shark in the Pacific Coast of Colombia. <i>Journal of Heredity</i> , 2015, 106, 448-458.	1.0	32
3024	Changes in spawning time led to the speciation of the broadcast spawning corals <i>Acropora digitifera</i> and the cryptic species <i>Acropora</i> sp. 1 with similar gamete recognition systems. <i>Coral Reefs</i> , 2015, 34, 1189-1198.	0.9	32
3025	Assessing patterns of admixture and ancestry in Canadian honey bees. <i>Insectes Sociaux</i> , 2015, 62, 479-489.	0.7	31
3026	Gene-associated markers can assign origin in a weakly structured fish, Atlantic herring. <i>ICES Journal of Marine Science</i> , 2015, 72, 1790-1801.	1.2	50
3027	Genetic characterization of hybridization between native and invasive bittersweet vines ( <i>Celastrus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.2	14
3028	Phylogeography and population genetics of black alder ( <i>Alnus glutinosa</i> (L.) Gaertn.) in Ireland: putting it in a European context. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	18
3029	COI gene sequence analysis for testing cyclical mating in securing genetic diversity of <i>Macrobrachium rosenbergii</i> . <i>Biochemical Systematics and Ecology</i> , 2015, 62, 178-185.	0.6	5
3030	Evaluating the impact of a fluoropolymer plant on a river macrobenthic community by a combined chemical, ecological and genetic approach. <i>Science of the Total Environment</i> , 2015, 538, 654-663.	3.9	10
3031	<i>IRF6</i> Is a Marker of Severity in Nonsyndromic Cleft Lip/Palate. <i>Journal of Dental Research</i> , 2015, 94, 226S-232S.	2.5	22
3032	Genetic variation and population structure of the Pacific oyster <i>Crassostrea gigas</i> in the northwestern Pacific inferred from mitochondrial COI sequences. <i>Fisheries Science</i> , 2015, 81, 1071-1082.	0.7	22
3033	Enriching the knowledge on East Asia populations: Characterization of male lineages from Macau and Shanghai. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e322-e324.	0.1	0
3034	Implementing genotypic AmpFlSTR Â® Identifier Â® Plus profiles to infer population groups. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e553-e554.	0.1	1

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3036	Genetic structure and diversity of breeding Montagu's harrier ( <i>Circus pygargus</i> ) in Europe. <i>European Journal of Wildlife Research</i> , 2015, 61, 691-701.	0.7	5
3037	Phylogeography of the Peninsula Crowned Snake ( <i>Tantilla relicta relicta</i> ) on the Lake Wales Ridge in Central Florida. <i>Journal of Herpetology</i> , 2015, 49, 415-419.	0.2	2
3038	HLA supertype variation across populations: new insights into the role of natural selection in the evolution of HLA-A and HLA-B polymorphisms. <i>Immunogenetics</i> , 2015, 67, 651-663.	1.2	42
3039	Patterns of genetic diversity of <i>Prunus africana</i> in Ethiopia: hot spot but not point of origin for range-wide diversity. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	12
3040	Development of microsatellites for the genus <i>Salamandrina</i> : A tool to discriminate between northern and southern spectacled salamanders ( <i>Salamandrina perspicillata</i> and <i>Salamandrina terdigitata</i> ) and their hybrids. <i>Biochemical Systematics and Ecology</i> , 2015, 63, 170-173.	0.6	2
3041	Microsatellite DNA reveals genetically different populations of Atlantic bonito <i>Sarda sarda</i> in the Mediterranean Basin. <i>Biochemical Systematics and Ecology</i> , 2015, 63, 174-182.	0.6	6
3042	Inferring the links between breeding and wintering grounds in a Palearctic African migratory bird, the Great Reed Warbler, using mitochondrial DNA data. <i>African Zoology</i> , 2015, 50, 241-248.	0.2	5
3043	Relationship between wild greylag and European domestic geese based on mitochondrial <i>cytb</i> DNA. <i>Animal Genetics</i> , 2015, 46, 485-497.	0.6	15
3044	First molecular characterization of <i>Sarcocystis tenella</i> in Tatra chamois ( <i>Rupicapra rupicapra tatrica</i> ) in Poland. <i>Parasitology Research</i> , 2015, 114, 3885-3892.	0.6	16
3045	Comparative transcriptomics of a complex of four European pine species. <i>BMC Genomics</i> , 2015, 16, 234.	1.2	40
3046	Exploring the relationship between lifestyles, diets and genetic adaptations in humans. <i>BMC Genetics</i> , 2015, 16, 55.	2.7	15
3047	Genetic diversity of 15 autosomal STR loci in the population of Southern Punjab Pakistan. <i>Forensic Science International: Genetics</i> , 2015, 19, e1-e2.	1.6	7
3048	Genotype and haplotype frequencies of the DRD4 VNTR polymorphism in the men with no history of ADHD, convicted of violent crimes. <i>Journal of Criminal Justice</i> , 2015, 43, 464-469.	1.5	6
3049	Ecological release leads to novel ontogenetic diet shift in kokanee ( <i>Oncorhynchus nerka</i> ). <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2015, 72, 1718-1730.	0.7	13
3050	Studies of East European populations with a 46-plex ancestry-informative indel set. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e16-e18.	0.1	1
3051	Selection on MHC class II supertypes in the New Zealand endemic Hochstetter's frog. <i>BMC Evolutionary Biology</i> , 2015, 15, 63.	3.2	26
3052	Genetic structure, diversity, and interisland dispersal in the endangered Mariana Common Moorhen ( <i>Gallinula chloropus guami</i> ). <i>Condor</i> , 2015, 117, 660-669.	0.7	8

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3053	Were sea level changes during the Pleistocene in the South Atlantic Coastal Plain a driver of speciation in <i>Petunia</i> (Solanaceae)? BMC Evolutionary Biology, 2015, 15, 92.	3.2	33
3054	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. American Journal of Botany, 2015, 102, 1647-1658.	0.8	3
3055	Complete mitochondrial genome reveals genetic diversity of <i>Angiostrongylus cantonensis</i> (Nematoda: Tj ETQq0 0 0 rgBT /Overlock 10	0.9	20
3056	Allele frequencies of 38 insertion/deletion polymorphisms in a population sample from the Federal District (Brazil)â€”A territory that arose from nothing. Forensic Science International: Genetics, 2015, 19, 79-80.	1.6	1
3057	Ancestry informative markers for distinguishing between Thai populations based on genome-wide association datasets. Legal Medicine, 2015, 17, 245-250.	0.6	15
3058	CYP2B6 poor metaboliser alleles involved in efavirenz and nevirapine metabolism: CYP2B6*9 and CYP2B6*18 distribution in HIV-exposed subjects from Dschang, Western Cameroon. Infection, Genetics and Evolution, 2015, 35, 122-126.	1.0	10
3059	Temperature niche conservatism and strong genetic structure are involved in the trans-Panamanian colonization of <i>Matudaea</i> (Hamamelidaceae) to Andean forests. Biochemical Systematics and Ecology, 2015, 63, 98-108.	0.6	2
3060	Analysis of the most efficient autosomal strs and genetic data for the locus se33 in ecuadorian population. Forensic Science International: Genetics Supplement Series, 2015, 5, e93-e95.	0.1	4
3061	Biogeography of the <i>Phalaenopsis amabilis</i> species complex inferred from nuclear and plastid DNAs. BMC Plant Biology, 2015, 15, 202.	1.6	13
3062	Environmental and genetic correlates of allocation to sexual reproduction in the circumpolar plant <i>Bistorta vivipara</i> . American Journal of Botany, 2015, 102, 1174-1186.	0.8	12
3063	Phylogeographic Study of Whip Scorpions (Chelicerata: Arachnida: Thelyphonida) in Japan and Taiwan. Zoological Science, 2015, 32, 352.	0.3	9
3064	Phytoplankton succession affects the composition of <i>Poly-nucleobacter</i> subtypes in humic lakes. Environmental Microbiology, 2015, 17, 816-828.	1.8	18
3065	Genotypingâ€”byâ€”sequencing approach indicates geographic distance as the main factor affecting genetic structure and gene flow in Brazilian populations of <i>Grapholita molesta</i> (Lepidoptera,) Tj ETQq0 0 0 rgBT /Overlock 10 1650 257 T	1.0	16
3066	Non-random expression of ribosomal DNA units in a grasshopper showing high intragenomic variation for the ITS2 region. Insect Molecular Biology, 2015, 24, 319-330.	1.0	2
3067	The biodiversity and genetic structure of Balearic sheep breeds. Journal of Animal Breeding and Genetics, 2015, 132, 268-276.	0.8	10
3068	Evidence of landâ€”sea transfer of the zoonotic pathogen <i>Campylobacter</i> to a wildlife marine sentinel species. Molecular Ecology, 2015, 24, 208-221.	2.0	25
3069	The origin of unique diversity in deglaciated areas: traces of <i>Pleistocene</i> processes in northâ€”European endemics from the <i>Galium pusillum</i> polyploid complex ( <i>Rubiaceae</i> ). Molecular Ecology, 2015, 24, 1311-1334.	2.0	13
3070	Stochastic modelling of shifts in allele frequencies reveals a strongly polygynous mating system in the reâ€”introduced <i>Asiatic</i> wild ass. Molecular Ecology, 2015, 24, 1433-1446.	2.0	11

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3071	<i>HLA-B*58:63</i> , a novel allele identified by sequence-based typing in a Chinese bone marrow voluntary donor. <i>Tissue Antigens</i> , 2015, 85, 73-75.	1.0	3
3072	Identification of a novel <i>HLA-A*24</i> allele, <i>A*24:289</i> , in a Chinese individual. <i>Tissue Antigens</i> , 2015, 85, 69-71.	1.0	3
3073	Simple sequence repeat analysis of genetic diversity among <i>Acetyl-CoA carboxylase inhibitor-resistant</i> and <i>susceptible</i> <i>Echinochloa crusgalli</i> and <i>E. oryzicola</i> populations in Korea. <i>Weed Research</i> , 2015, 55, 90-100.	0.8	10
3074	Patterns of genetic admixture between roe deer of different origin in central Italy. <i>Journal of Mammalogy</i> , 2015, 96, 827-838.	0.6	8
3075	Discovery and validation of gene-linked diagnostic <i>SNP</i> markers for assessing hybridization between <i>Largemouth bass</i> ( <i>Micropterus salmoides</i> ) and <i>Florida bass</i> ( <i>M. floridanus</i> ). <i>Molecular Ecology Resources</i> , 2015, 15, 395-404.	2.2	29
3076	Genetic analysis of the threatened American hart's-tongue fern ( <i>Asplenium scolopendrium</i> var.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i> conservation. <i>Biochemical Systematics and Ecology</i> , 2015, 62, 25-35.	0.6	9
3077	Possible association of rare polymorphism in the <i>ABCB1</i> gene with rifampin and ethambutol drug-resistant tuberculosis. <i>Tuberculosis</i> , 2015, 95, 532-537.	0.8	11
3078	Low genetic diversity despite multiple introductions of the invasive plant species <i>Impatiens glandulifera</i> in Europe. <i>BMC Genetics</i> , 2015, 16, 103.	2.7	62
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3082	Human platelet antigen genotyping of platelet donors in southern Brazil. <i>International Journal of Immunogenetics</i> , 2015, 42, 329-335.	0.8	11
3083	Black-spotted pond frog ( <i>Pelophylax nigromaculatus</i> ) on the Chinese Loess Plateau represents a cryptic species: Evidence from molecular phylogeny and ecological niche modeling. <i>Journal of Systematics and Evolution</i> , 2015, 53, 339-350.	1.6	8
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3088	Seascape genetics of saithe ( <i>Pollachius virens</i> ) across the North Atlantic using single nucleotide polymorphisms. <i>ICES Journal of Marine Science</i> , 2015, 72, 2732-2741.	1.2	16

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3097	Genetic characterization of 27 Y-STR loci in the native population of Ashaninka from Peru. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e220-e222.	0.1	7
3098	An investigation of 21 insertion deletion markers in United Arab Emirates population. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e261-e263.	0.1	0
3099	Y-STR haplotype background of Philippines: Comparison with other Southeast Asian populations. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e428-e429.	0.1	0
3100	Founding mothers of Chueta population. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e492-e494.	0.1	2
3101	Routine analysis of sexual assault cases in Brasília, Brazil, using 23 Y chromosomal markers. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e619-e621.	0.1	2
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3103	Comparative phylogeography between two generalist flea species reveal a complex interaction between parasite life history and host vicariance: parasite-host association matters. <i>BMC Evolutionary Biology</i> , 2015, 15, 105.	3.2	24
3104	The European Paleoendemic <i>Haberlea rhodopensis</i> (Gesneriaceae) Has an Oligocene Origin and a Pleistocene Diversification and Occurs in a Long-Persisting Refugial Area in Southeastern Europe. <i>International Journal of Plant Sciences</i> , 2015, 176, 499-514.	0.6	25
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3108	Population data for 15 autosomal STR loci in the Miao ethnic minority from Guizhou Province, Southwest China. <i>Forensic Science International: Genetics</i> , 2015, 16, e3-e4.	1.6	37
3109	Temporal genetic and demographic monitoring of pond-breeding amphibians in three contrasting population systems. <i>Conservation Genetics</i> , 2015, 16, 1335-1344.	0.8	9
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3113	Genetic diversity of a tropical rainforest understory bird in an urban fragmented landscape. <i>Condor</i> , 2015, 117, 447-459.	0.7	15
3114	Genetic diversity of Italian goat breeds assessed with a medium-density SNP chip. <i>Genetics Selection Evolution</i> , 2015, 47, 62.	1.2	72
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3123	Genetic diversity and genetic structure of the striped field mouse <i>Apodemus agrarius coreae</i> (Muridae, Rodentia) in Korea. <i>Gene</i> , 2015, 572, 292-297.	1.0	8
3124	How many species of <i>Siphonaria pectinata</i> (Gastropoda: Heterobranchia) are there?. <i>Journal of Molluscan Studies</i> , 0, , eyv038.	0.4	2

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3126	Genetic diversity and population structure of an Italian landrace of runner bean ( <i>Phaseolus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj 5	0.5	11
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3129	Genetic diversity of the swamp rat in South America: Population expansion after transgressive-regressive marine events in the Late Quaternary. <i>Mammalian Biology</i> , 2015, 80, 510-517.	0.8	5
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3131	Genetic diversity of <i>Viola cazorlensis</i> Gand., an endemic species of Mediterranean dolomitic habitats: implications for conservation. <i>Systematics and Biodiversity</i> , 2015, 13, 571-580.	0.5	15
3132	Population genetic structure in wild and hatchery populations of white cloud mountain minnow ( <i>Tanichthys albonubes</i> ): Recommendations for conservation. <i>Biochemical Systematics and Ecology</i> , 2015, 62, 142-150.	0.6	9
3133	Mitochondrial DNA Diversity and Phylogeography of <i>Lucania interioris</i> Inform Biodiversity Conservation in the Cuatro Ci�negas Basin, M�xico. <i>Western North American Naturalist</i> , 2015, 75, 200-208.	0.2	7
3134	Developing a genetic baseline for the yellowtail amberjack species complex, <i>Seriola lalandi</i> sensu lato, to assess and preserve variation in wild populations of these globally important aquaculture species. <i>Conservation Genetics</i> , 2015, 16, 1475-1488.	0.8	28
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3136	Genetic sources of individual variation in parental care behavior. <i>Behavioral Ecology and Sociobiology</i> , 2015, 69, 1933-1943.	0.6	15
3137	Population structure of large yellow croaker ( <i>Larimichthys crocea</i> ) revealed by single nucleotide polymorphisms. <i>Biochemical Systematics and Ecology</i> , 2015, 63, 136-142.	0.6	5
3138	Polymorphism analysis of 15 STR loci in a large sample of Guangdong (Southern China) Han population. <i>Legal Medicine</i> , 2015, 17, 489-492.	0.6	13
3139	De novo assembly and characterization of transcriptome using Illumina sequencing and development of twenty five microsatellite markers for an endemic tree <i>Juglans hopeiensis</i> Hu in China. <i>Biochemical Systematics and Ecology</i> , 2015, 63, 201-211.	0.6	41
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3145	A tree well travelled: global genetic structure of the invasive tree <i>Acacia saligna</i> . Journal of Biogeography, 2015, 42, 305-314.	1.4	30
3146	DNA analysis of ancient dogs of the Americas: Identifying possible founding haplotypes and reconstructing population histories. Journal of Human Evolution, 2015, 79, 105-118.	1.3	47
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3148	Trends in bowhead whales in West Greenland: Aerial surveys <i>vs</i> genetic capture-recapture analyses. Marine Mammal Science, 2015, 31, 133-154.	0.9	24
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3154	Reconstructing the demographic history of orangutans using Approximate Bayesian Computation. Molecular Ecology, 2015, 24, 310-327.	2.0	32
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3158	Reconstruction of two colonisation pathways of <i>Mantis religiosa</i> (Mantodea) in Germany using four mitochondrial markers. Genetica, 2015, 143, 11-20.	0.5	7
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3162	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
3163	The mitochondrial <i>DNA</i> history of a former native <i>American</i> village in northern <i>Uruguay</i> . <i>American Journal of Human Biology</i> , 2015, 27, 407-416.	0.8	8
3164	Genetic diversity of Cornigliese sheep breed using STR markers. <i>Small Ruminant Research</i> , 2015, 123, 62-69.	0.6	16
3165	Tracking footprints of selection associated with soybean adaptation to Central-East Europe environments. <i>Euphytica</i> , 2015, 203, 701-713.	0.6	9
3166	Genetic diversity across geographical scales in marine coastal ecosystems: <i>Holothuria arguinensis</i> a model species. <i>Journal of Experimental Marine Biology and Ecology</i> , 2015, 463, 158-167.	0.7	19
3167	The genetic diversity and introgression of <i>Juglans regia</i> and <i>Juglans sigillata</i> in Tibet as revealed by SSR markers. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	121
3168	Molecular taxonomy and naming of five cryptic species of <i>Alviniconcha</i> snails (Gastropoda: Tj ETQq1 1 0.784314 rgBT, Overlooked	0.5	78
3169	Population structure and identification of two matrilinear and one patrilinear mitochondrial lineages in the mussel <i>Mytella charruana</i> . <i>Estuarine, Coastal and Shelf Science</i> , 2015, 156, 165-174.	0.9	13
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3172	Characterization of the <i>Campylobacter jejuni</i> Population in the Barnacle Geese Reservoir. <i>Zoonoses and Public Health</i> , 2015, 62, 209-221.	0.9	19
3173	Non-random distribution of 17 Y-chromosome STR loci in different areas of Sardinia. <i>Forensic Science International: Genetics</i> , 2015, 16, 26-28.	1.6	7
3174	Population genetic data for 15 autosomal STR markers in Turkish Cypriots from Cyprus. <i>Forensic Science International: Genetics</i> , 2015, 14, e1-e3.	1.6	12
3175	Genetic structure and consequences of stock exploitation of <i>Chrysoblephus puniceus</i> , a commercially important sparid in the South West Indian Ocean. <i>Fisheries Research</i> , 2015, 164, 64-72.	0.9	6
3176	Investigating the puzzling genetic structure of mallard populations ( <i>Anas platyrhynchos</i> L.) in Italy. <i>European Journal of Wildlife Research</i> , 2015, 61, 81-89.	0.7	10
3177	Marker-trait associations for survival, growth, and flowering components in <i>Eucalyptus cladocalyx</i> under arid conditions. <i>Biologia Plantarum</i> , 2015, 59, 389-393.	1.9	7
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3180	Mitochondrial DNA perspective of Serbian genetic diversity. <i>American Journal of Physical Anthropology</i> , 2015, 156, 449-465.	2.1	15
3181	Ancient <scp>DNA</scp> from the <scp>S</scp>child site in <scp>I</scp>llinois: Implications for the <scp>M</scp>ississippian transition in the <scp>L</scp>ower <scp>I</scp>llinois <scp>R</scp>iver <scp>V</scp>alley. <i>American Journal of Physical Anthropology</i> , 2015, 156, 434-448.	2.1	6
3182	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
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3185	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
3186	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
3187	Use of genotyping by sequencing data to develop a high-throughput and multifunctional <scp>SNP</scp> panel for conservation applications in Pacific lamprey. <i>Molecular Ecology Resources</i> , 2015, 15, 187-202.	2.2	75
3188	Genetic differentiation of brackish water populations of cod <i>Gadus morhua</i> in the southern Baltic, inferred from genotyping using SNP-arrays. <i>Marine Genomics</i> , 2015, 19, 17-22.	0.4	36
3189	Genetic structure of <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> in different regions from Brazil. <i>Plant Pathology</i> , 2015, 64, 137-146.	1.2	24
3190	Population-level perspectives on global change: genetic and demographic analyses indicate various scales, timing, and causes of scyphozoan jellyfish blooms. <i>Biological Invasions</i> , 2015, 17, 851-867.	1.2	34
3191	Genetic polymorphism of the 26 short tandem repeat loci in the Chinese Hebei Han population using two commercial forensic kits. <i>Molecular Biology Reports</i> , 2015, 42, 217-225.	1.0	8
3192	Dispersal is linked to habitat use in 59 species of water beetles (Coleoptera: Adepaga) on Madagascar. <i>Ecography</i> , 2015, 38, 732-739.	2.1	22
3193	Portuguese mitochondrial DNA genetic diversity—An update and a phylogenetic revision. <i>Forensic Science International: Genetics</i> , 2015, 15, 27-32.	1.6	10
3194	Low genetic variability in <i>S</i>clerotinia sclerotiorum<i></i> populations from common bean fields in <scp>M</scp>inas <scp>G</scp>erais <scp>S</scp>tate, <scp>B</scp>razil, at regional, local and micro-scales. <i>Plant Pathology</i> , 2015, 64, 921-931.	1.2	37
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3196	Local Evolution of Pyrethroid Resistance Offsets Gene Flow Among <i>Aedes aegypti</i> Collections in Yucatan State, Mexico. <i>American Journal of Tropical Medicine and Hygiene</i> , 2015, 92, 201-209.	0.6	42

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3197	The sampling scheme matters: <i>Pan troglodytes troglodytes</i> and <i>P. t. t.</i> <i>schweinfurthii</i> are characterized by clinal genetic variation rather than a strong subspecies break. <i>American Journal of Physical Anthropology</i> , 2015, 156, 181-191.	2.1	24
3198	The relationship between distance and genetic similarity among invasive rat populations in the Falkland Islands. <i>Conservation Genetics</i> , 2015, 16, 125-135.	0.8	11
3199	West <i>versus</i> <i>E. ast M. editerranean S. ea</i> : origin and genetic differentiation of the sea cucumber <i>H. olothuria polii</i> . <i>Marine Ecology</i> , 2015, 36, 485-495.	0.4	24
3200	Origin and genome evolution of polyploid green toads in Central Asia: evidence from microsatellite markers. <i>Heredity</i> , 2015, 114, 300-308.	1.2	18
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3342	Shared phylogeographical breaks in a Caribbean coral reef sponge and its invertebrate commensals. Journal of Biogeography, 2016, 43, 2136-2146.	1.4	28
3343	Urban population genetics of the invasive black rats in Franceville, Gabon. Journal of Zoology, 2016, 299, 183-190.	0.8	11
3344	Genetic variability, local selection and demographic history: genomic evidence of evolving towards allopatric speciation in Asian seabass. Molecular Ecology, 2016, 25, 3605-3621.	2.0	32
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3346	Population genetic structure and demographic history of the black fly vector, <i>Simulium nodosum</i> in Thailand. Medical and Veterinary Entomology, 2016, 30, 286-292.	0.7	5
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3348	Using genetic monitoring to inform best practice in a captive breeding programme: inbreeding and potential genetic rescue in the freshwater pearl mussel <i>Margaritifera margaritifera</i> . Conservation Genetics, 2016, 17, 1323-1332.	0.8	6
3349	Genetic polymorphic investigation of 21 autosomal short tandem repeat loci in the Chinese Li ethnic group. Forensic Science International: Genetics, 2016, 24, e17-e18.	1.6	5
3350	HLA-G coding region and 3' untranslated region (3'UTR) in two Chinese Han populations. Immunology Letters, 2016, 176, 65-71.	1.1	3
3351	Insights into the molecular phylogeny and historical biogeography of the white-clawed crayfish (Decapoda, Astacidae). Molecular Phylogenetics and Evolution, 2016, 103, 26-40.	1.2	36
3352	Nuclear locus divergence at the early stages of speciation in the Orchard Oriole complex. Ecology and Evolution, 2016, 6, 4307-4317.	0.8	1
3353	Major histocompatibility complex class II DAB alleles associated with intestinal parasite load in the vulnerable Chinese egret ( <i>Egretta eulophotes</i> ). Ecology and Evolution, 2016, 6, 4421-4434.	0.8	9
3354	Geographical isolation and genetic differentiation: the case of <i>Orestias ascotansensis</i> (Teleostei: Tj ETQq1 1 0.784314 rgBT /Over Society, 2016, 117, 747-759.	0.7	9
3355	Higher genetic diversity on mountain tops: the role of historical and contemporary processes in shaping genetic variation in the bank vole. Biological Journal of the Linnean Society, 2016, 118, 233-244.	0.7	12
3356	Genetic isolation among mountains but not between stream types in a tropical high-altitude mayfly. Freshwater Biology, 2016, 61, 702-714.	1.2	30
3357	The role of environment and core-margin effects on range-wide phenotypic variation in a montane grasshopper. Journal of Evolutionary Biology, 2016, 29, 2129-2142.	0.8	16
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3360	Contrasting support for alternative models of genomic variation based on microhabitat preference: species-specific effects of climate change in alpine sedges. <i>Molecular Ecology</i> , 2016, 25, 3974-3986.	2.0	55
3361	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
3362	Genetic heritage of Croatians in the Southeastern European gene pool: Y chromosome analysis of the Croatian continental and Island population. <i>American Journal of Human Biology</i> , 2016, 28, 837-845.	0.8	10
3363	Exploring the mitochondrial DNA variability of the Amazonian Yanomami. <i>American Journal of Human Biology</i> , 2016, 28, 846-856.	0.8	0
3364	Antiquity and diversity of aboriginal Australian Y-chromosomes. <i>American Journal of Physical Anthropology</i> , 2016, 159, 367-381.	2.1	26
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3366	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
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3368	Between-site and year variation in the relative susceptibility of native Scottish <i>Pinus sylvestris</i> populations to dothistroma needle blight. <i>Plant Pathology</i> , 2016, 65, 369-379.	1.2	10
3369	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
3370	Genomic architecture of phenotypic divergence between two hybridizing plant species along an elevational gradient. <i>AoB PLANTS</i> , 2016, 8, .	1.2	11
3371	Conservation genetics assessment and phylogenetic relationships of critically endangered <i>Hucho bleekeri</i> in China. <i>Journal of Applied Ichthyology</i> , 2016, 32, 343-349.	0.3	10
3372	Genetic and paleomodelling evidence of the population expansion of the cattle egret <i>Bubulcus ibis</i> in Africa during the climatic oscillations of the Late Pleistocene. <i>Journal of Avian Biology</i> , 2016, 47, 846-857.	0.6	6
3373	Mitochondrial DNA variation of indigenous goats in Nark and Siolo counties of Kenya. <i>Journal of Animal Breeding and Genetics</i> , 2016, 133, 238-247.	0.8	20
3374	Seascape features, rather than dispersal traits, predict spatial genetic patterns in co-distributed reef fishes. <i>Journal of Biogeography</i> , 2016, 43, 256-267.	1.4	48
3375	A bridge too far: dispersal barriers and cryptic speciation in an Arabian Peninsula grouper ( <i>Cephalopholis hemistiktos</i> ). <i>Journal of Biogeography</i> , 2016, 43, 820-832.	1.4	24
3376	Population structure of two rabies hosts relative to the known distribution of rabies virus variants in Alaska. <i>Molecular Ecology</i> , 2016, 25, 675-688.	2.0	22

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3380	Analysis of <i>Amblyomma sculptum</i> haplotypes in an area endemic for Brazilian spotted fever. <i>Medical and Veterinary Entomology</i> , 2016, 30, 342-350.	0.7	12
3381	Differentiation in populations of the apple scab fungus <i>Venturia inaequalis</i> on cultivars in a mixed orchard remain over time. <i>Plant Pathology</i> , 2016, 65, 1133-1141.	1.2	12
3382	Phylogeography of <i>Asparagopsis taxiformis</i> revisited: Combined mtDNA data provide novel insights into population structure in Japan. <i>Phycological Research</i> , 2016, 64, 95-101.	0.8	4
3383	Integrative taxonomy of the Italian pine voles, <i>Microtus savii</i> group ( <i>Cricetidae</i> , <i>Arvicolinae</i> ). <i>Zoologica Scripta</i> , 2016, 45, 225-236.	0.7	16
3384	Budding speciation via peripheral isolation: the <i>Psorodonotus venosus</i> (Orthoptera, Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5	0.7	17
3385	HLA class I molecular variation and peptide-binding properties suggest a model of joint divergent asymmetric selection. <i>Immunogenetics</i> , 2016, 68, 401-416.	1.2	31
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3389	Mitochondrial DNA variation of <i>Protosalanx hyalocranius</i> in the Huaihe River. <i>Animal Genetics</i> , 2016, 47, 388-389.	0.6	2
3390	A rapid and inexpensive DNA extraction protocol for oysters. <i>Animal Genetics</i> , 2016, 47, 389-390.	0.6	3
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3392	Genetic signature of the northward expansion of the Egyptian mongoose <i>Herpestes ichneumon</i> (Herpestidae) in the Iberian Peninsula. <i>Biological Journal of the Linnean Society</i> , 2016, 118, 686-697.	0.7	6
3393	Species-specific phylogeographical patterns and Pleistocene east-west divergence in <i>Annona</i> (Annonaceae) in the Brazilian Cerrado. <i>Botanical Journal of the Linnean Society</i> , 2016, 181, 21-36.	0.8	33
3394	Congruence of phenotypic and genetic variation at the subspecific level in a Neotropical passerine. <i>Ibis</i> , 2016, 158, 844-856.	1.0	10

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3396	Comparative population structure of two dominant species, <i>Shinkaia crosnieri</i> (Munidopsidae) Tj ETQq1 1 0.784314 rgBT /Over both deep-sea vent and cold seep inferred from mitochondrial multi-genes. <i>Ecology and Evolution</i> , 2016, 6, 3571-3582.	0.8	27
3397	Expansion of a SNaPshot assay to a 55-SNP multiplex: Assay enhancements, validation, and power in forensic science. <i>Electrophoresis</i> , 2016, 37, 1310-1317.	1.3	25
3398	Genetic diversity of HPV16 and HPV18 in Brazilian patients with invasive cervical cancer. <i>Journal of Medical Virology</i> , 2016, 88, 1279-1287.	2.5	18
3399	Intraspecific diversity matters in bryophyte conservation – internal transcribed spacer and <i>rpl16</i> G2 intron variation in some European mosses. <i>Journal of Bryology</i> , 2016, 38, 173-182.	0.4	13
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3406	Evolutionary and contemporary responses to habitat fragmentation detected in a mesic zone marsupial, the long-nosed potoroo ( <i>Potorous tridactylus</i> ) in south-eastern Australia. <i>Journal of Biogeography</i> , 2016, 43, 653-665.	1.4	18
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3409	Evidence of divergent selection for drought and cold tolerance at landscape and local scales in <i>Abies alba</i> Mill. in the French Mediterranean Alps. <i>Molecular Ecology</i> , 2016, 25, 776-794.	2.0	64
3410	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
3411	The invasive bighead goby <i>Puntius ticto</i> displays large-scale genetic similarities and small-scale genetic differentiation in relation to shipping patterns. <i>Molecular Ecology</i> , 2016, 25, 1925-1943.	2.0	12
3412	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

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3415	Exceptional maternal lineage diversity in brown bears ( <i>Ursus arctos</i> ) from Turkey. <i>Zoological Journal of the Linnean Society</i> , 2016, 176, 463-477.	1.0	44
3416	Variability of innate immune system genes in Native American populations—relationship with history and epidemiology. <i>American Journal of Physical Anthropology</i> , 2016, 159, 722-728.	2.1	6
3417	Mitochondrial DNA polymorphism of atlantic cod of the Barents and White seas. <i>Biology Bulletin</i> , 2016, 43, 235-243.	0.1	4
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3425	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
3426	Peripheral genetic structure of <i>Helicoverpa zea</i> indicates asymmetrical panmixia. <i>Ecology and Evolution</i> , 2016, 6, 3198-3207.	0.8	25
3427	Y chromosome diversity in a linguistic isolate (Mirandese, NE Portugal). <i>American Journal of Human Biology</i> , 2016, 28, 671-680.	0.8	2
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3429	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
3430	Population structure of the golden snub-nosed monkey <i>Rhinopithecus roxellana</i> in the Qinling Mountains, central China. <i>Integrative Zoology</i> , 2016, 11, 350-360.	1.3	19



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3435	Ecological change predicts population dynamics and genetic diversity over 120 000 years. <i>Global Change Biology</i> , 2016, 22, 1737-1745.	4.2	6
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3437	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
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3440	A genetic delineation of Patchouli ( <i>Pogostemon cablin</i> ) revealed by specific locus amplified fragment sequencing. <i>Journal of Systematics and Evolution</i> , 2016, 54, 491-501.	1.6	16
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3442	Red and white Chinook salmon: genetic divergence and mate choice. <i>Molecular Ecology</i> , 2016, 25, 1259-1274.	2.0	25
3444	Landscape genetics, adaptive diversity and population structure in <i>Phaseolus vulgaris</i> . <i>New Phytologist</i> , 2016, 209, 1781-1794.	3.5	86
3445	<i>HLA-B*46:02</i> , a novel <i>HLA-B*46</i> allele identified in a Chinese individual by sequence-based typing. <i>Hla</i> , 2016, 87, 462-464.	0.4	4
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3449	Recombinant MHC tetramers for isolation of virus-specific CD8+ cells from healthy donors: Potential approach for cell therapy of posttransplant cytomegalovirus infection. <i>Biochemistry (Moscow)</i> , 2016, 81, 1371-1383.	0.7	8

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3451	Analysis of genetic diversity in Rose's mountain toadlet ( <i>Capensibufo rosei</i> ) using novel microsatellite markers. African Journal of Herpetology, 2016, 65, 69-82.	0.3	4
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3463	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. Invertebrate Systematics, 2016, 30, 635.	0.5	47
3464	Paternal Genetic Structure in Contemporary Mennonite Communities from the American Midwest. Human Biology, 2016, 88, 95.	0.4	16
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3467	Phylogeography of a semi-aquatic bug, <i>Microvelia horvathi</i> (Hemiptera: Veliidae): an evaluation of historical, geographical and ecological factors. Scientific Reports, 2016, 6, 21932.	1.6	25

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3470	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
3471	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
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3474	Implications for management and conservation of the population genetic structure of the wedge clam <i>Donax trunculus</i> across two biogeographic boundaries. <i>Scientific Reports</i> , 2016, 6, 39152.	1.6	27
3475	Chloroplast DNA-Based Phylogeography of <i>Tilia americana</i> (Malvaceae). <i>Systematic Botany</i> , 2016, 41, 865-880.	0.2	6
3476	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
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3480	Genetic analyses reveal declining trends and low effective population size in an overfished South African sciaenid species, the dusky kob ( <i>Argyrosomus japonicus</i> ). <i>Marine and Freshwater Research</i> , 2016, 67, 266.	0.7	20
3481	Mitigating Chinese-Indian rhesus macaque ( <i>Macaca mulatta</i> ) hybridity at the California National Primate Research Center (CNPRC). <i>Journal of Medical Primatology</i> , 2016, 45, 333-335.	0.3	1
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3488	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
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3500	MHC-dependent mate choice is linked to a trace-amine-associated receptor gene in a mammal. <i>Scientific Reports</i> , 2016, 6, 38490.	1.6	41
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3504	Contrasting and complex evolutionary histories within the terapontid grunter genus <i>Hephaestus</i> revealed by nuclear and mitochondrial genes. <i>Marine and Freshwater Research</i> , 2016, 67, 1813.	0.7	7

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3506	Broad-scale genetic homogeneity in natural populations of common hazel ( <i>Corylus avellana</i> ) in Ireland. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	10
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3515	A genome-wide perspective about the diversity and demographic history of seven Spanish goat breeds. <i>Genetics Selection Evolution</i> , 2016, 48, 52.	1.2	63
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3523	Fine-scale habitat preferences influence within-river population connectivity: a case study using two sympatric <i>scp&gt;N&lt;/scp&gt;ew &lt;scp&gt;Z&lt;/scp&gt;ealand &lt;i&gt;&lt;scp&gt;G&lt;/scp&gt;alaxias&lt;/i&gt;</i> fish species. <i>Freshwater Biology</i> , 2016, 61, 51-56.	1.2	15

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3525	The role of parasite-driven selection in shaping landscape genomic structure in red grouse ( <i>Lagopus lagopus scotica</i> ). Molecular Ecology, 2016, 25, 324-341.	2.0	16
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3527	The art of traditional native PAGE: The APLP 48-ID assay for human identification. Legal Medicine, 2016, 19, 28-31.	0.6	2
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3532	The impact of selection, gene flow and demographic history on heterogeneous genomic divergence: three-spine sticklebacks in divergent environments. Molecular Ecology, 2016, 25, 238-259.	2.0	74
3533	Population genetics of the olive-winged bulbul ( <i>Pycnonotus plumosus</i> ) in a tropical urban-fragmented landscape. Ecology and Evolution, 2016, 6, 78-90.	0.8	15
3534	Incongruent range dynamics between co-occurring Asian temperate tree species facilitated by life history traits. Ecology and Evolution, 2016, 6, 2346-2358.	0.8	10
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3536	Role of genetic background in the introgressive hybridization of rainbow trout ( <i>Oncorhynchus mykiss</i> ). Overlooked 10 Tf 50 26	0.8	8
3537	Phylogeographic-based conservation implications for the New Zealand long-tailed bat, ( <i>Chalinolobus</i> ). Conservation Genetics, 2016, 17, 1067-1079.	0.8	14
3538	Identification of candidate AFLP markers for shell color of the Pacific oyster ( <i>Crassostrea gigas</i> ) under artificial selection. Biochemical Systematics and Ecology, 2016, 66, 209-215.	0.6	4
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3541	Population genetic structure of <i>Rhizoctonia solani</i> AG 3-PT from potatoes in South Africa. Fungal Biology, 2016, 120, 701-710.	1.1	6



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3543	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
3544	Genetic basis of adult migration timing in anadromous steelhead discovered through multivariate association testing. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20153064.	1.2	107
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3546	Genetic variation within and among asexual populations of <i>Porphyra umbilicalis</i> (Bangiales, Rhodophyta) in the Gulf of Maine, USA. <i>Botanica Marina</i> , 2016, 59, 1-12.	0.6	4
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3550	Population data of 21 autosomal STR loci in Chinese Han population from Hubei province in Central China. <i>Forensic Science International: Genetics</i> , 2016, 20, e13-e14.	1.6	41
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3553	Comparative phylogeography of two monogenean species ( <i>Mazocraeidae</i> ) on the host of chub mackerel, <i>Scomber japonicus</i> , along the coast of China. <i>Parasitology</i> , 2016, 143, 594-605.	0.7	10
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3555	Corncrake conservation genetics at a European scale: The impact of biogeographical and anthropological processes. <i>Biological Conservation</i> , 2016, 198, 210-219.	1.9	12
3556	Genetic diversity and population structure of endangered endemic <i>Paeonia jishanensis</i> in China and conservation implications. <i>Biochemical Systematics and Ecology</i> , 2016, 66, 319-325.	0.6	18
3557	Haplotype analysis of non-HLA immunogenetic loci in Turkish and worldwide populations. <i>Gene</i> , 2016, 587, 132-136.	1.0	6
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3562	Genetic diversity and population structure of the endangered medicinal plant <i>Phellodendron amurense</i> in China revealed by SSR markers. <i>Biochemical Systematics and Ecology</i> , 2016, 66, 286-292.	0.6	21
3563	Multiple evolutionary units and demographic stability during the last glacial maximum in the <i>Scytalopus speluncae</i> complex (Aves: Rhinocryptidae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 102, 86-96.	1.2	15
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3565	Phylogeography of East Asian <i>Lespedeza buergeri</i> (Fabaceae) based on chloroplast and nuclear ribosomal DNA sequence variations. <i>Journal of Plant Research</i> , 2016, 129, 793-805.	1.2	16
3566	Bayesian analyses of Pacific swordfish ( <i>Xiphias gladius</i> L.) genetic differentiation using multilocus single nucleotide polymorphism (SNP) data. <i>Journal of Experimental Marine Biology and Ecology</i> , 2016, 482, 1-17.	0.7	13
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3573	Detection and characterisation of the biopollutant <i>Xenostrobus securis</i> (Lamarck 1819) Asturian population from DNA Barcoding and eBarcoding. <i>Marine Pollution Bulletin</i> , 2016, 105, 23-29.	2.3	31
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3575	Cross-species amplification of microsatellite loci for non-invasive genetic monitoring of the snowy owl ( <i>Bubo scandiacus</i> ). <i>European Journal of Wildlife Research</i> , 2016, 62, 247-249.	0.7	0
3576	NGMSelect, and Investigator Argus X-12 analysis in population samples from Albania, Iraq, Lithuania, Slovenia, and Turkey. <i>Forensic Science International: Genetics</i> , 2016, 22, 110-112.	1.6	16
3577	Pure species in a continuum of genetic and morphological variation: sympatric oaks at the edge of their range. <i>Annals of Botany</i> , 2016, 117, 541-549.	1.4	21
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3581	Conservation genetics in Chinese sheep: diversity of fourteen indigenous sheep ( <i>Ovis aries</i> ) using microsatellite markers. <i>Ecology and Evolution</i> , 2016, 6, 810-817.	0.8	19
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3592	Population genetic structure of the shovel-nosed lobster <i>Thenus unimaculatus</i> (Decapoda). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 102 T</i> 766, 225-236.	1.0	9
3593	Patterns and mechanisms of dispersal in a keystone seagrass species. <i>Marine Environmental Research</i> , 2016, 117, 54-62.	1.1	28
3594	HaploGrep 2: mitochondrial haplogroup classification in the era of high-throughput sequencing. <i>Nucleic Acids Research</i> , 2016, 44, W58-W63.	6.5	688
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3598	Colonization of the Scottish islands via long-distance Neolithic transport of red deer ( <i>Cervus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.2	23
3599	Genetic diversity of native and introduced populations of the invasive house crow ( <i>Corvus splendens</i> ) in Asia and Africa. <i>Biological Invasions</i> , 2016, 18, 1867-1881.	1.2	8
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3604	Genetic diversity and population structure of the roughskin sculpin ( <i>Trachidermus fasciatus</i> Heckel) inferred from microsatellite analyses: implications for its conservation and management. <i>Conservation Genetics</i> , 2016, 17, 921-930.	0.8	21
3605	Conservation genetics of the endangered San Francisco Bay endemic salt marsh harvest mouse ( <i>Reithrodontomys raviventris</i> ). <i>Conservation Genetics</i> , 2016, 17, 1055-1066.	0.8	15
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3610	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
3611	Population data of 17 short tandem repeat loci in 2923 individuals from the Han population of Nantong in East China. <i>International Journal of Legal Medicine</i> , 2016, 130, 1195-1197.	1.2	5
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3613	Population data of 23 STR loci (PowerPlex® Fusion System) in Mexican Mestizos from the West Region. <i>International Journal of Legal Medicine</i> , 2016, 130, 1489-1491.	1.2	27
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3749	Assessment of genetic diversity and population differentiation of <i>Achyranthes bidentata</i> (Amaranthaceae) in Dao Di and its surrounding region based on microsatellite markers. <i>Biochemical Systematics and Ecology</i> , 2016, 69, 27-32.	0.6	6
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3756	Making sense of the relationships between Ne, Nb and Nc towards defining conservation thresholds in Atlantic salmon ( <i>Salmo salar</i> ). <i>Heredity</i> , 2016, 117, 268-278.	1.2	46
3757	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
3758	Global diversity in the TAS2R38 bitter taste receptor: revisiting a classic evolutionary PROPosal. <i>Scientific Reports</i> , 2016, 6, 25506.	1.6	69



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3760	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
3761	Population Structure Among and Within Iowa, Missouri, Ohio, and South Dakota Populations of <i>Phytophthora sojae</i> . <i>Plant Disease</i> , 2016, 100, 367-379.	0.7	50
3762	Association of Putative Fungal Effectors in <i>Fusarium oxysporum</i> with Wilt Symptoms in Soybean. <i>Phytopathology</i> , 2016, 106, 762-773.	1.1	12
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3769	Genetic diversity and population structure of common walnut ( <i>Juglans regia</i> ) in China based on EST-SSRs and the nuclear gene phenylalanine ammonia-lyase (PAL). <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	47
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3778	Association between <i>RAPH1</i> Gene Haplotypes and <i>CHE2</i> Locus Phenotypes. <i>Annals of Human Genetics</i> , 2016, 80, 203-209.	0.3	2
3779	Dispersal and genetic structure of <i>Boccardia polybranchia</i> and <i>Polydora hoplura</i> (Annelida:). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662 To</i>	1.7	21
3780	Identification of two lineages of host-associated eriophyoid mites predisposed to different levels of host diversification. <i>Molecular Phylogenetics and Evolution</i> , 2016, 105, 235-240.	1.2	20
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3787	A Community of Clones: Snow Algae Are Diverse Communities of Spatially Structured Clones. <i>International Journal of Plant Sciences</i> , 2016, 177, 432-439.	0.6	52
3788	Species distributions represent intraspecific genetic diversity of freshwater fish in conservation assessments. <i>Freshwater Biology</i> , 2016, 61, 1707-1719.	1.2	12
3789	Mitochondrial DNA control region haplotype and haplogroup diversity in South Eastern Turkey. <i>Forensic Science International: Genetics</i> , 2016, 24, 176-179.	1.6	16
3790	On the Bantu expansion. <i>Gene</i> , 2016, 593, 48-57.	1.0	4
3791	RAD SNP markers as a tool for conservation of dolphinfish <i>Coryphaena hippurus</i> in the Mediterranean Sea: Identification of subtle genetic structure and assessment of populations sex-ratios. <i>Marine Genomics</i> , 2016, 28, 57-62.	0.4	15
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3794	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

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3796	The mitochondrial DNA makeup of Romanians: A forensic mtDNA control region database and phylogenetic characterization. <i>Forensic Science International: Genetics</i> , 2016, 24, 136-142.	1.6	20
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3798	A tug-of-war between tolerance and rejection – New evidence for 3'UTR HLA-G haplotypes influence in recurrent pregnancy loss. <i>Human Immunology</i> , 2016, 77, 892-897.	1.2	25
3799	Contrasting levels of strays and contemporary gene flow among anadromous populations of Arctic charr, <i>Salvelinus alpinus</i> (L.), in northern Norway. <i>Hydrobiologia</i> , 2016, 783, 269-281.	1.0	8
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3801	Effects of Pleistocene climate changes on species ranges and evolutionary processes in the Neotropical Atlantic Forest. <i>Biological Journal of the Linnean Society</i> , 2016, 119, 856-872.	0.7	91
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3805	Genetic structure in two <i>Phascolosoma</i> species in the Pacific Ocean. <i>Marine Biology Research</i> , 2016, 12, 739-747.	0.3	4
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3810	Present-Day Genetic Structure of the Holoparasite <i>Conopholis americana</i> (Orobanchaceae) in Eastern North America and the Location of Its Refugia during the Last Glacial Cycle. <i>International Journal of Plant Sciences</i> , 2016, 177, 132-144.	0.6	4
3811	Genetic structuring in a relictual population of screaming hairy armadillo ( <i>Chaetophractus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf,50 102 Td	0.5	7
3812	Genetic analyses reveal high levels of seed and pollen flow in hawthorn ( <i>Crataegus monogyna</i> Jacq.), a key component of hedgerows. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	16

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3814	Population genetics of Atlantic bluefin tuna, <i>Thunnus thynnus</i> (Linnaeus, 1758), in the Mediterranean: implications for its conservation management. <i>Journal of Applied Ichthyology</i> , 2016, 32, 523-531.	0.3	12
3815	Phylogeographic insights into the invasion history and secondary spread of the signal crayfish in Japan. <i>Ecology and Evolution</i> , 2016, 6, 5366-5382.	0.8	13
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3817	Genetic polymorphisms study of pharmacogenomic VIP variants in Han ethnic of China's Shaanxi province. <i>Environmental Toxicology and Pharmacology</i> , 2016, 46, 27-35.	2.0	8
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3821	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
3822	ISO 17025 validation of a next-generation sequencing assay for relationship testing. <i>Electrophoresis</i> , 2016, 37, 2822-2831.	1.3	52
3823	The Genetic Signature of Range Expansion in a Disease Vector—The Black-Legged Tick. <i>Journal of Heredity</i> , 2017, 108, esw073.	1.0	9
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3825	RNF213 Is Associated with Intracranial Aneurysms in the French-Canadian Population. <i>American Journal of Human Genetics</i> , 2016, 99, 1072-1085.	2.6	49
3826	Occurrence of islands in genomes of <i>Sinorhizobium meliloti</i> native isolates. <i>Russian Journal of Genetics</i> , 2016, 52, 1015-1022.	0.2	3
3827	Assessment of genetic diversity in natural European hophornbeam ( <i>Ostrya carpinifolia</i> Scop.) populations in Turkey. <i>Biotechnology and Biotechnological Equipment</i> , 2016, 30, 948-955.	0.5	1
3828	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
3829	Population genetic structure and post-LGM expansion of the plant bug <i>Nesidiocoris tenuis</i> (Hemiptera: Tj ETQq0 0.0 rgBT /Overlock 10	1.6	16
3830	Genetic diversity and population differentiation of small giant clam <i>Tridacna maxima</i> in Comoros islands assessed by microsatellite markers. <i>SpringerPlus</i> , 2016, 5, 1852.	1.2	5

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3832	Morphological and molecular variation among populations of tidewater ( <i>Menidia peninsulae</i> ) and inland ( <i>M. beryllina</i> ) silversides: insight into drivers of adaptation and speciation of silverside fishes. Environmental Biology of Fishes, 2016, 99, 857-871.	0.4	5
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3835	Genetic variation assessed with microsatellites in mass selection lines of the Pacific oyster ( <i>Crassostrea gigas</i> ) in China. Journal of Ocean University of China, 2016, 15, 1039-1045.	0.6	11
3836	Inter- and intra-genetic diversity in the Polish Konik horse: implications for the conservation program. Canadian Journal of Animal Science, 2016, 96, 570-580.	0.7	10
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3838	Population structure and conservation genetics of anadromous white-spotted char ( <i>Salvelinus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 2016, 99, 513-525.	0.4	6
3839	Genetic variation and population structure of the oriental fruit moth <i>Grapholita molesta</i> in Shanxi, a major pome fruits growing region in North China. Journal of Asia-Pacific Entomology, 2016, 19, 1131-1137.	0.4	2
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3841	Subtle genetic population structure in Pacific halibut <i>Hippoglossus stenolepis</i> . Journal of Fish Biology, 2016, 89, 2571-2594.	0.7	7
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3843	Genetic diversity patterns of the orchid <i>Anacamptis pyramidalis</i> at the edges of its distribution range. Plant Systematics and Evolution, 2016, 302, 1227-1238.	0.3	6
3844	Genetic Diversity in Gorkhas: an Autosomal STR Study. Scientific Reports, 2016, 6, 32494.	1.6	17
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3847	Intrapopulation genomics in a model mutualist: Population structure and candidate symbiosis genes under selection in <i>Medicago truncatula</i> . Evolution; International Journal of Organic Evolution, 2016, 70, 2704-2717.	1.1	16
3848	Genetic structure and diversity in an isolated population of an endemic mole salamander ( <i>Ambystoma</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 15	0.5	15

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3850	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
3851	Contrasted levels of genetic diversity in a benthic Mediterranean octocoral: Consequences of different demographic histories?. <i>Ecology and Evolution</i> , 2016, 6, 8665-8678.	0.8	20
3852	Survey of genetic diversity and seed germination rates of the southeastern endemic <i>Symphyotrichum georgianum</i> (Alexander) G.L. Nesom (Asteraceae) from large and small populations <sup>1,2</sup> . <i>Journal of the Torrey Botanical Society</i> , 2016, 143, 274.	0.1	1
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3854	Ancient DNA reveals selection acting on genes associated with hypoxia response in pre-Columbian Peruvian Highlanders in the last 8500 years. <i>Scientific Reports</i> , 2016, 6, 23485.	1.6	26
3855	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
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3857	Geographical distance and barriers explain population genetic patterns in an endangered island perennial. <i>AoB PLANTS</i> , 2016, 8, plw072.	1.2	16
3858	Genetic characterization and population genetic structure of the Antarctic minke whale <i>Balaenoptera bonaerensis</i> in the Indo-Pacific region of the Southern Ocean. <i>Fisheries Science</i> , 2016, 82, 873-886.	0.7	9
3859	Anthropogenic Stressors Shape Genetic Structure: Insights from a Model Freshwater Population along a Land Use Gradient. <i>Environmental Science &amp; Technology</i> , 2016, 50, 11346-11356.	4.6	36
3860	Global population divergence and admixture of the brown rat ( <i>Rattus norvegicus</i> ). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161762.	1.2	119
3861	Population structure and genetic diversity of <i>Lithocarpus litseifolius</i> (Fagaceae) assessed using microsatellite markers. <i>Nordic Journal of Botany</i> , 2016, 34, 752-760.	0.2	2
3862	Contrasting patterns of selection between <i>MHC</i> I and <i>II</i> across populations of Humboldt and Magellanic penguins. <i>Ecology and Evolution</i> , 2016, 6, 7498-7510.	0.8	13
3863	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
3864	Genetic Ancestry and Natural Selection Drive Population Differences in Immune Responses to Pathogens. <i>Cell</i> , 2016, 167, 657-669.e21.	13.5	419
3865	Genetic Variations of the Parasitic Dinoflagellate <i>Hematodinium</i> Infecting Cultured Marine Crustaceans in China. <i>Protist</i> , 2016, 167, 597-609.	0.6	4
3866	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



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3867	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
3868	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
3869	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
3870	Detecting a hierarchical genetic population structure via Multi-InDel markers on the X chromosome. <i>Scientific Reports</i> , 2016, 6, 32178.	1.6	16
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3872	Genetic variation in the massive coral <i>Porites lobata</i> . <i>Marine Biology</i> , 2016, 163, 1.	0.7	5
3873	Evolutionary potential and adaptation of <i>Banksia attenuata</i> (Proteaceae) to climate and fire regime in southwestern Australia, a global biodiversity hotspot. <i>Scientific Reports</i> , 2016, 6, 26315.	1.6	8
3874	Morphological and genetic characterisation of Pagliarola breed and its genetic relationships with other three indigenous Italian sheep breeds. <i>Italian Journal of Animal Science</i> , 2016, 15, 47-54.	0.8	5
3875	Population genetic structure and demographic history of <i>Streptococcus mutans</i> (Bacteria). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4</i>	0.7	1
3876	Biomass traits and candidate genes for bioenergy revealed through association genetics in coppiced European <i>Populus nigra</i> (L.). <i>Biotechnology for Biofuels</i> , 2016, 9, 195.	6.2	36
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3878	Multispecies assessment of genetic differentiation of aquatic insects in intermittent river revealed by next-generation sequencing. <i>Journal of Japan Society of Civil Engineers Ser G (Environmental)</i> <i>Tj ETQq1 1 0.784314rgBT /Overlock 10 Tf 50 4</i>	0.7	1
3879	Are migratory behaviours of bats socially transmitted?. <i>Royal Society Open Science</i> , 2016, 3, 150658.	1.1	8
3880	Genetic structure of remnant black poplar ( <i>Populus nigra</i> L.) populations along biggest rivers in Serbia assessed by SSR markers. <i>Silvae Genetica</i> , 2016, 65, 12-19.	0.4	7
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3922	Genomic scanning using <i>scn</i> AFLP to detect loci under selection in the moss <i>Funaria hygrometrica</i> along a climate gradient in the Sierra Nevada Mountains, Spain. <i>Plant Biology</i> , 2016, 18, 280-288.	1.8	27
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3927	Long-term persisting hybrid swarm and geographic difference in hybridization pattern: genetic consequences of secondary contact between two <i>Vincetoxicum</i> species (Apocynaceae "Asclepiadoideae"). <i>BMC Evolutionary Biology</i> , 2016, 16, 20.	3.2	11
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3931	Evidence for adaptation of porcine Toll-like receptors. <i>Immunogenetics</i> , 2016, 68, 179-189.	1.2	7
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3935	Diverse rates of gene flow and long-distance migration in two moose <i>Alces alces</i> subpopulations in Europe. <i>Mammal Research</i> , 2016, 61, 171-178.	0.6	11
3936	Mitochondrial DNA variations in Korean <i>Apis cerana</i> (Hymenoptera: Apidae) and development of another potential marker. <i>Apidologie</i> , 2016, 47, 123-134.	0.9	13
3937	Mitochondrial DNA genetic diversity of honey bees, <i>Apis mellifera</i> , in Hawaii. <i>Apidologie</i> , 2016, 47, 679-687.	0.9	12
3938	Imbalanced presence of <i>Borrelia burgdorferi</i> s.l. multilocus sequence types in clinical manifestations of Lyme borreliosis. <i>Infection, Genetics and Evolution</i> , 2016, 42, 66-76.	1.0	59
3939	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

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3948	Genetic polymorphism of 22 autosomal STR markers in a Han population of Southern China. Forensic Science International: Genetics, 2016, 24, e14-e16.	1.6	18
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3954	Analysis of the genetic structure of allopatric populations of <i>Lutzomyia umbratilis</i> using the period clock gene. Acta Tropica, 2016, 154, 149-154.	0.9	10
3955	Genetic diversity of the red-spotted tokay gecko ( <i>Gekko gecko</i> Linnaeus, 1758) (Squamata: Gekkonidae) in Southeast Asia determined with multilocus enzyme electrophoresis. Journal of Asia-Pacific Biodiversity, 2016, 9, 63-68.	0.2	6
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3968	Connectivity of the squat lobsters <i>Shinkaia crosnieri</i> (Crustacea: Decapoda:)	0.4	24
3969	The genetic landscape of <i>Ceratocystis albifundus</i> populations in South Africa reveals a recent fungal introduction event. <i>Fungal Biology</i> , 2016, 120, 690-700.	1.1	37
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3972	Genetic structure of island and mainland populations of a Neotropical bumble bee species. <i>Journal of Insect Conservation</i> , 2016, 20, 383-394.	0.8	18
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3977	Genetic diversity of widespread moss-dwelling nematode species in German beech forests. <i>European Journal of Soil Biology</i> , 2016, 74, 23-31.	1.4	11
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3988	Population genetic structure and temporal stability among <i>Trypanosoma brucei rhodesiense</i> isolates in Uganda. <i>Parasites and Vectors</i> , 2016, 9, 259.	1.0	7
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3996	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
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3998	Geographic independence and phylogenetic diversity of red shiner introductions. <i>Conservation Genetics</i> , 2016, 17, 795-809.	0.8	7
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4000	Signatures of natural selection on <i>Pinus cembra</i> and <i>P. mugo</i> along elevational gradients in the Alps. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	22
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4007	Demographic history and adaptation account for clock gene diversity in humans. <i>Heredity</i> , 2016, 117, 165-172.	1.2	9
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4009	Geographic variation, null hypotheses, and subspecies limits in the California Gnatcatcher: A response to McCormack and Maley. <i>Auk</i> , 2016, 133, 59-68.	0.7	14
4010	<i>HLA-A</i> , <i>HLA-B</i> , <i>HLA-C</i> , <i>DRB1</i> allele and haplotype frequencies of 14529 Chinese Han bone marrow donors living in Dalian, China. <i>International Journal of Immunogenetics</i> , 2016, 43, 79-85.	0.8	6
4011	Shaped by uneven Pleistocene climate: mitochondrial phylogeographic pattern and population history of white wagtail <i>Motacilla alba</i> (Aves: Passeriformes). <i>Journal of Avian Biology</i> , 2016, 47, 263-274.	0.6	21

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4014	Tracking changes in chromosomal arrangements and their genetic content during adaptation. <i>Journal of Evolutionary Biology</i> , 2016, 29, 1151-1167.	0.8	16
4015	Genetic divergence and isolation by thermal environment in geothermal populations of an aquatic invertebrate. <i>Journal of Evolutionary Biology</i> , 2016, 29, 1701-1712.	0.8	16
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4018	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
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4021	Genomic survey provides insights into the evolutionary changes that occurred during European expansion of the invasive mosquitofish ( <i>Gambusia holbrooki</i> ). <i>Molecular Ecology</i> , 2016, 25, 1089-1105.	2.0	38
4022	New view of population genetics of zooplankton: $\text{RAD-seq}$ analysis reveals population structure of the North Atlantic planktonic copepod <i>Centropages typicus</i> . <i>Molecular Ecology</i> , 2016, 25, 1566-1580.	2.0	56
4023	Selection against recombinant hybrids maintains reproductive isolation in hybridizing <i>Populus</i> species despite $F_1$ fertility and recurrent gene flow. <i>Molecular Ecology</i> , 2016, 25, 2482-2498.	2.0	95
4024	Amphibian-killing chytrid in Brazil comprises both locally endemic and globally expanding populations. <i>Molecular Ecology</i> , 2016, 25, 2978-2996.	2.0	82
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4027	Strong dispersal in a parasitoid wasp overwhelms habitat fragmentation and host population dynamics. <i>Molecular Ecology</i> , 2016, 25, 3344-3355.	2.0	18
4028	Narrow endemics on coastal plains: Miocene divergence of the critically endangered genus <i>Avellara</i> (Compositae). <i>Plant Biology</i> , 2016, 18, 729-738.	1.8	16
4029	Molecular phylogeography of white-lipped tree viper ( <i>Trimeresurus</i> ; Viperidae). <i>Zoologica Scripta</i> , 2016, 45, 252-262.	0.7	17

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4031	Contrasting phylogeographic signatures in two Australo-Papuan bowerbird species complexes (Aves: Tj ETQq1 1.0, 784314, rgBT / Over 2F	0.7	21
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4033	Genetic diversity of reef fishes around Cuba: a multispecies assessment. <i>Marine Biology</i> , 2016, 163, 1.	0.7	4
4034	Phenotypic and Molecular Assessment of Drug Resistance Profile and Genetic Diversity of Waterborne <i>Escherichia coli</i> . <i>Water, Air, and Soil Pollution</i> , 2016, 227, 146.	1.1	20
4035	Low genetic variability of the edible dormouse ( <i>Glis glis</i> ) in Stolowe Mountains National Park (Poland) – preliminary results. <i>Mammal Research</i> , 2016, 61, 409-415.	0.6	7
4036	HLA-A, -B, -C, -DRB1 and -DQB1 allele and haplotype frequencies in a population of 432 healthy unrelated individuals from Albania. <i>Human Immunology</i> , 2016, 77, 620-621.	1.2	8
4037	An integrated linkage map reveals candidate genes underlying adaptive variation in Chinook salmon ( <i>Oncorhynchus tshawytscha</i> ). <i>Molecular Ecology Resources</i> , 2016, 16, 769-783.	2.2	49
4038	Spatially explicit summary statistics for historical population genetic inference. <i>Methods in Ecology and Evolution</i> , 2016, 7, 418-427.	2.2	21
4039	Recent and rapid diversification of the small carpenter bees in eastern North America. <i>Biological Journal of the Linnean Society</i> , 2016, 117, 633-645.	0.7	28
4040	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
4041	Molecular phylogeny and DNA barcoding confirm cryptic species in the African freshwater oyster <i>Etheria elliptica</i> Lamarck, 1807 (Bivalvia: Etheriidae). <i>Biological Journal of the Linnean Society</i> , 2016, 118, 369-381.	0.7	20
4042	Temporal and spatial mosaics: deep host association and shallow geographic drivers shape genetic structure in a widespread pinworm, <i>Rauschtneria eutamii</i> (Nematoda: Oxyuridae). <i>Biological Journal of the Linnean Society</i> , 2016, 119, 397-413.	0.7	10
4043	Strong signature of selection in seeder populations but not in resprouters of the fynbos heath <i>Erica coccinea</i> (Ericaceae). <i>Botanical Journal of the Linnean Society</i> , 2016, 181, 115-126.	0.8	7
4044	Census and effective population sizes of white-spotted charr ( <i>Salvelinus leucomaenis</i> ) in a fragmented landscape. <i>Ecology of Freshwater Fish</i> , 2016, 25, 612-621.	0.7	6
4045	Phenotypic shifts in urban areas in the tropical lizard <i>Anolis cristatellus</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1009-1022.	1.1	162
4046	Evolutionary history and population genetic structure of the endemic tree frog <i>Hyla tsinlingensis</i> (Amphibia: Anura: Hylidae) inferred from mitochondrial gene analysis. <i>Mitochondrial DNA</i> , 2016, 27, 1348-1357.	0.6	6
4047	DNA barcode based wildlife forensics for resolving the origin of claw samples using a novel primer cocktail. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3932-3935.	0.7	13

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4049	Genetic monitoring of deep-water exploited banks of the precious Sardinia coral <i>Corallium rubrum</i> (L., 1758): useful data for a sustainable management. Aquatic Conservation: Marine and Freshwater Ecosystems, 2016, 26, 236-250.	0.9	26
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4051	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
4052	The Global AIMs Nano set: A 31-plex SNaPshot assay of ancestry-informative SNPs. Forensic Science International: Genetics, 2016, 22, 81-88.	1.6	57
4053	Effective number of breeders, effective population size and their relationship with census size in an iteroparous species, <i>Salvelinus fontinalis</i> . Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20152601.	1.2	47
4054	Do hatchery-reared sea urchins pose a threat to genetic diversity in wild populations?. Heredity, 2016, 116, 378-383.	1.2	17
4055	Multi-locus genotyping reveals absence of genetic structure in field populations of the brown ear tick ( <i>Rhipicephalus appendiculatus</i> ) in Kenya. Ticks and Tick-borne Diseases, 2016, 7, 26-35.	1.1	17
4056	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
4057	Performing monkeys of Bangladesh: characterizing their source and genetic variation. Primates, 2016, 57, 221-230.	0.7	3
4058	Phylogeography of a widespread species: pre-glacial vicariance, refugia, occasional blocking straits and long-distance migrations. AoB PLANTS, 2016, 8, .	1.2	16
4059	Predicting the genetic consequences of future climate change: The power of coupling spatial demography, the coalescent, and historical landscape changes. American Journal of Botany, 2016, 103, 153-163.	0.8	43
4060	Genetic analysis of 17 Y-STR loci in Han and Korean populations from Jilin Province, Northeast China. Forensic Science International: Genetics, 2016, 22, 8-10.	1.6	21
4061	Geographic patterns of genetic diversity in two species complexes of Canadian marine bivalves. Journal of Molluscan Studies, 2016, 82, 282-291.	0.4	13
4062	Origin and introduction history of self-sustaining rainbow trout populations in Europe as inferred from mitochondrial DNA and a Y-linked marker. Hydrobiologia, 2016, 770, 129-144.	1.0	7
4063	Cryptic species of cardinalfish with evidence for old and new divergence. Coral Reefs, 2016, 35, 437-450.	0.9	8
4064	The application of genomics to inform conservation of a functionally important reef fish ( <i>Scarus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 1	0.8	19
4065	Geographic population structure and subspecific boundaries in a tidal marsh sparrow. Conservation Genetics, 2016, 17, 603-613.	0.8	7

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4067	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
4068	Should ecomorphs be conserved? The case of <i>Nostoc flagelliforme</i> , an endangered extremophile cyanobacteria. <i>Journal for Nature Conservation</i> , 2016, 30, 52-64.	0.8	19
4070	A comparative study of insertion/deletion polymorphisms applied among Southwest, South and Northwest Chinese populations using Investigator® DIPlex. <i>Forensic Science International: Genetics</i> , 2016, 21, 10-14.	1.6	45
4071	High-quality mtDNA control region sequences from 680 individuals sampled across the Netherlands to establish a national forensic mtDNA reference database. <i>Forensic Science International: Genetics</i> , 2016, 21, 158-167.	1.6	20
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4073	Identification of a major Quantitative Trait Locus determining resistance to the organophosphate temephos in the dengue vector mosquito <i>Aedes aegypti</i> . <i>Genomics</i> , 2016, 107, 40-48.	1.3	17
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4075	Comparative phylogeography of the western Indian Ocean reef fauna. <i>Acta Oecologica</i> , 2016, 72, 72-86.	0.5	35
4076	Molecular characterization and phylogenetic analysis of <i>Fasciola hepatica</i> from Peru. <i>Parasitology International</i> , 2016, 65, 171-174.	0.6	21
4077	Analysis of 24 Y-STR haplotype data in a Chinese Han population from Guangdong Province. <i>International Journal of Legal Medicine</i> , 2016, 130, 689-691.	1.2	7
4078	Genetic and morphological differences among the three species of the genus <i>Rastrelliger</i> (Perciformes: Scombridae). <i>Ichthyological Research</i> , 2016, 63, 275-287.	0.5	9
4079	Geographic variation in bird songs: examination of the effects of sympatric related species on the acoustic structure of songs. <i>Acta Ethologica</i> , 2016, 19, 81-90.	0.4	15
4080	Phylogeography, Genetic Diversity, and Management Units of Hawksbill Turtles in the Indo-Pacific. <i>Journal of Heredity</i> , 2016, 107, 199-213.	1.0	49
4081	High genetic diversity but low population structure in the frog <i>Pseudopaludicola falcipes</i> (Hensel, 1916). <i>Journal of Herpetology</i> , 2016, 50, 137-151.	1.2	22
4082	Cellar-Associated <i>Saccharomyces cerevisiae</i> Population Structure Revealed High-Level Diversity and Perennial Persistence at Sauternes Wine Estates. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2909-2918.	1.4	66
4083	Isolation, characterization and multiplex PCR development of Bean Goose ( <i>Anser fabalis</i> ) microsatellite loci. <i>Journal of Ornithology</i> , 2016, 157, 641-646.	0.5	5
4084	Analysis of ANKK1 (rs1800497) and DRD2 (rs1079597, rs1800498) variants in five ethnic groups from Punjab, North-West India. <i>Gene</i> , 2016, 584, 69-74.	1.0	10



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4086	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
4087	Genetic distribution of 15 autosomal STR markers in the Punjabi population of Pakistan. <i>International Journal of Legal Medicine</i> , 2016, 130, 1487-1488.	1.2	7
4088	Genetic structure of a disjunct peripheral population of mountain sucker <i>Pantosteus jordani</i> in the Black Hills, South Dakota, USA. <i>Conservation Genetics</i> , 2016, 17, 775-784.	0.8	2
4089	Population Structure of <i>Candida albicans</i> from Three Teaching Hospitals in Ghana. <i>Medical Mycology</i> , 2016, 54, 197-206.	0.3	3
4090	Stable populations in unstable habitats: temporal genetic structure of the introduced ascidian <i>Styela plicata</i> in North Carolina. <i>Marine Biology</i> , 2016, 163, 1.	0.7	20
4091	Fine-scale patterns of genetic variation in a widespread clonal seagrass species. <i>Marine Biology</i> , 2016, 163, 1.	0.7	23
4092	An integrated genetic and morphological approach to clarify the conservation status of the threatened Italian endemic species <i>Alburnus albidus</i> (Cypriniformes: Cyprinidae). <i>Hydrobiologia</i> , 2016, 770, 73-87.	1.0	6
4093	Geographic origins and population genetics of bats killed at windâ€¦energy facilities. <i>Ecological Applications</i> , 2016, 26, 1381-1395.	1.8	28
4094	Genetic diversity and structure of the globally invasive tree, <i>Paraserianthes lophantha</i> subspecies <i>lophantha</i> , suggest an introduction history characterised by varying propagule pressure. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	7
4095	Red River barrier and Pleistocene climatic fluctuations shaped the genetic structure of <i>Microhyla fissipes</i> complex (Anura: Microhylidae) in southern China and Indochina. <i>Environmental Epigenetics</i> , 2016, 62, 531-543.	0.9	47
4096	Population genomics of divergence among extreme and intermediate color forms in a polymorphic insect. <i>Ecology and Evolution</i> , 2016, 6, 1075-1091.	0.8	31
4097	High genetic diversity of common toad ( <i>Bufo bufo</i> ) populations under strong natural fragmentation on a northern archipelago. <i>Ecology and Evolution</i> , 2016, 6, 1626-1636.	0.8	13
4098	Toxicity and population structure of the Roughâ€¦skinned Newt ( <i>Taricha granulosa</i> ) outside the range of an arms race with resistant predators. <i>Ecology and Evolution</i> , 2016, 6, 2714-2724.	0.8	18
4099	Evolution in situ: hybrid origin and establishment of willows ( <i>Salix</i> L.) on alpine glacier forefields. <i>Heredity</i> , 2016, 116, 531-541.	1.2	35
4100	Lifeâ€¦history traits and geographical divergence in wild rice ( <i>Oryza rufipogon</i> ) gene pool in Indochina Peninsula region. <i>Annals of Applied Biology</i> , 2016, 168, 52-65.	1.3	5
4101	Ecological and historical determinants of population genetic structure and diversity in the Mediterranean shrub <i>Rosmarinus officinalis</i> (Lamiaceae). <i>Botanical Journal of the Linnean Society</i> , 2016, 180, 50-63.	0.8	17
4102	Reduced genetic diversity and increased reproductive isolation follow population-level loss of larval dispersal in a marine gastropod. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 18-37.	1.1	25

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4103	The role of fire and a long-lived soil seed bank in maintaining persistence, genetic diversity and connectivity in a fire-prone landscape. <i>Journal of Biogeography</i> , 2016, 43, 70-84.	1.4	13
4104	Phylogeographic analysis of the brown alga <i>Cutleria multifida</i> ( <i>Chlorophyta</i> , <i>Chlorophyceae</i> ) suggests a complicated introduction history. <i>Phycological Research</i> , 2016, 64, 3-10.	0.8	6
4105	Extreme genetic diversity in asexual grass thrips populations. <i>Journal of Evolutionary Biology</i> , 2016, 29, 887-899.	0.8	18
4106	Intraspecific Variation in <i>Antherina suraka</i> (Lepidoptera: Saturniidae), an Endemic Resident of Endangered Forests in Madagascar. <i>Annals of the Entomological Society of America</i> , 2016, 109, 384-395.	1.3	1
4107	The Genetic History of Peruvian Quechua <i>Lamias</i> and Chankas: Uniparental DNA Patterns among Autochthonous Amazonian and Andean Populations. <i>Annals of Human Genetics</i> , 2016, 80, 88-101.	0.3	29
4108	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
4109	The importance of effective sampling for exploring the population dynamics of haploid-diploid seaweeds. <i>Journal of Phycology</i> , 2016, 52, 1-9.	1.0	25
4110	Morphology, molecules and taxonomy: extreme incongruence in pleurocerids ( <i>Gastropoda</i> , <i>Cerithioidea</i> , <i>Pleuroceridae</i> ). <i>Zoologica Scripta</i> , 2016, 45, 62-87.	0.7	23
4111	Population differentiation at a regional scale in spadefoot toads: contributions of distance and divergent selective environments. <i>Environmental Epigenetics</i> , 2016, 62, 193-206.	0.9	4
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4113	Genetic predisposition in patients with hypertension and normal ejection fraction to oxidative stress. <i>Journal of the American Society of Hypertension</i> , 2016, 10, 124-132.	2.3	8
4114	Y Chromosome STR haplotypes in different ethnic groups of Vietnam. <i>Forensic Science International: Genetics</i> , 2016, 22, e18-e20.	1.6	7
4115	Demographic history and asynchronous spawning shape genetic differentiation among populations of the hard coral <i>Acropora tenuis</i> in Western Australia. <i>Molecular Phylogenetics and Evolution</i> , 2016, 98, 89-96.	1.2	20
4116	Understanding intra and inter-archipelago population genetic patterns within a recently evolved insular endemic lineage. <i>Plant Systematics and Evolution</i> , 2016, 302, 367-384.	0.3	20
4117	Genetic diversity and spatial genetic structure of African wild dogs ( <i>Lycaon pictus</i> ) in the Greater Limpopo transfrontier conservation area. <i>Conservation Genetics</i> , 2016, 17, 785-794.	0.8	13
4118	High levels of genetic diversity and population structure in an endemic and rare species: implications for conservation. <i>AoB PLANTS</i> , 2016, 8, .	1.2	52
4119	Low genetic diversity, restricted dispersal, and elevation-specific patterns of population decline in American pikas in an atypical environment. <i>Journal of Mammalogy</i> , 2016, 97, 464-472.	0.6	21
4120	Local habitat condition rather than geographic distance determines the genetic structure of <i>Tamarix chinensis</i> populations in Yellow River Delta, China. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	11

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4122	Responses of plants to changes in Qinghai-Tibetan Plateau and glaciations: Evidence from phylogeography of a <i>Sibiraea</i> (Rosaceae) complex. <i>Biochemical Systematics and Ecology</i> , 2016, 65, 72-82.	0.6	22
4123	Genetic stock compositions and natal origin of green turtle ( <i>Chelonia mydas</i> ) foraging at Brunei Bay. <i>Global Ecology and Conservation</i> , 2016, 6, 16-24.	1.0	23
4124	Association of HLA-G untranslated region variants with type 1 diabetes mellitus. <i>Human Immunology</i> , 2016, 77, 358-364.	1.2	20
4125	Genetic connectivity and self-replenishment of inshore and offshore populations of the endemic anemonefish, <i>Amphiprion latezonatus</i> . <i>Coral Reefs</i> , 2016, 35, 959-970.	0.9	7
4126	Genetic population structure and low genetic diversity in the over-exploited sea cucumber <i>Holothuria edulis</i> Lesson, 1830 (Echinodermata: Holothuroidea) in Okinawa Island. <i>Conservation Genetics</i> , 2016, 17, 811-821.	0.8	22
4127	Allele frequencies for fifteen autosomal STR loci in a Nakhi population from Yunnan Province, Southwest China. <i>Forensic Science International: Genetics</i> , 2016, 21, e13-e14.	1.6	10
4128	Population genetic analysis of the GlobalFiler STR loci in 748 individuals from the Kazakh population of Xinjiang in northwest China. <i>International Journal of Legal Medicine</i> , 2016, 130, 1187-1189.	1.2	27
4129	Genetic diversity and conservation status of managed vicuña ( <i>Vicugna vicugna</i> ) populations in Argentina. <i>Genetica</i> , 2016, 144, 85-97.	0.5	9
4130	Low Major Histocompatibility Complex Class II Variation in the Endangered Indo-Pacific Humpback Dolphin ( <i>Sousa chinensis</i> ): Inferences About the Role of Balancing Selection. <i>Journal of Heredity</i> , 2016, 107, 143-152.	1.0	34
4131	Ancient, but not recent, population declines have had a genetic impact on alpine yellow-bellied toad populations, suggesting potential for complete recovery. <i>Conservation Genetics</i> , 2016, 17, 727-743.	0.8	6
4132	Levels of genetic diversity and taxonomic status of <i>Epinephelus</i> species in United Arab Emirates fish markets. <i>Marine Pollution Bulletin</i> , 2016, 105, 540-545.	2.3	9
4133	High resolution SNPs selection in <i>Engraulis encrasicolus</i> through Taqman OpenArray. <i>Fisheries Research</i> , 2016, 177, 31-38.	0.9	9
4134	Genetic analysis of 17 Y-STR loci in Han population from Shandong Province in East China. <i>Forensic Science International: Genetics</i> , 2016, 22, e15-e17.	1.6	14
4135	Great ape Y Chromosome and mitochondrial DNA phylogenies reflect subspecies structure and patterns of mating and dispersal. <i>Genome Research</i> , 2016, 26, 427-439.	2.4	27
4136	Phylogeography of <i>Cnesterodon decemmaculatus</i> (Cyprinodontiformes: poeciliidae) in Southern Pampas, Argentina: ancient versus recent patterns in freshwater fishes. <i>Environmental Biology of Fishes</i> , 2016, 99, 293-307.	0.4	13
4137	Predictable allele frequency changes due to habitat fragmentation in the Glanville fritillary butterfly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2678-2683.	3.3	66
4138	Genetic Correlates of Individual Differences in Sleep Behavior of Free-Living Great Tits ( <i>Parus</i> ). <i>Trends in Ecology and Evolution</i> , 2016, 31, 107-114.	0.8	16

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4139	Genetic diversity and hybridization in the two species <i>Inga ingoides</i> and <i>Inga edulis</i> : potential applications for agroforestry in the Peruvian Amazon. <i>Annals of Forest Science</i> , 2016, 73, 425-435.	0.8	9
4140	Habitat quality limits gene flow between populations of <i>Bombus ruderus</i> in the South Island, New Zealand. <i>Conservation Genetics</i> , 2016, 17, 703-713.	0.8	4
4141	Comprehensive Screening for Naturally Occurring Hepatitis C Virus Resistance to Direct-Acting Antivirals in the NS3, NS5A, and NS5B Genes in Worldwide Isolates of Viral Genotypes 1 to 6. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 2402-2416.	1.4	52
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4143	Genetic variability and structure of jaguar ( <i>Panthera onca</i> ) in Mexican zoos. <i>Genetica</i> , 2016, 144, 59-69.	0.5	9
4144	DEFB1 polymorphisms and susceptibility to recurrent tonsillitis in Italian children. <i>International Journal of Pediatric Otorhinolaryngology</i> , 2016, 83, 12-15.	0.4	6
4145	Pleistocene events and present environmental factors have shaped the phylogeography of the intertidal limpet <i>Cellana toreuma</i> (Reeve, 1855) (Gastropoda: Nacellidae) in Southeast Asia and China. <i>Journal of Molluscan Studies</i> , 2016, 82, 378-390.	0.4	13
4146	Invader or resident? Ancient-DNA reveals rapid species turnover in New Zealand little penguins. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20152879.	1.2	22
4147	Postglacial expansion pathways of red mangrove, <i>Rhizophora mangle</i> , in the Caribbean Basin and Florida. <i>American Journal of Botany</i> , 2016, 103, 260-276.	0.8	41
4148	Genetic consequences of allopatric and sympatric divergence in Arctic charr ( <i>Salvelinus alpinus</i> (L.)) from Fjellfr�svatn as inferred by microsatellite markers. <i>Hydrobiologia</i> , 2016, 783, 257-267.	1.0	11
4149	The phylogenetic diversity of <i>Spirometra erinaceieuropaei</i> isolates from southwest China revealed by multi genes. <i>Acta Tropica</i> , 2016, 156, 108-114.	0.9	25
4150	Forensic and population genetic analysis of Xinjiang Uyghur population on 21 short tandem repeat loci of 6-dye GlobalFiler� PCR Amplification kit. <i>Forensic Science International: Genetics</i> , 2016, 22, 22-24.	1.6	26
4151	Population genetics and ecological niche of invasive <i>Aedes albopictus</i> in Mexico. <i>Acta Tropica</i> , 2016, 157, 30-41.	0.9	29
4152	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
4153	Contrasting and congruent patterns of genetic structuring in two <i>Microtus</i> vole species using museum specimens. <i>Mammal Research</i> , 2016, 61, 141-152.	0.6	17
4154	Effect of major histocompatibility complex haplotype matching by C4 and MICA genotyping on acute graft versus host disease in unrelated hematopoietic stem cell transplantation. <i>Human Immunology</i> , 2016, 77, 176-183.	1.2	7
4155	A rose by any other name: systematics and diversity in the Chilean giant barnacle <i>Austromegabalanus psittacus</i> (Molina, 1782) (Cirripedia). <i>Journal of Crustacean Biology</i> , 2016, 36, 180-188.	0.3	2
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4158	Insights into the Introduction History and Population Genetic Dynamics of the Nile Monitor ( <i>Varanus niloticus</i> ) in Florida. <i>Journal of Heredity</i> , 2016, 107, 349-362.	1.0	7
4159	Malagasy bats shelter a considerable genetic diversity of pathogenic <i>Leptospira</i> suggesting notable host-specificity patterns. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw037.	1.3	40
4160	A genome-wide association study reveals novel elite allelic variations in seed oil content of <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2016, 129, 1203-1215.	1.8	185
4161	Growing Cassava ( <i>Manihot esculenta</i> ) in Mato Grosso, Brazil: Genetic Diversity Conservation in Small-Scale Agriculture. <i>Economic Botany</i> , 2016, 70, 15-28.	0.8	10
4162	Y chromosome haplotype diversity in Mongolic-speaking populations and gene conversion at the duplicated STR DYS385a,b in haplogroup C3-M407. <i>Journal of Human Genetics</i> , 2016, 61, 491-496.	1.1	7
4163	Phylogeographic and population genetic structure of bighorn sheep ( <i>Ovis canadensis</i> ) in North American deserts. <i>Journal of Mammalogy</i> , 2016, 97, 823-838.	0.6	39
4164	Forensic genetic value of a 27 Y-STR loci multiplex (Yfiler® Plus kit) in an Italian population sample. <i>Forensic Science International: Genetics</i> , 2016, 21, e1-e5.	1.6	37
4165	The mitochondrial landscape of African Americans: An examination of more than 2500 control region haplotypes from 22 U.S. locations. <i>Forensic Science International: Genetics</i> , 2016, 22, 139-148.	1.6	10
4166	Genetic evaluation of hatchery stocks of Honmoroko <i>Gnathopogon caerulescens</i> by mitochondrial DNA sequence for stock enhancement. <i>Fisheries Science</i> , 2016, 82, 269-278.	0.7	8
4167	Genetic population structure of the mottled spinefoot <i>Siganus fuscescens</i> in Japan. <i>Fisheries Science</i> , 2016, 82, 289-301.	0.7	3
4168	Substructuring of Scots pine in Europe based on polymorphism at chloroplast microsatellite loci. <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2016, 220, 142-149.	0.6	14
4169	Genetic Structure and Effective Population Sizes in European Red Deer ( <i>Cervus elaphus</i> ) at a Continental Scale: Insights from Microsatellite DNA. <i>Journal of Heredity</i> , 2016, 107, 318-326.	1.0	43
4170	Identification of Korean-specific SNP markers from whole-exome sequencing data. <i>International Journal of Legal Medicine</i> , 2016, 130, 669-677.	1.2	3
4171	Analysis of 27 Y-chromosomal STR haplotypes in a Han population of Henan province, Central China. <i>International Journal of Legal Medicine</i> , 2016, 130, 1191-1194.	1.2	17
4172	Recent expansion and relic survival: Phylogeography of the land snail genus <i>Helix</i> (Mollusca). <i>Tj ETQq1 1 0.784314 192 / Overlock 10 Tf</i>	1.2	19
4173	A SNP panel for identity and kinship testing using massive parallel sequencing. <i>International Journal of Legal Medicine</i> , 2016, 130, 905-914.	1.2	55
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4176	Population data of 24 STRs in Mexican-Mestizo population from Monterrey, Nuevo Leon (Northeast.) <i>Tj ETQq1 1 0.784314 rgBT /Over</i> 2016, 21, e15-e17.	1.6	30
4177	Genetic diversity of the NE Atlantic sea urchin <i>Strongylocentrotus droebachiensis</i> unveils chaotic genetic patchiness possibly linked to local selective pressure. <i>Marine Biology</i> , 2016, 163, 36.	0.7	10
4178	SNP discovery in common bean by restriction-associated DNA (RAD) sequencing for genetic diversity and population structure analysis. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1277-1291.	1.0	18
4179	Genetic analyses of overfished silver kob <i>Argyrosomus inodorus</i> (Scieanidae) stocks along the southern African coast. <i>Fisheries Research</i> , 2016, 176, 100-106.	0.9	8
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4181	Allopatric speciation in the flightless <i>Phoberus capensis</i> (Coleoptera: Trogidae) group, with description of two new species. <i>Insect Systematics and Evolution</i> , 2016, 47, 149-179.	0.2	6
4182	Taxonomic status and origin of the Egyptian weasel ( <i>Mustela subpalmata</i> ) inferred from mitochondrial DNA. <i>Genetica</i> , 2016, 144, 191-202.	0.5	5
4183	A contribution to the phylogeography of <i>Pinctada imbricata radiata</i> (Leach, 1814) (Bivalvia:) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i> <i>Journal of Zoology</i> , 2016, 83, 113-120.	0.6	6
4184	Comparative genetic population structure of three endangered giant clams (Cardiidae: <i>Tridacna</i> species) throughout the Indo-West Pacific: implications for divergence, connectivity and conservation. <i>Journal of Molluscan Studies</i> , 2016, 82, 403-414.	0.4	44
4185	Ecological genomics of mutualism decline in nitrogen-fixing bacteria. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20152563.	1.2	45
4186	Rapid morphological changes, admixture and invasive success in populations of Ring-necked parakeets ( <i>Psittacula krameri</i> ) established in Europe. <i>Biological Invasions</i> , 2016, 18, 1581-1598.	1.2	18
4187	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
4188	Genetic variation of the 20 STRs in Han population from Yunnan-Kweichow plateau of China. <i>Forensic Science International: Genetics</i> , 2016, 23, e10-e11.	1.6	22
4189	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
4190	Methodological assessment of 2b-RAD genotyping technique for population structure inferences in yellowfin tuna ( <i>Thunnus albacares</i> ). <i>Marine Genomics</i> , 2016, 25, 43-48.	0.4	56
4191	Birds, nutrients, and climate change: mtDNA haplotype diversity of Arctic <i>Daphnia</i> on Svalbard revisited. <i>Polar Biology</i> , 2016, 39, 1425-1437.	0.5	8
4192	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



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4195	Myth or relict: Does ancient DNA detect the enigmatic Upland seal?. <i>Molecular Phylogenetics and Evolution</i> , 2016, 97, 101-106.	1.2	15
4196	Nesting phenology, mate choice, and genetic divergence within a partially migratory population of American Kestrels. <i>Auk</i> , 2016, 133, 99-109.	0.7	16
4197	Indigenous Arabs are descendants of the earliest split from ancient Eurasian populations. <i>Genome Research</i> , 2016, 26, 151-162.	2.4	89
4198	18S rRNA and COI haplotype diversity of <i>Trichodorus obtusus</i> from turfgrass in South Carolina. <i>Nematology</i> , 2016, 18, 53-65.	0.2	7
4199	Population genetics of the widespread shrub <i>Forsythia suspensa</i> (Oleaceae) in warm-temperate China using microsatellite loci: implication for conservation. <i>Plant Systematics and Evolution</i> , 2016, 302, 1-9.	0.3	7
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4201	Identification and characterization of five polymorphic microsatellite loci in the freshwater copepod <i>Hemidiaptomus gurneyi</i> (Copepoda: Calanoida: Diaptomidae). <i>Italian Journal of Zoology</i> , 2016, 83, 146-150.	0.6	6
4202	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
4203	Distribution of genetic variants of oxidative stress metabolism genes: Paraoxonase 1 ( <i>PON1</i> ) and Glutathione S-transferase ( <i>GSTM1/GSTT1</i> ) in a population from Southeastern Mexico. <i>Annals of Human Biology</i> , 2016, 43, 554-562.	0.4	6
4204	Allele and haplotype diversity of 17 Y-STRs loci in the northern region Pashtun (Pathans) population of Pakistan. <i>Australian Journal of Forensic Sciences</i> , 2016, 48, 273-278.	0.7	0
4205	Fitchi: haplotype genealogy graphs based on the Fitch algorithm. <i>Bioinformatics</i> , 2016, 32, 1250-1252.	1.8	35
4206	Genetic population structure of the Japanese torrent catfish <i>Liobagrus reinii</i> (Amblycipitidae) inferred from mitochondrial cytochrome b variations. <i>Ichthyological Research</i> , 2016, 63, 333-346.	0.5	17
4207	Genetic variations of Turkish bank vole, <i>Myodes glareolus</i> (Mammalia: Rodentia) inferred from mtDNA. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4372-4379.	0.7	5
4208	Northward genetic penetration across the Himalayas viewed from Sherpa people. <i>Mitochondrial DNA</i> , 2016, 27, 342-349.	0.6	7
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4210	Evaluation of genetic diversity amongst <i>Descurainia sophia</i> L. genotypes by inter-simple sequence repeat (ISSR) marker. <i>Physiology and Molecular Biology of Plants</i> , 2016, 22, 97-105.	1.4	8

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4213	Absence of population genetic structure in <i>Heterakis gallinarum</i> of chicken from Sichuan, inferred from mitochondrial cytochrome c oxidase subunit I gene. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3612-3617.	0.7	7
4214	A first report on coexistence and hybridization of <i>Mytilus trossulus</i> and <i>M. edulis</i> mussels in Greenland. Polar Biology, 2016, 39, 343-355.	0.5	52
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4219	Genetic structure and diversity of the island-restricted endangered land crab, <i>Johngarthia lagostoma</i> (H. Milne Edwards, 1837). Journal of Experimental Marine Biology and Ecology, 2016, 474, 204-209.	0.7	16
4220	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. Mammalian Biology, 2016, 81, 163-175.	0.8	17
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4223	Coevolution of genes and languages and high levels of population structure among the highland populations of Daghestan. Journal of Human Genetics, 2016, 61, 181-191.	1.1	27
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4225	Folktale transmission in the Arctic provides evidence for high bandwidth social learning among hunter-gatherer groups. Evolution and Human Behavior, 2016, 37, 47-53.	1.4	28
4226	Genetic diversity is maintained in the endangered New Zealand long-tailed bat ( <i>Chalinolobus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Genetics, 2016, 17, 91-102.	0.8	17
4227	Genetic Diversity and Population Structure Patterns in Chinese Cherry ( <i>Prunus pseudocerasus</i> Lindl) Landraces. Plant Molecular Biology Reporter, 2016, 34, 440-453.	1.0	21
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4231	Species composition and abundance of copepods in the morphologically cryptic genus <i>Pseudocalanus</i> in the Bering Sea. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2016, 134, 173-180.	0.6	9
4232	No divergent evolution, despite restricted connectivity, between Atlantic and Indian Ocean goby populations. <i>Marine Biodiversity</i> , 2016, 46, 465-471.	0.3	10
4233	Phylogeographic patterns in suckermouth catfish <i>Hypostomus ancistroides</i> (Loricariidae): dispersion, vicariance and species complexity across a Neotropical biogeographic region. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3590-3596.	0.7	9
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4235	Loss of <i>Wolbachia</i> but not <i>Cardinium</i> in the invasive range of the Australian thrips species, <i>Pezothrips kellyanus</i> . <i>Biological Invasions</i> , 2016, 18, 197-214.	1.2	31
4236	Pacifplex : an ancestry-informative SNP panel centred on Australia and the Pacific region. <i>Forensic Science International: Genetics</i> , 2016, 20, 71-80.	1.6	60
4237	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
4238	Revealing latitudinal patterns of mitochondrial DNA diversity in Chileans. <i>Forensic Science International: Genetics</i> , 2016, 20, 81-88.	1.6	20
4239	Study of Genetic Polymorphism at 8 STR Loci in the Jat Sikh Population of Madhya Pradesh. <i>SpringerBriefs in Applied Sciences and Technology</i> , 2016, , 15-25.	0.2	0
4240	The paternal ancestry of Uttarakhand does not imitate the classical caste system of India. <i>Journal of Human Genetics</i> , 2016, 61, 167-172.	1.1	4
4241	NAT2 gene diversity and its evolutionary trajectory in the Americas. <i>Pharmacogenomics Journal</i> , 2016, 16, 559-565.	0.9	18
4242	Data for 27 Y-chromosome STR loci in the Basque Country autochthonous population. <i>Forensic Science International: Genetics</i> , 2016, 20, e10-e12.	1.6	19
4243	EurEAs_Gplex – A new SNaPshot assay for continental population discrimination and gender identification. <i>Forensic Science International: Genetics</i> , 2016, 20, 89-100.	1.6	26
4244	Genetic analysis of 17 Y-STR loci from 1019 individuals of six Han populations in East China. <i>Forensic Science International: Genetics</i> , 2016, 20, 101-102.	1.6	33
4245	Variability and distribution of COL1A2 (type I collagen) polymorphisms in the central-eastern Mediterranean Basin. <i>Annals of Human Biology</i> , 2016, 43, 73-77.	0.4	1
4246	Phylogeography of the common pandora <i>Pagellus erythrinus</i> in the central Mediterranean Sea: sympatric mitochondrial lineages and genetic homogeneity. <i>Marine Biology Research</i> , 2016, 12, 4-15.	0.3	11

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4248	Genetic structure of Onchidium œstruma (Mollusca: Gastropoda: Eupulmonata) from the coastal area of China based on mtCOI. Mitochondrial DNA, 2016, 27, 1319-1323.	0.6	3
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4253	Revisiting the evolutionary events in Allium subgenus Cyathophora (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. Molecular Phylogenetics and Evolution, 2016, 94, 802-813.	1.2	27
4254	Mitochondrial DNA analysis of Iranian brown bears (Ursus arctos) reveals new phylogeographic lineage. Mammalian Biology, 2016, 81, 1-9.	0.8	64
4255	DNA barcoding of Iberian Peninsula and North Africa Tawny Owls <i>Strix aluco</i> suggests the Strait of Gibraltar as an important barrier for phylogeography. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4475-4478.	0.7	6
4256	Does population size affect genetic diversity? A test with sympatric lizard species. Heredity, 2016, 116, 92-98.	1.2	87
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4260	Characterisation of genetic structure of the Mayan population in Guatemala by autosomal STR analysis. Annals of Human Biology, 2016, 43, 457-468.	0.4	7
4261	Western Eurasian genetic influences in the Indonesian archipelago. Quaternary International, 2016, 416, 243-248.	0.7	8
4262	CYP2C9, CYP2C19, ABCB1 genetic polymorphisms and phenytoin plasma concentrations in Mexican-Mestizo patients with epilepsy. Pharmacogenomics Journal, 2016, 16, 286-292.	0.9	22
4263	The maternal perspective for five Slovenian regions: The importance of regional sampling. Annals of Human Biology, 2016, 43, 57-66.	0.4	4
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4266	Frequent haplotypes of caged <i>Caligus rogercresseyi</i> in the austral south of Chile: The result of a long term serial passage experiment?. <i>Aquaculture</i> , 2016, 450, 143-153.	1.7	3
4267	Limited genetic structure in a wood frog ( <i>Lithobates sylvaticus</i> ) population in an urban landscape inhabiting natural and constructed wetlands. <i>Conservation Genetics</i> , 2016, 17, 19-30.	0.8	21
4268	Molecular evidence supports recent anthropogenic introduction of the Algerian hedgehog <i>Atelerix algirus</i> in Spain, Balearic and Canary islands from North Africa. <i>Mammalia</i> , 2016, 80, .	0.3	7
4269	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
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4275	Genetic diversity and connectivity patterns of harvested and aquacultured molluscs in estuaries from Asturias (northern Spain). Implications for management strategies. <i>Aquaculture Research</i> , 2016, 47, 2937-2950.	0.9	15
4276	Effects of domestication bottleneck and selection on fatty acid desaturases in Indian sesame germplasm. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2016, 14, 81-90.	0.4	4
4277	Investigation of control region sequences of mtDNA in a Chinese Maonan population. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 350-354.	0.7	4
4278	Patterns of SSR variation in bread wheat ( <i>Triticum aestivum</i> L.) seeds under ex situ genebank storage and accelerated ageing. <i>Genetic Resources and Crop Evolution</i> , 2017, 64, 277-290.	0.8	12
4279	Origins of <i>Semisulcospira libertina</i> (gastropoda: semisulcospiridae) in Taiwan. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 518-525.	0.7	17
4280	Mitochondrial DNA variation in the Sindh population of Pakistan. <i>Australian Journal of Forensic Sciences</i> , 2017, 49, 201-216.	0.7	15
4281	Linking between genetic structure and geographical distance: Study of the maternal gene pool in the Ethiopian population. <i>Annals of Human Biology</i> , 2017, 44, 53-69.	0.4	8
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4285	Genetic structure and diversity of migratory freshwater fish in a fragmented Neotropical river system. <i>Reviews in Fish Biology and Fisheries</i> , 2017, 27, 209-231.	2.4	49
4286	DNA and dispersal models highlight constrained connectivity in a migratory marine megavertebrate. <i>Ecography</i> , 2017, 40, 586-597.	2.1	23
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4288	Lemonpeel ( <i>Centropyge flavissima</i> ) and yellow ( <i>C. heraldi</i> ) pygmy angelfishes each consist of two geographically isolated sibling species. <i>Marine Biodiversity</i> , 2017, 47, 831-845.	0.3	4
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4290	Life cycle and population genetics of bird cherry-oat aphids <i>Rhopalosiphum padi</i> in China: an important pest on wheat crops. <i>Journal of Pest Science</i> , 2017, 90, 103-116.	1.9	30
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4295	Genetic diversity in sorghum [ <i>Sorghum bicolor</i> (L.) Moench] germplasm from Southern Africa as revealed by microsatellite markers and agro-morphological traits. <i>Genetic Resources and Crop Evolution</i> , 2017, 64, 599-610.	0.8	19
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4297	Phylogeographical structure in mitochondrial DNA of whitefly, <i>Bemisia tabaci</i> Gennadius (Hemiptera: Aleyrodidae) in southern India and Southeast Asia. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 621-631.	0.7	10
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4299	Population structuring of the ubiquitous stingless bee <i>Tetragonisca angustula</i> in southern Brazil as revealed by microsatellite and mitochondrial markers. <i>Insect Science</i> , 2017, 24, 877-890.	1.5	9
4300	Genetic variability of <i>Fusarium fujikuroi</i> populations associated with bakanae of rice in Italy. <i>Plant Pathology</i> , 2017, 66, 469-479.	1.2	12



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4302	Environmental heterogeneity promotes microgeographic genetic divergence in the Mediterranean killifish <i>Aphanius fasciatus</i> (Cyprinodontidae). <i>Ethology Ecology and Evolution</i> , 2017, 29, 367-386.	0.6	4
4303	Contrasting genetic effects of red mangrove ( <i>Rhizophora mangle</i> L.) range expansion along West and East Florida. <i>Journal of Biogeography</i> , 2017, 44, 335-347.	1.4	34
4304	Genetic variants involved in oxidative stress, base excision repair, DNA methylation, and folate metabolism pathways influence myeloid neoplasias susceptibility and prognosis. <i>Molecular Carcinogenesis</i> , 2017, 56, 130-148.	1.3	15
4305	Genetic characterization of the Asian clam species complex ( <i>Corbicula</i> ) invasion in the Iberian Peninsula. <i>Hydrobiologia</i> , 2017, 784, 349-365.	1.0	16
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4309	The population genomic signature of environmental association and gene flow in an ecologically divergent tree species <i>Metrosideros polymorpha</i> (Myrtaceae). <i>Molecular Ecology</i> , 2017, 26, 1515-1532.	2.0	22
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4316	Adaptive evolution and demographic history contribute to the divergent population genetic structure of <i>Potato virus Y</i> between China and Japan. <i>Evolutionary Applications</i> , 2017, 10, 379-390.	1.5	40
4317	Special case among passerine birds: long-tailed tits keep family bonds during migration. <i>Behavioral Ecology and Sociobiology</i> , 2017, 71, 1.	0.6	4
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4320	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
4321	Identification of amino acids in antigen-binding site of class II HLA proteins independently associated with hepatitis B vaccine response. <i>Vaccine</i> , 2017, 35, 703-710.	1.7	31
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4324	Population genetic analyses and evaluation of 22 autosomal STRs in Indian populations. <i>International Journal of Legal Medicine</i> , 2017, 131, 971-973.	1.2	24
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4329	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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4331	Genetic polymorphism of 21 non-CODIS STR loci for Guangdong (Southern China) Han population. <i>Forensic Science International: Genetics</i> , 2017, 27, 180-181.	1.6	10
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4333	<i>Anisakis simplex</i> complex: ecological significance of recombinant genotypes in an allopatric area of the Adriatic Sea inferred by genome-derived simple sequence repeats. <i>International Journal for Parasitology</i> , 2017, 47, 215-223.	1.3	22
4334	Balancing selection on allorecognition genes in the colonial ascidian <i>Botryllus schlosseri</i> . <i>Developmental and Comparative Immunology</i> , 2017, 69, 60-74.	1.0	10
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4338	Mitochondrial <i>&lt;scp&gt;DNA&lt;/scp&gt;</i> phylogeography of least cisco <i>&lt;i&gt;&lt;scp&gt;C&lt;/scp&gt; oregonus sardinella&lt;/i&gt;</i> in <i>&lt;scp&gt;A&lt;/scp&gt;</i> laska. <i>Journal of Fish Biology</i> , 2017, 90, 1001-1020.	0.7	2
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4340	Analysis of 12 X-STR loci in the population of south Croatia. <i>Molecular Biology Reports</i> , 2017, 44, 183-189.	1.0	5
4341	Phylogeography of the smooth-coated otter ( <i>Lutrogale perspicillata</i> ): distinct evolutionary lineages and hybridization with the Asian small-clawed otter ( <i>Aonyx cinereus</i> ). <i>Scientific Reports</i> , 2017, 7, 41611.	1.6	15
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4344	Staying close to home? Genetic differentiation of rough-toothed dolphins near oceanic islands in the central Pacific Ocean. <i>Conservation Genetics</i> , 2017, 18, 33-51.	0.8	14
4345	Molecular phylogeography and population evolution analysis of <i>Citrus ichangensis</i> (Rutaceae). <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	15
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4349	Novel Genetic Variants in Carboxylesterase 1 Predict Severe Earlyâ€“Onset Capecitabineâ€“Related Toxicity. <i>Clinical Pharmacology and Therapeutics</i> , 2017, 102, 796-804.	2.3	30
4350	Restricted gene flow and local adaptation highlight the vulnerability of highâ€“latitude reefs to rapid environmental change. <i>Global Change Biology</i> , 2017, 23, 2197-2205.	4.2	54
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4356	Population genetics of pike, genus <i>Esox</i> (Actinopterygii, Esocidae), in Northern Italy: evidence for mosaic distribution of native, exotic and introgressed populations. <i>Hydrobiologia</i> , 2017, 794, 73-92.	1.0	14
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4358	Genetic analysis of <i>Phytophthora sojae</i> populations in Fujian, China. <i>Plant Pathology</i> , 2017, 66, 1182-1190.	1.2	18
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4361	Genetic diversity and population structure of <i>Anastrepha striata</i> (Diptera: Tephritidae) in three natural regions of southwestern Colombia using mitochondrial sequences. <i>Genetica</i> , 2017, 145, 79-89.	0.5	13
4362	Population genetics of the Manila clam ( <i>Ruditapes philippinarum</i> ) introduced in North America and Europe. <i>Scientific Reports</i> , 2017, 7, 39745.	1.6	62
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4396	Genetic signatures of natural selection in a model invasive ascidian. Scientific Reports, 2017, 7, 44080.	1.6	30
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4405	Genetic Polymorphism of Drug-Metabolizing Enzymes <i>CYP2C9</i> and <i>CYP2C19</i> in Moroccan Population. Genetic Testing and Molecular Biomarkers, 2017, 21, 298-304.	0.3	8
4406	Low genetic but high morphological variation over more than 1000 km coastline refutes omnipresence of cryptic diversity in marine nematodes. BMC Evolutionary Biology, 2017, 17, 71.	3.2	23
4407	Nuclear genetic diversity and population structure of a vulnerable and endemic orchid ( <i>Cymbidium</i> ) Tj ETQq1 1 0.784314 rgBT /Overlo	1.7	11
4408	Hidden diversity and phylogeographic history provide conservation insights for the edible seaweed <i>Sargassum fusiforme</i> in the Northwest Pacific. Evolutionary Applications, 2017, 10, 366-378.	1.5	51
4409	Genetic population structure of Indian oil sardine, <i>Sardinella longiceps</i> assessed using microsatellite markers. Conservation Genetics, 2017, 18, 951-964.	0.8	8



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4411	Colour polymorphism and genetic relationships among twelve subspecies of <i>Callosciurus finlaysonii</i> in Thailand. <i>Mammalian Biology</i> , 2017, 85, 6-13.	0.8	12
4412	Molecular identification and distribution of leatherjackets (<scp>D</scp>iptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667 Td (<scp>T</scp> 2017, 19, 400-407.	0.7	3
4413	Biogeographical evidence for common vicariance and rare dispersal in a southern Appalachian harvestman ( <i>Sabaconidae</i> , <i>Sabacon cavicolens</i>). <i>Journal of Biogeography</i> , 2017, 44, 1665-1678.	1.4	23
4414	quaddRAD: a new highâ€multiplexing and PCR duplicate removal ddRAD protocol produces novel evolutionary insights in a nonradiating cichlid lineage. <i>Molecular Ecology</i> , 2017, 26, 2783-2795.	2.0	57
4415	Conservation implications of long-distance migration routes: Regional metapopulation structure, asymmetrical dispersal, and population declines. <i>Biological Conservation</i> , 2017, 209, 263-272.	1.9	22
4416	Genetic dissection of five ethnic groups from Punjab, North-West Indiaâ€A study based on Autosomal Markers. <i>Legal Medicine</i> , 2017, 26, 25-32.	0.6	3
4417	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
4418	Population data for 20 autosomal STR loci in the Yi ethnic minority from Yunnan Province, Southwest China. <i>Forensic Science International: Genetics</i> , 2017, 28, e43-e44.	1.6	24
4419	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
4420	Population expansions dominate demographic histories of endemic and widespread Pacific reef fishes. <i>Scientific Reports</i> , 2017, 7, 40519.	1.6	32
4421	Habitat segregation and cryptic adaptation of species of <i>Periophthalmus</i> (Gobioidae: Gobiidae). <i>Journal of Fish Biology</i> , 2017, 90, 1926-1943.	0.7	1
4422	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
4423	Species identification and comparative population genetics of four coastal houndsharks based on novel NGSâ€mined microsatellites. <i>Ecology and Evolution</i> , 2017, 7, 1462-1486.	0.8	24
4424	Differential landscape effects on the fine-scale genetic structure of populations of a montane conifer from central Mexico. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	13
4425	The leaf turtle population of Phnom Kulen National Park (northwestern Cambodia) has genetic and morphological signatures of hybridization. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2017, 55, 167-174.	0.6	5
4426	An interstate highway affects gene flow in a top reptilian predator ( <i>Crotalus atrox</i> ) of the Sonoran Desert. <i>Conservation Genetics</i> , 2017, 18, 911-924.	0.8	15
4427	Is the Kuroshio Current a strong barrier for the dispersal of the gizzard shad ( <i>Konosirus punctatus</i> ) in the East China Sea?. <i>Marine and Freshwater Research</i> , 2017, 68, 810.	0.7	12

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4429	Island life and isolation: The population genetics of Pacific Wrens on the North Pacific Rim. <i>Condor</i> , 2017, 119, 131-142.	0.7	3
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4432	Extinctions, genetic erosion and conservation options for the black rhinoceros ( <i>Diceros bicornis</i> ). <i>Scientific Reports</i> , 2017, 7, 41417.	1.6	44
4433	Effect of domestication on the genetic diversity and structure of <i>Saccharina japonica</i> populations in China. <i>Scientific Reports</i> , 2017, 7, 42158.	1.6	44
4434	Molecular Genetics Informs Spatial Segregation of Two Desert Stream <i>Gila</i> Species. <i>Transactions of the American Fisheries Society</i> , 2017, 146, 47-59.	0.6	5
4435	One species for one island? Unexpected diversity and weak connectivity in a widely distributed tropical hydrozoan. <i>Heredity</i> , 2017, 118, 385-394.	1.2	24
4436	A separate lowstand lake at the northern edge of Lake Tanganyika? Evidence from phylogeographic patterns in the cichlid genus <i>Tropheus</i> . <i>Hydrobiologia</i> , 2017, 791, 51-68.	1.0	9
4437	Ancestry and demography and descendants of Iron Age nomads of the Eurasian Steppe. <i>Nature Communications</i> , 2017, 8, 14615.	5.8	96
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4439	Life-history, substrate choice and Cytochrome Oxidase I variations in sandy beach peracaridans along the Rio de la Plata estuary. <i>Estuarine, Coastal and Shelf Science</i> , 2017, 187, 152-159.	0.9	11
4440	Evolutionary constraints limiting the variation of Expressed Sequence Tag-linked microsatellite loci, prevent the detection of local adaptation in Mediterranean Bluefin tuna. <i>Fisheries Research</i> , 2017, 190, 157-163.	0.9	5
4441	Population genetics for 17 Y-STR loci in Hui ethnic minority from Liaoning Province, Northeast China. <i>Forensic Science International: Genetics</i> , 2017, 28, e36-e37.	1.6	18
4442	Forensic characteristics and phylogenetic analyses of the Chinese Yi population via 19 X-chromosomal STR loci. <i>International Journal of Legal Medicine</i> , 2017, 131, 1243-1246.	1.2	44
4443	Genetic diversity and population structure of the primary malaria vector <i>Anopheles sinensis</i> (Diptera: Tj ETQq1 1 0,784314 rgBT /Overlo	1.0	24
4444	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
4445	Population genomics of an endemic Mediterranean fish: differentiation by fine scale dispersal and adaptation. <i>Scientific Reports</i> , 2017, 7, 43417.	1.6	83

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4448	Panmixia and dispersal from the Mediterranean Basin to Macaronesian Islands of a macrolichen species. <i>Scientific Reports</i> , 2017, 7, 40879.	1.6	38
4449	Phylogeography and phylogeny of the genus <i>Acanthonyx</i> (Decapoda, Epialtidae) in the north-east Atlantic and Mediterranean. <i>Zoologica Scripta</i> , 2017, 46, 571-583.	0.7	3
4450	Ecological genomics of local adaptation in <i>Cornus florida</i> L. by genotyping by sequencing. <i>Ecology and Evolution</i> , 2017, 7, 441-465.	0.8	43
4451	Population genetic structure and interspecific differentiation between <i>Acer davidii</i> Franchi. and <i>A. morrisonense</i> Hayata (Aceraceae) based on SSR markers. <i>Biochemical Systematics and Ecology</i> , 2017, 71, 42-49.	0.6	7
4452	Mitochondrial control region diversity in Sindhi ethnic group of Pakistan. <i>Legal Medicine</i> , 2017, 26, 11-13.	0.6	10
4453	<i>Brachylaima ezohelicis</i> sp. nov. (Trematoda: Brachylaimidae) found from the land snail <i>Ezohelix gainesi</i> , with a note of an unidentified <i>Brachylaima</i> species in Hokkaido, Japan. <i>Parasitology International</i> , 2017, 66, 240-249.	0.6	32
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4457	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
4458	Gene flow between vicariant tree species: insights into savanna-forest evolutionary relationships. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	10
4459	Low genetic diversity and strong population structure shaped by anthropogenic habitat fragmentation in a critically endangered primate, <i>Trachypithecus leucocephalus</i> . <i>Heredity</i> , 2017, 118, 542-553.	1.2	30
4460	Spatial assessment of wolf-dog hybridization in a single breeding period. <i>Scientific Reports</i> , 2017, 7, 42475.	1.6	33
4461	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
4462	Human management and hybridization shape treegourd fruits in the Brazilian Amazon Basin. <i>Evolutionary Applications</i> , 2017, 10, 577-589.	1.5	9
4463	Sweet vernal grasses ( <i>Anthoxanthum</i> ) colonized African mountains along two fronts in the Late Pliocene, followed by secondary contact, polyploidization and local extinction in the Pleistocene. <i>Molecular Ecology</i> , 2017, 26, 3513-3532.	2.0	8

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4465	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
4466	Population Genomic Analysis of the Blue Crab <i>Callinectes sapidus</i> Using Genotyping-By-Sequencing. <i>Journal of Shellfish Research</i> , 2017, 36, 249-261.	0.3	14
4467	Patterns of Diversity and Spatial Variability of $\beta$ -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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4471	Stuck in fragments: Population genetics of the Endangered collared brown lemur <i>Eulemur collaris</i> in the Malagasy littoral forest. <i>American Journal of Physical Anthropology</i> , 2017, 163, 542-552.	2.1	8
4472	It's about time: Insights into temporal genetic patterns in oceanic zooplankton from biodiversity indices. <i>Limnology and Oceanography</i> , 2017, 62, 1836-1852.	1.6	6
4473	Population genetics for 17 Y-STR loci in Northern Han Chinese from Liaoning Province, Northeast China. <i>Forensic Science International: Genetics</i> , 2017, 29, e35-e37.	1.6	8
4474	Elucidation of fine-scale genetic structure of sandfish ( <i>Holothuria scabra</i> ) populations in Papua New Guinea and northern Australia. <i>Marine and Freshwater Research</i> , 2017, 68, 1901.	0.7	11
4475	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
4476	Population genomics meet Lagrangian simulations: Oceanographic patterns and long larval duration ensure connectivity among <i>Paracentrotus lividus</i> populations in the Adriatic and Ionian seas. <i>Ecology and Evolution</i> , 2017, 7, 2463-2479.	0.8	43
4477	Genetic distribution of 21 STR loci in the Chinese Han population from Hainan Island using Goldeneye® DNA ID 22NC Kit. <i>Forensic Science International: Genetics</i> , 2017, 29, e19-e20.	1.6	14
4478	HLA-A, -B and -C allele and haplotype frequencies defined by next generation sequencing in a population of 519 English blood donors. <i>Human Immunology</i> , 2017, 78, 397-398.	1.2	6
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4481	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

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4483	Genetic Characterization of Atlantic Blue Crab ( <i>Callinectes sapidus</i> ) in Charleston Harbor, South Carolina. Journal of Shellfish Research, 2017, 36, 243-247.	0.3	3
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4485	Genetic variability of the banded murex ( <i>Hexaplex trunculus</i> ) revealed by ND2 and ITS2 sequences. Russian Journal of Marine Biology, 2017, 43, 92-98.	0.2	3
4486	Genetic structure and diversity of western flower thrips, <i>Frankliniella occidentalis</i> in a French bean agroecosystem of Kenya. International Journal of Tropical Insect Science, 2017, 37, 71-78.	0.4	5
4487	Genetic structure and signatures of selection in grey reef sharks ( <i>Carcharhinus amblyrhynchos</i> ). Heredity, 2017, 119, 142-153.	1.2	53
4488	Genetic diversity and gene flow decline with elevation in montane mayflies. Heredity, 2017, 119, 107-116.	1.2	42
4489	Neutral Genetic Processes Influence MHC Evolution in Threatened Gopher Tortoises ( <i>Gopherus</i> ) Tj ETQq1 1 0.784314 rgBT /Qoverlock 10	1.0	5
4490	Genetic polymorphisms of 20 autosomal STR loci in the Vietnamese population from Yunnan Province, Southwest China. International Journal of Legal Medicine, 2017, 131, 661-662.	1.2	16
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4495	Assessing the scope for genetic rescue of an endangered butterfly: the case of the Eltham copper. Insect Conservation and Diversity, 2017, 10, 399-414.	1.4	10
4496	Severe consequences of habitat fragmentation on genetic diversity of an endangered Australian freshwater fish: A call for assisted gene flow. Evolutionary Applications, 2017, 10, 531-550.	1.5	119
4497	Chloroplast DNA assessment of anagenetic speciation in <i>Rubus takesimensis</i> (Rosaceae) on Ulleung Island, Korea. Journal of Plant Biology, 2017, 60, 163-174.	0.9	8
4498	Lineage divergence, local adaptation across a biogeographic break, and artificial transport, shape the genetic structure in the ascidian <i>Pyura chilensis</i> . Scientific Reports, 2017, 7, 44559.	1.6	16
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4501	Climate change and human colonization triggered habitat loss and fragmentation in Madagascar. <i>Molecular Ecology</i> , 2017, 26, 5203-5222.	2.0	56
4502	Population structure of Purple Sandpipers ( <i>Calidris maritima</i> ) as revealed by mitochondrial <i>cytb</i> DNA and microsatellites. <i>Ecology and Evolution</i> , 2017, 7, 3225-3242.	0.8	6
4503	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
4504	Population structure and gene flow in a newly harvested gray wolf ( <i>Canis lupus</i> ) population. <i>Conservation Genetics</i> , 2017, 18, 1091-1104.	0.8	14
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4506	Low population viability in small endangered orchid populations: Genetic variation, seedling recruitment and stochasticity. <i>Biological Conservation</i> , 2017, 210, 174-183.	1.9	22
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4516	Phylogeography of the mouth-brooding freshwater fish <i>Glossamia aprion</i> (Apogonidae) in northern and eastern Australia: historical biogeography and allopatric speciation. <i>Biological Journal of the Linnean Society</i> , 2017, 121, 833-848.	0.7	4
4517	Phylogeography of the spider <i>Araneus venatrix</i> (Araneidae) suggests past connections between Amazon and Atlantic rainforests. <i>Biological Journal of the Linnean Society</i> , 2017, 121, 771-785.	0.7	21



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4519	Reconstructing the introduction history of an invasive fish predator in South Africa. <i>Biological Invasions</i> , 2017, 19, 2261-2276.	1.2	19
4520	Genetic diversity and population structure of pummelo ( <i>Citrus maxima</i> ) germplasm in China. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	16
4521	<i>Tabula rasa</i> in the Patagonian Channels? The phylogeography of <i>Oreobolus obtusangulus</i> (Cyperaceae). <i>Molecular Ecology</i> , 2017, 26, 4027-4044.	2.0	9
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4524	Genetic structure among greater white-fronted goose populations of the Pacific Flyway. <i>Ecology and Evolution</i> , 2017, 7, 2956-2968.	0.8	15
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4526	Two haplotype clusters of <i>Echinococcus granulosus sensu stricto</i> in northern Iraq (Kurdistan) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422	0.9	25
4527	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
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4532	Phylogenetic and population-based approaches to mitogenome variation do not support association with male infertility. <i>Journal of Human Genetics</i> , 2017, 62, 361-371.	1.1	3
4533	Mitochondrial DNA diversity of present-day Aboriginal Australians and implications for human evolution in Oceania. <i>Journal of Human Genetics</i> , 2017, 62, 343-353.	1.1	24
4534	A genome scan for selection signatures comparing farmed Atlantic salmon with two wild populations: Testing colocalization among outlier markers, candidate genes, and quantitative trait loci for production traits. <i>Evolutionary Applications</i> , 2017, 10, 276-296.	1.5	55
4535	Ecological and physical barriers shape genetic structure of the Alpine porcini ( <i>Boletus reticulocephus</i> ). <i>Mycorrhiza</i> , 2017, 27, 261-272.	1.3	10

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4536	Population genetic data for 27 Y-STR loci in the Zhuang ethnic minority from Guangxi Zhuang Autonomous Region in the south of China. <i>Forensic Science International: Genetics</i> , 2017, 27, 182-183.	1.6	28
4537	The <scp>HLA</scp>â€A, â€B and â€<scp>DRB1</scp> polymorphism in a large dataset of South Brazil bone marrow donors from Rio Grande do Sul. <i>Hla</i> , 2017, 89, 29-38.	0.4	7
4538	Unexpected hybridization patterns in Near Eastern terrapins (<i>Mauremys caspica</i>,<i> M.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66). <i>Herpetologica</i> , 2017, 73, 401-413.	0.7	13
4539	Genetic Population Structure across the Range of Endangered Northeastern Bulrush,<i>Scirpus ancistrochaetus</i>. <i>International Journal of Plant Sciences</i> , 2017, 178, 67-78.	0.6	3
4540	Multiple processes drive genetic structure of humpback whale (<i>Megaptera novaeangliae</i>) populations across spatial scales. <i>Molecular Ecology</i> , 2017, 26, 977-994.	2.0	29
4541	Molecular characterization and phylogenetic analysis of <i>Fasciola gigantica</i> from Nigeria. <i>Parasitology International</i> , 2017, 66, 893-897.	0.6	25
4542	<i><scp>HLA</scp>â€G</i> 3â€2 untranslated region polymorphic sites associated with increased <scp>HLA</scp>â€G production are more frequent in patients exhibiting differentiated thyroid tumours. <i>Clinical Endocrinology</i> , 2017, 86, 597-605.	1.2	10
4543	Distributional shifts â€“ not geographic isolation â€“ as a probable driver of montane species divergence. <i>Ecography</i> , 2017, 40, 1475-1485.	2.1	47
4544	Microevolutionary analyses of <i>Pythium insidiosum</i> isolates of Brazil and Thailand based on exo-1,3-Î²-glucanase gene. <i>Infection, Genetics and Evolution</i> , 2017, 48, 58-63.	1.0	17
4545	The role of dispersal for genetic and phenotypic variation: insights from comparisons of sympatric pygmy grasshoppers. <i>Biological Journal of the Linnean Society</i> , 2017, 122, 84-97.	0.7	9
4547	Large and fine scale population structure in European hake ( <i>Merluccius merluccius</i> ) in the Northeast Atlantic. <i>ICES Journal of Marine Science</i> , 2017, 74, 1300-1310.	1.2	6
4548	Different genetic structures revealed resident populations of a specialist parasitoid wasp in contrast to its migratory host. <i>Ecology and Evolution</i> , 2017, 7, 5400-5409.	0.8	10
4549	Insights into the origin of parthenogenesis in oligochaetes: Strong genetic structure in a cosmopolitan earthworm is not related to reproductive mode. <i>European Journal of Soil Biology</i> , 2017, 81, 31-38.	1.4	9
4550	Mitogenomic diversity in Russians and Poles. <i>Forensic Science International: Genetics</i> , 2017, 30, 51-56.	1.6	17
4551	Genetic population diversity of European eel <i>Anguilla anguilla</i> elvers in two Egyptian water bodies, Rosetta (Rachid) estuary and Burullus Lake. <i>Genes and Genomics</i> , 2017, 39, 1035-1045.	0.5	3
4552	Phylogeny and systematics of Anatolian mountain frogs. <i>Biochemical Systematics and Ecology</i> , 2017, 73, 26-34.	0.6	5
4553	Population genetics of wild <i>Siniperca kneri</i> Garman, 1912 in China as evaluated by microsatellites. <i>Journal of Applied Ichthyology</i> , 2017, 33, 991-997.	0.3	1
4554	Lifeâ€history predicts past and present population connectivity in two sympatric sea stars. <i>Ecology and Evolution</i> , 2017, 7, 3916-3930.	0.8	17

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4556	Population genetics analysis of the Nuijiang catfish <i>Creteuchiloglanis macropterus</i> through a genome-wide single nucleotide polymorphisms resource generated by RAD-seq. <i>Scientific Reports</i> , 2017, 7, 2813.	1.6	16
4557	Unique postglacial evolution of the hornbeam ( <i>Carpinus betulus</i> L.) in the Carpathians and the Balkan Peninsula revealed by chloroplast DNA. <i>Science of the Total Environment</i> , 2017, 599-600, 1493-1502.	3.9	11
4558	<i>Alu</i> insertion polymorphisms in the African Sahel and the origin of Fulani pastoralists. <i>Annals of Human Biology</i> , 2017, 44, 537-545.	0.4	10
4559	High-throughput sequencing of transposable element insertions suggests adaptive evolution of the invasive Asian tiger mosquito towards temperate environments. <i>Molecular Ecology</i> , 2017, 26, 3968-3981.	2.0	34
4560	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
4561	Using a Population Genetics Approach for a Preliminary Investigation concerning Species Boundaries in <i>Herbertia</i> (Iridaceae). <i>International Journal of Plant Sciences</i> , 2017, 178, 439-449.	0.6	6
4562	Allopatric divergence and secondary contact without genetic admixture for <i>Perimela</i> ( <i>Lepidoptera: Geometridae</i> ), an alpine moth endemic to the Himalayas. <i>Systematic Entomology</i> , 2017, 42, 703-713.	1.7	4
4563	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
4564	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
4565	Narrow endemics in Mediterranean scrublands: high gene flow buffers genetic impoverishment in the annual monospecific <i>Castrilanthemum</i> (Asteraceae). <i>Biodiversity and Conservation</i> , 2017, 26, 2607-2626.	1.2	4
4566	Phylogenetic analysis of an epidemic outbreak of acute hepatitis C in HIV-infected patients by ultra-deep pyrosequencing. <i>Journal of Clinical Virology</i> , 2017, 92, 42-47.	1.6	17
4567	Non-parallel divergence across freshwater and marine three-spined stickleback <i>Gasterosteus aculeatus</i> populations. <i>Journal of Fish Biology</i> , 2017, 91, 175-194.	0.7	12
4568	A possible genetic basis for vulnerability in <i>Euphydryas maturna</i> (Lepidoptera: Nymphalidae). <i>Genetica</i> , 2017, 145, 151-161.	0.5	3
4569	Population Structure of <i>Colletotrichum truncatum</i> in Himachal Pradesh and Identification of Broad-Spectrum Resistant Sources in <i>Capsicum</i> . <i>Agricultural Research</i> , 2017, 6, 296-303.	0.9	5
4570	Population Structure of Digestive Trypsin Phenotypes in Hatcheries for Pacific White Shrimp and Their Frequencies during Growth in Commercial Culture. <i>North American Journal of Aquaculture</i> , 2017, 79, 261-266.	0.7	1
4571	Landscape genetics of a raccoon ( <i>Procyon lotor</i> ) metapopulation in an undeveloped coastal island system. <i>Journal of Mammalogy</i> , 2017, 98, 1137-1155.	0.6	5
4572	Genome architecture enables local adaptation of Atlantic cod despite high connectivity. <i>Molecular Ecology</i> , 2017, 26, 4452-4466.	2.0	130

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4574	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
4575	Phylogeographical structure and demographic expansion in the endemic alpine stream salamander ( <i>Hynobiidae: Batrachuperus</i> ) of the Qinling Mountains. <i>Scientific Reports</i> , 2017, 7, 1871.	1.6	23
4576	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
4577	Intensive Management and Natural Genetic Variation in Red Deer ( <i>Cervus elaphus</i> ). <i>Journal of Heredity</i> , 2017, 108, 496-504.	1.0	8
4578	Comparative assessment of the genetic variation in selectively bred generations from two geographic populations of ivory shell ( <i>Babylonia areolata</i> ). <i>Aquaculture Research</i> , 2017, 48, 4205-4218.	0.9	11
4579	The genetic structure of six-rowed naked barley landraces from the Qinghai-Tibetan Plateau is correlated with variation for ecogeographical factors. <i>Canadian Journal of Plant Science</i> , 0, , .	0.3	0
4580	Phylogeography and population dynamics of Antbirds (Thamnophilidae) from Amazonian fluvial islands. <i>Journal of Biogeography</i> , 2017, 44, 2284-2294.	1.4	30
4581	Origins and Genetic Diversity of Introduced Populations of the Puerto Rican Red-Eyed Coqui, <i>Eleutherodactylus antillensis</i> , in Saint Croix (U.S. Virgin Islands) and Panamá. <i>Copeia</i> , 2017, 105, 220-228.	1.4	4
4582	Watershed characteristics shape the landscape genetics of brook stickleback ( <i>Culaea</i> ). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i>	0.8	3
4583	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
4584	Genetic Resources of Neotropical Fishes. , 2017, , .		13
4585	Characterization of Genetic Resources. , 2017, , 55-117.		1
4586	Mitochondrial and nuclear intraspecific variation in the rusty blenny ( <i>Parablennius sanguinolentus</i> ). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i>	1.0	6
4587	Ecology and management history drive spatial genetic structure in Scots pine. <i>Forest Ecology and Management</i> , 2017, 400, 68-76.	1.4	18
4588	Local populations and inaccuracies: Determining the relevant mitochondrial haplotype distributions for North West European cats. <i>Forensic Science International: Genetics</i> , 2017, 30, 71-80.	1.6	2
4589	Population genetics of the deep-sea bluntnose sixgill shark, <i>Hexanchus griseus</i> , revealing spatial genetic heterogeneity. <i>Marine Genomics</i> , 2017, 36, 25-32.	0.4	10
4590	SSR marker analysis points to population admixture and continuum of genetic variation among Indian landraces of brinjal ( <i>Solanum melongena</i> L.). <i>Scientia Horticulturae</i> , 2017, 224, 68-73.	1.7	4

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4592	Development of 18 microsatellite markers for the white-streaked grouper, <i>Epinephelus ongus</i> (Bloch, 1793). <i>Journal of Heredity</i> , 2017, 108, 103-114.	0.3	1
4593	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
4594	Geographically distinct patterns of reproductive isolation and hybridization in two sympatric species of the <i>Jaera albifrons</i> complex (marine isopods). <i>Ecology and Evolution</i> , 2017, 7, 5352-5365.	0.8	11
4595	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
4596	Evolutionary and ecological forces influencing population diversification in Bornean montane passerines. <i>Molecular Phylogenetics and Evolution</i> , 2017, 113, 139-149.	1.2	9
4597	Extraordinarily rapid speciation in a marine fish. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 6074-6079.	3.3	99
4598	Safeguarding Our Genetic Resources with Libraries of Doubled-Haploid Lines. <i>Genetics</i> , 2017, 206, 1611-1619.	1.2	24
4599	Local adaptation shapes pattern of mitochondrial population structure in <i>Sebastiscus marmoratus</i> . <i>Environmental Biology of Fishes</i> , 2017, 100, 763-774.	0.4	15
4600	Contribution of spatial heterogeneity in effective population sizes to the variance in pairwise measures of genetic differentiation. <i>Methods in Ecology and Evolution</i> , 2017, 8, 1866-1877.	2.2	32
4601	Do plant populations on distinct inselbergs talk to each other? A case study of genetic connectivity of a bromeliad species in an Ocbil landscape. <i>Ecology and Evolution</i> , 2017, 7, 4704-4716.	0.8	35
4602	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
4603	Cryptic diversity in the Japanese mantis shrimp <i>Oratosquilla oratoria</i> (Crustacea: Squillidae): Allopatric diversification, secondary contact and hybridization. <i>Scientific Reports</i> , 2017, 7, 1972.	1.6	36
4604	Ancient Egyptian mummy genomes suggest an increase of Sub-Saharan African ancestry in post-Roman periods. <i>Nature Communications</i> , 2017, 8, 15694.	5.8	131
4605	Genetic and phenotypic variability in <i>Stenoperla prasina</i> (Newman, 1845) (Plecoptera: Eustheniidae) in relation to latitude and altitude in New Zealand. <i>Aquatic Insects</i> , 2017, 38, 49-65.	0.6	7
4606	Isolation by distance and isolation by environment contribute to population differentiation in <i>Protea repens</i> (Proteaceae L.), a widespread South African species. <i>American Journal of Botany</i> , 2017, 104, 674-684.	0.8	21
4607	A genotype–phenotype association approach to reveal thermal adaptation in <i>Daphnia galeata</i> . <i>Journal of Experimental Zoology Part A: Ecological and Integrative Physiology</i> , 2017, 327, 53-65.	0.9	8
4608	Signatures of temporal genetic differentiation of the small yellow croaker ( <i>Larimichthys polyactis</i> ) revealed by microsatellite markers. <i>Fisheries Research</i> , 2017, 194, 50-54.	0.9	5

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4610	Spinocerebellar ataxia type 10: common haplotype and disease progression rate in Peru and Brazil. <i>European Journal of Neurology</i> , 2017, 24, 892.	1.7	12
4611	Estimation of Evolutionary Rates of Mitochondrial DNA in Two Japanese Wood Mouse Species Based on Calibrations with Quaternary Environmental Changes. <i>Zoological Science</i> , 2017, 34, 201-210.	0.3	22
4612	Genetic diversity and population structure in the Barrens Topminnow ( <i>Fundulus julisia</i> ): implications for conservation and management of a critically endangered species. <i>Conservation Genetics</i> , 2017, 18, 1347-1358.	0.8	6
4613	Screening of duplicated loci reveals hidden divergence patterns in a complex salmonid genome. <i>Molecular Ecology</i> , 2017, 26, 4509-4522.	2.0	18
4614	Genetic studies in the recently divergent <i>Eligmodontia puerulus</i> and <i>E. moreni</i> (Rodentia, Cricetidae). <i>Tj ETQq1 1 0.784314 rgBT /Overlo</i>	0.8	4
4615	Natural genetic polymorphism and phylogeography of Siberian sturgeon <i>Acipenser baerii</i> Brandt, 1869. <i>Russian Journal of Genetics</i> , 2017, 53, 358-368.	0.2	7
4616	Run to the hills: gene flow among mountain areas leads to low genetic differentiation in the Norwegian lemming. <i>Biological Journal of the Linnean Society</i> , 2017, 121, 1-14.	0.7	10
4617	Coincidence of genotypes at two loci in two parthenogenetic rock lizards: how backcrosses might trigger adaptive speciation. <i>Biological Journal of the Linnean Society</i> , 2017, 121, 365-378.	0.7	21
4618	Rates of gene flow in a freshwater snail and the evolution of phenotypic plasticity. <i>Biological Journal of the Linnean Society</i> , 2017, 121, 764-770.	0.7	1
4619	Morphological convergence in the recently diversified <i>Silene gigantea</i> complex (Caryophyllaceae) in the Balkan Peninsula and south-western Turkey, with the description of a new subspecies. <i>Botanical Journal of the Linnean Society</i> , 2017, 183, 474-493.	0.8	9
4620	Signatures of adaptive molecular evolution in American pikas ( <i>Ochotona princeps</i> ). <i>Journal of Mammalogy</i> , 2017, 98, 1156-1167.	0.6	7
4621	Genetic diversity and population structure of the invasive plant <i>Solanum rostratum</i> in China. <i>Russian Journal of Ecology</i> , 2017, 48, 134-142.	0.3	4
4622	Identification of bakanae disease resistance loci in japonica rice through genome wide association study. <i>Rice</i> , 2017, 10, 29.	1.7	43
4623	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
4624	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
4625	Strong population structure in a species manipulated by humans since the Neolithic: the European fallow deer ( <i>Dama dama dama</i> ). <i>Heredity</i> , 2017, 119, 16-26.	1.2	30
4626	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



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4628	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
4629	Bone marrow transplant donor recruitment strategies to maximize, optimize, and equalize recipient chances of an acceptable match. <i>Revista Brasileira De Hematologia E Hemoterapia</i> , 2017, 39, 177-179.	0.7	4
4630	Population genetic data and mutations of 22 autosomal STR loci in Guizhou Han population. <i>Forensic Science International: Genetics</i> , 2017, 29, e29-e30.	1.6	33
4631	Genetic variation of 17 autosomal STR loci in the Zhuang ethnic minority from Guangxi Zhuang Autonomous Region in the south of China. <i>Forensic Science International: Genetics</i> , 2017, 28, e51-e52.	1.6	13
4632	Population genetic analysis of Xiamen Han population on 21 short tandem repeat loci. <i>Legal Medicine</i> , 2017, 26, 41-44.	0.6	20
4633	Genetic divergence with ongoing gene flow is maintained by the use of different hosts in phytophagous ladybird beetles genus <i>Henosepilachna</i> . <i>Journal of Evolutionary Biology</i> , 2017, 30, 1110-1123.	0.8	3
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4635	Natural variation in CTB4a enhances rice adaptation to cold habitats. <i>Nature Communications</i> , 2017, 8, 14788.	5.8	192
4636	Genetic diversity of the Pacific walrus ( <i>Odobenus rosmarus divergens</i> ) in the western part of the Chukchi Sea. <i>Russian Journal of Genetics</i> , 2017, 53, 242-251.	0.2	4
4637	Development and characterization of 24 polymorphic microsatellite markers for bluegill sunfish, <i>Lepomis macrochirus</i> . <i>Genes and Genomics</i> , 2017, 39, 637-644.	0.5	1
4638	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
4639	Molecular Population Genetics. <i>Genetics</i> , 2017, 205, 1003-1035.	1.2	100
4640	Population genetic structure and comparative diversity of smallmouth bass <i>Micropterus dolomieu</i> : congruent patterns from two genomes. <i>Journal of Fish Biology</i> , 2017, 90, 2125-2147.	0.7	11
4641	High genetic diversity and distinct origin of recently fragmented Scots pine ( <i>Pinus sylvestris</i> L.) populations along the Carpathians and the Pannonian Basin. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	26
4642	Genome-wide data delimits multiple climate-determined species ranges in a widespread Australian fish, the golden perch ( <i>Macquaria ambigua</i> ). <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 65-75.	1.2	42
4643	Retention of gene diversity during the spread of a non-native plant species. <i>Molecular Ecology</i> , 2017, 26, 3141-3150.	2.0	5
4644	Population structure and historical demography of <i>Dipteronia dyeriana</i> (Sapindaceae), an extremely narrow palaeoendemic plant from China: implications for conservation in a biodiversity hot spot. <i>Heredity</i> , 2017, 119, 95-106.	1.2	47

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4647	Genetic variation during range expansion: effects of habitat novelty and hybridization. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20170007.	1.2	37
4648	<sc>RAD</sc> sequencing reveals genomewide divergence between independent invasions of the European green crab (<i>Carcinus maenas</i>) in the Northwest Atlantic. Ecology and Evolution, 2017, 7, 2513-2524.	0.8	42
4649	Pervasive genetic differentiation among Central European populations of the threatened <i>Arnica montana</i> L. and genetic erosion at lower elevations. Perspectives in Plant Ecology, Evolution and Systematics, 2017, 27, 45-56.	1.1	16
4650	The systematics of the Mexican populations of <i>Macrobrachium digueti</i> (Bouvier, 1895) (Decapoda: Tj ETQq1 1 0.784314 rgBT /Overl	0.3	7
4651	Effects of fragmentation and anthropic pressure on the genetic structure of <i>Canthon</i> ( <i>Peltecanthon</i> ) <i>staigi</i> (Coleoptera: Scarabaeidae) populations in the Atlantic Forest domain. Journal of Insect Conservation, 2017, 21, 267-276.	0.8	6
4652	Do larval types affect genetic connectivity at sea? Testing hypothesis in two sibling marine gastropods with contrasting larval development. Marine Environmental Research, 2017, 127, 92-101.	1.1	25
4653	Expansion after expansion: dissecting the phylogeography of the widely distributed spur-thighed tortoise, <i>Testudo graeca</i> (Testudines: Testudinidae). Biological Journal of the Linnean Society, 2017, 121, 641-654.	0.7	24
4654	OsLG3 contributing to rice grain length and yield was mined by Ho-LAMap. BMC Biology, 2017, 15, 28.	1.7	100
4655	Population structure of Han nationality in Central-Southern China. Forensic Science International: Genetics, 2017, 29, e1-e3.	1.6	2
4656	Temporal patterns of genetic diversity in <i>Baetis tricaudatus</i> (Ephemeroptera:Baetidae) from the Russian River, northern California. Freshwater Science, 2017, 36, 351-363.	0.9	3
4657	Do ecological communities disperse across biogeographic barriers as a unit?. Molecular Ecology, 2017, 26, 3533-3545.	2.0	35
4658	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47
4659	Comparative population genetics of two dominant plant species of high Andean wetlands reveals complex evolutionary histories and conservation perspectives in Chile's Norte Chico. Conservation Genetics, 2017, 18, 1047-1060.	0.8	6
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4661	All roads lead to weediness: Patterns of genomic divergence reveal extensive recurrent weedy rice origins from South Asian <i>Oryza</i>. Molecular Ecology, 2017, 26, 3151-3167.	2.0	51
4662	Ancient DNA analysis of the extinct North American flat-headed peccary ( <i>Platygonus compressus</i> ). Molecular Phylogenetics and Evolution, 2017, 112, 258-267.	1.2	10

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4664	Massive Extraction of the Orchid <i>Laelia speciosa</i> (HBK) Schltr. for Trading in Local Markets Affect Its Population Genetic Structure in a Fragmented Landscape in Central Mexico. <i>Tropical Conservation Science</i> , 2017, 10, 194008291769323.	0.6	7
4665	Regional pattern of genetic variation in the Eastern Central European populations of <i>Euphydryas maturna</i> (Lepidoptera: Nymphalidae). <i>Journal of Insect Conservation</i> , 2017, 21, 171-181.	0.8	2
4666	Cytochrome c oxidase subunit I haplotype diversity of <i>Angiostrongylus cantonensis</i> (Nematoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.9	16
4667	Persistence of historical population structure in an endangered species despite near-complete biome conversion in California's San Joaquin Desert. <i>Molecular Ecology</i> , 2017, 26, 3618-3635.	2.0	23
4668	Correlation Between Environmental Factors, a Life History Trait, Phenotypic Cohesion, and Gene Flow Levels in Natural Populations of <i>Micropogonias furnieri</i> : Is Salinity the Main Factor Driving Divergence?. <i>Estuaries and Coasts</i> , 2017, 40, 1717-1731.	1.0	4
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4671	The genetic diversity of burbot ( <i>Lota lota</i> L., 1758) of Western Siberia (the analysis of the mtDNA) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.2	4
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4773	The complex evolutionary history and phylogeography of <i>Caridina typus</i> (Crustacea: Decapoda): long-distance dispersal and cryptic allopatric species. <i>Scientific Reports</i> , 2017, 7, 9044.	1.6	13
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4958	Genetic structure and phenotypic variation of <i>Anopheles darlingi</i> in northwest Colombia. <i>Infection, Genetics and Evolution</i> , 2017, 56, 143-151.	1.0	7
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4995	Microsatellite analysis of population structure in <i>Eucalyptus globulus</i> . <i>Genome</i> , 2017, 60, 770-777.	0.9	12
4996	Estimates of genetic variability and inbreeding in experimentally selected populations of European sea bass. <i>Aquaculture</i> , 2017, 479, 742-749.	1.7	16
4997	Genome-wide population genetic analysis identifies evolutionary forces establishing continuous population divergence. <i>Ecological Research</i> , 2017, 32, 461-468.	0.7	1
4998	Association of MITF loci with coat color spotting patterns in Ethiopian cattle. <i>Genes and Genomics</i> , 2017, 39, 285-293.	0.5	7
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5001	Genetic characterization of <i>Brycon hilarii</i> (Characiformes) populations within the Pantanal: Aspects of their conservation within a globally important neotropical wetland. <i>Journal of Ichthyology</i> , 2017, 57, 434-444.	0.2	9
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5021	Demographic history and population genetic structure of <i>Hagenia abyssinica</i> (Rosaceae), a tropical tree endemic to the Ethiopian highlands and eastern African mountains. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	8
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5026	Lake level fluctuations and divergence of cichlid fish ecomorphs in Lake Tanganyika. <i>Hydrobiologia</i> , 2017, 791, 21-34.	1.0	14
5027	Demographic structure and genetic variability throughout the distribution of <i>Platte thistle</i> ( <i>Cirsium canescens</i> Asteraceae). <i>Journal of Biogeography</i> , 2017, 44, 375-385.	1.4	8
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5037	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
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5044	Displacement of native Patagonian freshwater silverside populations ( <i>Odontesthes hatcheri</i> ), Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667 2017, 19, 971-988.	1.2	13
5045	InvestigatorÂ® HDplex (Qiagen) reference population database for forensic use in Argentina. <i>Forensic Science International: Genetics</i> , 2017, 26, 91-95.	1.6	8
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5047	From Alaska to Antarctica: Species boundaries and genetic diversity of <i>Prasiola</i> (Trebouxiophyceae), a foliose chlorophyte associated with the bipolar lichen-forming fungus <i>Mastodia tessellata</i> . <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 117-131.	1.2	57
5048	Genetic data on 16 X-chromosomal STR loci in three population samples from China. <i>Forensic Science International: Genetics</i> , 2017, 26, e17-e18.	1.6	2
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5050	Association between HLA genes and dust mite sensitivity in a Brazilian population. <i>Human Immunology</i> , 2017, 78, 88-94.	1.2	11
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5053	Population genetic data for 12 X-STR loci in the Northern Han Chinese and StatsX package as tools for population statistics on X-STR. <i>Forensic Science International: Genetics</i> , 2017, 26, e1-e8.	1.6	24
5054	Highly restricted gene flow between disjunct populations of the skunk clownfish ( <i>Amphiprion</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 0.4 17	0.4	17
5055	Geographic distribution and environmental control of vertebral count in <i>Ammodytes</i> spp. along the northern Pacific coast of Japan. <i>Journal of Fish Biology</i> , 2017, 90, 773-785.	0.7	6
5056	Population subdivision in the tropical spiny lobster <i>Panulirus ornatus</i> throughout its Indo-West Pacific distribution. <i>ICES Journal of Marine Science</i> , 2017, 74, 759-768.	1.2	11
5057	Invasion genetics of <i>Senecio vulgaris</i> : loss of genetic diversity characterizes the invasion of a selfing annual, despite multiple introductions. <i>Biological Invasions</i> , 2017, 19, 255-267.	1.2	14
5058	Satellite DNA content illuminates the ancestry of a supernumerary (B) chromosome. <i>Chromosoma</i> , 2017, 126, 487-500.	1.0	36
5059	Are species genetically more sensitive to habitat fragmentation on the periphery of their range compared to the core? A case study on the sand lizard ( <i>Lacerta agilis</i> ). <i>Landscape Ecology</i> , 2017, 32, 131-145.	1.9	9



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5061	Genomic landscape of early ecological speciation initiated by selection on nuptial colour. <i>Molecular Ecology</i> , 2017, 26, 7-24.	2.0	26
5062	Population genetic inferences using immune gene SNPs mirror patterns inferred by microsatellites. <i>Molecular Ecology Resources</i> , 2017, 17, 481-491.	2.2	17
5063	Phylogeography of <i>Quercus aquifolioides</i> provides novel insights into the Neogene history of a major global hotspot of plant diversity in southâ€“west China. <i>Journal of Biogeography</i> , 2017, 44, 294-307.	1.4	113
5064	Does population distribution matter? Influence of a patchy versus continuous distribution on genetic patterns in a windâ€“pollinated shrub. <i>Journal of Biogeography</i> , 2017, 44, 361-374.	1.4	16
5065	Neogene and Pleistocene history of <i>Agave lechuguilla</i> in the Chihuahuan Desert. <i>Journal of Biogeography</i> , 2017, 44, 322-334.	1.4	60
5066	Origin of a divergent mtDNA lineage of a freshwater snail species, <i>Radix balthica</i> , in Iceland: cryptic glacial refugia or a postglacial founder event?. <i>Hydrobiologia</i> , 2017, 787, 73-98.	1.0	41
5067	Genetic population structure in Greenland halibut ( <i>Reinhardtius hippoglossoides</i> ) and its relevance to fishery management. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2017, 74, 475-485.	0.7	15
5068	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
5069	Targeted reâ€“sequencing confirms the importance of chemosensory genes in aphid host race differentiation. <i>Molecular Ecology</i> , 2017, 26, 43-58.	2.0	27
5070	An assessment of spatio-temporal genetic variation in the South African abalone ( <i>Haliotis midae</i> ), using SNPs: implications for conservation management. <i>Conservation Genetics</i> , 2017, 18, 17-31.	0.8	14
5071	Isolation-by-time population structure in potamodromous <i>Dourado Salminus brasiliensis</i> in southern Brazil. <i>Conservation Genetics</i> , 2017, 18, 67-76.	0.8	34
5072	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
5073	Going, going, gone? Loss of genetic diversity in two critically endangered Australian freshwater fishes, <i>Scaturiginichthys vermeilipinnis</i> and <i>Chlamydogobius squamigenus</i> , from Great Artesian Basin springs at Edgbaston, Queensland, Australia. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2017, 27, 39-50.	0.9	25
5074	The Mediterranean Sea hosts endemic haplotypes and a distinct population of the dolphinfish <i>Coryphaena hippurus</i> Linnaeus, 1758 (Perciformes, Coryphaenidae). <i>Fisheries Research</i> , 2017, 186, 151-158.	0.9	11
5075	Genetic diversity and connectivity within <i>Mytilus</i> spp. in the subarctic and Arctic. <i>Evolutionary Applications</i> , 2017, 10, 39-55.	1.5	70
5076	Conservation implications of small population size and habitat fragmentation in an endangered lupine. <i>Conservation Genetics</i> , 2017, 18, 77-88.	0.8	6
5077	On the role played by the carrying capacity and the ancestral population size during a range expansion. <i>Heredity</i> , 2017, 118, 143-153.	1.2	4

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5079	Genetic characterization of wild and farmed European seabass in the Adriatic sea: assessment of farmed escapees using a Bayesian approach. <i>ICES Journal of Marine Science</i> , 2017, 74, 369-378.	1.2	24
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5081	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
5082	Experimentally provided conspecific cues boost bird territory density but not breeding performance. <i>Behavioral Ecology</i> , 2017, 28, 174-185.	1.0	17
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5084	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
5085	Golden Eagle fatalities and the continentalâ€scale consequences of local windâ€energy generation. <i>Conservation Biology</i> , 2017, 31, 406-415.	2.4	46
5086	A new Eurasian phylogeographical paradigm? Limited contribution of southern populations to the recolonization of high latitude populations in <i>Juniperus communis</i> L. (Cupressaceae). <i>Journal of Biogeography</i> , 2017, 44, 271-282.	1.4	32
5087	Concordance of microsatellite and mitochondrial <i>scp</i> DNA markers in detecting genetic population structure in the boring giant clam <i>Tridacna crocea</i> across the Indoâ€Malay Archipelago. <i>Marine Ecology</i> , 2017, 38, e12389.	0.4	21
5088	Population expansion, current and past gene flow in Gouldâ€™s petrel: implications for conservation. <i>Conservation Genetics</i> , 2017, 18, 105-115.	0.8	4
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5090	Landscape genetics reveals inbreeding and genetic bottlenecks in the extremely rare short-globose cacti <i>Mammillaria pectinifera</i> (Cactaceae) as a result of habitat fragmentation. <i>Plant Diversity</i> , 2017, 39, 13-19.	1.8	10
5091	Slow motion extinction: inbreeding, introgression, and loss in the critically endangered mangrove finch ( <i>Camarhynchus heliobates</i> ). <i>Conservation Genetics</i> , 2017, 18, 159-170.	0.8	27
5092	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
5093	Origin and introduction history of the least weasel ( <i>Mustela nivalis</i> ) on Mediterranean and Atlantic islands inferred from genetic data. <i>Biological Invasions</i> , 2017, 19, 399-421.	1.2	9
5094	Where do animals come from during postâ€fire population recovery? Implications for ecological and genetic patterns in postâ€fire landscapes. <i>Ecography</i> , 2017, 40, 1325-1338.	2.1	36
5095	Novel microsatellite markers for <i>Dalechampia scandens</i> (Euphorbiaceae) and closely related taxa: application to studying a species complex. <i>Plant Species Biology</i> , 2017, 32, 179-186.	0.6	7

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5097	Genetic variation and local differences in Pacific cod <i>Gadus macrocephalus</i> around Japan. <i>Journal of Fish Biology</i> , 2017, 90, 61-79.	0.7	15
5098	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
5099	<i>genepopedit</i> : a simple and flexible tool for manipulating multilocus molecular data in R. <i>Molecular Ecology Resources</i> , 2017, 17, 12-18.	2.2	52
5100	Characterization of <i>Monilinia</i> species associated with brown rot in stone fruit in Brazil. <i>Plant Pathology</i> , 2017, 66, 423-436.	1.2	16
5101	Mitochondrial and Nuclear DNA Based Genetic Assessment Indicated Distinct Variation and Low Genetic Exchange Among the Three Subspecies of Swamp Deer ( <i>Rucervus duvaucelii</i> ). <i>Evolutionary Biology</i> , 2017, 44, 31-42.	0.5	19
5102	Genetic erosion in the snail <i>Littoraria subvittata</i> (Reid, 1986) due to mangrove deforestation. <i>Journal of Molluscan Studies</i> , 2017, 83, 1-10.	0.4	16
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5105	Genetic diversity and population differentiation within and between island populations of two sympatric <i>Petroica</i> robins, the Chatham Island black robin and tomtit. <i>Conservation Genetics</i> , 2017, 18, 275-285.	0.8	8
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5107	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
5108	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
5109	Landscape genetics informs mesohabitat preference and conservation priorities for a surrogate indicator species in a highly fragmented river system. <i>Heredity</i> , 2017, 118, 374-384.	1.2	16
5110	Red blood cell alloimmunization in patients with sickle cell disease: correlation with HLA and cytokine gene polymorphisms. <i>Transfusion</i> , 2017, 57, 379-389.	0.8	56
5111	Genetic diversity and population genetic structure of <i>Python bivittatus</i> in China. <i>Journal of Forestry Research</i> , 2017, 28, 621-628.	1.7	2
5112	Introgression and selection shaped the evolutionary history of sympatric sister species of coral reef fishes (genus: <i>Haemulon</i> ). <i>Molecular Ecology</i> , 2017, 26, 639-652.	2.0	29
5113	High performance computation of landscape genomic models including local indicators of spatial association. <i>Molecular Ecology Resources</i> , 2017, 17, 1072-1089.	2.2	112

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5115	Demographic modelling with whole-genome data reveals parallel origin of similar <i>Pundamilia</i> cichlid species after hybridization. <i>Molecular Ecology</i> , 2017, 26, 123-141.	2.0	106
5116	Population genetic structure of cotton pink bollworm, <i>Pectinophora gossypiella</i> (Saunders) (Lepidoptera: Gelechiidae) using mitochondrial cytochrome oxidase I ( <i>COL</i> ) gene sequences from India. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 941-948.	0.7	7
5117	An overview of Australia's temperate marine phylogeography, with new evidence from high-dispersal gastropods. <i>Journal of Biogeography</i> , 2017, 44, 217-229.	1.4	26
5118	Genetic population structure of the fluvial eight-barbel loach <i>Lefua</i> sp. 1 in the three river systems in central Honshu, Japan, revealed by microsatellite DNA markers. <i>Ichthyological Research</i> , 2017, 64, 232-239.	0.5	0
5119	Genome-wide analysis highlights genetic dilution in Algerian sheep. <i>Heredity</i> , 2017, 118, 293-301.	1.2	30
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5121	Allopatric speciation in the desert: diversification of cichlids at their geographical and ecological range limit in Iran. <i>Hydrobiologia</i> , 2017, 791, 193-207.	1.0	9
5122	Identifying patterns of dispersal, connectivity and selection in the sea scallop, <i>Placopecten magellanicus</i> , using RAD-seq-derived SNPs. <i>Evolutionary Applications</i> , 2017, 10, 102-117.	1.5	82
5123	<i>Pemphigus vulgaris</i> and <i>pemphigus foliaceus</i> determined by CD86 and CTLA4 polymorphisms. <i>Clinics in Dermatology</i> , 2017, 35, 236-241.	0.8	13
5124	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
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5127	Range-wide genetic structure of <i>Arabidopsis halleri</i> (Brassicaceae): glacial persistence in multiple refugia and origin of the Northern Hemisphere disjunction. <i>Botanical Journal of the Linnean Society</i> , 2017, 185, 321-342.	0.8	39
5128	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
5129	Population status of Greenland halibut <i>Reinhardtius hippoglossoides</i> (Walbaum, 1793) of the Laptev Sea. <i>Doklady Biochemistry and Biophysics</i> , 2017, 477, 349-353.	0.3	6
5130	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
5131	Search for genetic markers of climatic adaptation in populations of North Eurasia. <i>Russian Journal of Genetics</i> , 2017, 53, 1172-1183.	0.2	14

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5133	Genetic Diversity of an Invasive Invertebrate in an Urban Environment, as Exemplified by the Harlequin <i>&lt;i&gt;Ladybird Harmonia&lt;/i&gt;</i> Axyridis (Pallas, 1773). <i>Annales Zoologici</i> , 2017, 67, 759-772.	0.1	3
5134	Extensive gene flow of white-backed planthopper in the Greater Mekong Subregion as revealed by microsatellite markers. <i>Scientific Reports</i> , 2017, 7, 15905.	1.6	6
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5136	Early-Mid Pleistocene genetic differentiation and range expansions as exemplified by invasive Eurasian <i>Bunias orientalis</i> (Brassicaceae) indicates the Caucasus as key region. <i>Scientific Reports</i> , 2017, 7, 16764.	1.6	14
5137	Microsatellite markers revealed moderate genetic diversity and population differentiation of moso bamboo ( <i>Phyllostachys edulis</i> )â€”a primarily asexual reproduction species in China. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	19
5138	Phylogeography of the Mantled Howler Monkey ( <i>Alouatta palliata</i> ; Atelidae, Primates) across Its Geographical Range by Means of Mitochondrial Genetic Analyses and New Insights about the Phylogeny of <i>Alouatta</i> . <i>Folia Primatologica</i> , 2017, 88, 421-454.	0.3	11
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5142	An integrative mating system assessment of a nonmodel, economically important Pacific rockfish ( <i>&lt;i&gt;Sebastes melanops&lt;/i&gt;</i> ) reveals nonterritorial polygamy and conservation implications for a large species flock. <i>Ecology and Evolution</i> , 2017, 7, 11277-11291.	0.8	8
5143	Understanding population structure and historical demography of <i>Litsea auriculata</i> (Lauraceae), an endangered species in east China. <i>Scientific Reports</i> , 2017, 7, 17343.	1.6	8
5144	Variation in Major Histocompatibility Complex diversity in invasive cane toad populations. <i>Wildlife Research</i> , 2017, 44, 565.	0.7	7
5145	Maintaining genetic integrity of coexisting wild and domestic populations: Genetic differentiation between wild and domestic <i>&lt;i&gt;Rangifer&lt;/i&gt;</i> with long traditions of intentional interbreeding. <i>Ecology and Evolution</i> , 2017, 7, 6790-6802.	0.8	24
5146	Highly contrasted population genetic structures in a hostâ€”parasite pair in the Caribbean Sea. <i>Ecology and Evolution</i> , 2017, 7, 9267-9280.	0.8	13
5147	Insight into the population structure of hardhead silverside, <i>&lt;i&gt;Atherinomorus stipes&lt;/i&gt;</i> (Teleostei:) Tj ETQq1 1 0.784314 rgBT /Overlo	0.8	5
5148	Numerous mitochondrial DNA haplotypes reveal multiple independent polyploidy origins of hexaploids in <i>&lt;i&gt;Carassius&lt;/i&gt;</i> species complex. <i>Ecology and Evolution</i> , 2017, 7, 10604-10615.	0.8	26
5149	Strong population genetic structure of an invasive species, <i>&lt;i&gt;Rhynchophorus ferrugineus&lt;/i&gt;</i> (Olivier), in southern China. <i>Ecology and Evolution</i> , 2017, 7, 10770-10781.	0.8	22

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5151	Microsatellite polymorphic loci reveal genetic structure of cultivated pears in East Asia. <i>Acta Horticulturae</i> , 2017, , 107-114.	0.1	0
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5153	Population genetic structure in <i>Sabatieria</i> (Nematoda) reveals intermediary gene flow and admixture between distant cold seeps from the Mediterranean Sea. <i>BMC Evolutionary Biology</i> , 2017, 17, 154.	3.2	6
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5155	Human-mediated processes affecting distribution and genetic structure of <i>Squalidus multimaculatus</i> , a freshwater cyprinid with small spatial range. <i>Animal Cells and Systems</i> , 2017, 21, 349-357.	0.8	4
5156	Patterns of fungal-algal symbiont association in <i>Usnea aurantiaco-atra</i> reveal the succession of lichen-moss communities in Fildes Peninsula, Antarctica. <i>Polar Research</i> , 2017, 36, 1374123.	1.6	3
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5159	Geographical distance and local environmental conditions drive the genetic population structure of a freshwater microalga (Bathycoccaceae; Chlorophyta) in Patagonian lakes. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	12
5160	Paternal phylogeographic structure of the brown bear ( <i>Ursus arctos</i> ) in northeastern Asia and the effect of male-mediated gene flow to insular populations. <i>Zoological Letters</i> , 2017, 3, 21.	0.7	42
5161	Genetic population structure of sheepshead, <i>Archosargus probatocephalus</i> (Sparidae), a coastal marine fish off the southeastern United States: multiple population clusters based on species-specific microsatellite markers. <i>Bulletin of Marine Science</i> , 2017, 93, 691-713.	0.4	7
5162	Conservation Genetics of the Capercaillie <i>Tetrao urogallus</i> in Poland – Diversity of Mitochondrial DNA in Remnant and Extinct Populations. <i>Acta Ornithologica</i> , 2017, 52, 179-196.	0.1	3
5163	Genetic diversity and population genetic analysis of <i>Donax vittatus</i> (Mollusca: Bivalvia) and phylogeny of the genus with mitochondrial and nuclear markers. <i>Estuarine, Coastal and Shelf Science</i> , 2017, 197, 126-135.	0.9	17
5164	Implications of fidelity and philopatry for the population structure of female black-tailed deer. <i>Behavioral Ecology</i> , 2017, 28, 983-990.	1.0	22
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5166	Siberian Roe Deer ( <i>Capreolus pygargus</i> Pallas, 1771) in Ukraine: Analysis of the Mitochondrial and Nuclear DNA. <i>Biology Bulletin</i> , 2017, 44, 575-583.	0.1	4
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5170	Ontogenetic changes in mouth morphology triggers conflicting hypotheses of relationships in characid fishes (Ostariophysi: Characiformes). <i>Neotropical Ichthyology</i> , 2017, 15, .	0.5	7
5171	Polimorfismo S19W (Ser19Ter) de la APOA5 y su relación con la hipertrigliceridemia en una población de Colombia. <i>Revista De La Universidad Industrial De Santander Salud</i> , 2017, 49, 29-35.	0.0	0
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5174	Invasive Everywhere? Phylogeographic Analysis of the Globally Distributed Tree Pathogen <i>Lasiodiplodia theobromae</i> . <i>Forests</i> , 2017, 8, 145.	0.9	31
5175	Genetic characterization of coat color genes in Brazilian Crioula sheep from a conservation nucleus. <i>Pesquisa Agropecuaria Brasileira</i> , 2017, 52, 615-622.	0.9	7
5176	Small-Scale Habitat-Specific Variation and Adaptive Divergence of Photosynthetic Pigments in Different Alkali Soils in Reed Identified by Common Garden and Genetic Tests. <i>Frontiers in Plant Science</i> , 2016, 7, 2016.	1.7	28
5177	Local Climate Heterogeneity Shapes Population Genetic Structure of Two Undifferentiated Insular <i>Scutellaria</i> Species. <i>Frontiers in Plant Science</i> , 2017, 8, 159.	1.7	12
5178	Solar Radiation-Associated Adaptive SNP Genetic Differentiation in Wild Emmer Wheat, <i>Triticum dicoccoides</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 258.	1.7	12
5179	Population Structure and Phylogenetic Relationships in a Diverse Panel of <i>Brassica rapa</i> L.. <i>Frontiers in Plant Science</i> , 2017, 8, 321.	1.7	53
5180	Species Delimitation and Lineage Separation History of a Species Complex of Aspens in China. <i>Frontiers in Plant Science</i> , 2017, 8, 375.	1.7	35
5181	Deciphering Genomic Regions for High Grain Iron and Zinc Content Using Association Mapping in Pearl Millet. <i>Frontiers in Plant Science</i> , 2017, 8, 412.	1.7	72
5182	Landscape Population Genomics of <i>Forsythia</i> ( <i>Forsythia suspensa</i> ) Reveal That Ecological Habitats Determine the Adaptive Evolution of Species. <i>Frontiers in Plant Science</i> , 2017, 8, 481.	1.7	18
5183	Elevation Shift in <i>Abies</i> Mill. (Pinaceae) of Subtropical and Temperate China and Vietnam—Corroborative Evidence from Cytoplasmic DNA and Ecological Niche Modeling. <i>Frontiers in Plant Science</i> , 2017, 8, 578.	1.7	15
5184	Genetic Diversity, Population Structure, and Linkage Disequilibrium of an Association-Mapping Panel Revealed by Genome-Wide SNP Markers in Sesame. <i>Frontiers in Plant Science</i> , 2017, 8, 1189.	1.7	36
5185	Genotyping-by-Sequencing (GBS) Revealed Molecular Genetic Diversity of Iranian Wheat Landraces and Cultivars. <i>Frontiers in Plant Science</i> , 2017, 8, 1293.	1.7	125

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5187	Development and Application of Transcriptome-Derived Microsatellites in <i>Actinidia eriantha</i> (Actinidiaceae). <i>Frontiers in Plant Science</i> , 2017, 8, 1383.	1.7	18
5188	Testing Domestication Scenarios of Lima Bean ( <i>Phaseolus lunatus</i> L.) in Mesoamerica: Insights from Genome-Wide Genetic Markers. <i>Frontiers in Plant Science</i> , 2017, 8, 1551.	1.7	37
5189	Genetic Variation and Population Structure of <i>Oryza glaberrima</i> and Development of a Mini-Core Collection Using DArTseq. <i>Frontiers in Plant Science</i> , 2017, 8, 1748.	1.7	71
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5195	Comparative genome-wide polymorphic microsatellite markers in Antarctic penguins through next generation sequencing. <i>Genetics and Molecular Biology</i> , 2017, 40, 676-687.	0.6	9
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#	ARTICLE	IF	CITATIONS
5331	Development and Characterization of 12 Novel Polymorphic Microsatellite Loci for the Mammal Chewing Louse <i>Geomydoecus aurei</i> (Insecta: Phthiraptera) and a Comparison of Next-Generation Sequencing Approaches for Use in Parasitology. <i>Journal of Parasitology</i> , 2018, 104, 89-95.	0.3	4
5332	Human beta defensin-1 is involved in the susceptibility to adeno-tonsillar hypertrophy. <i>International Journal of Pediatric Otorhinolaryngology</i> , 2018, 107, 135-139.	0.4	6
5333	A divergent lineage among <i>Octopus minor</i> (Sasaki, 1920) populations in the Northwest Pacific supported by DNA barcoding. <i>Marine Biology Research</i> , 2018, 14, 335-344.	0.3	7
5334	Spatial population genetic structure of a bacterial parasite in close coevolution with its host. <i>Molecular Ecology</i> , 2018, 27, 1371-1384.	2.0	20
5335	Rediscovery and a Redescription of the Crooked-Acklins Boa, <i>Chilabothrus schwartzi</i> (Buden,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.2	6
5336	Mitochondrial and nuclear genetic structure in <i>Rhodeus ocellatus</i> (Teleostei: Cyprinidae) with approximate Bayesian computation. <i>Environmental Biology of Fishes</i> , 2018, 101, 829-841.	0.4	7
5337	A biting commentary: Integrating tooth characters with molecular data doubles known species diversity in a lineage of sea slugs that consume "killer algae". <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 356-370.	1.2	12
5338	Nuclear, chloroplast, and mitochondrial data of a US cannabis DNA database. <i>International Journal of Legal Medicine</i> , 2018, 132, 713-725.	1.2	15
5339	Genetic differentiation between insular and continental populations of migratory and resident warblers, the Great Reed Warbler <i>Acrocephalus arundinaceus</i> and Cetti's Warbler <i>Cettia cetti</i> . <i>Journal of Ornithology</i> , 2018, 159, 703-712.	0.5	2
5340	Interindividual Differences in the Expression of ATP-Binding Cassette and Solute Carrier Family Transporters in Human Skin: DNA Methylation Regulates Transcriptional Activity of the Human ABCC3 Gene. <i>Drug Metabolism and Disposition</i> , 2018, 46, 628-635.	1.7	17
5341	Molecular phylogeography and population history of <i>Crassostrea sikamea</i> (Amemiya, 1928) based on mitochondrial DNA. <i>Journal of Experimental Marine Biology and Ecology</i> , 2018, 503, 23-30.	0.7	7
5342	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
5343	Genetic evidences of non-reproductive shoaling in the freshwater fish <i>Salminus brasiliensis</i> . <i>Hydrobiologia</i> , 2018, 815, 65-72.	1.0	4
5344	Genetic diversity of Norway spruce ( <i>Picea abies</i> (L.) Karst.) seed orchard crops: Effects of number of parents, seed year, and pollen contamination. <i>Forest Ecology and Management</i> , 2018, 411, 132-141.	1.4	23
5345	The genomic footprint of climate adaptation in <i>Chironomus riparius</i> . <i>Molecular Ecology</i> , 2018, 27, 1439-1456.	2.0	54
5346	Molecular and climate data reveal expansion and genetic differentiation of Mexican Violet-ear Colibri <i>thalassinus thalassinus</i> (Aves: Trochilidae) populations separated by the Isthmus of Tehuantepec. <i>Journal of Ornithology</i> , 2018, 159, 687-702.	0.5	7
5347	Genetic structure of <i>Leucojum aestivum</i> L. in the Po Valley (N-Italy) drives conservation management actions. <i>Conservation Genetics</i> , 2018, 19, 827-838.	0.8	6
5348	Variable dispersal histories across the Drake Passage: The case of coastal benthic Foraminifera. <i>Marine Micropaleontology</i> , 2018, 140, 81-94.	0.5	6

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5349	Genomic diversity and population structure of three autochthonous Greek sheep breeds assessed with genome-wide DNA arrays. <i>Molecular Genetics and Genomics</i> , 2018, 293, 753-768.	1.0	13
5350	Enlarging the gene-geography of Europe and the Mediterranean area to STR loci of common forensic use: longitudinal and latitudinal frequency gradients. <i>Annals of Human Biology</i> , 2018, 45, 77-85.	0.4	5
5351	Dinucleotide (CA) <sub>n</sub> tandem repeats on the human X-chromosome and the history of the Mediterranean populations. <i>Annals of Human Biology</i> , 2018, 45, 72-76.	0.4	4
5352	Conservation implications of spatial genetic structure in two species of oribatid mites from the Antarctic Peninsula and the Scotia Arc. <i>Antarctic Science</i> , 2018, 30, 105-114.	0.5	12
5353	River damming drives population fragmentation and habitat loss of the threatened Danube streber ( <i>Zingel streber</i> ): Implications for conservation. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2018, 28, 587-599.	0.9	19
5354	New insights from Thailand into the maternal genetic history of Mainland Southeast Asia. <i>European Journal of Human Genetics</i> , 2018, 26, 898-911.	1.4	53
5355	Post-mortem analysis of suicide victims shows ABCB1 haplotype 1236Tâ€“2677Tâ€“3435T as a candidate predisposing factor behind adverse drug reactions in females. <i>Pharmacogenetics and Genomics</i> , 2018, 28, 99-106.	0.7	11
5356	HLA-B*07, HLA-DRB1*07, HLA-DRB1*12, and HLA-C*03:02 Strongly Associate With BMI: Data From 1.3 Million Healthy Chinese Adults. <i>Diabetes</i> , 2018, 67, 861-871.	0.3	9
5357	Hybridization between <i>Tithonia tubaeformis</i> and <i>T. rotundifolia</i> (Asteraceae) evidenced by nSSR and secondary metabolites. <i>Plant Systematics and Evolution</i> , 2018, 304, 313-326.	0.3	7
5358	Lack of spatial structure for phenotypic and genetic variation despite high self-fertilization in <i>Aquilegia canadensis</i> (Ranunculaceae). <i>Heredity</i> , 2018, 121, 605-615.	1.2	2
5359	High genetic diversity and demographic stability in <i>Aechmea kertesziae</i> (Bromeliaceae), a species of sandy coastal plains (restinga habitat) in southern Brazil. <i>Botanical Journal of the Linnean Society</i> , 2018, 186, 374-388.	0.8	13
5360	Integrated genetic and morphological data support ecoâ€“evolutionary divergence of Angolan and South African populations of <i>Diplodus hottentotus</i> . <i>Journal of Fish Biology</i> , 2018, 92, 1163-1176.	0.7	7
5361	Forensic parameters and admixture in Mestizos from five geographic regions of Mexico based on 20 autosomal STRs (Powerplex 21 system). <i>International Journal of Legal Medicine</i> , 2018, 132, 1293-1296.	1.2	17
5362	Phylogeographic pattern of <i>Liza affinis</i> populations in Chinese coastal waters: estimation of larval dispersal potential. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 1253-1260.	0.7	5
5363	Genetic diversity of farmed and wild populations of the reefâ€“building coral, <i>Acropora tenuis</i> . <i>Restoration Ecology</i> , 2018, 26, 1195-1202.	1.4	8
5364	Novel microsatellite markers for the endangered neotropical fish <i>Brycon orbignyanus</i> and cross-amplification in related species. <i>Italian Journal of Animal Science</i> , 2018, 17, 916-920.	0.8	7
5365	Caught in the act: Incipient speciation across a latitudinal gradient in a semifossorial mammal from Madagascar, the mole tenrec <i>Oryzorictes hova</i> (Tenrecidae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 74-84.	1.2	10
5366	Triplicate parallel life cycle divergence despite gene flow in periodical cicadas. <i>Communications Biology</i> , 2018, 1, 26.	2.0	9

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5367	Novel microsatellite markers reveal multiple origins of <i>Botryosphaeria dothidea</i> causing the Chinese grapevine trunk disease. <i>Fungal Ecology</i> , 2018, 33, 134-142.	0.7	9
5368	Genetic diversity analysis of the oriental river prawn ( <i>Macrobrachium nipponense</i> ) in Huaihe River. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 737-744.	0.7	12
5369	Genetic Structure of <i>Zymoseptoria tritici</i> in Northern France at Region, Field, Plant, and Leaf Layer Scales. <i>Phytopathology</i> , 2018, 108, 1114-1123.	1.1	13
5370	Selection outweighs drift at a fine scale: Lack of <i>MHC</i> differentiation within a family living lizard across geographically close but disconnected rocky outcrops. <i>Molecular Ecology</i> , 2018, 27, 2204-2214.	2.0	9
5371	Plastid DNA diversity and genetic divergence within <i>Rhododendron dauricum</i> s.l. ( <i>R. dauricum</i> s.s., <i>R.</i> ) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422 1</i> 763-774.	0.3	11
5372	Parallel evolution and adaptation to environmental factors in a marine flatfish: Implications for fisheries and aquaculture management of the turbot ( <i>Scophthalmus maximus</i> ). <i>Evolutionary Applications</i> , 2018, 11, 1322-1341.	1.5	54
5373	Multilocus phylogeography of <i>Patella caerulea</i> (Linnaeus, 1758) reveals contrasting connectivity patterns across the Eastern–Western Mediterranean transition. <i>Journal of Biogeography</i> , 2018, 45, 1301-1312.	1.4	5
5374	Characterization and transferability of microsatellites for <i>Gentiana lawrencei</i> var. <i>farreri</i> (Gentianaceae). <i>Applications in Plant Sciences</i> , 2018, 6, e1015.	0.8	12
5375	Population genomics and geographical parthenogenesis in Japanese harvestmen (Opiliones,) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422 1</i>	0.8	11
5376	Population genetic structure of the endemic rosewoods <i>Dalbergia cochinchinensis</i> and <i>D.Âoliveri</i> at a regional scale reflects the Indochinese landscape and life–history traits. <i>Ecology and Evolution</i> , 2018, 8, 530-545.	0.8	22
5377	Genetic Population Structure of Shoal Bass within their Native Range. <i>North American Journal of Fisheries Management</i> , 2018, 38, 549-564.	0.5	7
5378	Genomic analyses identify multiple Asian origins and deeply diverged mitochondrial clades in inbred brown rats ( <i>Rattus norvegicus</i> ). <i>Evolutionary Applications</i> , 2018, 11, 718-726.	1.5	12
5379	Detecting signatures of positive selection in non-model species using genomic data. <i>Zoological Journal of the Linnean Society</i> , 2018, 184, 528-583.	1.0	67
5380	Genetic diversity and phylogenetic characteristics of Chinese Tibetan and Yi minority ethnic groups revealed by non-CODIS STR markers. <i>Scientific Reports</i> , 2018, 8, 5895.	1.6	31
5381	Genes from the TAS1R and TAS2R Families of Taste Receptors: Looking for Signatures of Their Adaptive Role in Human Evolution. <i>Genome Biology and Evolution</i> , 2018, 10, 1139-1152.	1.1	18
5382	Genetic characteristics of coastal cutthroat trout inhabiting an urban watershed. <i>Environmental Biology of Fishes</i> , 2018, 101, 799-811.	0.4	1
5383	Genetic characteristics of broodstock and offspring of the seven-band grouper ( <i>Hyporthodus</i> ) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 0</i> United Kingdom, 2018, 98, 261-267.	0.4	0
5384	Survival in northern microrefugia in an endemic Carpathian gammarid (Crustacea: Amphipoda). <i>Zoologica Scripta</i> , 2018, 47, 357-372.	0.7	18



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5385	Preliminary assessment of genetic diversity and population connectivity of the Mugger Crocodile in Iran. <i>Amphibia - Reptilia</i> , 2018, 39, 126-131.	0.1	6
5386	Extensive gene flow along the urban-rural gradient in a migratory colonial bird. <i>Journal of Avian Biology</i> , 2018, 49, .	0.6	6
5387	Range contraction and increasing isolation of a polar bear subpopulation in an era of sea-ice loss. <i>Ecology and Evolution</i> , 2018, 8, 2062-2075.	0.8	38
5388	Population genetic structure, introgression, and hybridization in the genus <i>Rhizophora</i> along the Brazilian coast. <i>Ecology and Evolution</i> , 2018, 8, 3491-3504.	0.8	53
5389	Forensic molecular genetic diversity analysis of Chinese Hui ethnic group based on a novel STR panel. <i>International Journal of Legal Medicine</i> , 2018, 132, 1297-1299.	1.2	22
5390	Comparative analysis of rhizobial chromosomes and plasmids to estimate their evolutionary relationships. <i>Plasmid</i> , 2018, 96-97, 13-24.	0.4	19
5391	Genetic analysis reveals harvested <i>Lethrinus nebulosus</i> in the Southwest Indian Ocean comprise two cryptic species. <i>ICES Journal of Marine Science</i> , 2018, 75, 1465-1472.	1.2	4
5392	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
5393	Testing Wallace's intuition: water type, reproductive isolation and divergence in an Amazonian fish. <i>Journal of Evolutionary Biology</i> , 2018, 31, 882-892.	0.8	16
5394	Genome-wide screen for universal individual identification SNPs based on the HapMap and 1000 Genomes databases. <i>Scientific Reports</i> , 2018, 8, 5553.	1.6	9
5395	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
5396	Population genetic analysis of the recently rediscovered Hula painted frog ( <i>Latonia nigriventer</i> ) reveals high genetic diversity and low inbreeding. <i>Scientific Reports</i> , 2018, 8, 5588.	1.6	14
5397	Loss of genetic variability in the captive stocks of tambaqui, <i>Colossoma macropomum</i> (Cuvier), Tj ETQq0 0 0 rgBT /Overlock 10 Tf Research, 2018, 49, 1914-1925.	0.9	17
5398	Origin, Genetic Diversity, and Population History of a Marine Population (Chanidae: <i>Chanos chanos</i> ) in an Enclosed Lagoon in French Polynesia. <i>Pacific Science</i> , 2018, 72, 223-231.	0.2	1
5399	Exploring the phylogeography of a hexaploid freshwater fish by <i>scp</i> RAD sequencing. <i>Ecology and Evolution</i> , 2018, 8, 2326-2342.	0.8	17
5400	Unconstrained gene flow between populations of a widespread epiphytic lichen <i>Usnea subfloridana</i> (Parmeliaceae, Ascomycota) in Estonia. <i>Fungal Biology</i> , 2018, 122, 731-737.	1.1	5
5401	Genetic Structure of <i>Dytiscus sharpi</i> in North and South Hokuriku in Japan Inferred from Mitochondrial and Nuclear Gene Sequence. <i>Zoological Science</i> , 2018, 35, 134-139.	0.3	1
5402	Cryptic species and parallel genetic structuring in Lethrinid fish: Implications for conservation and management in the southwest Indian Ocean. <i>Ecology and Evolution</i> , 2018, 8, 2182-2195.	0.8	16

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5403	Population structure of the Townsend's big-eared bat ( <i>Corynorhinus townsendii townsendii</i> ) in California. <i>Journal of Mammalogy</i> , 2018, 99, 646-658.	0.6	8
5404	Comparison of the rookery connectivity and migratory connectivity: insight into movement and colonization of the green turtle ( <i>Chelonia mydas</i> ) in Pacific Southeast Asia. <i>Marine Biology</i> , 2018, 165, 1.	0.7	12
5405	Assessment of spatial-temporal variation in natural populations of <i>Brassica incana</i> in south Italy: implications for conservation. <i>Plant Systematics and Evolution</i> , 2018, 304, 731-745.	0.3	4
5406	Resolving relationships and phylogeographic history of the <i>Nyssa sylvatica</i> complex using data from RAD-seq and species distribution modeling. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 1-16.	1.2	39
5407	The genetic diversity within the 1.4 kb HLA-G 5' upstream regulatory region moderately impacts on cellular microenvironment responses. <i>Scientific Reports</i> , 2018, 8, 5652.	1.6	16
5408	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
5409	Distribution of mating-type alleles and genetic variability in field populations of <i>Leptosphaeria maculans</i> in western Canada. <i>Journal of Phytopathology</i> , 2018, 166, 438-447.	0.5	0
5410	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
5411	Natural selection and neutral evolutionary processes contribute to genetic divergence in leaf traits across a precipitation gradient in the tropical oak <i>Quercus oleoides</i> . <i>Molecular Ecology</i> , 2018, 27, 2176-2192.	2.0	43
5412	Local Introgression of Mitochondrial DNA in Eight-Barbel Loaches of the Genus <i>Lefua</i> (Balitoridae, Cypriniformes). <i>Zoological Science</i> , 2018, 35, 140-148.	0.3	1
5413	Human cytochrome P450 2B6 genetic variability in Botswana: a case of haplotype diversity and convergent phenotypes. <i>Scientific Reports</i> , 2018, 8, 4912.	1.6	7
5414	The demographic history of Atlantic salmon ( <i>Salmo salar</i> ) across its distribution range reconstructed from approximate Bayesian computations*. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 1261-1277.	1.1	75
5415	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
5416	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
5417	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
5418	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
5419	De novo SNP discovery and strong genetic structuring between upstream and downstream populations of <i>Paratya australiensis</i> Kemp, 1917 (Decapoda: Caridea: Atyidae). <i>Journal of Crustacean Biology</i> , 2018, 38, 166-172.	0.3	1
5420	Spatial dynamics and mixing of bluefin tuna in the Atlantic Ocean and Mediterranean Sea revealed using next-generation sequencing. <i>Molecular Ecology Resources</i> , 2018, 18, 620-638.	2.2	34

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5421	Does the Mid-Atlantic Ridge affect the distribution of abyssal benthic crustaceans across the Atlantic Ocean?. Deep-Sea Research Part II: Topical Studies in Oceanography, 2018, 148, 91-104.	0.6	37
5422	Genetic Differentiation and Demographic History of the Northern Rufous Mouse Lemur ( <i>Microcebus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 Primates, 2018, 39, 65-89.	0.9	16
5423	Forensic genetic informativeness of an SNP panel consisting of 19 multi-allelic SNPs. Forensic Science International: Genetics, 2018, 34, 49-56.	1.6	19
5424	From conservation genetics to conservation genomics: a genome-wide assessment of blue whales ( <i>Balaenoptera musculus</i> ) in Australian feeding aggregations. Royal Society Open Science, 2018, 5, 170925.	1.1	41
5425	Archaeogenetics of Late Iron Age Anatolia, Batman: Investigating maternal genetic continuity in north Mesopotamia since the Neolithic. American Journal of Physical Anthropology, 2018, 166, 196-207.	2.1	9
5426	No distinct barrier effects of highways and a wide river on the genetic structure of the Alpine newt ( <i>Ichthyosaura alpestris</i> ) in densely settled landscapes. Conservation Genetics, 2018, 19, 673-685.	0.8	13
5427	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). Tree Genetics and Genomes, 2018, 14, 1.	0.6	11
5428	Eco-Evolutionary Processes Generating Diversity Among Bottlenose Dolphin, <i>Tursiops truncatus</i> , Populations off Baja California, Mexico. Evolutionary Biology, 2018, 45, 223-236.	0.5	12
5429	Population Genomics of Marine Zooplankton. Population Genomics, 2018, , 61-102.	0.2	24
5430	Polymorphism of Chloroplast DNA and Phylogeography of Green Alder ( <i>Alnus alnobetula</i> (Ehrh.) K.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 Society of Washington, 2018, 131, 36-46.	0.2	4
5431	Population genetic structure of the intertidal kinorhynch <i>Echinoderes marthae</i> (Kinorhyncha) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Society of Washington, 2018, 131, 36-46.	0.3	4
5432	The prevalence of HLA alleles in a lupus nephritis population. Transplant Immunology, 2018, 47, 37-43.	0.6	15
5433	The reunion of two lineages of the Neotropical brown stink bug on soybean lands in the heart of Brazil. Scientific Reports, 2018, 8, 2496.	1.6	33
5434	High genetic diversity and strong differentiation in dramatically fluctuating populations of <i>Zostera japonica</i> (Zosteraceae): implication for conservation. Journal of Plant Ecology, 2018, 11, 789-797.	1.2	8
5435	Genetic structuring and secondary contact in the white-chested <i>Amazilia</i> hummingbird species complex. Journal of Avian Biology, 2018, 49, jav-01536.	0.6	15
5436	Historical divergences associated with intermittent land bridges overshadow isolation by larval dispersal in co-distributed species of <i>Tridacna</i> giant clams. Journal of Biogeography, 2018, 45, 848-858.	1.4	18
5437	Phylogeography of the Asian lesser white-toothed shrew, <i>Crocivura shantungensis</i> , in East Asia: role of the Korean Peninsula as refugium for small mammals. Genetica, 2018, 146, 211-226.	0.5	9
5438	A mosaic genetic structure of the human population living in the South Baltic region during the Iron Age. Scientific Reports, 2018, 8, 2455.	1.6	13

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5439	The CÂ€Sâ€A 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
5440	Contrasting maternal and paternal genetic variation of hunter-gatherer groups in Thailand. <i>Scientific Reports</i> , 2018, 8, 1536.	1.6	23
5441	Genetic variability and population structure of <i>Passiflora contracta</i> , a bat-pollinated species from a fragmented rainforest. <i>Botanical Journal of the Linnean Society</i> , 2018, 186, 247-258.	0.8	4
5442	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
5443	Genetic variation in populations from central Argentina based on mitochondrial and Y chromosome DNA evidence. <i>Journal of Human Genetics</i> , 2018, 63, 493-507.	1.1	20
5444	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
5445	Patterns of nuclear and chloroplast genetic diversity and structure of manioc along major Brazilian Amazonian rivers. <i>Annals of Botany</i> , 2018, 121, 625-639.	1.4	26
5446	Low rates of hybridization between European wildcats and domestic cats in a humanâ€dominated landscape. <i>Ecology and Evolution</i> , 2018, 8, 2290-2304.	0.8	27
5447	Genetic Variation and Structure in an Endemic Island Oak, <i>Quercus tomentella</i> , and Mainland Canyon Oak, <i>Quercus chrysolepis</i> . <i>International Journal of Plant Sciences</i> , 2018, 179, 151-161.	0.6	11
5448	Phenotypic divergence despite low genetic differentiation in house sparrow populations. <i>Scientific Reports</i> , 2018, 8, 394.	1.6	14
5449	Atlantic salmon <i>Salmo salar</i> in the chalk streams of England are genetically unique. <i>Journal of Fish Biology</i> , 2018, 92, 621-641.	0.7	7
5450	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
5451	Mitochondrial diversity and phylogeography of <i>Acrossocheilus paradoxus</i> (Teleostei: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 Td	0.7	13
5452	Migration-Selection Balance Drives Genetic Differentiation in Genes Associated with High-Altitude Function in the Speckled Teal ( <i>Anas flavirostris</i> ) in the Andes. <i>Genome Biology and Evolution</i> , 2018, 10, 14-32.	1.1	18
5453	Genetic diversity analyses for population structuring in <i>Channa striata</i> using mitochondrial and microsatellite DNA regions with implication to their conservation in Indian waters. <i>Meta Gene</i> , 2018, 16, 28-38.	0.3	8
5454	Biases of STRUCTURE software when exploring introduction routes of invasive species. <i>Heredity</i> , 2018, 120, 485-499.	1.2	12
5455	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
5456	Population genetic structure of the sword prawn <i>Parapenaeopsis hardwickii</i> (Miers, 1878) (Decapoda: Tj ETQq1 1 0.784314 rgBT /Over	0.3	13

#	ARTICLE	IF	CITATIONS
5457	<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
5458	Genetic homogeneity in the deep-sea grenadier <i>Macrourus berglax</i> across the North Atlantic Ocean. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2018, 132, 60-67.	0.6	5
5459	Genetic analyses favour an ancient and natural origin of elephants on Borneo. <i>Scientific Reports</i> , 2018, 8, 880.	1.6	11
5460	Phylogeography of the pelagic snail <i>Limacina helicina</i> (Gastropoda: Thecosomata) in the subarctic western North Pacific. <i>Journal of Molluscan Studies</i> , 2018, 84, 30-37.	0.4	14
5461	Population genetics of an island invasion by Japanese Bush-Warblers in Hawaii, USA. <i>Auk</i> , 2018, 135, 171-180.	0.7	3
5462	High diversity and low genetic structure of feather mites associated with a phenotypically variable bird host. <i>Parasitology</i> , 2018, 145, 1243-1250.	0.7	4
5463	Investigating the population structure and genetic differentiation of livestock guard dog breeds. <i>Animal</i> , 2018, 12, 2009-2016.	1.3	7
5464	Ancient Human Migrations to and through Jammu Kashmir- India were not of Males Exclusively. <i>Scientific Reports</i> , 2018, 8, 851.	1.6	21
5465	Conservation Genetics of Two Highly Endangered and Poorly Known Species of <i>Zamia</i> (Zamiaceae): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.0	5
5466	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
5467	Genomics of end-Pleistocene population replacement in a small mammal. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20172624.	1.2	26
5468	Human migration and the spread of malaria parasites to the New World. <i>Scientific Reports</i> , 2018, 8, 1993.	1.6	76
5469	Genetic variations and phylogeography of the swallowtail butterfly <i>Papilio machaon</i> on the Japanese Islands. <i>Entomological Science</i> , 2018, 21, 248-259.	0.3	7
5470	Seascape genomics reveals adaptive divergence in a connected and commercially important mollusc, the greenlip abalone ( <i>Haliotis laevigata</i> ), along a longitudinal environmental gradient. <i>Molecular Ecology</i> , 2018, 27, 1603-1620.	2.0	95
5471	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
5472	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
5473	Flickers of speciation: Sympatric colour morphs of the arcá€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
5474	Microsatellite DNA analysis reveals lower than expected genetic diversity in the threatened leopard cat ( <i>Prionailurus bengalensis</i> ) in South Korea. <i>Genes and Genomics</i> , 2018, 40, 521-530.	0.5	6

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5475	Genetic characteristics and phylogenetic analysis of three Chinese ethnic groups using the Huaxia Platinum System. <i>Scientific Reports</i> , 2018, 8, 2429.	1.6	35
5476	Restricted gene flow among western Indian Ocean populations of the mangrove whelk <i>Terebralia palustris</i> (Linnaeus, 1767) (Caenogastropoda: Potamididae). <i>Journal of Molluscan Studies</i> , 2018, 84, 163-169.	0.4	10
5477	Extreme streams: species persistence and genomic change in montane insect populations across a flooding gradient. <i>Ecology Letters</i> , 2018, 21, 525-535.	3.0	35
5478	From individual heterogeneity to population-level overdispersion: quantifying the relative roles of host exposure and parasite establishment in driving aggregated helminth distributions. <i>International Journal for Parasitology</i> , 2018, 48, 309-318.	1.3	14
5479	Genomic tools for management and conservation of Atlantic cod in a coastal marine protected area. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2018, 75, 1915-1925.	0.7	11
5480	Spatio-environmental determinants of the genetic structure of three steppe species in a highly fragmented landscape. <i>Basic and Applied Ecology</i> , 2018, 28, 48-59.	1.2	10
5481	Deep intraspecific divergence in <i>Drosophila meridionalis</i> , a cactophilic member of the New World <i>Drosophila</i> repleta group. <i>Biological Journal of the Linnean Society</i> , 2018, 123, 163-178.	0.7	6
5482	An experimental test of alternative population augmentation scenarios. <i>Conservation Biology</i> , 2018, 32, 838-848.	2.4	24
5483	Detection of mitochondrial haplogroups in a small avarâ€slavic population from the eighthâ€“ninth century AD. <i>American Journal of Physical Anthropology</i> , 2018, 165, 536-553.	2.1	12
5484	Genetic structure and diversity of the koala population in South Gippsland, Victoria: a remnant population of high conservation significance. <i>Conservation Genetics</i> , 2018, 19, 713-728.	0.8	9
5485	Variable Molecular Markers for the Order Mantophasmatodea (Insecta). <i>Journal of Heredity</i> , 2018, 109, 477-483.	1.0	3
5486	Genetic analysis of 17 Y-STR loci from 1026 individuals of Han populations in Jilin Province, Northeast China. <i>International Journal of Legal Medicine</i> , 2018, 132, 1309-1311.	1.2	6
5487	Hierarchical metapopulation structure in a highly mobile marine predator: the southern Australian coastal bottlenose dolphin ( <i>Tursiops cf. australis</i> ). <i>Conservation Genetics</i> , 2018, 19, 637-654.	0.8	22
5488	The Evolutionary History of Nebraska Deer Mice: Local Adaptation in the Face of Strong Gene Flow. <i>Molecular Biology and Evolution</i> , 2018, 35, 792-806.	3.5	76
5489	Residence rule flexibility and descent groups dynamics shape uniparental genetic diversities in South East Asia. <i>American Journal of Physical Anthropology</i> , 2018, 165, 480-491.	2.1	13
5490	Rapid range expansion of the Brazilian free-tailed bat in the southeastern United States, 2008â€“2016. <i>Journal of Mammalogy</i> , 2018, 99, 312-320.	0.6	33
5491	Genetic assessment of milkfish ( <i>Chanos chanos</i> Forsskal) stocks based on novel short tandem repeats for marker-aided broodstock management. <i>Aquaculture Research</i> , 2018, 49, 1557-1568.	0.9	1
5492	Demography and selection shape transcriptomic divergence in field crickets. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 553-567.	1.1	6



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5493	Phylogeography of the Ibero-Maghrebian red-eyed grass snake ( <i>Natrix astreptophora</i> ). <i>Organisms Diversity and Evolution</i> , 2018, 18, 143-150.	0.7	16
5494	Environmental effects on fine-scale spatial genetic structure in four Alpine keystone forest tree species. <i>Molecular Ecology</i> , 2018, 27, 647-658.	2.0	15
5495	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
5496	Genomic data reveal cryptic lineage diversification and introgression in Californian golden cup oaks (section <i>Protobalanus</i> ). <i>New Phytologist</i> , 2018, 218, 804-818.	3.5	56
5497	Demographic history influences spatial patterns of genetic diversity in recently expanded coyote ( <i>Canis latrans</i> ) populations. <i>Heredity</i> , 2018, 120, 183-195.	1.2	18
5498	Genetic differentiation of <i>Actinidia chinensis</i> and analysis of gene flow barriers in the Qinling Mountains, the species' northern distribution boundary. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 881-895.	0.8	6
5499	Do multiple karyomorphs and population genetics of freshwater darter characines ( <i>Apareiodon</i> )	0.4	20
5500	Comparing the genetic diversity and structure of indigenous Korean and Chinese populations of <i>Laodelphax striatellus</i> Fallén using mitochondrial haplotypes. <i>Journal of Asia-Pacific Entomology</i> , 2018, 21, 233-238.	0.4	7
5501	Population genetic data of 22 autosomal STRs in Guizhou Bouyei population, Southwestern China. <i>Forensic Science International: Genetics</i> , 2018, 33, e11-e12.	1.6	3
5502	Local differentiation in the origin of stranded loggerhead turtles, <i>Caretta caretta</i> , within an eastern Turkey foraging area. <i>Ocean and Coastal Management</i> , 2018, 153, 70-75.	2.0	11
5503	Population genomic analysis suggests strong influence of river network on spatial distribution of genetic variation in invasive saltcedar across the southwestern United States. <i>Molecular Ecology</i> , 2018, 27, 636-646.	2.0	18
5504	Genetic characterization of grey wolves ( <i>Canis lupus</i> L. 1758) from Bosnia and Herzegovina: implications for conservation. <i>Conservation Genetics</i> , 2018, 19, 755-760.	0.8	5
5505	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
5506	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
5507	Independent introductions and sequential founder events shape genetic differentiation and diversity of the invasive green anole ( <i>Anolis carolinensis</i> ) on Pacific Islands. <i>Diversity and Distributions</i> , 2018, 24, 666-679.	1.9	22
5508	A mountain range is a strong genetic barrier between populations of <i>Afzelia quanzensis</i> (pod)	0.6	10
5509	Mitochondrial genome and polymorphic microsatellite markers from the abyssal sponge <i>Plenaster craigi</i> Lim & Wiklund, 2017: tools for understanding the impact of deep-sea mining. <i>Marine Biodiversity</i> , 2018, 48, 621-630.	0.3	3
5510	Development of 13 microsatellite markers for <i>Castanopsis tribuloides</i> (Fagaceae) using next-generation sequencing. <i>Molecular Biology Reports</i> , 2018, 45, 27-30.	1.0	5

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5511	Analysis of mainland Japanese and Okinawan Japanese populations using the precision ID Ancestry Panel. <i>Forensic Science International: Genetics</i> , 2018, 33, 106-109.	1.6	16
5512	Association between the polymorphism of HLA and ESRD in Dalian Han population located in north of China. <i>Immunological Investigations</i> , 2018, 47, 212-219.	1.0	8
5513	Genetic admixture of mitten crabs in the Northeast Asia hybrid zones. <i>Hydrobiologia</i> , 2018, 806, 203-214.	1.0	7
5514	Ripples on the surface. Surnames and genes in Sicily and Southern Italy. <i>Annals of Human Biology</i> , 2018, 45, 57-65.	0.4	5
5515	Allele and haplotype diversity of 12 X-STRs in Sardinia. <i>Forensic Science International: Genetics</i> , 2018, 33, e1-e3.	1.6	12
5516	Strong trans-Pacific break and local conservation units in the Galapagos shark ( <i>Carcharhinus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.2	37
5517	Demographic expansion of two <i>Tamarix</i> species along the Yellow River caused by geological events and climate change in the Pleistocene. <i>Scientific Reports</i> , 2018, 8, 60.	1.6	7
5518	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
5519	Phylogeography and demographic history of the Pacific smelt <i>Osmerus dentex</i> inferred from mitochondrial DNA variation. <i>Polar Biology</i> , 2018, 41, 877-896.	0.5	12
5520	Contrasting genetic metrics and patterns among naturalized rainbow trout ( <i>Oncorhynchus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Evolution, 2018, 8, 273-285.	0.8	10
5521	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
5522	Human-mediated and natural dispersal of an invasive fish in the eastern Great Lakes. <i>Heredity</i> , 2018, 120, 533-546.	1.2	18
5523	Colonization history of the western corn rootworm ( <i>Diabrotica virgifera virgifera</i> ) in North America: insights from random forest ABC using microsatellite data. <i>Biological Invasions</i> , 2018, 20, 665-677.	1.2	26
5524	Allelic and haplotype diversity of 12 X-STRs in the United Arab Emirates. <i>Forensic Science International: Genetics</i> , 2018, 33, e4-e6.	1.6	15
5525	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
5526	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
5527	Long-term genetic consequences of mammal reintroductions into an Australian conservation reserve. <i>Biological Conservation</i> , 2018, 219, 1-11.	1.9	43
5528	Ice sheets and genetics: Insights into the phylogeography of Scottish Atlantic salmon, <i>Salmo salar</i> L.. <i>Journal of Biogeography</i> , 2018, 45, 51-63.	1.4	8

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5529	Long-distance dispersal or postglacial contraction? Insights into disjunction between Himalaya–Hengduan Mountains and Taiwan in a cold-adapted herbaceous genus, <i>Triplostegia</i> . Ecology and Evolution, 2018, 8, 1131-1146.	0.8	23
5530	Comparative phylogeography of six red algae along the Antarctic Peninsula: extreme genetic depletion linked to historical bottlenecks and recent expansion. Polar Biology, 2018, 41, 827-837.	0.5	19
5531	Genetic variation and forensic characterization of highland Tibetan ethnicity revealed by autosomal STR markers. International Journal of Legal Medicine, 2018, 132, 1097-1102.	1.2	26
5532	Holarctic phylogeography of golden eagles ( <i>Aquila chrysaetos</i> ) and evaluation of alternative North American management approaches. Biological Journal of the Linnean Society, 2018, 123, 471-482.	0.7	7
5533	Integrated tool for microsatellite isolation and validation from the reference genome and their application in the study of breeding turnover in an endangered avian population. Integrative Zoology, 2018, 13, 553-568.	1.3	11
5534	Colonization and diversification of the white-browed shortwing (Aves: Muscicapidae: Brachypteryx) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 50	1.2	5
5535	Cryptic diversity in the <i>Oecomys roberti</i> complex: revalidation of <i>Oecomys tapajinus</i> (Rodentia,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50	0.6	8
5536	Matriclans shape populations: Insights from the Angolan Namib Desert into the maternal genetic history of southern Africa. American Journal of Physical Anthropology, 2018, 165, 518-535.	2.1	22
5537	Genetic population structure of the Hokkai shrimp <i>Pandalus latirostris</i> Rathbun, 1902 (Decapoda:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50	0.3	3
5538	Looking at genetic structure and selection signatures of the Mexican chicken population using single nucleotide polymorphism markers. Poultry Science, 2018, 97, 791-802.	1.5	8
5539	The Comoros Show the Earliest Austronesian Gene Flow into the Swahili Corridor. American Journal of Human Genetics, 2018, 102, 58-68.	2.6	32
5540	<i>Myotis myotis</i> (Chiroptera: Vespertilionidae) diverges into two distinct, Anatolian and European, populations. Zoological Journal of the Linnean Society, 2018, 183, 226-235.	1.0	6
5541	Population-level assessment of genetic diversity and habitat fragmentation in critically endangered <i>Gorilla gorilla gorilla</i> gorillas. American Journal of Physical Anthropology, 2018, 165, 565-575.	2.1	14
5542	Estimating the age of Hb Gâ€Coushatta [Î22(B4)Gluâ€Ala] mutation by haplotypes of Î2â€globin gene cluster in Denizli, Turkey. Molecular Genetics & Genomic Medicine, 2018, 6, 547-554.	0.6	3
5543	Genetic Diversity and Antifungal Susceptibility of <i>Candida parapsilosis</i> Sensu Stricto Isolated from Bloodstream Infections in Turkish Patients. Mycopathologia, 2018, 183, 701-708.	1.3	7
5544	Patterns of geographic variation of thermal adapted candidate genes in <i>Drosophila subobscura</i> sex chromosome arrangements. BMC Evolutionary Biology, 2018, 18, 60.	3.2	11
5545	Haplotype analysis of APOE intragenic SNPs. BMC Neuroscience, 2018, 19, 16.	0.8	43
5546	Meta-populational demes constitute a reservoir for large MHC allele diversity in wild house mice ( <i>Mus musculus</i> ). Frontiers in Zoology, 2018, 15, 15.	0.9	11

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5547	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
5548	Signatures of historical selection on MHC reveal different selection patterns in the moor frog ( <i>Rana</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	1.2	17
5549	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
5550	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
5551	Decreasing proportion of <i>Anopheles darlingi</i> biting outdoors between long-lasting insecticidal net distributions in peri-liquitos, Amazonian Peru. <i>Malaria Journal</i> , 2018, 17, 86.	0.8	32
5552	Along for the ride or missing it altogether: exploring the host specificity and diversity of haemogregarines in the Canary Islands. <i>Parasites and Vectors</i> , 2018, 11, 190.	1.0	12
5553	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
5554	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
5555	Age-dependent, negative heterozygosity-fitness correlations and local effects in an endangered Caribbean reptile, <i>Iguana delicatissima</i> . <i>Ecology and Evolution</i> , 2018, 8, 2088-2096.	0.8	10
5556	Genetic differentiation between local populations of <i>Ips typographus</i> in the high Tatra Mountains range. <i>Scandinavian Journal of Forest Research</i> , 2018, 33, 215-221.	0.5	4
5557	Contemporary factors influencing genetic diversity in the Alaska humpback whitefish <i>Coregonus clupeaformis</i> complex. <i>Journal of Fish Biology</i> , 2018, 92, 1065-1081.	0.7	0
5558	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
5559	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
5560	Seascape genetics of a flatfish reveals local selection under high levels of gene flow. <i>ICES Journal of Marine Science</i> , 2018, 75, 675-689.	1.2	40
5561	Oceanographic variation influences spatial genomic structure in the sea scallop, <i>Placopecten magellanicus</i> . <i>Ecology and Evolution</i> , 2018, 8, 2824-2841.	0.8	12
5562	Strong population structure but no equilibrium yet: Genetic connectivity and phylogeography in the kelp <i>Saccharina latissima</i> (Laminariales, Phaeophyta). <i>Ecology and Evolution</i> , 2018, 8, 4265-4277.	0.8	17
5563	Genetic Divergence of Nearby Walleye Spawning Groups in Central Lake Erie: Implications for Management. <i>North American Journal of Fisheries Management</i> , 2018, 38, 783-793.	0.5	11
5564	HLA -A, -C, -B, -DRB1, -DQB1 and -DPB1 allele and haplotype frequencies in 4514 healthy Norwegians. <i>Human Immunology</i> , 2018, 79, 527-529.	1.2	16

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5565	Significant loss of mitochondrial diversity within the last century due to extinction of peripheral populations in eastern gorillas. <i>Scientific Reports</i> , 2018, 8, 6551.	1.6	28
5566	Twenty-five years after: post-introduction association of <i>Mecinus janthinus</i> s.l. with invasive host toadflaxes <i>Linaria vulgaris</i> and <i>Linaria dalmatica</i> in North America. <i>Annals of Applied Biology</i> , 2018, 173, 16-34.	1.3	11
5567	Uncovering the geographical and host impacts on the classification of <i>Vibrio vulnificus</i> . <i>Evolutionary Applications</i> , 2018, 11, 883-890.	1.5	6
5568	Defining conservation units with enhanced molecular tools to reveal fine scale structuring among Mediterranean green turtle rookeries. <i>Biological Conservation</i> , 2018, 222, 253-260.	1.9	21
5569	Phylogenetics of Merkel-cell polyomavirus and human polyomavirus 6: A long-term history with humans. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 210-220.	1.2	12
5570	Mainland and Island Populations of <i>Coccothrinax argentata</i> (Arecaceae): Revisiting a Common Garden Experiment in its 18th Year. <i>Systematic Botany</i> , 2018, 43, 153-161.	0.2	0
5571	Forensic applicability of multi-allelic InDels with mononucleotide homopolymer structures. <i>Electrophoresis</i> , 2018, 39, 2136-2143.	1.3	16
5572	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
5573	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
5574	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
5575	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
5576	High-resolution HLA allele and haplotype frequencies in majority and minority populations of Costa Rica and Nicaragua: Differential admixture proportions in neighboring countries. <i>Hla</i> , 2018, 91, 514-529.	0.4	20
5577	Genetic polymorphism of <i>Baylisascaris procyonis</i> in host infrapopulations and component populations in the Central USA. <i>Parasitology International</i> , 2018, 67, 392-396.	0.6	1
5578	Sequence polymorphism data of the hypervariable regions of mitochondrial DNA in the Yadav population of Haryana. <i>Data in Brief</i> , 2018, 18, 164-171.	0.5	2
5579	Levels of genetic diversity and inferred origins of <i>Penaeus vannamei</i> culture resources in China: Implications for the production of a broad synthetic base population for genetic improvement. <i>Aquaculture</i> , 2018, 491, 221-231.	1.7	22
5580	Ancient DNA reveals temporal population structure within the South-Central Andes area. <i>American Journal of Physical Anthropology</i> , 2018, 166, 851-860.	2.1	3
5581	Genetic impacts of a commercial aquaculture lease on adjacent oyster populations. <i>Aquaculture</i> , 2018, 491, 310-320.	1.7	6
5582	Fishing in troubled waters: Revealing genomic signatures of local adaptation in response to freshwater pollutants in two macroinvertebrates. <i>Science of the Total Environment</i> , 2018, 633, 875-891.	3.9	15

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5583	Genomics of Parallel Ecological Speciation in Lake Victoria Cichlids. <i>Molecular Biology and Evolution</i> , 2018, 35, 1489-1506.	3.5	103
5584	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
5585	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
5586	Genetic characterisation of 19 autosomal STR loci in a population sample from the Southeastern Anatolia Region of Turkey. <i>Annals of Human Biology</i> , 2018, 45, 148-159.	0.4	1
5587	Structure and genetic variation among populations of <i>Euschistus heros</i> from different geographic regions in Brazil. <i>Entomologia Experimentalis Et Applicata</i> , 2018, 166, 191-203.	0.7	10
5588	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
5589	Which species, how many, and from where: Integrating habitat suitability, population genomics, and abundance estimates into species reintroduction planning. <i>Global Change Biology</i> , 2018, 24, 3729-3748.	4.2	30
5590	Across rather than between river genetic structure in Atlantic salmon <i>Salmo salar</i> in north-east Scotland, UK: potential causes and management implications. <i>Journal of Fish Biology</i> , 2018, 92, 607-620.	0.7	5
5591	How many daddies: microsatellite genotyping reveals polyandry in a live-bearing clinid fish <i>Muraenoclinus dorsalis</i> . <i>Journal of Fish Biology</i> , 2018, 92, 1435-1445.	0.7	5
5592	A comprehensive mitochondrial DNA mixed-stock analysis clarifies the composition of loggerhead turtle aggregates in the Adriatic Sea. <i>Marine Biology</i> , 2018, 165, 1.	0.7	15
5593	Expanded Croatian 12 X-STR loci database with an overview of anomalous profiles. <i>Forensic Science International: Genetics</i> , 2018, 34, 249-256.	1.6	10
5594	Genetic differentiation and forensic efficiency evaluation for Chinese Salar ethnic minority based on a 5-dye multiplex insertion and deletion panel. <i>Gene</i> , 2018, 660, 41-50.	1.0	10
5595	The analysis of mitochondrial data indicates the existence of population substructure in Karayaka sheep. <i>Small Ruminant Research</i> , 2018, 162, 25-29.	0.6	8
5596	Morphological and genetic correlates in the left-right asymmetric scale-eating cichlid fish of Lake Tanganyika. <i>Biological Journal of the Linnean Society</i> , 2018, 124, 67-84.	0.7	13
5597	Dispersal mechanisms for zebra mussels: population genetics supports clustered invasions over spread from hub lakes in Minnesota. <i>Biological Invasions</i> , 2018, 20, 2461-2484.	1.2	10
5598	Mitochondrial signatures revealed panmixia in <i>Lutjanus argentimaculatus</i> (Forsskål 1775). <i>Journal of Genetics</i> , 2018, 97, 179-187.	0.4	2
5599	Metabolic and genetic markers' associations with elevated levels of alanine aminotransferase in adolescents. <i>Journal of Pediatric Endocrinology and Metabolism</i> , 2018, 31, 407-414.	0.4	5
5600	The comparative phylogeography of shore crabs and their acanthocephalan parasites. <i>Marine Biology</i> , 2018, 165, 1.	0.7	8



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5601	From wild to domestic reindeer – Genetic evidence of a non-native origin of reindeer pastoralism in northern Fennoscandia. <i>Journal of Archaeological Science: Reports</i> , 2018, 19, 279-286.	0.2	27
5602	Self-reported color-race and genomic ancestry in an admixed population: A contribution of a nationwide survey in patients with type 1 diabetes in Brazil. <i>Diabetes Research and Clinical Practice</i> , 2018, 140, 245-252.	1.1	29
5603	<i>Bathynomus giganteus</i> (Isopoda: Cirolanidae) and the canyon: a population genetics assessment of De Soto Canyon as a glacial refugium for the giant deep-sea isopod. <i>Hydrobiologia</i> , 2018, 825, 211-225.	1.0	5
5604	High genetic diversity in a threatened clonal species, <i>Cypripedium calceolus</i> (Orchidaceae), enables long-term stability of the species in different biogeographical regions in Estonia. <i>Botanical Journal of the Linnean Society</i> , 2018, 186, 560-571.	0.8	24
5605	Case study of microsatellite polymorphism of European perch in selected commercially important lakes of Latvia. <i>Biologia (Poland)</i> , 2018, 73, 273-280.	0.8	2
5606	A partition of <i>Toxoplasma gondii</i> genotypes across spatial gradients and among host species, and decreased parasite diversity towards areas of human settlement in North America. <i>International Journal for Parasitology</i> , 2018, 48, 611-619.	1.3	42
5607	Different Selected Mechanisms Attenuated the Inhibitory Interaction of KIR2DL1 with C2+ HLA-C in Two Indigenous Human Populations in Southern Africa. <i>Journal of Immunology</i> , 2018, 200, 2640-2655.	0.4	32
5608	Effects of the Tanaka Line on the genetic structure of <i>Bombax ceiba</i> (Malvaceae) in dry-hot valley areas of southwest China. <i>Ecology and Evolution</i> , 2018, 8, 3599-3608.	0.8	17
5609	High-throughput analysis of satellite DNA in the grasshopper <i>Pyrgomorpha conica</i> reveals abundance of homologous and heterologous higher-order repeats. <i>Chromosoma</i> , 2018, 127, 323-340.	1.0	29
5610	Investigation of 12 X-STR loci in Mongolian and Eastern Han populations of China with comparison to other populations. <i>Scientific Reports</i> , 2018, 8, 4287.	1.6	16
5611	Genetic differentiation, races and interracial admixture in avocado ( <i>Persea americana</i> Mill.), and <i>Persea</i> spp. evaluated using SSR markers. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 1195-1215.	0.8	41
5612	Plant macrofossils from lake sediment as the material to assess ancient genetic diversity: Did deforestation influence Norway spruce ( <i>Picea abies</i> ) in the South Carpathians?. <i>Quaternary International</i> , 2018, 477, 106-116.	0.7	5
5613	Mitochondrial DNA analyses and ecological niche modeling reveal post- <i>LGM</i> 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
5614	Genetic diversity and population structure of <i>Theileria parva</i> in South Sudan. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 806-813.	1.1	11
5615	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
5616	Infection patterns and molecular data reveal host and tissue specificity of <i>Posthodiplostomum</i> species in centrarchid hosts. <i>Parasitology</i> , 2018, 145, 1458-1468.	0.7	13
5617	A pantropically introduced tree is followed by specific ectomycorrhizal symbionts due to pseudo-vertical transmission. <i>ISME Journal</i> , 2018, 12, 1806-1816.	4.4	23
5618	The demographic history and mutational load of African hunter-gatherers and farmers. <i>Nature Ecology and Evolution</i> , 2018, 2, 721-730.	3.4	38

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5619	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
5620	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
5621	Sex ratio rather than population size affects genetic diversity in <i>Antennaria dioica</i> . <i>Plant Biology</i> , 2018, 20, 789-796.	1.8	18
5622	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
5623	New insights on geographical/ecological populations within <i>Coilia nasus</i> (Clupeiformes): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 587	0.7	7
5624	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
5625	Population data of 23 autosomal STR loci in the Chinese Han population from Guangdong Province in southern China. <i>International Journal of Legal Medicine</i> , 2018, 132, 133-135.	1.2	21
5626	Resolving the ambiguities in the identification of two smooth-hound sharks ( <i>Mustelus mustelus</i> and) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 262	0.3	19
5627	The critical role of local refugia in postglacial colonization of Chinese pine: joint inferences from DNA analyses, pollen records, and species distribution modeling. <i>Ecography</i> , 2018, 41, 592-606.	2.1	26
5628	Invasion of the Hawaiian Islands by a parasite infecting imperiled stream fishes. <i>Ecography</i> , 2018, 41, 528-539.	2.1	8
5629	Polymorphisms, differentiation, and phylogeny of 10 Tibetan goat populations inferred from mitochondrial D-loop sequences. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 439-445.	0.7	12
5630	Historical mitochondrial diversity in African leopards ( <i>Panthera pardus</i> ) revealed by archival museum specimens. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 455-473.	0.7	15
5631	Four evolutionarily significant units among narrow-barred Spanish mackerel ( <i>Scomberomorus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262	0.3	6
5632	The population structure and genetic divergence of <i>Labeo gonius</i> (Hamilton, 1822) analyzed through mitochondrial DNA cytochrome b gene for conservation in Indian waters. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 543-551.	0.7	9
5633	Characterization of mitochondrial DNA polymorphisms in the Han population in Liaoning Province, Northeast China. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 250-255.	0.7	3
5634	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 ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 262	0.3	19
5635	Genetic diversity of <i>Nephtys hombergii</i> (Phyllodocida, Polychaeta) associated with environmental factors in a highly fluctuating ecosystem. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2018, 98, 777-789.	0.4	1
5636	Geographic variation in the spotted-wing drosophila, <i>Drosophila suzukii</i> (Diptera): Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 262	0.7	10

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5637	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
5638	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
5639	Genetic diversity and population demography of the endemic species <i>Acrossocheilus longipinnis</i> (Teleostei, Cyprinidae) based on mtDNA COI and cyt <i>b</i> gene sequences. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 403-408.	0.7	5
5640	Mitochondrial DNA sequence variation in Iranian native dogs. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 394-402.	0.7	1
5641	With no gap to mind: a shallow genealogy within the world's most widespread small pelagic fish. Ecology, 2018, 41, 491-504.	2.1	16
5642	Evaluation of Genetic Diversity, Population Structure, and Relationship Between Legendary Vechur Cattle and Crossbred Cattle of Kerala State, India. Animal Biotechnology, 2018, 29, 50-58.	0.7	20
5643	Population structure, genetic diversity, and sexual state of the rice brown spot pathogen <i>Bipolaris oryzae</i> from three Asian countries. Plant Pathology, 2018, 67, 181-192.	1.2	26
5644	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
5645	Phylogeography of Lionfishes (Pterois) Indicate Taxonomic Over Splitting and Hybrid Origin of the Invasive <i>Pterois volitans</i> . Journal of Heredity, 2018, 109, 162-175.	1.0	39
5646	Population data of 17 Y-STRs (Yfiler) from Punjabis and Kashmiris of Pakistan. International Journal of Legal Medicine, 2018, 132, 137-138.	1.2	22
5647	Cytochrome c oxidase subunit I haplotype reveals high genetic diversity of <i>Angiostrongylus malaysiensis</i> (Nematoda: Angiostrongylidae). Journal of Helminthology, 2018, 92, 254-259.	0.4	11
5648	Heart failure and endothelial nitric oxide synthase G894T gene polymorphism frequency variations within ancestries. Nitric Oxide - Biology and Chemistry, 2018, 73, 60-65.	1.2	0
5649	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
5650	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
5651	Signature of postglacial colonization on contemporary genetic structure and diversity of <i>Quadrula quadrula</i> (Bivalvia: Unionidae). Hydrobiologia, 2018, 810, 207-225.	1.0	15
5652	Small-scale intraspecific patterns of adaptive immunogenetic polymorphisms and neutral variation in Lake Superior lake trout. Immunogenetics, 2018, 70, 53-66.	1.2	7
5653	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
5654	Genetic analysis of ciliates living on the groundwater amphipod <i>Crangonyx islandicus</i> (Amphipoda: Crangonyctidae). Acta Zoologica, 2018, 99, 188-198.	0.6	7

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5655	Linking genetic and ecological differentiation in an ungulate with a circumpolar distribution. <i>Ecography</i> , 2018, 41, 922-937.	2.1	15
5656	Yellow sigatoka epidemics caused by a panmictic population of <i>Mycosphaerella musicola</i> in Brazil. <i>Plant Pathology</i> , 2018, 67, 295-302.	1.2	7
5657	From river to farm: an evaluation of genetic diversity in wild and aquaculture stocks of <i>Brycon amazonicus</i> (Spix & Agassiz, 1829), Characidae, Bryconinae. <i>Hydrobiologia</i> , 2018, 805, 75-88.	1.0	22
5658	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
5659	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
5660	Spatial genetic structure and body size divergence in endangered <i>Gymnogobius isaza</i> in ancient Lake Biwa. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 756-764.	0.7	1
5661	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
5662	Molecular Characterization of the Indigenous Stingless Bees ( <i>Tetragonula</i> spp. Complex) Using ISSR Marker from Southern Peninsular India. <i>Neotropical Entomology</i> , 2018, 47, 106-117.	0.5	3
5663	Population genetic analysis of a 21-plex DIP panel in seven Chinese ethnic populations. <i>International Journal of Legal Medicine</i> , 2018, 132, 145-147.	1.2	4
5664	Population genetic analysis of the Globalfiler STR loci in 3032 individuals from the Altay Han population of Xinjiang in northwest China. <i>International Journal of Legal Medicine</i> , 2018, 132, 141-143.	1.2	14
5665	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
5666	Elevational divergence in the great tit complex revealed by major hemoglobin genes. <i>Environmental Epigenetics</i> , 2018, 64, 455-464.	0.9	7
5667	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
5668	Genetic variation of the land-locked freshwater shrimp <i>Caridina pseudodenticulata</i> (Decapoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10 29, 687-694.	0.7	3
5669	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
5670	Genetic analysis of 12 X-STR loci in the Serbian population from Vojvodina Province. <i>International Journal of Legal Medicine</i> , 2018, 132, 405-408.	1.2	11
5671	Army imposters: diversification of army ant-mimicking beetles with their Eciton hosts. <i>Insectes Sociaux</i> , 2018, 65, 59-75.	0.7	7
5672	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

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5673	Phylogeography of the sandy beach amphipod <i>Haustorioides japonicus</i> along the Sea of Japan: Paleogeographical signatures of cryptic regional divergences. <i>Estuarine, Coastal and Shelf Science</i> , 2018, 200, 19-30.	0.9	17
5674	SNP typing using the HID-Ion AmpliSeq <sup>®</sup> Identity Panel in a southern Chinese population. <i>International Journal of Legal Medicine</i> , 2018, 132, 997-1006.	1.2	22
5675	Relative Contribution of Seed Tuber- and Soilborne Inoculum to Potato Disease Development and Changes in the Population Genetic Structure of <i>Rhizoctonia solani</i> AG 3-PT under Field Conditions in South Africa. <i>Plant Disease</i> , 2018, 102, 60-66.	0.7	6
5676	Genetic evidence of fragmented populations and inbreeding in the Colombian endemic Dahlia <sup>™</sup> s toad-headed turtle ( <i>Mesoclemmys dahlia</i> ). <i>Conservation Genetics</i> , 2018, 19, 221-233.	0.8	9
5677	Fire Does Not Strongly Affect Genetic Diversity or Structure of a Common Treefrog in the Endangered Florida Scrub. <i>Journal of Heredity</i> , 2018, 109, 243-252.	1.0	7
5678	High-resolution mitochondrial DNA analysis sheds light on human diversity, cultural interactions, and population mobility in Northwestern Amazonia. <i>American Journal of Physical Anthropology</i> , 2018, 165, 238-255.	2.1	42
5679	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
5680	Phylogeography and Population Genetic Analyses in the Iberian Toothcarp ( <i>Aphanius iberus</i> ) Tj ETQq1 1 0.784314 ggBT /Overlock 10 Tf	1.0	11
5681	Spatial and Temporal Scales of Range Expansion in Wild <i>Phaseolus vulgaris</i> . <i>Molecular Biology and Evolution</i> , 2018, 35, 119-131.	3.5	76
5682	A GHEP-ISFG collaborative study on the genetic variation of 38 autosomal indels for human identification in different continental populations. <i>Forensic Science International: Genetics</i> , 2018, 32, 18-25.	1.6	12
5683	Repeated expansions and fragmentations linked to Pleistocene climate changes shaped the genetic structure of a woody climber, <i>Actinidia arguta</i> (Actinidiaceae). <i>Botany</i> , 2018, 96, 19-31.	0.5	17
5684	Pedigree reconstruction using molecular data reveals an early warning sign of gene diversity loss in an island population of Tasmanian devils ( <i>Sarcophilus harrisii</i> ). <i>Conservation Genetics</i> , 2018, 19, 439-450.	0.8	27
5685	Microbial sequence typing in the genomic era. <i>Infection, Genetics and Evolution</i> , 2018, 63, 346-359.	1.0	50
5686	Genetic variability of CYP2D6, CYP2B6, CYP2C9 and CYP2C19 genes across the Italian Peninsula. <i>Annals of Human Biology</i> , 2018, 45, 66-71.	0.4	10
5687	Genetic divergence among and within Arctic char ( <i>Salvelinus alpinus</i> ) populations inhabiting landlocked and sea-accessible sites in Labrador, Canada. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2018, 75, 1256-1269.	0.7	20
5688	Inbreeding in the exploited limpet <i>Patella aspera</i> across the Macaronesia archipelagos (NE Atlantic): Implications for conservation. <i>Fisheries Research</i> , 2018, 198, 180-188.	0.9	11
5689	Effect of coffee agriculture management on the population structure of a forest dwelling rodent ( <i>Heteromys desmarestianus goldmani</i> ). <i>Conservation Genetics</i> , 2018, 19, 495-499.	0.8	10
5690	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

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5691	Confirmation of a unique and genetically diverse “heritage” strain of brook trout ( <i>Salvelinus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.8	5
5692	Conservation and genetic characterisation of common bean landraces from Cilento region (southern) Tj ETQq1 1 0 784314 rgBT /Overlock 13	0.5	3
5693	Genetic differentiation in populations of lane snapper ( <i>Lutjanus synagris</i> “Lutjanidae) from Western Atlantic as revealed by multilocus analysis. Fisheries Research, 2018, 198, 138-149.	0.9	12
5694	Cryptic speciation in the <i>Merodon luteomaculatus</i> complex (Diptera: Syrphidae) from the eastern Mediterranean. Journal of Zoological Systematics and Evolutionary Research, 2018, 56, 170-191.	0.6	25
5695	Genetic characteristics and possible introduced origin of the paradise fish <i>Macropodus opercularis</i> in the Ryukyu Archipelago, Japan. Ichthyological Research, 2018, 65, 134-141.	0.5	5
5696	The impact of successive mass selection on population genetic structure in the Pacific oyster ( <i>Crassostrea gigas</i> ) revealed by microsatellite markers. Aquaculture International, 2018, 26, 113-125.	1.1	9
5697	Population data and mutation rates of 20 autosomal STR loci in a Chinese Han population from Yunnan Province, Southwest China. International Journal of Legal Medicine, 2018, 132, 1083-1085.	1.2	15
5698	Geography, geology and ecology influence population genetic diversity and structure in the endangered endemic Azorean Ammi ( <i>Apiaceae</i> ). Plant Systematics and Evolution, 2018, 304, 163-176.	0.3	5
5699	Rapid discovery of SNPs that differentiate hatchery steelhead trout from ESA-listed natural-origin steelhead trout using a 57K SNP array. Canadian Journal of Fisheries and Aquatic Sciences, 2018, 75, 1160-1168.	0.7	8
5700	Conservation genetics of redbside dace ( <i>Clinostomus elongatus</i> ): phylogeography and contemporary spatial structure. Conservation Genetics, 2018, 19, 409-424.	0.8	7
5701	Forensic features and phylogenetic analyses of Sichuan Han population via 23 autosomal STR loci included in the Huaxia Platinum System. International Journal of Legal Medicine, 2018, 132, 1079-1082.	1.2	60
5702	Population data and forensic efficiency of 21 autosomal STR loci included in AGCU EX22 amplification system in the Wanzhou Han population. International Journal of Legal Medicine, 2018, 132, 153-155.	1.2	5
5703	Origin and phylogeography of African savannah elephants ( <i>Loxodonta africana</i> ) in Kruger and nearby parks in southern Africa. Conservation Genetics, 2018, 19, 155-167.	0.8	8
5704	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). Systematics and Biodiversity, 2018, 16, 171-187.	0.5	35
5705	Population genetics and distribution data reveal conservation concerns to the sky island endemic <i>Pithecopus megacephalus</i> (Anura, Phyllomedusidae). Conservation Genetics, 2018, 19, 99-110.	0.8	16
5706	Population genetic structure of the parasite <i>Anisakis simplex</i> (s. s.) collected in <i>Clupea harengus</i> L. from North East Atlantic fishing grounds. Fisheries Research, 2018, 202, 103-111.	0.9	16
5707	Single-nucleotide polymorphism data describe contemporary population structure and diversity in allochronic lineages of pink salmon ( <i>Oncorhynchus gorbuscha</i> ). Canadian Journal of Fisheries and Aquatic Sciences, 2018, 75, 987-997.	0.7	15
5708	Genetic connectivity in a herbivorous coral reef fish ( <i>Acanthurus leucosternon</i> Bennet, 1833) in the Eastern African region. Hydrobiologia, 2018, 806, 237-250.	1.0	13



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5709	Cryptic genetic divergence in <i>Scolopsis taenioptera</i> (Perciformes: Nemipteridae) in the western Pacific Ocean. <i>Ichthyological Research</i> , 2018, 65, 92-100.	0.5	8
5710	Conservation genetics of an endemic and threatened amphibian ( <i>Capensibufo rosei</i> ): a leap towards establishing a genetic monitoring framework. <i>Conservation Genetics</i> , 2018, 19, 349-363.	0.8	4
5711	Demographic inference and genetic diversity of <i>Octopus mimus</i> (Cephalopoda: Octopodidae) throughout the Humboldt Current System. <i>Hydrobiologia</i> , 2018, 808, 125-135.	1.0	12
5712	<i>Maculinea rebeli</i> (<sc>H</sc>irschke) – A phantom or reality? Novel contribution to a long-standing debate over the taxonomic status of an enigmatic <sc>L</sc>ycaenidae butterfly. <i>Systematic Entomology</i> , 2018, 43, 166-182.	1.7	14
5713	Population genetic structure of lumpfish along the Norwegian coast: aquaculture implications. <i>Aquaculture International</i> , 2018, 26, 49-60.	1.1	15
5714	Bank vole immunoheterogeneity may limit <i>Nephropatia Epidemica</i> emergence in a French non-endemic region. <i>Parasitology</i> , 2018, 145, 393-407.	0.7	14
5715	Genetic variation of complete mitochondrial genome sequences of the Sumatran rhinoceros ( <i>Dicerorhinus sumatrensis</i> ). <i>Conservation Genetics</i> , 2018, 19, 397-408.	0.8	8
5716	Intracontinental plant invader shows matching genetic and chemical profiles and might benefit from high defence variation within populations. <i>Journal of Ecology</i> , 2018, 106, 714-726.	1.9	25
5717	Multidisciplinary approaches for species delimitation in <i>Sisyrinchium</i> (<sc>I</sc>ridaceae). <i>Plant Species Biology</i> , 2018, 33, 3-15.	0.6	4
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5719	X-chromosomal STR-based genetic structure of Sichuan Tibetan minority ethnicity group and its relationships to various groups. <i>International Journal of Legal Medicine</i> , 2018, 132, 409-413.	1.2	48
5720	Contemporary range expansion of the Virginia opossum (<i>Didelphis</i> <i>virginiana</i>) impacted by humans and snow cover. <i>Canadian Journal of Zoology</i> , 2018, 96, 107-115.	0.4	19
5721	First microsatellite data on <sc><i>Proteus anguinus</i></sc> reveal weak genetic structure between the caves of Postojna and Planina. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2018, 28, 241-246.	0.9	10
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5723	Comparative phylogeography of a vulnerable bat and its ectoparasite reveals dispersal of a non-mobile parasite among distinct evolutionarily significant units of the host. <i>Conservation Genetics</i> , 2018, 19, 481-494.	0.8	15
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5725	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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5731	Lack of genetic population structure of slimy sculpin in a large, fragmented lake. <i>Ecology of Freshwater Fish</i> , 2018, 27, 699-709.	0.7	5
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5735	Fine-scale population structure of <i>Lobatus gigas</i> in Jamaica's exclusive economic zone considering hydrodynamic influences. <i>Fisheries Research</i> , 2018, 199, 53-62.	0.9	10
5736	Population genetics of traditional landraces of <i>Cucurbita pepo</i> L., 1753 in the cloud forest in Baja Verapaz, Guatemala. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 979-991.	0.8	7
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5738	Tau haplotypes support the Asian ancestry of the Roma population settled in the Basque Country. <i>Heredity</i> , 2018, 120, 91-99.	1.2	6
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5743	Climatic suitability, isolation by distance and river resistance explain genetic variation in a Brazilian whiptail lizard. <i>Heredity</i> , 2018, 120, 251-265.	1.2	39
5744	Looking back to go forward: genetics informs future management of captive and reintroduced populations of the black-footed rock-wallaby <i>Petrogale lateralis</i> . <i>Conservation Genetics</i> , 2018, 19, 235-247.	0.8	13

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5751	The Eastern side of the Westernmost Europeans: Insights from subclades within Y-chromosome haplogroup J-M304. <i>American Journal of Human Biology</i> , 2018, 30, e23082.	0.8	17
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5755	Inferring Chinese surnames with Y-STR profiles. <i>Forensic Science International: Genetics</i> , 2018, 33, 66-71.	1.6	12
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5761	Genetic diversity and population history of <i>Tanichthys albonubes</i> (Teleostei). <i>Journal of Heredity</i> , 2018, 109, 422-434.	0.9	12
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5848	Yâ€chromosome haplotype analysis revealing multiple paternal origins in swamp buffaloes of China and Southeast Asia. <i>Journal of Animal Breeding and Genetics</i> , 2018, 135, 442-449.	0.8	3
5849	Bottlenecks in the transmission of porcine reproductive and respiratory syndrome virus (PRRSV1) to naïve pigs and the quasi-species variation of the virus during infection in vaccinated pigs. <i>Veterinary Research</i> , 2018, 49, 107.	1.1	11
5850	Ancient east-west divergence, recent admixture, and multiple marginal refugia shape genetic structure of a widespread oak species ( <i>Quercus acutissima</i> ) in China. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	19
5851	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
5852	Genotyping-by-sequencing supports a genetic basis for wing reduction in an alpine New Zealand stonefly. <i>Scientific Reports</i> , 2018, 8, 16275.	1.6	17

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5853	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
5854	Whole-genome sequencing and analysis of <i>Plasmodium falciparum</i> isolates from China-Myanmar border area. <i>Infectious Diseases of Poverty</i> , 2018, 7, 118.	1.5	18
5855	The Antarctic Circumpolar Current isolates and connects: Structured circumpolarity in the sea star <i>Glabaster antarctica</i> . <i>Ecology and Evolution</i> , 2018, 8, 10621-10633.	0.8	21
5856	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
5857	Diversity of the CO1 Gene of Mitochondrial DNA in Representatives of Genus <i>Antimora</i> (Moridae). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	0.3	6
5858	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
5859	Hotspots of recent hybridization between pigs and wild boars in Europe. <i>Scientific Reports</i> , 2018, 8, 17372.	1.6	53
5860	Population Connectivity and Traces of Mitochondrial Introgression in New Zealand Black-Billed Gulls ( <i>Larus bulleri</i> ). <i>Genes</i> , 2018, 9, 544.	1.0	6
5861	Genome-wide SNP profiling of worldwide goat populations reveals strong partitioning of diversity and highlights post-domestication migration routes. <i>Genetics Selection Evolution</i> , 2018, 50, 58.	1.2	87
5862	Genetic diversity of populations of the dioecious <i>Myrsine coriacea</i> (Primulaceae) in the Atlantic Forest. <i>Acta Botanica Brasilica</i> , 2018, 32, 376-385.	0.8	13
5863	Range-wide genomic data synthesis reveals transatlantic vicariance and secondary contact in Atlantic cod. <i>Ecology and Evolution</i> , 2018, 8, 12140-12152.	0.8	7
5864	Genetic structure of cultivated <i>Zanthoxylum</i> species investigated with SSR markers. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	8
5865	Genetic evidence of human mediated, historical seed transfer from the Tyrolean Alps to the Romanian Carpathians in <i>Larix decidua</i> (Mill.) forests. <i>Annals of Forest Science</i> , 2018, 75, 1.	0.8	9
5866	Intraspecific Polymorphism of the Mitochondrial DNA Control Region and Phylogeography of Little Ground Squirrel ( <i>Spermophilus pygmaeus</i> , Scuridae, Rodentia). <i>Russian Journal of Genetics</i> , 2018, 54, 1332-1341.	0.2	3
5867	Genetic diversity and population structure of <i>Haloxylon salicornicum</i> moq. in Kuwait by ISSR markers. <i>PLoS ONE</i> , 2018, 13, e0207369.	1.1	26
5868	Genotype frequency contributions of Mx1 gene in eight chicken breeds under different selection pressures. <i>3 Biotech</i> , 2018, 8, 483.	1.1	5
5869	Phylogeography and demographic history of the Chagas disease vector <i>Rhodnius nasutus</i> (Hemiptera:). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	1.3	6
5870	Genetic diversity mirrors trophic ecology in coral reef fish feeding guilds. <i>Molecular Ecology</i> , 2018, 27, 5004-5018.	2.0	5

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5872	A survey of molecular diversity and population genetic structure in North American clearwing moths (Lepidoptera: Sesiidae) using cytochrome c oxidase I. <i>PLoS ONE</i> , 2018, 13, e0202281.	1.1	6
5873	Genetic Diversity among Clouded Salamanders ( <i>Hynobius nebulosus</i> ) in Shiga Prefecture. <i>Zoological Science</i> , 2018, 35, 427.	0.3	2
5874	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
5875	Mitogenomic data indicate admixture components of Central-Inner Asian and Srubnaya origin in the conquering Hungarians. <i>PLoS ONE</i> , 2018, 13, e0205920.	1.1	26
5876	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
5877	Unexpected patterns of segregation distortion at a selfish supergene in the fire ant <i>Solenopsis invicta</i> . <i>BMC Genetics</i> , 2018, 19, 101.	2.7	22
5878	Genetic structuring of the coastal herb <i>Arthropodium cirratum</i> (Asparagaceae) is shaped by low gene flow, hybridization and prehistoric translocation. <i>PLoS ONE</i> , 2018, 13, e0204943.	1.1	4
5879	Reinterpretation of an endangered taxon based on integrative taxonomy: The case of <i>Cynara baetica</i> (Compositae). <i>PLoS ONE</i> , 2018, 13, e0207094.	1.1	7
5880	Maternal genetic and phylogenetic characteristics of domesticated cattle in northwestern China. <i>PLoS ONE</i> , 2018, 13, e0209645.	1.1	6
5881	Fine-scale population genetic structure of sugar kelp, <i>Saccharina latissima</i> (Laminariales), Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 34	0.6	26
5882	Investigating the genetic diversity and differentiation patterns in the <i>Penstemon scariosus</i> species complex under different sample sizes using AFLPs and SSRs. <i>Conservation Genetics</i> , 2018, 19, 1335-1348.	0.8	18
5883	Seascape genetics of the spiny lobster <i>Panulirus homarus</i> in the Western Indian Ocean: Understanding how oceanographic features shape the genetic structure of species with high larval dispersal potential. <i>Ecology and Evolution</i> , 2018, 8, 12221-12237.	0.8	21
5884	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
5885	Forensic parameters and admixture in seven geographical regions of the Guerrero state (South,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 1	0.4	6
5886	Association mapping of quantitative resistance to charcoal root rot in mulberry germplasm. <i>PLoS ONE</i> , 2018, 13, e0200099.	1.1	18
5887	Comparative analysis of adaptive and neutral markers of <i>Drosophila mediopunctata</i> populations dispersed among forest fragments. <i>Ecology and Evolution</i> , 2018, 8, 12681-12693.	0.8	1
5888	UDP-glucuronosyltransferase genetic variation in North African populations: a comparison with African and European data. <i>Annals of Human Biology</i> , 2018, 45, 516-523.	0.4	4

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5890	Mitochondrial characterisation of two Spanish populations from the Vera and Bejar valleys (Central) Tj ETQq1 1 0.784314 rgBT /Overlacc	0.4	0
5891	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
5892	Porous barriers? Assessment of gene flow within and among sympatric long-eared bat species. <i>Ecology and Evolution</i> , 2018, 8, 12841-12854.	0.8	16
5893	Supercolonial structure of invasive populations of the tawny crazy ant <i>Nylanderia fulva</i> in the US. <i>BMC Evolutionary Biology</i> , 2018, 18, 209.	3.2	38
5894	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
5895	Contrasting patterns of neutral and functional genetic diversity in stable and disturbed environments. <i>Ecology and Evolution</i> , 2018, 8, 12073-12089.	0.8	17
5896	Congruent population genetic structure but differing depths of divergence for three alpine stoneflies with similar ecology and geographic distributions. <i>Freshwater Biology</i> , 2019, 64, 335-347.	1.2	14
5897	Limited Genetic Structure of Gypsy Moth Populations Reflecting a Recent History in Europe. <i>Insects</i> , 2018, 9, 143.	1.0	2
5898	Genetic population structure of Japanese river sculpin <i>Cottus pollux</i> (Cottidae) large-egg type, inferred from mitochondrial DNA sequences. <i>Journal of Fish Biology</i> , 2018, 94, 325-329.	0.7	2
5899	Contrasting population genetic structure in three aggregating groupers (Percoidei: Epinephelidae) in the Indo-West Pacific: the importance of reproductive mode. <i>BMC Evolutionary Biology</i> , 2018, 18, 180.	3.2	15
5900	Demographic and genetic description of Greenland's only indigenous Atlantic salmon <i>Salmo salar</i> population. <i>Journal of Fish Biology</i> , 2018, 94, 154-164.	0.7	4
5901	Investigation of the genetic diversity of <i>Phytophthora capsici</i> in China using a universal fluorescent labelling method. <i>Journal of Phytopathology</i> , 2019, 167, 111-122.	0.5	4
5902	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
5903	Gene expression is implicated in the ability of pikas to occupy Himalayan elevational gradient. <i>PLoS ONE</i> , 2018, 13, e0207936.	1.1	9
5904	Management of Biodiversity Conservation Based on Genetic Diversity in Ecological and Agricultural Restoration. , 2018, , .		0
5905	Population Genetic Diversity and Phylogenetic Characteristics for High-Altitude Adaptive Kham Tibetan Revealed by DNATyper™ 19 Amplification System. <i>Frontiers in Genetics</i> , 2018, 9, 630.	1.1	17
5906	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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5908	Genetic diversity of Myanmar cattle breeds using complete mitochondrial D-loop sequence. <i>Journal of Animal Genetics</i> , 2018, 46, 57-67.	0.5	5
5909	Molecular signatures of divergence and selection in closely related pine taxa. <i>Tree Genetics and Genomes</i> , 2018, 14, 83.	0.6	15
5910	Paternal portrait of populations of the middle Magdalena River region (Tolima and Huila, Colombia): New insights on the peopling of Central America and northernmost South America. <i>PLoS ONE</i> , 2018, 13, e0207130.	1.1	9
5911	Genetic and structural characterization of 20 autosomal short tandem repeats in the Chinese Qinghai Han population and its genetic relationships and interpopulation differentiations with other reference populations. <i>Forensic Sciences Research</i> , 2018, 3, 145-152.	0.9	7
5912	Distribution and Genetic Diversity of the Rare Plant <i>Veratrum woodii</i> (Liliales: Melanthiaceae) in Georgia: A Preliminary Study with AFLP Fingerprint Data. <i>Systematic Botany</i> , 2018, 43, 858-869.	0.2	6
5913	Detecting the QTL-Allele System of Seed Oil Traits Using Multi-Locus Genome-Wide Association Analysis for Population Characterization and Optimal Cross Prediction in Soybean. <i>Frontiers in Plant Science</i> , 2018, 9, 1793.	1.7	19
5914	Assessing the Speciation of a Cold Water Species, Japanese Sand Lance <i>Ammodytes personatus</i> , in the Northwestern Pacific by AFLP Markers. <i>Animals</i> , 2018, 8, 224.	1.0	4
5915	Short-distance barriers affect genetic variability of <i>Rhizophora mangle</i> L. in the Yucatan Peninsula. <i>Ecology and Evolution</i> , 2018, 8, 11083-11099.	0.8	12
5916	The multiple maternal legacy of the Late Iron Age group of Urville-Nacqueville (France, Normandy) documents a long-standing genetic contact zone in northwestern France. <i>PLoS ONE</i> , 2018, 13, e0207459.	1.1	10
5917	Genomic divergence between Spanish <i>Littorina saxatilis</i> ecotypes unravels limited admixture and extensive parallelism associated with population history. <i>Ecology and Evolution</i> , 2018, 8, 8311-8327.	0.8	27
5918	Genetic diagnosis of a rare myrmecochorous species, <i>Plagiorhegma dubium</i> (Berberidaceae): Historical genetic bottlenecks and strong spatial structures among populations. <i>Ecology and Evolution</i> , 2018, 8, 8791-8802.	0.8	3
5919	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
5920	Association of STAT4, TGF $\beta$ 1, SH2B3 and PTPN22 polymorphisms with autoimmune hepatitis. <i>Experimental and Molecular Pathology</i> , 2018, 105, 279-284.	0.9	17
5921	Genetic structure and diversity within lethally managed populations of two mesopredators in South Africa. <i>Journal of Mammalogy</i> , 0, , .	0.6	5
5922	Comparative mitogenomic analyses of Amazona parrots and Psittaciformes. <i>Genetics and Molecular Biology</i> , 2018, 41, 593-604.	0.6	5
5923	The ectoparasites of hybrid ducks in New Zealand (Mallard x Grey Duck). <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2018, 7, 335-342.	0.6	2
5924	Hierarchical structuring of genetic variation at differing geographic scales in the cultivated sugar kelp <i>Saccharina latissima</i> . <i>Marine Environmental Research</i> , 2018, 142, 108-115.	1.1	9



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5926	Genetic structure and polymorphisms of Gelao ethnicity residing in southwest china revealed by X-chromosomal genetic markers. Scientific Reports, 2018, 8, 14585.	1.6	19
5927	Zostera noltii in the Canary Islands: A Genetic Description for Conservation Purposes. Journal of Coastal Research, 2018, 345, 1129-1135.	0.1	0
5928	Population Structure of Riverine and Coastal Dolphins Sotalia fluviatilis and Sotalia guianensis: Patterns of Nuclear and Mitochondrial Diversity and Implications for Conservation. Journal of Heredity, 2018, 109, 757-770.	1.0	6
5929	Genetic diversity in the camellia weevil, <i>Curculio chinensis</i> Chevrolat (Coleptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 587 Td (C Science, 2018, 21, 447-460.	0.3	10
5930	Biogeography and Distribution of the Cryptic Species Rosyface ShinerNotropis rubellusand Carmine ShinerNotropis percobromusin Illinois. Copeia, 2018, 106, 524-531.	1.4	1
5931	Conservation status of the two cryptic species of <i>Hamatocaulis vernicosus</i> (Bryophyta) in Sweden. Journal of Bryology, 2018, 40, 307-315.	0.4	12
5932	Genetic structure of South African Nguni (Zulu) sheep populations reveals admixture with exotic breeds. PLoS ONE, 2018, 13, e0196276.	1.1	14
5933	Forensic characterization and genetic polymorphisms of 19 X-chromosomal STRs in 1344 Han Chinese individuals and comprehensive population relationship analyses among 20 Chinese groups. PLoS ONE, 2018, 13, e0204286.	1.1	39
5934	The Phytogeographic History of Common Walnut in China. Frontiers in Plant Science, 2018, 9, 1399.	1.7	39
5935	Flyway structure in the circumpolar greater white-fronted goose. Ecology and Evolution, 2018, 8, 8490-8507.	0.8	12
5936	Genetic variability of <i>Panstrongylus geniculatus</i> (Reduviidae: Triatominae) in the Metropolitan District of Caracas, Venezuela. Infection, Genetics and Evolution, 2018, 66, 236-244.	1.0	7
5937	Variation in the regulatory region of <i>FZP</i> causes increases in secondary inflorescence branching and grain yield in rice domestication. Plant Journal, 2018, 96, 716-733.	2.8	65
5938	Positive selection at sites of chemosensory genes is associated with the recent divergence and local ecological adaptation in cactophilic <i>Drosophila</i> . BMC Evolutionary Biology, 2018, 18, 144.	3.2	5
5939	Genes reveal traces of common recent demographic history for most of the Uralic-speaking populations. Genome Biology, 2018, 19, 139.	3.8	67
5940	Cytosuclear incongruences hamper species delimitation in the socially polymorphic desert ants of the <i>Cataglyphis albicans</i> group in Israel. Journal of Evolutionary Biology, 2018, 31, 1828-1842.	0.8	11
5941	Population genomics of <i>Fundulus grandis</i> exposed to oil from Deepwater Horizon. Journal of Experimental Marine Biology and Ecology, 2018, 509, 82-90.	0.7	3
5942	Morphological and genetic divergence between two lineages of <i>Magnolia salicifolia</i> (Magnoliaceae) in Japan. Biological Journal of the Linnean Society, 0, , .	0.7	1

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5944	Variabilidad genética de Aedes aegypti 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
5945	Insights into the diversity of Hormogastridae (Annelida, Oligochaeta) with descriptions of six new species. Zootaxa, 2018, 4496, 65-95.	0.2	4
5946	Identification of novel haplotypes and interpretation of gene flow of mitochondrial DNA control region of Eurasian otter ( <i>Lutra lutra</i> ) for the effective conservation. Journal of Veterinary Medical Science, 2018, 80, 1791-1800.	0.3	2
5947	At the confluence of vicariance and dispersal: Phylogeography of cavernicolous springtails (Collembola: Arrhopalitidae, Tomoceridae) codistributed across a geologically complex karst landscape in Illinois and Missouri. Ecology and Evolution, 2018, 8, 10306-10325.	0.8	20
5948	Population structure of North Atlantic and North Pacific sei whales ( <i>Balaenoptera borealis</i> ) inferred from mitochondrial control region DNA sequences and microsatellite genotypes. Conservation Genetics, 2018, 19, 1007-1024.	0.8	14
5949	Insights into the introduction history and population genetic dynamics of the Argentine black-and-white tegu ( <i>Salvator merianae</i> ) in Florida. Genetica, 2018, 146, 443-459.	0.5	1
5950	Agricultural landscapes and the Loire River influence the genetic structure of the marbled newt in Western France. Scientific Reports, 2018, 8, 14177.	1.6	8
5951	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) <i>Tj ETQq0 0 0 rgBT / Overlock 10 16 50 97 To</i>	0.8	10
5952	The Influence of Selection on MHC DQA and DQB Haplotypes in the Endemic New Zealand Hector's and Maui Dolphins. Journal of Heredity, 2018, 109, 744-756.	1.0	3
5953	Polymorphism in merozoite surface protein-7E of Plasmodium vivax in Thailand: Natural selection related to protein secondary structure. PLoS ONE, 2018, 13, e0196765.	1.1	6
5954	Molecular evidence of hybridization in sympatric populations of the Enantia jethys complex (Lepidoptera: Pieridae). PLoS ONE, 2018, 13, e0197116.	1.1	10
5955	Spatial genetic structure of an endangered orchid <i>Cypripedium calceolus</i> (Orchidaceae) at a regional scale: limited gene flow in a fragmented landscape. Conservation Genetics, 2018, 19, 1449-1460.	0.8	25
5956	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
5957	Large-scale mitochondrial DNA analysis reveals new light on the phylogeography of Central and Eastern-European Brown hare ( <i>Lepus europaeus</i> Pallas, 1778). PLoS ONE, 2018, 13, e0204653.	1.1	15
5958	Effective population size and the genetic consequences of commercial whaling on the humpback whales ( <i>Megaptera novaeangliae</i> ) from Southwestern Atlantic Ocean. Genetics and Molecular Biology, 2018, 41, 253-262.	0.6	3
5959	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> ) <i>Tj ETQq0 0 0 rgBT / Overlock 10 16 50 97 To</i>	1.1	16
5960	Genomic data recover previously undetectable fragmentation effects in an endangered amphibian. Molecular Ecology, 2018, 27, 4430-4443.	2.0	43

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5962	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
5963	Phylogeography of Endangered Bitterling <i>Acheilognathus melanogaster</i> Endemic to Eastern Japan. <i>Zoological Science</i> , 2018, 35, 396-401.	0.3	1
5964	Genetic structure of populations of several endangered and endemic <i>Dianthus</i> species revealed by microsatellite markers. <i>Acta Botanica Croatica</i> , 2018, 77, 181-188.	0.3	3
5965	Clones or no clones: genetic structure of riparian <i>Populus euphratica</i> forests in Central Asia. <i>Journal of Arid Land</i> , 2018, 10, 750-766.	0.9	7
5966	Genomic heterogeneity differentiates clinical and environmental subgroups of <i>Legionella pneumophila</i> sequence type 1. <i>PLoS ONE</i> , 2018, 13, e0206110.	1.1	9
5967	Cultural Innovations Influence Patterns of Genetic Diversity in Northwestern Amazonia. <i>Molecular Biology and Evolution</i> , 2018, 35, 2719-2735.	3.5	17
5968	Riverine barrier effects on population genetic structure of the Hanuman langur ( <i>Semnopithecus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.2	10
5969	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
5970	A comprehensive portrait of Y-STR diversity of Indian populations and comparison with 129 worldwide populations. <i>Scientific Reports</i> , 2018, 8, 15421.	1.6	24
5971	Phylogeography of the gall-inducing micromoth <i>Eucercospora minutus</i> BrÃthes (Cecidosidae) reveals lineage diversification associated with the Neotropical Peripampasic Orogenic Arc. <i>PLoS ONE</i> , 2018, 13, e0201251.	1.1	8
5972	Population genetics of the endangered Maugean skate ( <i>Zearaja maugeana</i> ) in Macquarie Harbour, Tasmania. <i>Conservation Genetics</i> , 2018, 19, 1505-1512.	0.8	6
5973	Isolation and characterization of species-specific microsatellite markers for blue and black wildebeest ( <i>Connochaetes taurinus</i> and <i>C. gnou</i> ). <i>Journal of Genetics</i> , 2018, 97, 101-109.	0.4	1
5974	Genetic diversity and population structure analyses of <i>Plectranthus edulis</i> (Vatke) Agnew collections from diverse agro-ecologies in Ethiopia using newly developed EST-SSRs marker system. <i>BMC Genetics</i> , 2018, 19, 92.	2.7	26
5975	Population genetic analysis of Chadian Guinea worms reveals that human and non-human hosts share common parasite populations. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006747.	1.3	46
5976	Evidence of a Genetically Distinct Population of Striped Bass within the Saint John River, New Brunswick, Canada. <i>North American Journal of Fisheries Management</i> , 2018, 38, 1339-1349.	0.5	11
5977	Genetic diversity and population structure analysis of eight local chicken breeds of Southern Xinjiang. <i>British Poultry Science</i> , 2018, 59, 629-635.	0.8	11
5978	Genetic Diversity Patterns and Heterosis Prediction Based on SSRs and SNPs in Hybrid Parents of Pearl Millet. <i>Crop Science</i> , 2018, 58, 2379-2390.	0.8	15

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5980	Genetic structure and shell shape variation within a rocky shore whelk suggest both diverging and constraining selection with gene flow. Biological Journal of the Linnean Society, 2018, , .	0.7	2
5981	Human variation in the shape of the birth canal is significant and geographically structured. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20181807.	1.2	62
5982	Genome-Wide Evolutionary Analysis of Natural History and Adaptation in the World's Tigers. Current Biology, 2018, 28, 3840-3849.e6.	1.8	60
5983	Using high-throughput sequencing to investigate the factors structuring genomic variation of a Mediterranean grasshopper of great conservation concern. Scientific Reports, 2018, 8, 13436.	1.6	12
5984	Genetic diversities and population structures of four popular Myanmar local cattle breeds. Animal Science Journal, 2018, 89, 1648-1655.	0.6	7
5985	Nunataks or massif de refuge? A phylogeographic study of <i>Rhodiola crenulata</i> (Crassulaceae) on the world's highest sky islands. BMC Evolutionary Biology, 2018, 18, 154.	3.2	19
5986	Description and post-glacial demography of <i>Gammarus jazdzewskii</i> sp. nov. (Crustacea: Tj ETQq1 1 0.784314 rgBT /Overlock 107	0.5	19
5987	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. International Journal of Plant Sciences, 2018, 179, 730-757.	0.6	7
5988	Genetic structure of Japanese sea cucumbers ( <i>Apostichopus japonicus</i> ) along the Sanriku coast supports the effect of earthquakes and related tsunamis. Genetica, 2018, 146, 497-503.	0.5	1
5989	Positive selection in coding regions and motif duplication in regulatory regions of bottlenose dolphin MHC class II genes. PLoS ONE, 2018, 13, e0203450.	1.1	20
5990	Recent Fragmentation May Not Alter Genetic Patterns in Endangered Long-Lived Species: Evidence From <i>Taxus cuspidata</i> . Frontiers in Plant Science, 2018, 9, 1571.	1.7	24
5991	Use of rapidly evolving molecular markers to distinguish species and clarify range uncertainties in the spearfishes (Istiophoridae, Tetrapturus). Bulletin of Marine Science, 2018, 94, 1355-1378.	0.4	2
5992	Susceptibility to <i>Plasmodium vivax</i> malaria associated with DARC (Duffy antigen) polymorphisms is influenced by the time of exposure to malaria. Scientific Reports, 2018, 8, 13851.	1.6	25
5993	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. Scientific Reports, 2018, 8, 15111.	1.6	11
5994	Multiple refugia from penultimate glaciations in East Asia demonstrated by phylogeography and ecological modelling of an insect pest. BMC Evolutionary Biology, 2018, 18, 152.	3.2	26
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5996	The flounder next door: Closer evolutionary relationship between allopatric than sympatric <i>Bothus</i> (Rafinesque, 1810) species (Pleuronectiformes, Bothidae). Zoologischer Anzeiger, 2018, 277, 131-142.	0.4	3

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5998	Genetic diversity and population structure of <i>Vriesea reitzii</i> (Bromeliaceae), a species from the Southern Brazilian Highlands. Genetics and Molecular Biology, 2018, 41, 308-317.	0.6	6
5999	Selection and Utility of Single Nucleotide Polymorphism Markers to Reveal Fine-Scale Population Structure in Human Malaria Parasite <i>Plasmodium falciparum</i> . Frontiers in Ecology and Evolution, 2018, 6, .	1.1	5
6000	Evidence for Introgression Among Three Species of the <i>Anastrepha fraterculus</i> Group, a Radiating Species Complex of Fruit Flies. Frontiers in Genetics, 2018, 9, 359.	1.1	15
6001	Haplotype Loci Under Selection in Canadian Durum Wheat Germplasm Over 60 Years of Breeding: Association With Grain Yield, Quality Traits, Protein Loss, and Plant Height. Frontiers in Plant Science, 2018, 9, 1589.	1.7	29
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6003	Diversidad genética y estructura poblacional de <i>Anopheles triannulatus</i> s.l. en Cárdena, Colombia, determinadas mediante el método de región de código de barras de ADN. Biomedica, 2018, 38, 117-126.	0.3	2
6004	Rates of population differentiation and speciation are decoupled in sea snakes. Biology Letters, 2018, 14, 20180563.	1.0	12
6005	<sc>SSR</sc> markers for <i>Filago</i> subg. <i>Filago</i> (Gnaphalieae: Asteraceae) and cross-amplification in three other subgenera. Applications in Plant Sciences, 2018, 6, e01171.	0.8	3
6006	Analysis of uniparental markers reveals a complex pattern of migration within Sardinia. Annals of Human Biology, 2018, 45, 354-358.	0.4	1
6007	Genetic evidence indicates ecological divergence rather than geographic barriers structure Florida fox squirrels. Journal of Mammalogy, 2018, , .	0.6	1
6008	Hybridization between Native and Introduced Individuals of Sika Deer in the Central Part of Toyama Prefecture. Mammal Study, 2018, 43, 269.	0.2	5
6009	The use of microsatellite markers for species delimitation in Antarctic <i>Usnea</i> subgenus <i>Neuropogon</i>. Mycologia, 2018, 110, 1047-1057.	0.8	17
6010	Climatic and Soil Factors Shape the Demographical History and Genetic Diversity of a Deciduous Oak ( <i>Quercus liaotungensis</i> ) in Northern China. Frontiers in Plant Science, 2018, 9, 1534.	1.7	26
6011	Range, population structure and morphological characterization of the small range endemic bush-cricket <i>Lluciapomaresius panteli</i> (Orthoptera: Tettigoniidae: Bradyporinae). Journal of Insect Conservation, 2018, 22, 659-674.	0.8	0
6012	Complex hybridization patterns in European pond turtles ( <i>Emys orbicularis</i> ) in the Pyrenean Region. Scientific Reports, 2018, 8, 15925.	1.6	17
6013	Speciation pattern of the horned ghost crab <i>Ocypode ceratophthalmus</i> (Pallas, 1772): An evaluation of the drivers of Indo-Pacific marine biodiversity using a widely distributed species. Journal of Biogeography, 2018, 45, 2658-2668.	1.4	7
6014	Connections and containers: Using genetic data to understand how watershed evolution and human activities influence cutthroat trout biogeography. PLoS ONE, 2018, 13, e0202043.	1.1	8

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6016	Genetic Structure of the Hyrcanian Wood Frog, <i>Rana pseudodalmatina</i> (Amphibia: Ranidae) Using mtDNA Gene Sequences. Russian Journal of Genetics, 2018, 54, 1221-1228.	0.2	8
6017	Combining mitochondrial and nuclear genome analyses to dissect the effects of colonization, environment, and geography on population structure in <i>Pinus tabuliformis</i> . Evolutionary Applications, 2018, 11, 1931-1945.	1.5	28
6018	Plastid DNA variation of the endemic species <i>Oxytropis glandulosa</i> Turcz. (Fabaceae). Turkish Journal of Botany, 2018, 42, 38-50.	0.5	12
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6020	Comparative Population Genetics of Red Imported Fire Ants ( <i>Solenopsis invicta</i> ) at the University of Central Oklahoma and Lake Arcadia, Edmond, Oklahoma. American Midland Naturalist, 2018, 180, 246-257.	0.2	0
6021	Deciphering the drivers of negative speciesâ€“genetic diversity correlation in Alpine amphibians. Molecular Ecology, 2018, 27, 4916-4930.	2.0	14
6022	Development of 17 polymorphic microsatellite loci from Jeju striped field mouse, <i>Apodemus agrarius chejuensis</i> (Rodentia: Muridae), by 454 pyrosequencing. Hereditas, 2018, 155, 30.	0.5	1
6023	Development and characterization of a microsatellite library for the freshwater crab <i>Potamonautes danielsi</i> Peer, Gouws, Lazo-Wasem, Perissinotto & Miranda, 2017 (Brachyura: Potamonautidae) and its transferability across three congeneric species. Journal of Crustacean Biology, 0, , .	0.3	1
6024	Clipperton Atoll as a model to study small marine populations: Endemism and the genomic consequences of small population size. PLoS ONE, 2018, 13, e0198901.	1.1	12
6025	Landscape genetics of the foundational salt marsh plant species black needlerush ( <i>Juncus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342 Td	1.9	13
6026	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. Regional Studies in Marine Science, 2018, 24, 278-287.	0.4	14
6027	The population genomics of yellowfin tuna ( <i>Thunnus albacares</i> ) at global geographic scale challenges current stock delineation. Scientific Reports, 2018, 8, 13890.	1.6	55
6028	Mitochondrial phylogeography and population structure of the cattle tick <i>Rhipicephalus appendiculatus</i> in the African Great Lakes region. Parasites and Vectors, 2018, 11, 329.	1.0	11
6029	Limited introgression supports division of giraffe into four species. Ecology and Evolution, 2018, 8, 10156-10165.	0.8	40
6030	Population structure of a global agricultural invasive pest, <i>Bactrocera dorsalis</i> (Diptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 40	1.5	40
6031	Comparative phylogeography of parasitic Laelaps mites contribute new insights into the specialist-generalist variation hypothesis (SGVH). BMC Evolutionary Biology, 2018, 18, 131.	3.2	15
6032	Population genomics and morphometric assignment of western honey bees ( <i>Apis mellifera</i> L.) in the Republic of South Africa. BMC Genomics, 2018, 19, 615.	1.2	18



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6034	Selection on the Colombian paso horse's gaits has produced kinematic differences partly explained by the DMRT3 gene. <i>PLoS ONE</i> , 2018, 13, e0202584.	1.1	15
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6036	Quantifying dispersal between marine protected areas by a highly mobile species, the bottlenose dolphin, <i>Tursiops truncatus</i> . <i>Ecology and Evolution</i> , 2018, 8, 9241-9258.	0.8	15
6037	Genetic Assignment of Brook Trout Reveals Rapid Success of Culvert Restoration in Headwater Streams. <i>North American Journal of Fisheries Management</i> , 2018, 38, 991-1003.	0.5	15
6038	Hybridization and Genetic Structure of Neosho Smallmouth Bass in the Ozark Highlands. <i>North American Journal of Fisheries Management</i> , 2018, 38, 1226-1240.	0.5	17
6039	HLA-A, -B, -DRB1, -DQA1, and -DQB1 profile in a population from southern Brazil. <i>Hla</i> , 2018, 92, 298-303.	0.4	14
6040	Novel Microsatellite Markers for the Invasive Golden Mussel <i>Limnoperna fortunei</i> . <i>Journal of Shellfish Research</i> , 2018, 37, 485-489.	0.3	4
6041	Spatial genetic variation and habitat association of <i>Rhinichthys cataractae</i> , the longnose dace, in the Driftless Area of the upper Mississippi River basin. <i>Conservation Genetics</i> , 2018, 19, 1367-1378.	0.8	1
6042	Mitogenomics of the jaguarundi ( <i>Puma yagouaroundi</i> , Felidae, Carnivora): Disagreement between morphological subspecies and molecular data. <i>Mammalian Biology</i> , 2018, 93, 153-168.	0.8	8
6043	Genetic diversity maintained among fragmented populations of a tree undergoing range contraction. <i>Heredity</i> , 2018, 121, 304-318.	1.2	22
6044	Hybridization between two bitterling fish species in their sympatric range and a river where one species is native and the other is introduced. <i>PLoS ONE</i> , 2018, 13, e0203423.	1.1	11
6045	DNA Barcodes Suggest Possible New Cryptic Species in the <i>Codatractus melon</i> Species Group (Hesperiidae: Eudaminae) in North America. <i>Journal of the Lepidopterists' Society</i> , 2018, 72, 203-211.	0.0	3
6046	Development of 12 microsatellite markers for <i>Bombina orientalis</i> based on RNA-Seq and their usefulness in population genetic diversity. <i>Molecular Biology Reports</i> , 2018, 45, 2811-2814.	1.0	3
6047	Can the choice of diet undermine the potential genetic risk of AT1R 1166A>C gene polymorphism?. <i>Gene</i> , 2018, 679, 291-296.	1.0	2
6048	Phylogeography of Muller's termite frog suggests the vicariant role of the Central Brazilian Plateau. <i>Journal of Biogeography</i> , 2018, 45, 2508-2519.	1.4	22
6049	Historical and Contemporary Gene Flow and the Genetic Structure of Muskellunge in the Ohio River Drainage. <i>Transactions of the American Fisheries Society</i> , 2018, 147, 1067-1077.	0.6	1
6050	Molecular and morphological data reveals new insights into genetic diversity and population structure of Chinese cherry ( <i>Prunus pseudocerasus</i> Lindl.) landraces. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 2169-2187.	0.8	7

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6052	Secondary Intergradation of Various Forms of Pidschian-Like Whitefishes ( <i>Coregonus lavaretus</i> sensu Tj ETQq1 1 0.784314 rgBT /Overl	0.4	5
6053	Recent northward range extension of <i>Nerita yoldii</i> (Gastropoda: Neritidae) on artificial rocky shores in China. <i>Journal of Molluscan Studies</i> , 2018, , .	0.4	0
6054	Neutral variation does not predict immunogenetic variation in the European grayling ( <i>Thymallus</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	2.0	3
6055	Reduced representation sequencing detects only subtle regional structure in a heavily exploited and rapidly recolonizing marine mammal species. <i>Ecology and Evolution</i> , 2018, 8, 8736-8749.	0.8	9
6056	Weak population structure of the Spot-tail shark <i>Carcharhinus sorrah</i> and the Blacktip shark <i>C. limbatus</i> along the coasts of the Arabian Peninsula, Pakistan, and South Africa. <i>Ecology and Evolution</i> , 2018, 8, 9536-9549.	0.8	7
6057	Population Structure and Genetic Diversity Within the Endangered Species <i>Pityopsis ruthii</i> (Asteraceae). <i>Frontiers in Plant Science</i> , 2018, 9, 943.	1.7	24
6058	Genotyping-by-Sequencing Enhances Genetic Diversity Analysis of Crested Wheatgrass [ <i>Agropyron cristatum</i> (L.) Gaertn.]. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2587.	1.8	14
6059	Evaluation of the Genetic Diversity and Differentiation of Black Locust ( <i>Robinia pseudoacacia</i> L.) Based on Genomic and Expressed Sequence Tag-Simple Sequence Repeats. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2492.	1.8	11
6060	Discovered and disappearing? Conservation genetics of a recently named Australian carnivorous marsupial. <i>Ecology and Evolution</i> , 2018, 8, 9413-9425.	0.8	4
6061	Genetic analysis of European red foxes reveals multiple distinct peripheral populations and central continental admixture. <i>Quaternary Science Reviews</i> , 2018, 197, 257-266.	1.4	11
6062	Cultural Transmission of Fine-Scale Fidelity to Feeding Sites May Shape Humpback Whale Genetic Diversity in Russian Pacific Waters. <i>Journal of Heredity</i> , 2018, 109, 724-734.	1.0	9
6063	Phylogeography of two closely related species of <i>Allium</i> endemic to East Asia: Population evolution in response to climate oscillations. <i>Ecology and Evolution</i> , 2018, 8, 7986-7999.	0.8	2
6064	Historical and recent reductions in genetic variation of the <i>Sarotherodon galilaeus</i> population in the Sea of Galilee. <i>Conservation Genetics</i> , 2018, 19, 1323-1333.	0.8	9
6065	Genetic diversity of 21 forensic autosomal STRs and DYS391 in the Han population from Shanghai, Eastern China. <i>Forensic Science International: Genetics</i> , 2018, 37, e23-e25.	1.6	1
6066	Environmental extremes drive population structure at the northern range limit of Atlantic salmon in North America. <i>Molecular Ecology</i> , 2018, 27, 4026-4040.	2.0	26
6067	Population connectivity among shallow and mesophotic <i>Montastraea cavernosa</i> corals in the Gulf of Mexico identifies potential for refugia. <i>Coral Reefs</i> , 2018, 37, 1183-1196.	0.9	40
6068	Recent low levels of differentiation in the native <i>Bombus ephippiatus</i> (Hymenoptera: Apidae) along two Neotropical mountain-ranges in Guatemala. <i>Biodiversity and Conservation</i> , 2018, 27, 3513-3531.	1.2	11

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6070	Genetic structure analysis of mantis shrimp <i>Oratosquilla oratoria</i> based on mitochondrial DNA control region sequence. <i>Genes and Genomics</i> , 2018, 40, 1001-1009.	0.5	2
6071	Can we identify the Mexican hairless dog in the archaeological record? Morphological and genetic insights from Tizayuca, Basin of Mexico. <i>Journal of Archaeological Science</i> , 2018, 98, 128-136.	1.2	4
6072	High level of genetic connectivity in a deep-water reef fish, <i>Caulolatilus microps</i> . <i>Journal of Fish Biology</i> , 2018, 93, 766-777.	0.7	3
6073	Genetic population structure of <i>Sphaeroma wadai</i> Nunomura, 1994 (Isopoda: Sphaeromatidae) along the Japanese coast. <i>Crustacean Research</i> , 2018, 47, 111-123.	0.2	0
6074	Evidence for shifting genetic structure among Caribbean giant barrel sponges in the Florida Keys. <i>Marine Biology</i> , 2018, 165, 1.	0.7	8
6075	Population genomics of the introduced and cultivated Pacific kelp <i>Undaria pinnatifida</i> : "Marinas" not "farms" drive regional connectivity and establishment in natural rocky reefs. <i>Evolutionary Applications</i> , 2018, 11, 1582-1597.	1.5	45
6076	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
6077	Population genetic analysis reveals barriers and corridors for gene flow within and among riparian populations of a rare plant. <i>AoB PLANTS</i> , 2018, 10, plx065.	1.2	14
6078	Evolutionary and demographic processes shaping geographic patterns of genetic diversity in a keystone species, the African forest elephant ( <i>Loxodonta cyclotis</i> ). <i>Ecology and Evolution</i> , 2018, 8, 4919-4931.	0.8	9
6079	Integrative systematic revision of a Mediterranean earthworm family: Hormogastridae (Annelida). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3</i>	0.5	17
6080	Population genetic subdivision of seagrasses, <i>Syringodium isoetifolium</i> and <i>Thalassia hemprichii</i> , in the Indonesian Archipelago. <i>Botanica Marina</i> , 2018, 61, 235-245.	0.6	13
6081	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
6082	Using of microsatellite DNA profiling to identify hatchery-reared seed and assess potential genetic risks associated with large-scale release of swimming crab <i>Portunus trituberculatus</i> in Panjin, China. <i>Fisheries Research</i> , 2018, 207, 187-196.	0.9	14
6083	Effects of water pollution and river fragmentation on population genetic structure of invasive mosquitofish. <i>Science of the Total Environment</i> , 2018, 637-638, 1372-1382.	3.9	19
6084	Evolutionary history of the chili pepper <i>Capsicum baccatum</i> L. (Solanaceae): domestication in South America and natural diversification in the Seasonally Dry Tropical Forests. <i>Biological Journal of the Linnean Society</i> , 2018, 124, 466-478.	0.7	22
6085	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
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6088	Evaluation of <i>ATG5</i> polymorphisms in Italian patients with systemic lupus erythematosus: contribution to disease susceptibility and clinical phenotypes. <i>Lupus</i> , 2018, 27, 1464-1469.	0.8	25
6089	Is genetic drift to blame for testicular dysgenesis syndrome in Semliki chimpanzees ( <i>Pan</i> )? <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662 T</i>	0.3	3
6090	Concerted Pleistocene dispersal and genetic differentiation in passerine birds from the Tres Mar��as Archipelago, Mexico. <i>Auk</i> , 2018, 135, 716-732.	0.7	10
6091	Mitochondrial DNA is unsuitable to test for isolation by distance. <i>Scientific Reports</i> , 2018, 8, 8448.	1.6	76
6092	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
6093	Antimicrobial resistance and the presence of extended-spectrum beta-lactamase genes in <i>Escherichia coli</i> isolated from the environment of horse riding centers. <i>Environmental Science and Pollution Research</i> , 2018, 25, 21789-21800.	2.7	19
6094	HLA-DQA1, -DQB1, and -DRB1 Alleles Associated with Acute Tubulointerstitial Nephritis in a Chinese Population: A Single-Center Cohort Study. <i>Journal of Immunology</i> , 2018, 201, 423-431.	0.4	11
6095	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
6096	Implications of a phylogeographic approach for the selection of <i>Ceutorhynchus assimilis</i> as a potential biological control agent for <i>Lepidium draba</i> . <i>Biological Control</i> , 2018, 123, 43-52.	1.4	1
6097	Mitochondrial DNA short tandem repeats unveil hidden population structuring and migration routes of an endangered marine turtle. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2018, 28, 788-797.	0.9	18
6098	Low Genetic Diversity and Low Gene Flow Corresponded to a Weak Genetic Structure of Ruddy-Breasted Crake ( <i>Porzana fusca</i> ) in China. <i>Biochemical Genetics</i> , 2018, 56, 586-617.	0.8	3
6099	Data on haplotype diversity in the hypervariable region I, II and III of mtDNA amongst the Brahmin population of Haryana. <i>Data in Brief</i> , 2018, 17, 305-313.	0.5	2
6100	Divergent evolutionary origins and biogeographic histories of two freshwater crabs (Brachyura): <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 662 T</i> <i>Phylogenetics and Evolution</i> , 2018, 127, 119-128.	1.2	14
6101	Temporal dynamics of genetic clines of invasive European green crab ( <i>Carcinus maenas</i> ) in eastern North America. <i>Evolutionary Applications</i> , 2018, 11, 1656-1670.	1.5	19
6102	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
6103	Ancient goat genomes reveal mosaic domestication in the Fertile Crescent. <i>Science</i> , 2018, 361, 85-88.	6.0	149
6104	Population declines, genetic bottlenecks and potential hybridization in sea snakes on Australia's Timor Sea reefs. <i>Biological Conservation</i> , 2018, 225, 66-79.	1.9	6

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6105	Human impact on the diversity and virulence of the ubiquitous zoonotic parasite <i>Toxoplasma gondii</i> . Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6956-E6963.	3.3	99
6106	Concordance between genetic diversity and marine biogeography in a highly mobile marine mammal, the Risso's dolphin. Journal of Biogeography, 2018, 45, 2092-2103.	1.4	11
6107	Tandem Action of Natural and Chemical Stressors in Stream Ecosystems: Insights from a Population Genetic Perspective. Environmental Science & Technology, 2018, 52, 7962-7971.	4.6	12
6108	Population Structure of Pacific Cod <i>Gadus macrocephalus</i> in the Southern Part of the Range Based on the Microsatellite Analyses. Russian Journal of Genetics, 2018, 54, 670-679.	0.2	8
6109	Human Leukocyte Antigen-A, B, C, DRB1, and DQB1 Allele and Haplotype Frequencies in a Subset of 237 Donors in the South African Bone Marrow Registry. Journal of Immunology Research, 2018, 2018, 1-8.	0.9	9
6110	Lessons from a natural experiment: Allopatric morphological divergence and sympatric diversification in the Midas cichlid species complex are largely influenced by ecology in a deterministic way. Evolution Letters, 2018, 2, 323-340.	1.6	39
6111	Phylogeography of the Northern Alligator Lizard (Squamata, Anguillidae): Hidden diversity in a western endemic. Zoologica Scripta, 2018, 47, 462-476.	0.7	8
6112	Genetic variation and population structure of <i>Diaphorina citri</i> using cytochrome oxidase I sequencing. PLoS ONE, 2018, 13, e0198399.	1.1	12
6113	Structural Polymorphism of <i>Sinorhizobium meliloti</i> Genes Related to Virulence and Salt Tolerance. Russian Journal of Genetics, 2018, 54, 525-535.	0.2	1
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6115	Genetic polymorphism analysis of MICB gene in Jing ethnic minority of Southern China. Hla, 2018, 92, 224-230.	0.4	0
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6120	Population genomic data reveal extreme geographic subdivision and novel conservation actions for the declining foothill yellow-legged frog. Heredity, 2018, 121, 112-125.	1.2	27
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6134	Mitogenome phylogeographic analysis of a planktonic crustacean. Molecular Phylogenetics and Evolution, 2018, 129, 138-148.	1.2	36
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6136	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. PLoS ONE, 2018, 13, e0194247.	1.1	19
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6142	Chinstrap penguin population genetic structure: one or more populations along the Southern Ocean?. <i>BMC Evolutionary Biology</i> , 2018, 18, 90.	3.2	7
6143	Genetic and phenotypic variability of iris color in Buenos Aires population. <i>Genetics and Molecular Biology</i> , 2018, 41, 50-58.	0.6	13
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6146	Inter-individual differences in contamination profiles as tracer of social group association in stranded sperm whales. <i>Scientific Reports</i> , 2018, 8, 10958.	1.6	5
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6150	Spatial versus temporal structure: Implications of inter-haul variation and relatedness in the North-east Atlantic spurdog <i>Squalus acanthias</i> . <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2018, 28, 1167-1180.	0.9	5
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6160	Species Boundaries Between Three Sympatric Oak Species: <i>Quercus aliena</i> , <i>Q. dentata</i> , and <i>Q. variabilis</i> at the Northern Edge of Their Distribution in China. <i>Frontiers in Plant Science</i> , 2018, 9, 414.	1.7	20
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6163	Phylogeography and Ecological Niche Modeling Reveal Reduced Genetic Diversity and Colonization Patterns of Skunk Cabbage ( <i>Symplocarpus foetidus</i> ; Araceae) From Glacial Refugia in Eastern North America. <i>Frontiers in Plant Science</i> , 2018, 9, 648.	1.7	10
6164	Comparative Genomics, Whole-Genome Re-sequencing and Expression Profile Analysis of Nucleobase:Cation Symporter 2 (NCS2) Genes in Maize. <i>Frontiers in Plant Science</i> , 2018, 9, 856.	1.7	6
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6166	Patterns and drivers of species diversity in the Indo-Pacific red seaweed <i>Portieria</i> . <i>Journal of Biogeography</i> , 2018, 45, 2299-2313.	1.4	46
6167	Stream flow alone does not predict population structure of diving beetles across complex tropical landscapes. <i>Molecular Ecology</i> , 2018, 27, 3541-3554.	2.0	8
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6169	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
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6181	Signs of continental ancestry in urban populations of Peru through autosomal STR loci and mitochondrial DNA typing. PLoS ONE, 2018, 13, e0200796.	1.1	8
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6187	Fine-scale geographic patterns of gene flow and reproductive character displacement in <i>Drosophila subquinaria</i> and <i>Drosophila recens</i> . Molecular Ecology, 2018, 27, 3655-3670.	2.0	14
6188	Novel insights on colonization routes and evolutionary potential of <i>Colletotrichum kahawae</i> , a severe pathogen of <i>Coffea arabica</i> . Molecular Plant Pathology, 2018, 19, 2488-2501.	2.0	22
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6191	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
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6193	Molecular Data Suggest Long-Term in Situ Antarctic Persistence Within Antarctica's Most Speciose Plant Genus, <i>Schistidium</i> . Frontiers in Ecology and Evolution, 2018, 6, .	1.1	32
6194	Genetic Diversity of the Endangered Neotropical Cichlid Fish ( <i>Gymnogeophagus setequedas</i> ) in Brazil. Frontiers in Genetics, 2018, 9, 13.	1.1	22
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6197	Population Genetic Analysis of <i>Theileria annulata</i> from Six Geographical Regions in China, Determined on the Basis of Micro- and Mini-satellite Markers. <i>Frontiers in Genetics</i> , 2018, 9, 50.	1.1	9
6198	New Insights on Water Buffalo Genomic Diversity and Post-Domestication Migration Routes From Medium Density SNP Chip Data. <i>Frontiers in Genetics</i> , 2018, 9, 53.	1.1	79
6199	Little Divergence Among Mitochondrial Lineages of <i>Prochilodus</i> (Teleostei, Characiformes). <i>Frontiers in Genetics</i> , 2018, 9, 107.	1.1	22
6200	Genetic Differentiation of North-East Argentina Populations Based on 30 Binary X Chromosome Markers. <i>Frontiers in Genetics</i> , 2018, 9, 208.	1.1	5
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6203	Genetic Diversity and Phylogenetic Relationships of Coevolving Symbiont-Harboring Insect Trypanosomatids, and Their Neotropical Dispersal by Invader African Blowflies (Calliphoridae). <i>Frontiers in Microbiology</i> , 2018, 9, 131.	1.5	10
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6205	Unveiling the History of a Peculiar Weevil-Plant Interaction in South America: A Phylogeographic Approach to <i>Hydnorobius hydnorae</i> (Belidae) Associated with <i>Prosopanche americana</i> (Aristolochiaceae). <i>Diversity</i> , 2018, 10, 33.	0.7	3
6206	Genetic Variation and Hybridisation among Eight Species of <i>kāwhai</i> ( <i>Sophora</i> : Fabaceae) from New Zealand Revealed by Microsatellite Markers. <i>Genes</i> , 2018, 9, 111.	1.0	11
6207	The Genetic Architecture Underlying the Evolution of a Rare Piscivorous Life History Form in Brown Trout after Secondary Contact and Strong Introgression. <i>Genes</i> , 2018, 9, 280.	1.0	23
6208	Investigating the Promoter of <i>FAT10</i> Gene in HCC Patients. <i>Genes</i> , 2018, 9, 319.	1.0	10
6209	Viruses as indicators of contemporary host dispersal and phylogeography: an example of feline immunodeficiency virus (<scp>FIV</sub></scp> <sub>le</sub>) in freeâ€ranging African lion (<i>Panthera leo</i>). <i>Journal of Evolutionary Biology</i> , 2018, 31, 1529-1543.	0.8	8
6210	Genetic diversity, phylogeography and molecular clock of the <i>Lutzomyia longipalpis</i> complex (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 T	1.3	28
6211	Widespread plant specialization in the polyphagous planthopper <i>Hyalesthes obsoletus</i> (Cixiidae), a major vector of stolbur phytoplasma: Evidence of cryptic speciation. <i>PLoS ONE</i> , 2018, 13, e0196969.	1.1	20
6212	Geographic variation of contact calls suggest distinct modes of vocal transmission in a leaf-roosting bat. <i>Behavioral Ecology and Sociobiology</i> , 2018, 72, 1.	0.6	3
6213	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

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6215	Multi-Environment Evaluation and Genetic Characterisation of Common Bean Breeding Lines for Organic Farming Systems. <i>Sustainability</i> , 2018, 10, 777.	1.6	14
6216	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
6217	Phenotypic, Genetic, and Cytogenetic Evidence of Hybridization Between Species of Trans-Andean Tamarins (Genus <i>Saguinus</i> ). <i>International Journal of Primatology</i> , 2018, 39, 1022-1038.	0.9	7
6218	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
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6220	Strong Association of the HLA-DR/DQ Locus with Childhood Steroid-Sensitive Nephrotic Syndrome in the Japanese Population. <i>Journal of the American Society of Nephrology: JASN</i> , 2018, 29, 2189-2199.	3.0	54
6221	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
6222	Phylogeography and population genomics of a lotic water beetle across a complex tropical landscape. <i>Molecular Ecology</i> , 2018, 27, 3346-3356.	2.0	12
6223	Low genetic diversity in an isolated red fox ( <i>Vulpes vulpes</i> ) population on Mt. Hakodate, Japan, revealed by microsatellite analyses of fecal samples. <i>Mammal Study</i> , 2018, 43, 141-152.	0.2	1
6224	Genetic structure of introduced American mink ( <i>Neovison vison</i> ) in Patagonia: colonisation insights and implications for control and management strategies. <i>Wildlife Research</i> , 2018, 45, 344.	0.7	14
6225	Gene flow and genetic structure in Nile perch, <i>Lates niloticus</i> , from African freshwater rivers and lakes. <i>PLoS ONE</i> , 2018, 13, e0200001.	1.1	10
6226	A novel multiplex assay of SNP-STR markers for forensic purpose. <i>PLoS ONE</i> , 2018, 13, e0200700.	1.1	20
6227	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
6228	Population genetic structure of the threatened tropical seagrass <i>Enhalus acoroides</i> in Hainan Island, China. <i>Aquatic Botany</i> , 2018, 150, 64-70.	0.8	15
6230	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
6231	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
6232	Population genetics of Alaska Common Raven show dispersal and isolation in the world's largest songbird. <i>Auk</i> , 2018, 135, 868-880.	0.7	3

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6234	Allele surfing shaped the genetic structure of the European pond turtle via colonization and population expansion across the Iberian Peninsula from Africa. <i>Journal of Biogeography</i> , 2018, 45, 2202-2215.	1.4	17
6235	Morphometric and Molecular Diversity of the Holarctic <i>Meromyza saltatrix</i> (L., 1761) (Diptera). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66</i>	0.1	2
6236	Going with the Flow: Testing the Role of Habitat Isolation among Three Ecologically Divergent Darter Species. <i>Copeia</i> , 2018, 106, 375-387.	1.4	8
6237	Contrasted patterns of divergence and gene flow among five fish species in a Mongolian rift lake following glaciation. <i>Biological Journal of the Linnean Society</i> , 2018, 125, 115-125.	0.7	12
6238	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
6239	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
6240	Sequence-based U.S. population data for 27 autosomal STR loci. <i>Forensic Science International: Genetics</i> , 2018, 37, 106-115.	1.6	75
6241	HLA-DRB1 allele frequency and immunological response in obstructive sleep apnea syndrome in Turkish population. <i>Clinical Respiratory Journal</i> , 2018, 12, 2505-2512.	0.6	2
6242	Regional variation in drivers of connectivity for two frog species ( <i>Rana pretiosa</i> and) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5</i>	2.0	23
6243	High genetic diversity and moderate genetic structure in the self-incompatible, clonal <i>Bromelia hieronymi</i> (Bromeliaceae). <i>Botanical Journal of the Linnean Society</i> , 2018, 187, 672-688.	0.8	33
6244	Homeologue-specific expression divergence in the recently formed tetraploid <i>Capsella bursa-pastoris</i> (Brassicaceae). <i>New Phytologist</i> , 2018, 220, 624-635.	3.5	10
6245	Evolutionary Significant Units within Populations of Neotropical Broad-Snouted Caimans ( <i>Caiman</i> ) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i>	0.2	19
6246	Genetic non-invasive sampling (gNIS) as a cost-effective tool for monitoring elusive small mammals. <i>European Journal of Wildlife Research</i> , 2018, 64, 1.	0.7	45
6247	Genetic structure and phylogeography of <i>Juniperus phoenicea</i> complex throughout Mediterranean and Macaronesian regions: different stories in one. <i>Annals of Forest Science</i> , 2018, 75, 1.	0.8	7
6248	Incipient signs of genetic differentiation among African elephant populations in fragmenting miombo ecosystems in south-western Tanzania. <i>African Journal of Ecology</i> , 2018, 56, 993-1002.	0.4	5
6249	Integrative approaches to guide conservation decisions: Using genomics to define conservation units and functional corridors. <i>Molecular Ecology</i> , 2018, 27, 3452-3465.	2.0	63
6250	Genetic structure in parasitic <i>Rhinanthus angustifolius</i> is determined by geographical distance rather than habitat – implications for taxonomy and conservation. <i>Nordic Journal of Botany</i> , 2018, 36, .	0.2	1



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6251	Genetic Diversity and Population Structure of Shortleaf Pine ( <i>Pinus echinata</i> ) in the Missouri Ozarks. <i>American Midland Naturalist</i> , 2018, 180, 37.	0.2	2
6252	Considerations for monitoring population trends of colonial waterbirds using the effective number of breeders and census estimates. <i>Ecology and Evolution</i> , 2018, 8, 8088-8101.	0.8	1
6253	How Population Decline Can Impact Genetic Diversity: a Case Study of Eelgrass ( <i>Zostera marina</i> ) in Morro Bay, California. <i>Estuaries and Coasts</i> , 2018, 41, 2356-2367.	1.0	7
6254	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
6255	Estimation of the Genetic Diversity of Willow Warbler Populations of the Subspecies <i>Phylloscopus trochilus acredula</i> (L.) in Different Parts of Its Nesting Area in the European Part of Russia. <i>Biology Bulletin</i> , 2018, 45, 320-324.	0.1	1
6256	Unraveling the genetic structure of Brazilian commercial sugarcane cultivars through microsatellite markers. <i>PLoS ONE</i> , 2018, 13, e0195623.	1.1	30
6257	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
6258	Single nucleotide polymorphisms in native South American Atlantic coast populations of smooth shelled mussels: hybridization with invasive European <i>Mytilus galloprovincialis</i> . <i>Genetics Selection Evolution</i> , 2018, 50, 5.	1.2	48
6259	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
6260	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
6261	Population Genetic Structure of Rock Bream ( <i>Oplegnathus fasciatus</i> Temminck & Schlegel, 1884) Revealed by mtDNA COI Sequence in Korea and China. <i>Ocean Science Journal</i> , 2018, 53, 261-274.	0.6	3
6262	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
6263	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
6264	Population structure and patterns of geographic differentiation of <i>Bactrocera oleae</i> (Diptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 T Analysis, 2018, 29, 1051-1062.	0.7	6
6265	Genetic Variability in Farmed Brood Stocks of the Siberian Sturgeon in Poland. , 2018, , 337-346.		0
6266	<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
6267	Environmental factors affecting population level genetic divergence of the striped field mouse ( <i>Apodemus agrarius</i> ) in South Korea. <i>Ecological Research</i> , 2018, 33, 989-999.	0.7	3
6268	Cytokine Gene Polymorphism Profiles in Kidney Transplant Patients - Association of +1188A/C RS3212227 SNP in the IL12B Gene Prevents Delayed Graft Function. <i>Archives of Medical Research</i> , 2018, 49, 101-108.	1.5	5

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6270	Population structure of <i>Venturia inaequalis</i> , a causal agent of apple scab, in response to heterogeneous apple tree cultivation. <i>BMC Evolutionary Biology</i> , 2018, 18, 5.	3.2	14
6271	HLA class I (-A, -B, -C) and class II (-DR, -DQ) polymorphism in the Mauritanian population. <i>BMC Medical Genetics</i> , 2018, 19, 2.	2.1	5
6272	Global sequence diversity of the lactate dehydrogenase gene in <i>Plasmodium falciparum</i> . <i>Malaria Journal</i> , 2018, 17, 16.	0.8	13
6273	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
6274	Contrasting life histories contribute to divergent patterns of genetic diversity and population connectivity in freshwater sculpin fishes. <i>BMC Evolutionary Biology</i> , 2018, 18, 52.	3.2	9
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6276	Invasion genetics of nutria ( <i>Myocastor coypus</i> ) in Okayama, Japan, inferred from mitochondrial and microsatellite markers. <i>European Journal of Wildlife Research</i> , 2018, 64, 1.	0.7	11
6277	Assessing introgressive hybridization between blue wildebeest ( <i>Connochaetes taurinus</i> ) and black wildebeest ( <i>Connochaetes gnou</i> ) from South Africa. <i>Conservation Genetics</i> , 2018, 19, 981-993.	0.8	12
6278	Genetic differentiation in <i>Cricetulus migratorius</i> Pallas, 1773 (Rodentia, Cricetidae). <i>Mammalian Biology</i> , 2018, 92, 115-119.	0.8	7
6279	Genetic diversity and demographic history of the Siberian lime ( <i>Tilia sibirica</i> ). <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2018, 33, 9-17.	1.1	8
6280	Phylogeography of the Japanese ratsnake, <i>Elaphe climacophora</i> (Serpentes: Colubridae): impacts of Pleistocene climatic oscillations and sea-level fluctuations on geographical range. <i>Biological Journal of the Linnean Society</i> , 2018, 124, 174-187.	0.7	3
6281	Phylogeography of Brazilian pine ( <i>Araucaria angustifolia</i> ): integrative evidence for pre-Columbian anthropogenic dispersal. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	27
6282	Allopatric speciation of <i>Meteterakis</i> (Heterakoidea: Heterakidae), a highly dispersible parasitic nematode, in the East Asian islands. <i>Parasitology International</i> , 2018, 67, 493-500.	0.6	4
6283	Surprising diversity in the Pannonian populations of Marsh Fritillary ( <i>Euphydryas aurinia</i> , Lepidoptera: Tj ETQqO 0 0 rgBT /Overlock 10 T Evolutionary Research, 2018, 56, 519-532.	0.6	3
6284	Several Subspecies or Phenotypic Plasticity? A Geometric Morphometric and Molecular Analysis of Variability of the Mayan Cichlid <i>Mayaheros urophthalmus</i> in the Yucatan. <i>Copeia</i> , 2018, 106, 268-278.	1.4	6
6285	Postglacial expansion of the Arctic keystone copepod <i>Calanus glacialis</i> . <i>Marine Biodiversity</i> , 2018, 48, 1027-1035.	0.3	15
6286	Short dispersal distance of males in a wild white-handed gibbon ( <i>Hylobates lar</i> ) population. <i>American Journal of Physical Anthropology</i> , 2018, 167, 61-71.	2.1	15

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6289	Early selection of bZIP73 facilitated adaptation of japonica rice to cold climates. <i>Nature Communications</i> , 2018, 9, 3302.	5.8	155
6290	A Multilocus Approach to Understanding Historical and Contemporary Demography of the Keystone Floodplain Species <i>Colossoma macropomum</i> (Teleostei: Characiformes). <i>Frontiers in Genetics</i> , 2018, 9, 263.	1.1	9
6291	Balancing selection and introgression of newt immune-response genes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20180819.	1.2	21
6292	Dog breed affiliation with a forensically validated canine STR set. <i>Forensic Science International: Genetics</i> , 2018, 37, 126-134.	1.6	12
6293	A genetic portrait of the South-Eastern Carpathians based on autosomal short tandem repeats loci used in forensics. <i>American Journal of Human Biology</i> , 2018, 30, e23139.	0.8	3
6294	Genetic polymorphism analysis of 40 Y-chromosomal STR loci in seven populations from South China. <i>Forensic Science International</i> , 2018, 291, 109-114.	1.3	14
6295	Genetic structure of a patchily distributed philopatric migrant: implications for management and conservation. <i>Biological Journal of the Linnean Society</i> , 2018, 124, 633-644.	0.7	5
6296	Preliminary data on the distribution, morphology and genetics of white-clawed crayfish and on their ectosymbionts in Lunigiana (Tuscany, Italy). <i>Knowledge and Management of Aquatic Ecosystems</i> , 2018, , 25.	0.5	0
6297	Phylogeography, mitochondrial DNA diversity, and demographic history of geladas ( <i>Theropithecus</i> ). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	1.1	27
6298	Human leukocyte antigen-G 3â™ untranslanted region polymorphisms are associated with asthma severity. <i>Molecular Immunology</i> , 2018, 101, 500-506.	1.0	9
6299	A cis-eQTL of HLA-DPB1 Affects Susceptibility to Type 1 Autoimmune Hepatitis. <i>Scientific Reports</i> , 2018, 8, 11924.	1.6	22
6300	Genetic analysis of 15 autosomal STRs in Yousafzai population of Pakistan. <i>International Journal of Legal Medicine</i> , 2018, 132, 1635-1636.	1.2	2
6301	Genetic diversity and maternal lineages of south Indian goats. <i>Molecular Biology Reports</i> , 2018, 45, 2741-2748.	1.0	7
6302	Hepatitis C virus early kinetics and resistance-associated substitution dynamics during antiviral therapy with direct-acting antivirals. <i>Journal of Viral Hepatitis</i> , 2018, 25, 1515-1525.	1.0	10
6303	Cytosuclear discordance in the Florida Everglades invasive Burmese python ( <i>Python bivittatus</i> ) population reveals possible hybridization with the Indian python ( <i>P. Amolurus</i> ). <i>Ecology and Evolution</i> , 2018, 8, 9034-9047.	0.8	10
6304	Examining the interglacial high-elevation refugia scenario in East Asian subtropical mountain systems with the frog species <i>Leptobrachium liui</i> . <i>Ecology and Evolution</i> , 2018, 8, 9326-9340.	0.8	5

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6307	Updated carrier rates for c.35delG (GJB2) associated with hearing loss in Russia and common c.35delG haplotypes in Siberia. <i>BMC Medical Genetics</i> , 2018, 19, 138.	2.1	16
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6309	Ancient DNA reveals evidence of abundant aurochs ( <i>Bos primigenius</i> ) in Neolithic Northeast China. <i>Journal of Archaeological Science</i> , 2018, 98, 72-80.	1.2	26
6310	Modern State of Populations of Endemic Oxytropis Species from Baikal Siberia and Their Phylogenetic Relationships Based on Chloroplast DNA Markers. <i>Russian Journal of Genetics</i> , 2018, 54, 805-815.	0.2	11
6311	Male-Driven Differences in Chimpanzee ( <i>Pan troglodytes</i> ) Population Genetic Structure Across Three Habitats in Cameroon and Nigeria. <i>International Journal of Primatology</i> , 2018, 39, 581-601.	0.9	2
6312	An ancient and a recent colonization of islands by an Australian sap-feeding insect. <i>Journal of Biogeography</i> , 2018, 45, 2389-2399.	1.4	1
6313	The ecology of immune state in a wild mammal, <i>Mus musculus domesticus</i> . <i>PLoS Biology</i> , 2018, 16, e2003538.	2.6	44
6314	Identifying QTL-allele system of seed protein content in Chinese soybean landraces for population differentiation studies and optimal cross predictions. <i>Euphytica</i> , 2018, 214, 1.	0.6	7
6315	Extended HLA-G genetic diversity and ancestry composition in a Brazilian admixed population sample: Implications for HLA-G transcriptional control and for case-control association studies. <i>Human Immunology</i> , 2018, 79, 790-799.	1.2	9
6316	Genetic patterns in fragmented habitats: a case study for two <i>Peromyscus</i> species in southern California. <i>Journal of Mammalogy</i> , 2018, 99, 923-935.	0.6	2
6317	Remarkable Geographic Structuring of Rheophilic Fishes of the Lower Araguaia River. <i>Frontiers in Genetics</i> , 2018, 9, 295.	1.1	13
6318	Unlocking the novel genetic diversity and population structure of synthetic Hexaploid wheat. <i>BMC Genomics</i> , 2018, 19, 591.	1.2	76
6319	Sequence diversity of the Rh blood group system in Basques. <i>European Journal of Human Genetics</i> , 2018, 26, 1859-1866.	1.4	5
6320	Global genomic diversity and conservation priorities for domestic animals are associated with the economies of their regions of origin. <i>Scientific Reports</i> , 2018, 8, 11677.	1.6	23
6321	Genetics of lineage diversification and the evolution of host usage in the economically important wheat curl mite, <i>Aceria tosichella</i> Keifer, 1969. <i>BMC Evolutionary Biology</i> , 2018, 18, 122.	3.2	25
6322	The genetic diversity of <i>Borrelia afzelii</i> is not maintained by the diversity of the rodent hosts. <i>Parasites and Vectors</i> , 2018, 11, 454.	1.0	17

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6324	Maternal genetic variation in the northeastern Hungarian fallow deer ( <i>Dama dama</i> ) population. <i>Mammalian Biology</i> , 2018, 93, 21-28.	0.8	6
6325	Genetic population structure of the spotted seatrout ( <i>Cynoscion nebulosus</i> ): simultaneous examination of the mtDNA control region and microsatellite marker results. <i>Bulletin of Marine Science</i> , 2018, 94, 47-71.	0.4	17
6326	Optimization of a reduced volume PCR amplification for PowerPlex® Fusion kit using FTA® cards and generation of population genetic data for Brunei population. <i>Electrophoresis</i> , 2018, 39, 2979-2990.	1.3	5
6327	Population genomics of <i>Culiseta melanura</i> , the principal vector of Eastern equine encephalitis virus in the United States. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006698.	1.3	5
6328	Forensic efficiency and genetic divergence of 30 autosomal InDels in Chinese Han population from Jiangsu province. <i>Forensic Science International: Genetics</i> , 2018, 37, e17-e19.	1.6	17
6329	Analysis of 23 Y-STRs in a population sample from eastern Paraguay. <i>Forensic Science International: Genetics</i> , 2018, 37, e20-e22.	1.6	7
6330	Positive selection and climatic effects on MHC class II gene diversity in hares ( <i>Lepus capensis</i> ) from a steep ecological gradient. <i>Scientific Reports</i> , 2018, 8, 11514.	1.6	18
6331	What is the relationship between the bioaccumulation of chemical contaminants in the variegated scallop <i>Mimachlamys varia</i> and its health status? A study carried out on the French Atlantic coast using the Path ComDim model. <i>Science of the Total Environment</i> , 2018, 640-641, 662-670.	3.9	19
6332	Pleistocene glacial cycles drive isolation, gene flow and speciation in the high-elevation Andes. <i>New Phytologist</i> , 2018, 219, 779-793.	3.5	96
6333	Forensic ancestry analysis in two Chinese minority populations using massively parallel sequencing of 165 ancestry-informative SNPs. <i>Electrophoresis</i> , 2018, 39, 2732-2742.	1.3	68
6334	Bayesian estimation of partial population continuity using ancient <i>scp</i> DNA and spatially explicit simulations. <i>Evolutionary Applications</i> , 2018, 11, 1642-1655.	1.5	10
6335	Diversification with gene flow and niche divergence in a lizard species along the South American ædiagonal of open formations. <i>Journal of Biogeography</i> , 2018, 45, 1688-1700.	1.4	19
6336	Neutral and functionally important genes shed light on phylogeography and the history of high-altitude colonization in a widespread New World duck. <i>Ecology and Evolution</i> , 2018, 8, 6515-6528.	0.8	3
6337	Phylogenetic conservatism of thermal traits explains dispersal limitation and genomic differentiation of <i>Streptomyces</i> sister-taxa. <i>ISME Journal</i> , 2018, 12, 2176-2186.	4.4	27
6338	Stock structure of <i>Lethrinus laticaudis</i> (Lethrinidae) across northern Australia determined using genetics, otolith microchemistry and parasite assemblage composition. <i>Marine and Freshwater Research</i> , 2018, 69, 487.	0.7	11
6339	Whole mitochondrial genome diversity in two Hungarian populations. <i>Molecular Genetics and Genomics</i> , 2018, 293, 1255-1263.	1.0	19
6340	Effects of Pleistocene climate change on genetic structure and diversity of <i>Shorea macrophylla</i> in Kalimantan Rainforest. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	15

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6342	Monitoring methods for the Golden Eagle <i>Aquila chrysaetos</i> in Norway. Bird Study, 2018, 65, S43-S51.	0.4	4
6343	Migratory ecology of skipjack tuna <i>Katsuwonus pelamis</i> caught off Kyushu Island, Japan – a potential size screening effect of the Kuroshio. Nippon Suisan Gakkaishi, 2018, 84, 630-640.	0.0	2
6344	Evolutionary Dynamics of Copy Number and Meiotic Recombination in Murine 5S rDNA: Possible Involvement of Natural Selection. Journal of Molecular Evolution, 2018, 86, 312-323.	0.8	3
6345	Adaptation to reef habitats through selection on the coral animal and its associated microbiome. Molecular Ecology, 2018, 27, 2956-2971.	2.0	94
6346	Possible Northward Introgression of a Tropical Lineage of <i>Rhipicephalus sanguineus</i> Ticks at a Site of Emerging Rocky Mountain Spotted Fever. Journal of Parasitology, 2018, 104, 240-245.	0.3	21
6347	Successful worldwide invasion of the veined rapa whelk, <i>Rapana venosa</i> , despite a dramatic genetic bottleneck. Biological Invasions, 2018, 20, 3297-3314.	1.2	17
6348	Role of oceanography in shaping the genetic structure in the North Pacific hake <i>Merluccius productus</i> . PLoS ONE, 2018, 13, e0194646.	1.1	20
6349	A spatial genetics approach to inform vector control of tsetse flies ( <i>Glossina fuscipes</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422 Td (f	0.8	8
6350	Genetic diversity of the Chinese goat in the littoral zone of the Yangtze River as assessed by microsatellite and mtDNA. Ecology and Evolution, 2018, 8, 5111-5123.	0.8	9
6351	Genetic differentiation of <i>Rubus chamaemorus</i> populations in the Czech Republic and Norway after the last glacial period. Ecology and Evolution, 2018, 8, 5701-5711.	0.8	6
6352	Mitochondrial nuclear discordance across a recent contact zone for California voles. Ecology and Evolution, 2018, 8, 6226-6241.	0.8	6
6353	Selection of the sex-linked inhibitor of apoptosis in mountain pine beetle ( <i>Dendroctonus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422 Td (f	0.8	4
6354	Genetic diversity, genetic structure and diet of ancient and contemporary red deer ( <i>Cervus elaphus</i> L.) from north-eastern France. PLoS ONE, 2018, 13, e0189278.	1.1	7
6355	Increased mitochondrial DNA diversity in ancient Columbia River basin Chinook salmon <i>Oncorhynchus tshawytscha</i> . PLoS ONE, 2018, 13, e0190059.	1.1	26
6356	The genetic tale of a recovering lion population ( <i>Panthera leo</i> ) in the Savā Valley region (Zimbabwe): A better understanding of the history and managing the future. PLoS ONE, 2018, 13, e0190369.	1.1	14
6357	Examination of Clock and Adcyap1 gene variation in a neotropical migratory passerine. PLoS ONE, 2018, 13, e0190859.	1.1	19
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6361	Migratory culture, population structure and stock identity in North Pacific beluga whales ( <i>Delphinapterus leucas</i> ). PLoS ONE, 2018, 13, e0194201.	1.1	44
6362	MDR1 gene polymorphisms are associated with ulcerative colitis in a cohort of Serbian patients with inflammatory bowel disease. PLoS ONE, 2018, 13, e0194536.	1.1	21
6363	Filipino DNA variation at 12 X-chromosome short tandem repeat markers. Forensic Science International: Genetics, 2018, 36, e8-e12.	1.6	20
6364	Genomic signatures of population bottleneck and recovery in Northwest Atlantic pinnipeds. Ecology and Evolution, 2018, 8, 6599-6614.	0.8	16
6365	Morphological and molecular evidence for a new shrimp species, <i>Atyaephyra vladoi</i> sp. nov. (Decapoda), Tj ETQq0 0 0 rgBT /Overlock 10 demographic history. Zoologischer Anzeiger, 2018, 275, 66-79.	0.4	11
6366	Phylogeography and species distribution modelling reveal the effects of the Pleistocene ice ages on an intertidal limpet from the south-eastern Pacific. Journal of Biogeography, 2018, 45, 1751-1767.	1.4	12
6367	Investigating Holocene human population history in North Asia using ancient mitogenomes. Scientific Reports, 2018, 8, 8969.	1.6	15
6368	Maintenance of species boundaries in three sympatric <i>Ligularia</i> (Senecioneae, Asteraceae) species. Journal of Integrative Plant Biology, 2018, 60, 986-999.	4.1	7
6369	Wide distributions and cryptic diversity within a <i>Microstomum</i> (Platyhelminthes) species complex. Zoologica Scripta, 2018, 47, 486-498.	0.7	7
6370	The ghost of introduction past: Spatial and temporal variability in the genetic diversity of invasive smallmouth bass. Evolutionary Applications, 2018, 11, 1609-1629.	1.5	9
6371	A genetics-based approach confirms immune associations with life history across multiple populations of an aquatic vertebrate ( <i>Gasterosteus aculeatus</i> ). Molecular Ecology, 2018, 27, 3174-3191.	2.0	7
6372	Genetic diversity and populational structure of the seahorse <i>Hippocampus reidi</i> (Syngnathidae) in north-eastern Brazil: A conservationist approach. Aquatic Conservation: Marine and Freshwater Ecosystems, 2018, 28, 1114-1122.	0.9	4
6373	Lower genetic diversity and hatchability in amphibian populations isolated by urbanization. Population Ecology, 2018, 60, 347-360.	0.7	5
6374	Mitochondrial diversity and phylogeographic structure of native cattle breeds from Yunnan, Southwestern China. Livestock Science, 2018, 214, 129-134.	0.6	15
6375	Population structure analysis of the neglected parasite <i>Thelazia callipaeda</i> revealed high genetic diversity in Eastern Asia isolates. PLoS Neglected Tropical Diseases, 2018, 12, e0006165.	1.3	18
6376	Allelic and haplotype diversity of HLA-A, HLA-B and HLA-DRB1 gene at high resolution in the Nanning Han population. International Journal of Immunogenetics, 2018, 45, 201-209.	0.8	5

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6378	Genetic diversity and distribution of <i>Senegalia senegal</i> (L.) Britton under climate change scenarios in West Africa. <i>PLoS ONE</i> , 2018, 13, e0194726.	1.1	10
6379	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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6885	Genetic Differentiation of the Arctic Phylogenetic Group of Charr from Northeast Asia and North America. Russian Journal of Genetics, 2019, 55, 349-359.	0.2	7
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6904	Allele frequency and forensic efficiency of 15 autosomal STR loci in the Sardinian population (Italy). <i>Forensic Science International: Genetics</i> , 2019, 41, e26-e29.	1.6	3
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6907	Who is biting you? DNA barcodes reveal cryptic diversity in human-biting black flies (Diptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.9	8
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6909	Supporting the existence of two isolated evolutionary lineages of Gerres (Perciformes: Gerreidae) in America. <i>Zoologica Scripta</i> , 2019, 48, 466-481.	0.7	3
6910	Evidence for frequencyâ€dependent selection maintaining polymorphism in the Batesian mimic <i>Papilio polytes</i> in multiple islands in the Ryukyus, Japan. <i>Ecology and Evolution</i> , 2019, 9, 5991-6002.	0.8	7
6911	California roach ( <i>Hesperoleucus symmetricus</i> ) in the Eel River of northwestern California: native or introduced?. <i>Environmental Biology of Fishes</i> , 2019, 102, 771-781.	0.4	1
6912	HLA concordance between hematopoietic stem cell transplantation patients and umbilical cord blood units: Implications for cord blood banking in admixed populations. <i>Human Immunology</i> , 2019, 80, 714-722.	1.2	4
6913	Contrasting patterns in trophic niche evolution of polymorphic Arctic charr populations in two subarctic Norwegian lakes. <i>Hydrobiologia</i> , 2019, 840, 281-299.	1.0	12
6914	SPLATCHE3: simulation of serial genetic data under spatially explicit evolutionary scenarios including long-distance dispersal. <i>Bioinformatics</i> , 2019, 35, 4480-4483.	1.8	41
6915	Genetic and phenotypic responses to genomic selection for timing of breeding in a wild songbird. <i>Functional Ecology</i> , 2019, 33, 1708-1721.	1.7	18
6916	Unravelling the global invasion routes of a worldwide invader, the red swamp crayfish (<i>Procambarus clarkii</i>). <i>Freshwater Biology</i> , 2019, 64, 1382-1400.	1.2	65
6917	Development of microsatellite markers and the genetic diversity of <i>Myocastor coypus</i> introduced to South Korea. <i>Journal of Veterinary Medical Science</i> , 2019, 81, 499-503.	0.3	1
6918	Phylogeography of <i>Potamon ibericum</i> (Brachyura: Potamidae) identifies Quaternary glacial refugia within the Caucasus biodiversity hot spot. <i>Ecology and Evolution</i> , 2019, 9, 4749-4759.	0.8	15
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6920	Genetic differentiation predicts body size divergence between island and mainland populations of common wall lizards ( <i>Podarcis muralis</i> ). <i>Biological Journal of the Linnean Society</i> , 2019, 127, 771-786.	0.7	3
6921	Genetic basis of amphibian larval development along a latitudinal gradient: Gene diversity, selection and links with phenotypic variation in transcription factor <i>C/EBP<math>\beta</math></i> . <i>Molecular Ecology</i> , 2019, 28, 2786-2801.	2.0	5
6922	Development and validation of a multiplex insertion/deletion marker panel, SifaInDel 45plex system. <i>Forensic Science International: Genetics</i> , 2019, 41, 128-136.	1.6	12
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6925	Polymorphisms of ADME-related genes and their implications for drug safety and efficacy in Amazonian Amerindians. <i>Scientific Reports</i> , 2019, 9, 7201.	1.6	23
6926	Mitochondrial Gene Heterogeneity and Population Genetics of <i>Haemaphysalis longicornis</i> (Acari: Tj ETQq0 0 0 rgBT /Overlock 5 10 Tf 50 5	0.4	5
6927	Unveiling the Diversity of Immunoglobulin Heavy Constant Gamma (IGHG) Gene Segments in Brazilian Populations Reveals 28 Novel Alleles and Evidence of Gene Conversion and Natural Selection. <i>Frontiers in Immunology</i> , 2019, 10, 1161.	2.2	31
6928	Screening of polymorphic microsatellites and their application for <i>Saccharina angustata</i> and <i>Saccharina longissima</i> population genetic analysis. <i>Journal of Applied Phycology</i> , 2019, 31, 3295-3301.	1.5	2
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6931	Humans and Chimpanzees Display Opposite Patterns of Diversity in <i>Arylamine N-Acetyltransferase</i> Genes. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2199-2224.	0.8	9
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6936	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
6937	Geographic patterns in morphometric and genetic variation for coyote populations with emphasis on southeastern coyotes. <i>Ecology and Evolution</i> , 2019, 9, 3389-3404.	0.8	21

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6938	Island biogeography theory explains the genetic diversity of a fragmented rock ptarmigan ( <i>Lagopus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.8	15
6939	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
6940	Diverse yet endangered: pollen dispersal and mating system reveal inbreeding in a narrow endemic plant. <i>Plant Ecology and Diversity</i> , 2019, 12, 169-180.	1.0	15
6941	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
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6943	Whole Genome Sequencing and Re-sequencing of the Sable Antelope ( <i>Hippotragus niger</i> ): A Resource for Monitoring Diversity in <i>ex Situ</i> and <i>in Situ</i> Populations. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1785-1793.	0.8	18
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6961	Assessment by microsatellite analysis of genetic diversity and population structure of <i>Enhalus acoroides</i> from the coast of Khanh Hoa Province, Vietnam. Acta Oceanologica Sinica, 2019, 38, 144-150.	0.4	4
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6975	Genetic variation of avian malaria in the tropical Andes: a relationship with the spatial distribution of hosts. <i>Malaria Journal</i> , 2019, 18, 129.	0.8	11
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6979	LEPR polymorphisms and haplotypes in Mexican patients with colorectal cancer. <i>Biomedica</i> , 2019, 39, 205-211.	0.3	1
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7042	HLA-A, -B, -C, -DRB1 and -DQB1 allele and haplotype frequencies of 1463 umbilical cord blood units typed in high resolution from Bogotá, Colombia. <i>Human Immunology</i> , 2019, 80, 425-426.	1.2	10
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7169	Mitochondrial D-loop Sequence Variability in Three Native Insular Griffon Vulture ( <i>Gyps</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.9	5
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7174	Genetic affinity of Muslim population in South India based on HLA-DQB1 and relationship with other Indian Populations. International Journal of Modern Anthropology, 2019, 2, 97.	0.3	0
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7214	Genetic distributions and diversity analyses of 23 Y-STR loci in Xiâ€™an Han population. <i>Legal Medicine</i> , 2019, 41, 101635.	0.6	3
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7222	NOS1AP SNPs related to sudden arrhythmic death syndrome. <i>Forensic Science International: Genetics Supplement Series</i> , 2019, 7, 569-571.	0.1	0
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7248	The genetic diversity and population structure of <i>Sophora alopecuroides</i> (Fabaceae) as determined by microsatellite markers developed from transcriptome. <i>PLoS ONE</i> , 2019, 14, e0226100.	1.1	12
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7254	The natural diversity of <i>Carica papaya</i> in Panama. <i>Acta Horticulturae</i> , 2019, , 99-110.	0.1	2
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7263	Integrative taxonomy reveals a new <i>Gammarus</i> species (Crustacea, Amphipoda) surviving in a previously unknown southeast European glacial refugium. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2019, 57, 272-297.	0.6	18
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7271	Genetic polymorphisms, forensic efficiency, and phylogenetic analysis of 15 autosomal STR loci in the Uyghur population of Ili Kazakh Autonomous Prefecture, Northwestern China. <i>Annals of Human Genetics</i> , 2019, 83, 46-53.	0.3	0
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7274	Genetic variations and population data on five supplementary STR markers in Lebanon. <i>Annals of Human Genetics</i> , 2019, 83, 82-85.	0.3	1
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7279	Testing the effectiveness of conservation management within biosphere reserves: the case of the Mexican deer mouse ( <i>Peromyscus mexicanus</i> ) as a bioindicator. <i>Integrative Zoology</i> , 2019, 14, 422-434.	1.3	2

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7281	Intraspecific DNA contamination distorts subtle population structure in a marine fish: Decontamination of herring samples before restriction site associated sequencing and its effects on population genetic statistics. <i>Molecular Ecology Resources</i> , 2019, 19, 1131-1143.	2.2	11
7282	Genetic Diversity and Structure of Channel Catfish from Continental Waters of Mexico. <i>North American Journal of Aquaculture</i> , 2019, 81, 74-80.	0.7	2
7283	Past hybridisation and introgression erased traces of mitochondrial lineages evolution in the Neotropical silver catfish <i>Rhamdia quelen</i> (Siluriformes: Heptapteridae). <i>Hydrobiologia</i> , 2019, 830, 161-177.	1.0	4
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7289	Genetic polymorphism investigation of 16 X-STR loci in a Han population in Central South China. <i>Forensic Science International: Genetics</i> , 2019, 39, e21-e23.	1.6	4
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7294	Genetic diversity and the origin of Mongolian native sheep. <i>Livestock Science</i> , 2019, 220, 17-25.	0.6	12
7295	Bayesian phylodynamic analysis reveals the dispersal patterns of tobacco mosaic virus in China. <i>Virology</i> , 2019, 528, 110-117.	1.1	23
7296	Multilocus phylogeography of the brown-spotted pitviper <i>Protobothrops mucrosquamatus</i> (Reptilia: Elapidae). <i>Molecular Biology and Evolution</i> , 2019, 133, 82-91.	1.2	19
7297	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

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7298	The distributions of HLA-A, HLA-B, HLA-C, HLA-DRB1 and HLA-DQB1 allele and haplotype at high-resolution level in Zhejiang Han population of China. <i>International Journal of Immunogenetics</i> , 2019, 46, 7-16.	0.8	46
7299	Has past climate change affected cold-specialized species differentially through space and time?. <i>Systematic Entomology</i> , 2019, 44, 571-587.	1.7	4
7300	Evaluation of 13 rapidly mutating Y-STRs in endogamous Punjabi and Sindhi ethnic groups from Pakistan. <i>International Journal of Legal Medicine</i> , 2019, 133, 799-802.	1.2	4
7301	Responses of fish assemblage structure to large-scale weir construction in riverine ecosystems. <i>Science of the Total Environment</i> , 2019, 657, 1334-1342.	3.9	25
7302	Witnessing extinction: Population genetics of the last European Rollers ( <i>Coracias garrulus</i> ) in Austria and a first phylogeographic analysis of the species across its distribution range. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2019, 57, 461-475.	0.6	4
7303	Deep mitochondrial lineage divergence among populations of the southern stingray ( <i>Hypanus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 Caribbean. <i>Marine Biodiversity</i> , 2019, 49, 1627-1634.	0.3	6
7304	Genetic signatures of small effective population sizes and demographic declines in an endangered rattlesnake, <i>Sistrurus catenatus</i> . <i>Evolutionary Applications</i> , 2019, 12, 664-678.	1.5	29
7305	Genetic structure of bank vole populations in the contact zone of two lineages in north-eastern Poland. <i>Mammalian Biology</i> , 2019, 96, 93-101.	0.8	7
7306	Mitochondrial D-loop DNA analyses of Norway lobster ( <i>Nephrops norvegicus</i> ) reveals genetic isolation between Atlantic and East Mediterranean populations. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2019, 99, 933-940.	0.4	9
7307	Challenges of next-generation sequencing in conservation management: Insights from long-term monitoring of corridor effects on the genetic diversity of mouse lemurs in a fragmented landscape. <i>Evolutionary Applications</i> , 2019, 12, 425-442.	1.5	9
7308	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
7309	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
7310	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
7311	Genetic diversity and hybrid formation in Central European club-mosses ( <i>Diphasiastrum</i> ,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 <i>Phylogenetics and Evolution</i> , 2019, 131, 181-192.	1.2	8
7312	Significant Asia-Europe divergence in the middle spotted woodpecker (Aves, Picidae). <i>Zoologica Scripta</i> , 2019, 48, 17-32.	0.7	13
7313	Low genetic differentiation between two morphologically and ecologically distinct giant-leaved Mexican oaks. <i>Plant Systematics and Evolution</i> , 2019, 305, 89-101.	0.3	16
7314	Implications of introgression for wildlife translocations: the case of North American martens. <i>Conservation Genetics</i> , 2019, 20, 153-166.	0.8	16
7315	Evolutionary history of the scorpionfly <i>Dicerapanorpa magna</i> (Mecoptera, Panorpidae). <i>Zoologica Scripta</i> , 2019, 48, 93-105.	0.7	8

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7316	Tangled banks: A landscape genomic evaluation of Wallace's Riverine barrier hypothesis for three Amazon plant species. <i>Molecular Ecology</i> , 2019, 28, 980-997.	2.0	21
7317	Demography and genetics suggest reversal of dolphin source-sink dynamics, with implications for conservation. <i>Marine Mammal Science</i> , 2019, 35, 732-759.	0.9	21
7318	Detailed insights into pan-European population structure and inbreeding in wild and hatchery Pacific oysters ( <i>Crassostrea gigas</i> ) revealed by genome-wide SNP data. <i>Evolutionary Applications</i> , 2019, 12, 519-534.	1.5	39
7319	Comparative mtDNA phylogeographic patterns reveal marked differences in population genetic structure between generalist and specialist ectoparasites of the African penguin ( <i>Spheniscus</i> )	0.784314	10
7320	The role of matrilineality in shaping patterns of Y chromosome and mtDNA sequence variation in southwestern Angola. <i>European Journal of Human Genetics</i> , 2019, 27, 475-483.	1.4	10
7321	Multiple Introductions Without Admixture of <i>Colletotrichum truncatum</i> Associated with Soybean Anthracnose in Brazil. <i>Phytopathology</i> , 2019, 109, 681-689.	1.1	19
7322	Quantitative analysis of connectivity in populations of a semi-aquatic mammal using kinship categories and network assortativity. <i>Molecular Ecology Resources</i> , 2019, 19, 310-326.	2.2	29
7323	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
7324	The genetic structure of a mouse lemur living in a fragmented habitat in Northern Madagascar. <i>Conservation Genetics</i> , 2019, 20, 229-243.	0.8	16
7325	Genetic variability of populations of the white-eared opossum, <i>Didelphis albiventris</i> Lund 1840 ( <i>Didelphimorphia</i> ; <i>Didelphidae</i> ) in Brazil. <i>Brazilian Journal of Biology</i> , 2019, 79, 594-602.	0.4	13
7326	Low population genetic differentiation in two <i>Tamarix</i> species ( <i>Tamarix austromongolica</i> and <i>Tamarix</i> )	0.5	5
7327	Two speed invasion: assisted and intrinsic dispersal of common mynas over 150 years of colonization. <i>Journal of Biogeography</i> , 2019, 46, 45-57.	1.4	16
7328	Genetic structure and effective size of an endangered population of woodland caribou. <i>Conservation Genetics</i> , 2019, 20, 203-213.	0.8	9
7329	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
7330	Fifteen novel microsatellite loci, developed using next-generation sequencing, reveal the lack of genetic structure in <i>Donax vittatus</i> from Iberian Peninsula. <i>Estuarine, Coastal and Shelf Science</i> , 2019, 217, 218-225.	0.9	3
7331	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
7332	Phylogeographic and diversification patterns of the white-nosed coati ( <i>Nasua narica</i> ): Evidence for south-to-north colonization of North America. <i>Molecular Phylogenetics and Evolution</i> , 2019, 131, 149-163.	1.2	12
7333	Demographic inferences after a range expansion can be biased: the test case of the blacktip reef shark ( <i>Carcharhinus melanopterus</i> ). <i>Heredity</i> , 2019, 122, 759-769.	1.2	21



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7334	Genetic diversity and structure of Northern Sheatfish ( <i>Silurus soldatovi</i> ) assessed by newly developed and cross-species microsatellites. <i>Aquaculture Research</i> , 2019, 50, 895-903.	0.9	1
7335	Genetic association with high-resolution climate data reveals selection footprints in the genomes of barley landraces across the Iberian Peninsula. <i>Molecular Ecology</i> , 2019, 28, 1994-2012.	2.0	22
7336	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
7337	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
7338	Phylogeographic variation within the Buff-browed Foliage-gleaner (Aves: Furnariidae: Syndactyla) in the Amazon. <i>Phylogenetics and Evolution</i> , 2019, 133, 198-213.	1.2	28
7339	QuantiNemo 2: a Swiss knife to simulate complex demographic and genetic scenarios, forward and backward in time. <i>Bioinformatics</i> , 2019, 35, 886-888.	1.8	19
7340	The <i>Sarracenia alata</i> pitcher plant system and obligate arthropod inquilines should be considered an evolutionary community. <i>Journal of Biogeography</i> , 2019, 46, 485-496.	1.4	6
7341	Genetic Structure and Haplotype Pattern of Marine Planktonic Ostracod ( <i>Porroecia spinirostris</i> ) from South China Sea Based on Mitochondrial COI Gene. <i>Ocean Science Journal</i> , 2019, 54, 107-116.	0.6	3
7342	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
7343	The population of <i>Sclerotinia sclerotiorum</i> affecting common bean in Brazil is structured by mycelial compatibility groups. <i>Tropical Plant Pathology</i> , 2019, 44, 41-52.	0.8	4
7344	Comparisons of molecular diversity indices, selective sweeps and population structure of African rice with its wild progenitor and Asian rice. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1145-1158.	1.8	16
7345	Genetic diversity patterns and domestication origin of soybean. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1179-1193.	1.8	44
7346	Population structure of the oviparous South-West European common lizard. <i>European Journal of Wildlife Research</i> , 2019, 65, 1.	0.7	4
7347	Geographic patterns of mtDNA and Z-linked sequence variation in the Common Chiffchaff and the "chiffchaff complex". <i>PLoS ONE</i> , 2019, 14, e0210268.	1.1	14
7348	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
7349	Molecular analysis of an ancient Thule population at Nuvuk, Point Barrow, Alaska. <i>American Journal of Physical Anthropology</i> , 2019, 168, 303-317.	2.1	12
7350	Genetic characterization of 32 X-InDels in a population sample from São Paulo State (Brazil). <i>International Journal of Legal Medicine</i> , 2019, 133, 1385-1388.	1.2	17
7351	Evolutionary aspects of direct or indirect selection for seed size and seed metabolites in <i>Brassica juncea</i> and diploid progenitor species. <i>Molecular Biology Reports</i> , 2019, 46, 1227-1238.	1.0	11

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7353	Genotyping of 49-plex autosomal SNP panel in Iranian Turkmen ethnic group. <i>Legal Medicine</i> , 2019, 37, 45-48.	0.6	2
7354	Genotypic and allelic effects of the myostatin gene (MSTN) on carcass, meat quality, and biometric traits in Colored Polish Merino sheep. <i>Meat Science</i> , 2019, 151, 4-17.	2.7	20
7355	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
7356	Recombination contributes to population diversification in the polyploid intestinal symbiont <i>Epulopiscium</i> sp. type B. <i>ISME Journal</i> , 2019, 13, 1084-1097.	4.4	15
7357	Convergent evolution on the hypoxia-inducible factor (HIF) pathway genes EGLN1 and EPAS1 in high-altitude ducks. <i>Heredity</i> , 2019, 122, 819-832.	1.2	52
7358	The evolution of sex determination associated with a chromosomal inversion. <i>Nature Communications</i> , 2019, 10, 145.	5.8	64
7359	Mitochondrial DNA diversity and population structure of the ocellate freshwater stingray <i>Potamotrygon motoro</i> (Müller & Henle, 1841) (Myliobatiformes: Potamotrygonidae) in the Colombian Amazon and Orinoco Basins. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2019, 30, 466-473.	0.7	4
7360	Development of a Standardized Molecular Tool and Estimation of Genetic Measures for Responsible Aquaculture-Based Fisheries Enhancement of American Shad in North and South Carolina. <i>Transactions of the American Fisheries Society</i> , 2019, 148, 148-162.	0.6	3
7361	Genetic legacies of translocation and relictual populations of American marten at the southeastern margin of their distribution. <i>Conservation Genetics</i> , 2019, 20, 275-286.	0.8	4
7362	Farmers Drive Genetic Diversity of Thai Purple Rice ( <i>Oryza sativa</i> L.) Landraces. <i>Economic Botany</i> , 2019, 73, 76-85.	0.8	11
7363	A genetic perspective on Longobard-Era migrations. <i>European Journal of Human Genetics</i> , 2019, 27, 647-656.	1.4	15
7364	Conservation and historical distribution of two bumblebee species from the Atlantic Forest. <i>Systematics and Biodiversity</i> , 2019, 17, 22-38.	0.5	5
7365	Genetic divergence, population differentiation and phylogeography of the cicada <i>Subpsaltria yangi</i> based on molecular and acoustic data: an example of the early stage of speciation?. <i>BMC Evolutionary Biology</i> , 2019, 19, 5.	3.2	19
7366	Spatial distribution, prevalence and diversity of haemosporidians in the rufous-collared sparrow, <i>Zonotrichia capensis</i> . <i>Parasites and Vectors</i> , 2019, 12, 2.	1.0	14
7367	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
7368	Genetic diversity of 21 experimental chicken lines with diverse origins and genetic backgrounds. <i>Experimental Animals</i> , 2019, 68, 177-193.	0.7	6
7369	Genetic diversity is retained in a bottlenecked Cinereous Vulture population in Turkey. <i>Ibis</i> , 2019, 161, 793-805.	1.0	4

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7370	Population data of 23 Y STRs from Manchu population of Liaoning Province, Northeast China. International Journal of Legal Medicine, 2019, 133, 785-788.	1.2	12
7371	Evolutionary history of a beautiful damselfly, <i>Matrona basilaris</i> , revealed by phylogeographic analyses: the first study of an odonate species in mainland China. Heredity, 2019, 122, 570-581.	1.2	4
7372	Genetic polymorphisms of 20 STR loci in a Chaoshan group from Jieyang, China. Legal Medicine, 2019, 36, 41-42.	0.6	0
7373	The evolutionary history of the goby <i>Elacatinus punctulatus</i> in the tropical eastern pacific: Effects of habitat discontinuities and local environmental variability. Molecular Phylogenetics and Evolution, 2019, 130, 269-285.	1.2	17
7374	Genetic potential for disease resistance in critically endangered amphibians decimated by chytridiomycosis. Animal Conservation, 2019, 22, 238-250.	1.5	29
7375	Diversification and historical demography of the rapid racerunner ( <i>Eremias velox</i> ) in relation to geological history and Pleistocene climatic oscillations in arid Central Asia. Molecular Phylogenetics and Evolution, 2019, 130, 244-258.	1.2	18
7376	Rapidly mutating Y-STRs in rapidly expanding populations: Discrimination power of the Yfiler Plus multiplex in northern Africa. Forensic Science International: Genetics, 2019, 38, 185-194.	1.6	23
7377	Population data for 21 autosomal STR loci (GlobalFiler kit) in two Mexican-Mestizo population from the northwest, Mexico. International Journal of Legal Medicine, 2019, 133, 781-783.	1.2	6
7378	Phylogeography and genetic connectivity of the marine macroalga <i>Sargassum ilicifolium</i> (Phaeophyceae, Ochrophyta) in the northwestern Pacific. Journal of Phycology, 2019, 55, 7-24.	1.0	17
7379	Population genetic analysis of 30 insertion-deletion (INDEL) loci in a Qinghai Tibetan group using the Investigator DIPplex Kit. International Journal of Legal Medicine, 2019, 133, 1039-1041.	1.2	12
7380	HLA-F displays highly divergent and frequent haplotype lineages associated with different mRNA expression levels. Human Immunology, 2019, 80, 112-119.	1.2	20
7381	Phylogeography Approach of <i>Diloboderus abderus</i> (Coleoptera: Melolonthidae) in the Southern Cone of America. Neotropical Entomology, 2019, 48, 332-339.	0.5	1
7382	Genetic analysis of 12 X-STRs for forensic purposes in Liaoning Manchu population from China. Gene, 2019, 683, 153-158.	1.0	10
7383	Recombination and purifying and balancing selection determine the evolution of major antigenic protein 1 (map 1) family genes in <i>Ehrlichia ruminantium</i> . Gene, 2019, 683, 216-224.	1.0	8
7384	Genetic diversity and patterns of demographic expansion in natural populations of milkfish, <i>Chanos chanos</i> (Forsskål, 1775), in the Philippines. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2019, 30, 312-324.	0.7	3
7385	Evolutionary potential varies across populations and traits in the neotropical oak <i>Quercus oleoides</i> . Tree Physiology, 2019, 39, 427-439.	1.4	14
7386	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. Aquaculture, 2019, 500, 338-346.	1.7	21
7387	Amended larval recruitment model for the Japanese spiny lobster <i>Panulirus japonicus</i> based on new larval records and population genetic data in Taiwan. Journal of Oceanography, 2019, 75, 273-282.	0.7	3

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7388	Spodoptera marima: a New Synonym of Spodoptera ornithogalli (Lepidoptera: Noctuidae), with Notes on Adult Morphology, Host Plant Use and Genetic Variation Along Its Geographic Range. Neotropical Entomology, 2019, 48, 433-448.	0.5	10
7389	FST between archaic and present-day samples. Heredity, 2019, 122, 711-718.	1.2	7
7390	Isolation on a remote island: genetic and morphological differentiation of a cosmopolitan odonate. Heredity, 2019, 122, 893-905.	1.2	10
7391	Y-STRsâ€™ genetic profiling of 1953 individuals from two Chinese Han populations (Guizhou and Shanxi). Forensic Science International: Genetics, 2019, 38, e8-e10.	1.6	24
7392	Canals as ecological corridors and hybridization zones for two cyprinid species. Hydrobiologia, 2019, 830, 1-16.	1.0	7
7393	Genomic comparisons reveal biogeographic and anthropogenic impacts in the koala (Phascolarctos) Tj ETQq1 1 0.784314 rgBT /Overl 122, 525-544.	1.2	29
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7395	Population genetics of 19 Yâ€STR loci in Yanbian Korean samples from China. Annals of Human Genetics, 2019, 83, 134-140.	0.3	1
7396	Chromosomal fusion and life historyâ€™associated genomic variation contribute to withinâ€™river local adaptation of Atlantic salmon. Molecular Ecology, 2019, 28, 1439-1459.	2.0	56
7397	Leopard tortoises in southern Africa have greater genetic diversity in the north than in the south (Testudinidae). Zoologica Scripta, 2019, 48, 57-68.	0.7	4
7398	Invasive range expansion of the small carpenter bee, Ceratina dentipes (Hymenoptera: Apidae) into Hawaii with implications for native endangered species displacement. Biological Invasions, 2019, 21, 1155-1166.	1.2	11
7399	The genetic diversity, individual relatedness and possible mating system of an isolated population of the Cyprinid species Megalobrama pellgrini in upper reaches of the Changjiang (Yangtze) River, China. Journal of Oceanology and Limnology, 2019, 37, 1042-1050.	0.6	4
7400	Molecular phylogeography and genetic diversity of Angiostrongylus cantonensis and A. malaysiensis (Nematoda: Angiostrongylidae) based on 66-kDa protein gene. Parasitology International, 2019, 68, 24-30.	0.6	7
7401	Genetic perspectives on the historical introduction of the European rabbit (Oryctolagus cuniculus) to Australia. Biological Invasions, 2019, 21, 603-614.	1.2	10
7402	Evidence for intra-mitochondrial variation in population genetic structure of <i>Platycephalus</i> sp.1 In the Northwestern Pacific. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2019, 30, 281-288.	0.7	9
7403	Characterizing patterns of introgressive hybridization between two species of Tyrannus following concurrent range expansion. Ibis, 2019, 161, 770-780.	1.0	3
7404	Genetic evidence for regional philopatry of the Bull Shark (Carcharhinus leucas), to nursery areas in estuaries of the Gulf of Mexico and western North Atlantic ocean. Fisheries Research, 2019, 209, 67-74.	0.9	22
7405	Morphological and molecular evaluation of the Far East fruit genetic resources of Lonicera caerulea L.â€™vegetation, ethnobotany, use and conservation. Genetic Resources and Crop Evolution, 2019, 66, 121-141.	0.8	12

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7406	Phylogeographic structure in the chromosomally polymorphic rodent <i>Cricetulus barabensis</i> sensu lato (Mammalia, Cricetidae). Journal of Zoological Systematics and Evolutionary Research, 2019, 57, 679-694.	0.6	9
7407	Selection, drift, and introgression shape MHC polymorphism in lizards. Heredity, 2019, 122, 468-484.	1.2	16
7408	Characterization of genetic diversity and structures in natural <i>Glycine tomentella</i> populations on the southeast islands of China. Genetic Resources and Crop Evolution, 2019, 66, 47-59.	0.8	2
7409	Investigating the genetic diversity and affinities of historical populations of Tibet. Gene, 2019, 682, 81-91.	1.0	8
7410	Trace of outbreeding between Biwa salmon ( <i>Oncorhynchus masou</i> subsp.) and amago ( <i>O. m. ishikawae</i> ) detected from the upper reaches of inlet streams within Lake Biwa water system, Japan. Ichthyological Research, 2019, 66, 67-78.	0.5	2
7411	Phylogeography of the highly invasive sugar beet nematode, <i>Heterodera schachtii</i> (Schmidt), Tj ETQq1 1 0.784314 rgBT /Overl	1.5	7
7412	Regional genetic structure of sandfish <i>Holothuria (Metriatyla) scabra</i> populations across the Philippine archipelago. Fisheries Research, 2019, 209, 143-155.	0.9	22
7413	Genetic Variation and Differentiation of <i>Hylesia metabus</i> (Lepidoptera: Saturniidae): Moths of Public Health Importance in French Guiana and in Venezuela. Journal of Medical Entomology, 2019, 56, 137-148.	0.9	2
7414	Mating system complexity and cryptic speciation in the seed bank pathogen <i>Pyrenophora semeniperda</i> . Plant Pathology, 2019, 68, 369-382.	1.2	1
7415	Genetic structure of lake and stream populations in a Pyrenean amphibian ( <i>Calotriton asper</i> ) reveals evolutionary significant units associated with paedomorphosis. Journal of Zoological Systematics and Evolutionary Research, 2019, 57, 418-430.	0.6	7
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7417	Genetic diversity of <i>Leishmania tropica</i> in Morocco: does the dominance of one haplotype signify its fitness in both predominantly anthropophilic <i>Phlebotomus sergenti</i> and human beings?. Transboundary and Emerging Diseases, 2019, 66, 373-380.	1.3	11
7418	Complex problems need detailed solutions: Harnessing multiple data types to inform genetic management in the wild. Evolutionary Applications, 2019, 12, 280-291.	1.5	28
7419	Northern areas as refugia for temperate species under current climate warming: Atlantic salmon ( <i>Salmo salar</i> L.) as a model in northern Europe. Journal of Fish Biology, 2019, 95, 304-310.	0.7	3
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7421	Phylogeography of Noah's giant clam. Marine Biodiversity, 2019, 49, 521-526.	0.3	7
7422	Relative importance of ocean currents and fronts in population structures of marine fish: a lesson from the cryptic lineages of the <i>Hippocampus mohnikei</i> complex. Marine Biodiversity, 2019, 49, 263-275.	0.3	13
7423	The genetic divergence of <i>Oratosquilla oratoria</i> between the East China Sea and Yellow Sea: physical barrier and possible local adaptation. Journal of the Marine Biological Association of the United Kingdom, 2019, 99, 631-638.	0.4	0

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7425	Population connectivity of hydrothermal-vent limpets along the northern Mid-Atlantic Ridge (Gastropoda: Neritimorpha: Phenacolepadidae). <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2019, 99, 179-185.	0.4	10
7426	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
7427	Genetic Structuring in Riverine Population of <i>Channa striata</i> (Bloch, 1793) from India using Cytochrome Oxidase I Gene. <i>Proceedings of the National Academy of Sciences India Section B - Biological Sciences</i> , 2019, 89, 303-312.	0.4	0
7428	Allele frequencies of 18 autosomal STR loci in the Uyghur population living in Kashgar Prefecture, Northwest China. <i>International Journal of Legal Medicine</i> , 2019, 133, 427-428.	1.2	0
7429	Population data of 19 autosomal STR loci in the Li population from Hainan Province in southernmost China. <i>International Journal of Legal Medicine</i> , 2019, 133, 429-431.	1.2	17
7430	StatsX v2.0: the interactive graphical software for population statistics on X-STR. <i>International Journal of Legal Medicine</i> , 2019, 133, 39-44.	1.2	36
7431	Genomic evidence for the population genetic differentiation of <i>Misgurnus anguillicaudatus</i> in the Yangtze River basin of China. <i>Genomics</i> , 2019, 111, 367-374.	1.3	11
7432	Genetic polymorphism of 29 STR loci in the Hunan Han population from China. <i>Forensic Sciences Research</i> , 2019, 4, 351-353.	0.9	7
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7457	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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7484	Second Sahelian amphibian endemism suggested by phylogeography of Groove crowned Bullfrog ( <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i> ) of <i>Zoological Systematics and Evolutionary Research</i> , 2020, 58, 262-274.	0.6	5
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7500	Genomic analyses reveal three independent introductions of the invasive brown rat ( <i>Rattus</i> ) to the United States. <i>PLoS ONE</i> , 2020, 15(12), e0241141. <a href="#">DOI: 10.1371/journal.pone.0241141</a>	1.2	12
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7539	Paternal genetic history of the Yong population in northern Thailand revealed by Y-chromosomal haplotypes and haplogroups. <i>Molecular Genetics and Genomics</i> , 2020, 295, 579-589.	1.0	3
7540	Not a marginal loss: genetic diversity of the endangered freshwater snail <i>Melanopsis etrusca</i> (Brot.) Tj ETQq1 1 0.784314 rgBT /Overlock 0.8 5	0.8	5
7541	A comprehensive phylogeographic study of <i>Arion vulgaris</i> Moquin-Tandon, 1855 (Gastropoda:) Tj ETQq0 0 0 rgBT /Overlock 0.7 11 Tf 50 42	0.7	11
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7562	The last primary forests of the Tertiary relict <i>Glyptostrobus pensilis</i> contain the highest genetic diversity. <i>Forestry</i> , 2020, 93, 359-375.	1.2	7
7563	Genetic diversity and distribution pattern of economic seaweeds <i>Pyropia yezoensis</i> and <i>Py. suborbiculata</i> (Bangiales, Rhodophyta) in the northwest Pacific. <i>Journal of Applied Phycology</i> , 2020, 32, 2495-2504.	1.5	5
7564	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: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 <i>Journal for Parasitology</i> , 2020, 50, 55-62.	1.3	12
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7568	Assessment of genetic polymorphism at 20 autosomal STR loci in scheduled caste population of Himachal Pradesh. <i>International Journal of Legal Medicine</i> , 2020, 134, 1329-1330.	1.2	1
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7572	Biogeographic origin prediction of three continental populations through 42 ancestry informative SNPs. <i>Electrophoresis</i> , 2020, 41, 235-245.	1.3	8
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7576	Comparative phylogeography of mainland and insular species of Neotropical molossid bats ( <i>Molossus</i> ). <i>Ecology and Evolution</i> , 2020, 10, 389-409.	0.8	9
7577	Fine scale population structure of hoverfly pollinator, <i>Eristalis arbustorum</i> : an integrative study. <i>Journal of Insect Conservation</i> , 2020, 24, 49-63.	0.8	3
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7590	Characterization of ancestry informative markers in the Tigray population of Ethiopia: A contribution to the identification process of dead migrants in the Mediterranean Sea. <i>Forensic Science International: Genetics</i> , 2020, 45, 102207.	1.6	6
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7601	Genomic evidence of population genetic differentiation in deep-sea squat lobster <i>Shinkaia crosnieri</i> (crustacea: Decapoda: Anomura) from Northwestern Pacific hydrothermal vent and cold seep. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2020, 156, 103188.	0.6	15
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7604	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
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7607	Too strict or too loose? Integrative taxonomic assessment of <i>Bombus lapidarius</i> complex (Hymenoptera: Apidae). <i>Zoologica Scripta</i> , 2020, 49, 187-196.	0.7	6
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7609	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
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7612	Phylogeographical structure and genetic diversity of <i>Adonis vernalis</i> L. (Ranunculaceae) across and beyond the Pannonian region. <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2020, 262, 151497.	0.6	12
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7620	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
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7622	Genomic footprints of a biological invasion: Introduction from Asia and dispersal in Europe of the topmouth gudgeon ( <i>Pseudorasbora parva</i> ). <i>Molecular Ecology</i> , 2020, 29, 71-85.	2.0	13
7623	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

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7631	Genetic diversity of <i>Nuphar lutea</i> in Lithuanian river populations. <i>Aquatic Botany</i> , 2020, 161, 103173.	0.8	6
7632	Significant population genetic structuring in <i>Rhyzopertha dominica</i> across Turkey: Biogeographic and practical implications. <i>Journal of Stored Products Research</i> , 2020, 85, 101536.	1.2	3
7633	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
7634	Pre-Quaternary diversification and glacial demographic expansions of <i>Cardiocrinum</i> (Liliaceae) in temperate forest biomes of Sino-Japanese Floristic Region. <i>Molecular Phylogenetics and Evolution</i> , 2020, 143, 106693.	1.2	26
7635	Crayfish populations genetically fragmented in streams impounded for 36–104 years. <i>Freshwater Biology</i> , 2020, 65, 768-785.	1.2	14
7636	Genetic diversity of two Southern African cichlids ( <i>Oreochromis</i> ) Tj ETQq0 0 0 rGBT /Overlock 10 Tf 50 267 Td (andersonii) and <i>Oreochromis</i> Ichthyology, 2020, 36, 62-74.	0.3	4
7637	Effects of Intronic SNPs in the Myostatin Gene on Growth and Carcass Traits in Colored Polish Merino Sheep. <i>Genes</i> , 2020, 11, 2.	1.0	18
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7639	Genetic Diversity of the Pearse's Mudskipper <i>Periophthalmus novemradiatus</i> (Perciformes: Gobiidae) and Characterization of its Complete Mitochondrial Genome. <i>Thalassas</i> , 2020, 36, 103-113.	0.1	9
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7644	Are population isolations and declines a threat to island endemic water striders? A lesson from demographic and niche modelling of <i>Metrocoris esakii</i> (Hemiptera: Gerridae). <i>Molecular Ecology</i> , 2020, 29, 4573-4587.	2.0	6
7645	Phylogeographic structure of the dunes sagebrush lizard, an endemic habitat specialist. <i>PLoS ONE</i> , 2020, 15, e0238194.	1.1	3
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7649	Paternal Origins and Migratory Episodes of Domestic Sheep. <i>Current Biology</i> , 2020, 30, 4085-4095.e6.	1.8	49
7650	Genetic connectivity of the scalloped hammerhead shark <i>Sphyrna lewini</i> across Indonesia and the Western Indian Ocean. <i>PLoS ONE</i> , 2020, 15, e0230763.	1.1	15
7651	Population connectivity of the hydrothermal-vent limpet <i>Shinkailepas tollmanni</i> in the Southwest Pacific (Gastropoda: Neritimorpha: Phenacolepadidae). <i>PLoS ONE</i> , 2020, 15, e0239784.	1.1	8
7652	Massively parallel sequencing of sex-chromosomal STRs in Saudi Arabia reveals patrilineage-associated sequence variants. <i>Forensic Science International: Genetics</i> , 2020, 49, 102402.	1.6	2
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7656	Genetic analysis of <i>Boletus edulis</i> suggests that intra-specific competition may reduce local genetic diversity as a woodland ages. <i>Royal Society Open Science</i> , 2020, 7, 200419.	1.1	1
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7661	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
7662	A layover in Europe: Reconstructing the invasion route of asexual lineages of a New Zealand snail to North America. <i>Molecular Ecology</i> , 2020, 29, 3446-3465.	2.0	13
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7664	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
7665	Genomic analysis reveals the genetic diversity, population structure, evolutionary history and relationships of Chinese pepper. <i>Horticulture Research</i> , 2020, 7, 158.	2.9	25
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7667	Phylogeography of split kelp <i>Hedophyllum nigripes</i> : northern ice-age refugia and trans-Arctic dispersal. <i>Polar Biology</i> , 2020, 43, 1829-1841.	0.5	7
7668	<i>Bathyraja</i> ( <i>Arctoraja</i> ) <i>sexoculata</i> sp. nov., a new softnose skate (Rajiformes: Arhynchobatidae) from Simushir Island, Kuril Islands (western North Pacific), with special reference to geographic variations in <i>Bathyraja</i> ( <i>Arctoraja</i> ) <i>smirnovi</i> . <i>Zootaxa</i> , 2020, 4861, zootaxa.4861.4.3.	0.2	6
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7670	Population data of 22 autosomal STR loci in Chinese Han individuals from Hebei Province in northern China. <i>Forensic Science International: Reports</i> , 2020, 2, 100119.	0.4	0
7671	Fine-scale population structure and evidence for local adaptation in Australian giant black tiger shrimp ( <i>Penaeus monodon</i> ) using SNP analysis. <i>BMC Genomics</i> , 2020, 21, 669.	1.2	14
7672	Starch Metabolism in Wheat: Gene Variation and Association Analysis Reveal Additive Effects on Kernel Weight. <i>Frontiers in Plant Science</i> , 2020, 11, 562008.	1.7	5
7673	Genetic connectivity and population structure of African savanna elephants ( <i>Loxodonta africana</i> ) in Tanzania. <i>Ecology and Evolution</i> , 2020, 10, 11069-11089.	0.8	13
7674	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
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7679	High phylogeographic and genetic diversity of <i>Tidestromia lanuginosa</i> supports full-glacial refugia for arid-adapted plants in southern and central Coahuila, Mexico. <i>American Journal of Botany</i> , 2020, 107, 1296-1308.	0.8	4
7680	Genetic structuring among colonies of a pantropical seabird: Implication for subspecies validation and conservation. <i>Ecology and Evolution</i> , 2020, 10, 11886-11905.	0.8	7
7681	Insights from Chloroplast DNA into the Progenitor-Derivative Relationship Between <i>Campanula punctata</i> and <i>C. takesimana</i> (Campanulaceae) in Korea. <i>Journal of Plant Biology</i> , 2020, 63, 431-444.	0.9	4
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7811	<i>Trifolium repens</i> -Associated Bacteria as a Potential Tool to Facilitate Phytostabilization of Zinc and Lead Polluted Waste Heaps. Plants, 2020, 9, 1002.	1.6	13
7812	HLAs associated with perampanel-induced psychiatric adverse effects in a Korean population. Scientific Reports, 2020, 10, 13667.	1.6	3
7813	Maternal origin and genetic diversity of Algerian domestic chicken ( <i>Gallus gallus domesticus</i> ) from North-Western Africa based on mitochondrial DNA analysis. Animal Biotechnology, 2022, 33, 457-467.	0.7	7
7814	Examination of unidentifiable spined loach individuals found in the overlap zone of two tetraploid species within a single river in Japan. Journal of Applied Ichthyology, 2020, 36, 668-674.	0.3	1
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7817	Genetic diversity and population structure of the endangered orchid <i>Pelatantheria scolopendrifolia</i> (Orchidaceae) in Korea. PLoS ONE, 2020, 15, e0237546.	1.1	16
7818	Genetic structure of the endemic <i>Papaver occidentale</i> indicates survival and immigration in the Western Prealps. Alpine Botany, 2020, 130, 129-140.	1.1	3
7819	Chloroplast DNA phylogeography of the Holly mangrove <i>Acanthus ilicifolius</i> in the Indo-West Pacific. Hydrobiologia, 2020, 847, 3591-3608.	1.0	7
7820	Comparative Phylogeography and Integrative Taxonomy of <i>Ochlerotatus caspius</i> (Dipera: Culicidae) and <i>Ochlerotatus dorsalis</i> . Journal of Medical Entomology, 2020, 58, 222-240.	0.9	0
7821	Egg spottiness reflects female condition, physiological stress, and ornament expression in a common rallid species. Auk, 2020, 137, .	0.7	4
7822	Ecotypes of <i>Hypnea pseudomusciformis</i> (Cystocloniaceae, Rhodophyta) revealed by physiological, morphological, and molecular data. Journal of Applied Phycology, 2020, 32, 4399-4409.	1.5	8

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7824	Geographic distribution of microsatellite alleles in geladas (Primates, Cercopithecidae): Evidence for three evolutionary units. <i>Zoologica Scripta</i> , 2020, 49, 659-667.	0.7	4
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7828	First evaluation of the population structure, genetic diversity and landscape connectivity of the Endangered Arabian tahr. <i>Mammalian Biology</i> , 2020, 100, 659-673.	0.8	7
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7835	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
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7837	Population genetic diversity in an Iraqi population and gene flow across the Arabian Peninsula. <i>Scientific Reports</i> , 2020, 10, 15289.	1.6	5
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7842	Molecular phylogenetic, population genetic and demographic studies of <i>Nodularia douglasiae</i> and <i>Nodularia breviconcha</i> based on COI and 16S rRNA. <i>Scientific Reports</i> , 2020, 10, 16572.	1.6	7
7843	Fine-scale landscape genetics unveiling contemporary asymmetric movement of red panda ( <i>Ailurus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.6	21
7844	Changes in transcriptomic response to salinity stress induce the brackish water adaptation in a freshwater snail. <i>Scientific Reports</i> , 2020, 10, 16049.	1.6	5
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7846	Co-haplotyping symbiont and host to unravel invasion pathways of the exotic pest <i>Halyomorpha halys</i> in Italy. <i>Scientific Reports</i> , 2020, 10, 18441.	1.6	3
7847	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
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7853	Genetic Diversity and Structure of Japanese Endemic Genus <i>Thujopsis</i> (Cupressaceae) Using EST-SSR Markers. <i>Forests</i> , 2020, 11, 935.	0.9	5
7854	A set of novel multi-allelic SNPs for forensic application developed through massively parallel sequencing and its examples of population genetic studies. <i>Electrophoresis</i> , 2020, 41, 2036-2046.	1.3	2
7855	Genetic structure and diversity in the freshwater gastropod <i>Chilina dombeiana</i> in the Biobío River, Chile. <i>Conservation Genetics</i> , 2020, 21, 1023-1036.	0.8	5
7856	Preliminary characterization of the <i>Quercus pubescens</i> complex in southern Italy using molecular markers. <i>Acta Botanica Croatica</i> , 2020, 79, 15-25.	0.3	12
7857	Latitudinal Biogeographic Structuring in the Globally Distributed Moss <i>Ceratodon purpureus</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 502359.	1.7	13
7859	Iterative taxonomic study of <i>Pareiorhaphis hystrix</i> (Siluriformes, Loricariidae) suggests a single, yet phenotypically variable, species in south Brazil. <i>PLoS ONE</i> , 2020, 15, e0237160.	1.1	7

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7861	Conservation Genomics of a Threatened <i>Rhododendron</i> : Contrasting Patterns of Population Structure Revealed From Neutral and Selected SNPs. <i>Frontiers in Genetics</i> , 2020, 11, 757.	1.1	23
7862	Sex-biased patterns shaped the genetic history of Roma. <i>Scientific Reports</i> , 2020, 10, 14464.	1.6	7
7863	Natal Origin Identification of Green Turtles in the North Pacific by Genome-Wide Population Analysis With Limited DNA Samples. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	7
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7865	Genetic diversity and population structure of <i>Croton urucurana</i> Baill. (Euphorbiaceae) in Central Brazil by ISSR markers. <i>Revista Brasileira De Botanica</i> , 2020, 43, 831-838.	0.5	5
7866	Genetic diversity and population structure of the endangered fish <i>Pseudobagrus brevicorpus</i> (Bagridae) using a newly developed 12-microsatellite marker. <i>Genes and Genomics</i> , 2020, 42, 1291-1298.	0.5	3
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7869	Distribution and genetic diversity of two species of <i>Pelargus</i> minnows (Leuciscidae) in southern Greece. <i>Knowledge and Management of Aquatic Ecosystems</i> , 2020, , 27.	0.5	7
7870	Large-scale connectivity, cryptic population structure, and relatedness in Eastern Pacific Olive ridley sea turtles ( <i>Lepidochelys olivacea</i> ). <i>Ecology and Evolution</i> , 2020, 10, 8688-8704.	0.8	7
7871	Major histocompatibility complex variation is similar in little brown bats before and after white-nose syndrome outbreak. <i>Ecology and Evolution</i> , 2020, 10, 10031-10043.	0.8	3
7872	Miocene diversification of a golden-thread nanmu tree species ( <i>Phoebe zhennan</i> , Lauraceae) around the Sichuan Basin shaped by the East Asian monsoon. <i>Ecology and Evolution</i> , 2020, 10, 10543-10557.	0.8	17
7873	Defining relictual biodiversity: Conservation units in speckled dace (Leuciscidae: <i>Rhinichthys</i> ) Tj ETQq1 1 0.784314 rgBT / Overlock 10	0.8	15
7874	Evidence of genetic isolation between two Mediterranean morphotypes of <i>Parazoanthus axinellae</i> . <i>Scientific Reports</i> , 2020, 10, 13938.	1.6	8
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7881	Recent and rapid anthropogenic habitat fragmentation increases extinction risk for freshwater biodiversity. <i>Evolutionary Applications</i> , 2020, 13, 2857-2869.	1.5	43
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7883	Distribution of maternal lineages in hunterâ€gathering societies of the southern coast of Tierra del Fuego, Argentina. <i>American Journal of Physical Anthropology</i> , 2020, 173, 709-720.	2.1	6
7884	Investigation of mechanisms underlying chaotic genetic patchiness in the intertidal marbled crab <i>Pachygrapsus marmoratus</i> (Brachyura: Grapsidae) across the Ligurian Sea. <i>BMC Evolutionary Biology</i> , 2020, 20, 108.	3.2	8
7885	Genetic tropicalisation following a marine heatwave. <i>Scientific Reports</i> , 2020, 10, 12726.	1.6	50
7886	Origin and cross-species transmission of bat coronaviruses in China. <i>Nature Communications</i> , 2020, 11, 4235.	5.8	264
7887	Signatures of local adaptation in the spatial genetic structure of the ascidian <i>Pyura chilensis</i> along the southeast Pacific coast. <i>Scientific Reports</i> , 2020, 10, 14098.	1.6	10
7888	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
7889	Genetic diversity analysis of a flax ( <i>Linum usitatissimum</i> L.) global collection. <i>BMC Genomics</i> , 2020, 21, 557.	1.2	28
7890	<i>Taenia hydatigena</i> cysticercosis in wild boar ( <i>Sus scrofa</i> ) from southern Italy: an epidemiological and molecular survey. <i>Parasitology</i> , 2020, 147, 1636-1642.	0.7	10
7891	Genotypic and phenotypic distinctness of restored and indigenous populations of <i>Pimpinella saxifraga</i> L. 8 or more years after restoration. <i>Plant Biology</i> , 2020, 22, 1092-1101.	1.8	1
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7897	Genome-wide insights of Ethiopian indigenous sheep populations reveal the population structure related to tail morphology and phylogeography. <i>Genes and Genomics</i> , 2020, 42, 1169-1178.	0.5	8
7898	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
7899	Genetic Diversity and Population Structure of <i>Brachiaria</i> (syn. <i>Urochloa</i> ) Ecotypes from Uganda. <i>Agronomy</i> , 2020, 10, 1193.	1.3	7
7900	Genomic diversity of the Muslim population from Telangana (India) inferred from 23 autosomal STRs. <i>Annals of Human Biology</i> , 2020, 47, 652-658.	0.4	0
7901	SNP discovery for genetic diversity and population structure analysis coupled with restriction-associated DNA (RAD) sequencing in walnut cultivars of Sichuan Province, China. <i>Biotechnology and Biotechnological Equipment</i> , 2020, 34, 652-664.	0.5	9
7902	Little genetic structure in a Bornean endemic small mammal across a steep ecological gradient. <i>Molecular Ecology</i> , 2020, 29, 4074-4090.	2.0	9
7903	Genetic diversity of avocado from the southern highlands of Tanzania as revealed by microsatellite markers. <i>Hereditas</i> , 2020, 157, 40.	0.5	9
7904	Population data for 20 insertion-null allele markers in the Li ethnic minority from Hainan Province. <i>International Journal of Legal Medicine</i> , 2020, 134, 2075-2077.	1.2	1
7905	Association of ERAP2 polymorphisms in Colombian HLA-B27+ or HLA-B15+ patients with SpA and its relationship with clinical presentation: axial or peripheral predominance. <i>RMD Open</i> , 2020, 6, e001250.	1.8	5
7906	Similar patterns of genetic diversity and linkage disequilibrium in Western chimpanzees (Pan) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 347 <i>BMC Evolutionary Biology</i> , 2020, 20, 119.	3.2	2
7907	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
7908	Mitochondrial genomics reveals the evolutionary history of the porpoises (Phocoenidae) across the speciation continuum. <i>Scientific Reports</i> , 2020, 10, 15190.	1.6	13
7909	Founder events influence structures of <i>Aspergillus flavus</i> populations. <i>Environmental Microbiology</i> , 2020, 22, 3522-3534.	1.8	10
7910	Most frequent South Asian haplotypes of ACE2 share identity by descent with East Eurasian populations. <i>PLoS ONE</i> , 2020, 15, e0238255.	1.1	26
7911	Evolutionary trajectory of fish <i>Piscine novirhabdovirus</i> (=Viral Hemorrhagic Septicemia Virus) across its Laurentian Great Lakes history: Spatial and temporal diversification. <i>Ecology and Evolution</i> , 2020, 10, 9740-9775.	0.8	5
7912	Contrasting mitochondrial diversity of European starlings (<i>Sturnus vulgaris</i>) across three invasive continental distributions. <i>Ecology and Evolution</i> , 2020, 10, 10186-10195.	0.8	17
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7915	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
7916	Does color matter? Molecular and ecological divergence in four sympatric color morphs of a coral reef fish. <i>Ecology and Evolution</i> , 2020, 10, 9663-9681.	0.8	6
7917	Drivers of molecular and morphometric variation in <i>Triatoma brasiliensis</i> (Hemiptera: Triatominae): the resolution of geometric morphometrics for populational structuring on a microgeographical scale. <i>Parasites and Vectors</i> , 2020, 13, 455.	1.0	15
7919	Systematics of the <i>Peripatopsis clavigera</i> species complex (Onychophora : Peripatopsidae) reveals cryptic cladogenic patterning, with the description of five new species. <i>Invertebrate Systematics</i> , 2020, , .	0.5	6
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7921	Vicariance in a generalist fish parasite driven by climate and salinity tolerance of hosts. <i>Parasitology</i> , 2020, 147, 1658-1664.	0.7	4
7922	Tracing the genetic history of the <i>Cañaris</i> ™ from Ecuador and Peru using uniparental DNA markers. <i>BMC Genomics</i> , 2020, 21, 413.	1.2	5
7923	Genetic Characterization of the Local Pirenaica Cattle for Parentage and Traceability Purposes. <i>Animals</i> , 2020, 10, 1584.	1.0	4
7924	Seascape genomics reveals population isolation in the reef-building honeycomb worm, <i>Sabellaria alveolata</i> (L.). <i>BMC Evolutionary Biology</i> , 2020, 20, 100.	3.2	1
7925	Incipient genetic divergence or cryptic speciation? <i>Procamallanus</i> (Nematoda) in freshwater fishes ( ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.7	6
7926	Range-wide population genetics study informs on conservation translocations and reintroductions for the endangered Murray hardyhead ( <i>Craterocephalus fluviatilis</i> ). <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2020, 30, 1959-1974.	0.9	3
7927	Analyzing population structure for forensic STR markers in next generation sequencing data. <i>Forensic Science International: Genetics</i> , 2020, 49, 102364.	1.6	17
7928	Genetic Diversity of <i>Orobancha crenata</i> Populations in Ethiopia Using Microsatellite Markers. <i>International Journal of Genomics</i> , 2020, 2020, 1-8.	0.8	6
7929	Sahelian pastoralism from the perspective of variants associated with lactase persistence. <i>American Journal of Physical Anthropology</i> , 2020, 173, 423-436.	2.1	13
7930	Intraspecific Structure of <i>Rhododendron camtschaticum</i> Pall. on the Kamchatka Peninsula: Genetic Aspect. <i>Russian Journal of Genetics</i> , 2020, 56, 758-762.	0.2	0
7931	Assessing the diversity and distribution of potential intermediate hosts snails for urogenital schistosomiasis: <i>Bulinus</i> spp. (Gastropoda: Planorbidae) of Lake Victoria. <i>Parasites and Vectors</i> , 2020, 13, 418.	1.0	9
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7934	New Genetic Insights About Hybridization and Population Structure of Hawksbill and Loggerhead Turtles From Brazil. Journal of Heredity, 2020, 111, 444-456.	1.0	13
7935	Cryptic variation in mole voles <i>Ellobius</i> (Arvicolinae, Rodentia) of Mongolia. Zoologica Scripta, 2020, 49, 535-548.	0.7	10
7936	Multi-Species Phylogeography of Arid-Zone Sminthopsinae (Marsupialia: Dasyuridae) Reveals Evidence of Refugia and Population Expansion in Response to Quaternary Change. Genes, 2020, 11, 963.	1.0	10
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7938	Molecular relationships of introduced <i>Aedes japonicus</i> (Diptera: Culicidae) populations in British Columbia, Canada using mitochondrial DNA. Journal of Vector Ecology, 2020, 45, 285-296.	0.5	3
7939	The Multiple Origins of Roe Deer Populations in Western Iberia and Their Relevance for Conservation. Animals, 2020, 10, 2419.	1.0	4
7940	GWAS Based on RNA-Seq SNPs and High-Throughput Phenotyping Combined with Climatic Data Highlights the Reservoir of Valuable Genetic Diversity in Regional Tomato Landraces. Genes, 2020, 11, 1387.	1.0	14
7941	Seascape Genomics of the Sugar Kelp <i>Saccharina latissima</i> along the North Eastern Atlantic Latitudinal Gradient. Genes, 2020, 11, 1503.	1.0	17
7942	Genetic structure of two <i>Plagiatus</i> species suggests recent expansion of <i>Chrysodeixis includens</i> in the American continent. Agricultural and Forest Entomology, 2021, 23, 250-260.	0.7	6
7943	Isolation and characterization of microsatellite loci in <i>Pimelodus microstoma</i> (Siluriformes: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342 To	0.3	1
7944	Variability at the 3' untranslated region of the HLA-G gene: a study on patients with AIDS and cytomegalovirus retinochoroiditis. Scientific Reports, 2020, 10, 18646.	1.6	1
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8007	New genetic predictors for abacavir tolerance in HLA-B*57:01 positive individuals. <i>Human Immunology</i> , 2020, 81, 300-304.	1.2	19
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8080	Genetic Diversity of the root-knot nematode <i>Meloidogyne enterolobii</i> in Mulberry Based on the Mitochondrial COI Gene. Ecology and Evolution, 2020, 10, 5391-5401.	0.8	5
8081	Distribution and genetic variability of young-of-the-year greater amberjack ( <i>Seriola dumerili</i> ) in the East China Sea. Environmental Biology of Fishes, 2020, 103, 833-846.	0.4	9
8082	Whole-genome resequencing of wild and domestic sheep identifies genes associated with morphological and agronomic traits. Nature Communications, 2020, 11, 2815.	5.8	142
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8087	Remaking a stand: Links between genetic diversity and tree growth in expanding Mountain pine populations. Forest Ecology and Management, 2020, 472, 118244.	1.4	11
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8093	Population Genetic Analysis for Stock Enhancement of Silver Sea Bream ( <i>Rhabdosargus sarba</i> ) in Taiwan. Fishes, 2020, 5, 19.	0.7	7
8094	Impact of Climate Change and Adaptive Genetic Potential of Norway Spruce at the South-eastern Range of Species Distribution. Agricultural and Forest Meteorology, 2020, 291, 108040.	1.9	13
8095	The influence of host dispersal on the gene flow and genetic diversity of generalist and specialist ectoparasites. African Zoology, 2020, 55, 119-126.	0.2	7
8096	Genetic diversity and structure of the Chinese lake gudgeon ( <i>Sarcocheilichthys sinensis</i> ). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2020, 31, 228-237.	0.7	2



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8098	Quaternary land bridges have not been universal conduits of gene flow. <i>Molecular Ecology</i> , 2020, 29, 2692-2706.	2.0	15
8099	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
8100	â€œA cleaner breakâ€: Genetic divergence between geographic groups and sympatric phenotypes revealed in ballan wrasse ( <i>Labrus bergylta</i> ). <i>Ecology and Evolution</i> , 2020, 10, 6120-6135.	0.8	9
8101	SNP genotyping reveals substructuring in weakly differentiated populations of Atlantic cod ( <i>Gadus</i> ) Tj ETQq0 0 0 rgBT /Overlook 10 Tf 5	1.6	10
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8103	Drift, selection and adaptive variation in small populations of a threatened rattlesnake. <i>Molecular Ecology</i> , 2020, 29, 2612-2625.	2.0	8
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8106	Can polyploidy confer invasive plants with a wider climatic tolerance? A test using <i>Solidago canadensis</i> . <i>Ecology and Evolution</i> , 2020, 10, 5617-5630.	0.8	11
8107	A Genetic Assessment of Missouri's Lake Sturgeon after 30 Years of Restoration Releases. <i>North American Journal of Fisheries Management</i> , 2020, 40, 700-712.	0.5	4
8108	Association study of common functional genetic polymorphisms in SLC6A4 (5-HTT) and MAOA genes with obesity in portuguese children. <i>Archives of Physiology and Biochemistry</i> , 2022, 128, 1510-1515.	1.0	2
8109	Disagreement in F ST estimators: A case study from sex chromosomes. <i>Molecular Ecology Resources</i> , 2020, 20, 1517-1525.	2.2	13
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8111	Genetic, chemical and morphological variability of chamomile ( <i>Chamomilla recutita</i> L.) populations of Latvia. <i>Industrial Crops and Products</i> , 2020, 154, 112614.	2.5	11
8112	Integrative taxonomy of the Changeable Hawk-Eagle <i>Nisaetus cirrhatus</i> complex (Accipitriformes:) Tj ETQq1 1 0.784314 rgBT /Overlook 0,2 4	0,2	4
8113	Genotypingâ€inâ€Thousands by sequencing reveals marked population structure in Western Rattlesnakes to inform conservation status. <i>Ecology and Evolution</i> , 2020, 10, 7157-7172.	0.8	13
8114	The Merodon planifacies subgroup (Diptera, Syrphidae): Congruence of molecular and morphometric evidences reveal new taxa in Drakensberg mountains valleys (Republic of South Africa). <i>Zoologischer Anzeiger</i> , 2020, 287, 105-120.	0.4	8

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8118	Pathways of Pelagic Connectivity: <i>Eukrohnia hamata</i> (Chaetognatha) in the Arctic Ocean. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	8
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8120	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
8121	Mixed stock assessment of lake-run Caspian Sea trout <i>Salmo caspius</i> in the Lar National Park, Iran. <i>Fisheries Research</i> , 2020, 230, 105644.	0.9	4
8122	Characterization of genetic polymorphisms in Nigerians residing in Guangzhou using massively parallel sequencing. <i>Forensic Science International: Genetics</i> , 2020, 48, 102323.	1.6	3
8123	Y-chromosome genetic diversity of <i>Bos indicus</i> cattle in close proximity to the centre of domestication. <i>Scientific Reports</i> , 2020, 10, 9992.	1.6	5
8124	Candidate gene SNP variation in floodplain populations of pedunculate oak ( <i>Quercus robur</i> L.) near the species' southern range margin: Weak differentiation yet distinct associations with water availability. <i>Molecular Ecology</i> , 2020, 29, 2359-2378.	2.0	17
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8126	Deep phylogeographic structure may indicate cryptic species within the Sparid genus <i>Spondyliosoma</i> . <i>Journal of Fish Biology</i> , 2020, 96, 1434-1443.	0.7	3
8127	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
8128	The evolution of metabolism: How to test evolutionary hypotheses at the genomic level. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 482-500.	1.9	36
8129	Janzen-Connell effects shape gene flow patterns and realized fitness in the tropical dioecious tree <i>Spondias purpurea</i> (ANACARDIACEAE). <i>Scientific Reports</i> , 2020, 10, 4584.	1.6	7
8130	Genetic diversity of 15 autosomal STRs in a sample of Berbers from AurÃ's region in the Northeast of Algeria and genetic relationships with other neighbouring samples. <i>Annals of Human Biology</i> , 2020, 47, 284-293.	0.4	2
8131	Spatial genetic structure of <i>Opsariichthys hainanensis</i> in South China. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2020, 31, 98-107.	0.7	7
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8135	Interacting Roles of Breeding Geography and Early-Life Settlement in Godwit Migration Timing. Frontiers in Ecology and Evolution, 2020, 8, .	1.1	10
8136	Genetic drift does not sufficiently explain patterns of electric signal variation among populations of the mormyrid electric fish <i>Paramormyrops kingsleyae</i> . Evolution; International Journal of Organic Evolution, 2020, 74, 911-935.	1.1	8
8137	Linking local movement and molecular analysis to explore philopatry and population connectivity of the southern stingray <i>Hypanus americanus</i> . Journal of Fish Biology, 2020, 96, 1475-1488.	0.7	11
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8140	Genetic structure of regional water vole populations and footprints of reintroductions: a case study from southeast England. Conservation Genetics, 2020, 21, 531-546.	0.8	2
8141	Recent kurua-induced female gene flow disrupted the coevolution of genes and languages in the Papua New Guinea highlands. American Journal of Physical Anthropology, 2020, 172, 87-98.	2.1	1
8142	Genetic diversity of <i>Tulipa suaveolens</i> (Liliaceae) and its evolutionary relationship with early cultivars of <i>T. gesneriana</i> . Plant Systematics and Evolution, 2020, 306, 1.	0.3	8
8143	Cryptic diversity within the African aquatic plant <i>Ottelia ulvifolia</i> (Hydrocharitaceae) revealed by population genetic and phylogenetic analyses. Journal of Plant Research, 2020, 133, 373-381.	1.2	11
8144	Multiplex microsatellite PCR panels and their application in genetic analyses of bighead carp ( <i>Hypophthalmichthys nobilis</i> ) and silver carp ( <i>H. molitrix</i> ). Journal of Applied Ichthyology, 2020, 36, 342-348.	0.3	2
8145	Molecular variability of watermelon mosaic virus isolates from Argentina. European Journal of Plant Pathology, 2020, 156, 1091-1099.	0.8	2
8146	Development and characterization of novel microsatellite markers in chestnut tiger butterfly <i>Parantica sita</i> (Lepidoptera: Nymphalidae) using next-generation sequencing. Applied Entomology and Zoology, 2020, 55, 281-286.	0.6	6
8147	<i>ALOX5</i> , <i>LPA</i> , <i>MMP9</i> and <i>TPO</i> gene polymorphisms increase atherothrombosis susceptibility in middle-aged Mexicans. Royal Society Open Science, 2020, 7, 190775.	1.1	2
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8149	Genetic Structure and Phylogeography of <i>Tuber magnatum</i> Populations. Diversity, 2020, 12, 44.	0.7	13
8150	Spatiotemporal population dynamics of the Caddo Madtom ( <i>Noturus taylori</i> ), a narrow-range endemic of the Ouachita Highlands. Conservation Genetics, 2020, 21, 431-442.	0.8	2

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8152	Population genetic structure of the grass puffer (Tetraodontiformes: Tetraodontidae) in the northwestern Pacific revealed by mitochondrial DNA sequences and microsatellite loci. <i>Marine Biodiversity</i> , 2020, 50, 1.	0.3	8
8153	Genetic diversification, population structure, and geophylogeny of the Scarface rockskipper <i>Istiblennius pox</i> (Teleostei: Blenniidae) in the Persian Gulf and Oman Sea. <i>Marine Biodiversity</i> , 2020, 50, 1.	0.3	9
8154	Genetic diversity analysis of <i>Rhanterium eppaposum</i> Oliv. by ISSRs reveals a weak population structure. <i>Current Plant Biology</i> , 2020, 21, 100138.	2.3	15
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8157	The Early Peopling of the Philippines based on mtDNA. <i>Scientific Reports</i> , 2020, 10, 4901.	1.6	15
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8159	Demographic Inference of Divergence and Gene Exchange Between <i>Castanopsis fabri</i> and <i>Castanopsis lamontii</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 198.	1.7	0
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8162	Genetic diversity and the origin of commercial plantation of Indonesian teak on Java Island. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	17
8163	Genetic structures across a biogeographical barrier reflect dispersal potential of four Southeast Asian mangrove plant species. <i>Journal of Biogeography</i> , 2020, 47, 1258-1271.	1.4	18
8164	Is Niagara Falls a barrier to gene flow in riverine fishes? A test using genome-wide SNP data from seven native species. <i>Molecular Ecology</i> , 2020, 29, 1235-1249.	2.0	15
8165	Strong genetic differentiation among populations of <i>Cheirotonus gestroi</i> (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 Mapping, Sequencing, and Analysis, 2020, 31, 108-119.	0.7	3
8166	Genetic structure, gene flow pattern, and association analysis of superior germplasm resources in domesticated upland cotton ( <i>Gossypium hirsutum</i> L.). <i>Plant Diversity</i> , 2020, 42, 189-197.	1.8	9
8167	Genetic diversity and inferred dispersal history of the Schlegel's Japanese Gecko ( <i>Gekko japonicus</i> ) in Northeast Asia based on population genetic analyses and paleo-species distribution modelling. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2020, 31, 120-130.	0.7	4
8168	Genetic variation and population structure analysis of Chinese Wuzhong Hui population using 30 Indels. <i>Annals of Human Biology</i> , 2020, 47, 300-303.	0.4	7

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8170	Genetic Variability of <i>Ceraeochrysa cincta</i> , <i>Ceraeochrysa claveri</i> , and <i>Ceraeochrysa cubana</i> (Neuroptera: Chrysopidae) Populations in Agroecosystems of Southeast Brazil. <i>Environmental Entomology</i> , 2020, 49, 765-775.	0.7	2
8171	Genome wide association mapping and candidate gene analysis for pod shatter resistance in <i>Brassica juncea</i> and its progenitor species. <i>Molecular Biology Reports</i> , 2020, 47, 2963-2974.	1.0	14
8172	The Y-chromosome of the Soliga, an ancient forest-dwelling tribe of South India. <i>Gene: X</i> , 2020, 5, 100026.	2.3	1
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8174	Population data of 21 autosomal STR loci in Malaysian populations for human identification. <i>International Journal of Legal Medicine</i> , 2020, 134, 1675-1678.	1.2	6
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8176	HLA-A, -B, -DRB1 and -DQB1 polymorphisms among Iraqi Arabs. <i>Human Immunology</i> , 2020, 81, 191-192.	1.2	3
8177	Hybridization and hybrid zone stability between two lizards explained by population genetics and niche quantification. <i>Zoological Journal of the Linnean Society</i> , 2020, 190, 757-769.	1.0	1
8178	High diversity and pan-oceanic distribution of deep-sea polychaetes: <i>Prionospio</i> and <i>Aurospio</i> (Annelida: Spionidae) in the Atlantic and Pacific Ocean. <i>Organisms Diversity and Evolution</i> , 2020, 20, 171-187.	0.7	16
8179	Genetic Diversity and Conservation Status of <i>Helianthus verticillatus</i> , an Endangered Sunflower of the Southern United States. <i>Frontiers in Genetics</i> , 2020, 11, 410.	1.1	10
8180	Discrepancies between genetic and ecological divergence patterns suggest a complex biogeographic history in a Neotropical genus. <i>Ecology and Evolution</i> , 2020, 10, 4726-4738.	0.8	2
8181	A resilient brooding coral in the broadcast spawning <i>Porites lobata</i> species complex: a new endemic, introduced species, mutant, or new adaptive potential?. <i>Coral Reefs</i> , 2020, 39, 809-818.	0.9	11
8182	Identification of HLA-A/B/DRB1 alleles in Iranian patients with Fanconi anemia. <i>Human Antibodies</i> , 2020, 28, 221-226.	0.6	0
8183	Allelic frequency database of 15 polymorphic autosomal STRs in the Malayalam-speaking population of Kerala, India. <i>International Journal of Legal Medicine</i> , 2020, 134, 1679-1681.	1.2	11
8184	The evolution of spring fen ecotypes in <i>Rhinanthus</i> : genetic evidence for parallel origins in Scandinavia after the last ice age. <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	2
8185	Genome-wide assessment of population structure and genetic diversity of <i>Eucalyptus urophylla</i> based on a multi-species single-nucleotide polymorphism chip analysis. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	3
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8189	Combining genome-wide association study and <i>F<sub>ST</sub></i> -based approaches to identify targets of <i>Borrelia</i> -mediated selection in natural rodent hosts. <i>Molecular Ecology</i> , 2020, 29, 1386-1397.	2.0	9
8190	Ecosystem size predicts the probability of speciation in migratory freshwater fish. <i>Molecular Ecology</i> , 2020, 29, 3071-3083.	2.0	6
8191	Genetic structure of the ethnic Lao groups from mainland Southeast Asia revealed by forensic microsatellites. <i>Annals of Human Genetics</i> , 2020, 84, 357-369.	0.3	7
8192	Spatial genetic structure of Rocky Mountain bighorn sheep ( <i>Ovis canadensis canadensis</i> ) at the northern limit of their native range. <i>Canadian Journal of Zoology</i> , 2020, 98, 317-330.	0.4	6
8193	The Origin of the Subtropical Coral <i>Alveopora japonica</i> (Scleractinia: Acroporidae) in High-Latitude Environments. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	16
8194	Comparing the Performance of Microsatellites and RADseq in Population Genetic Studies: Analysis of Data for Pike ( <i>Esox lucius</i> ) and a Synthesis of Previous Studies. <i>Frontiers in Genetics</i> , 2020, 11, 218.	1.1	80
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8196	Evolutionarily-Related <i>Helicobacter pylori</i> Genotypes and Gastric Intraepithelial Neoplasia in a High-Risk Area of Northern Italy. <i>Microorganisms</i> , 2020, 8, 324.	1.6	3
8197	Small-scale population genetic structure of the sand bubbler crab <i>Scopimera ryukyuensis</i> in the Ryukyu Islands, Japan. <i>Molecular Biology Reports</i> , 2020, 47, 2619-2626.	1.0	5
8198	Population genetics of sandfish ( <i>Holothuria scabra</i> ) in the Andaman Sea, Thailand inferred from 12S rDNA and microsatellite polymorphism. <i>Regional Studies in Marine Science</i> , 2020, 35, 101189.	0.4	3
8199	Highly regional population structure of <i>Spondyllosoma cantharus</i> depicted by nuclear and mitochondrial DNA data. <i>Scientific Reports</i> , 2020, 10, 4063.	1.6	4
8200	Comprehensive study based on mtDNA signature (nad1) providing insights on <i>Echinococcus granulosus</i> s.s. genotypes from Pakistan and potential role of buffalo-dog cycle. <i>Infection, Genetics and Evolution</i> , 2020, 81, 104271.	1.0	15
8201	Genome-wide discovery of microsatellite markers and, population genetic diversity inferences revealed high anthropogenic pressure on endemic populations of <i>Trillium govanianum</i> . <i>Industrial Crops and Products</i> , 2020, 154, 112698.	2.5	12
8202	Genetic characterisation and forensic importance of 20 Y-STRs in Han population from Anshan, Northeast of China. <i>Annals of Human Biology</i> , 2020, 47, 478-482.	0.4	0
8203	Phylogeography of Asian sockeye salmon ( <i>Oncorhynchus nerka</i> ) based on analysis of mtDNA control region polymorphism. <i>Journal of Applied Ichthyology</i> , 2020, 36, 643-654.	0.3	2
8204	<i>SnToxA</i> , <i>SnTox1</i> , and <i>SnTox3</i> originated in <i>Parastagonospora nodorum</i> in the Fertile Crescent. <i>Plant Pathology</i> , 2020, 69, 1482-1491.	1.2	16
8205	Genetic connectivity of black drum ( <i>Pogonias courbina</i> ) stocks in the southwestern Atlantic Ocean. <i>Environmental Biology of Fishes</i> , 2020, 103, 913-926.	0.4	9



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8206	Phylogenic analysis and forensic genetic characterization of Guizhou Miao tribes from 58 microareas via autosomal STR. <i>Legal Medicine</i> , 2020, 47, 101737.	0.6	5
8207	Mitochondrial genome diversity and population mitogenomics of polar cod ( <i>Boreogadus saida</i> ) and Arctic dwelling gadoids. <i>Polar Biology</i> , 2020, 43, 979-994.	0.5	7
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8283	Population genetics and taxonomic signatures of wild Tilapia in Japan based on mitochondrial DNA control region analysis. <i>Hydrobiologia</i> , 2020, 847, 1491-1504.	1.0	8
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8341	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
8342	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
8343	Extreme genetic structure in a relict cactus genus from campo rupestre landscapes: implications for conservation. <i>Biodiversity and Conservation</i> , 2020, 29, 1263-1281.	1.2	6
8344	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
8345	A helitron-induced RabGDI $\pm$ variant causes quantitative recessive resistance to maize rough dwarf disease. <i>Nature Communications</i> , 2020, 11, 495.	5.8	45
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8347	Phylogeographical patterns and a cryptic species provide new insights into Western Indian Ocean giant clams phylogenetic relationships and colonization history. <i>Journal of Biogeography</i> , 2020, 47, 1086-1105.	1.4	22
8348	Genetic Structure Analysis in Sugarcane ( <i>Saccharum</i> spp.) Using Target Region Amplification Polymorphism (TRAP) Markers Based on Sugar- and Lignin-Related Genes and Potential Application in Core Collection Development. <i>Sugar Tech</i> , 2020, 22, 641-654.	0.9	11
8349	Phylogeography, genetic stocks, and conservation implications for an Australian endemic marine turtle. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2020, 30, 440-460.	0.9	23
8350	Genetic structure and recent population expansion in the commercially harvested deep-sea decapod, <i>Metanephrops challenger</i> (Crustacea: Decapoda). <i>New Zealand Journal of Marine and Freshwater Research</i> , 2020, 54, 251-270.	0.8	2
8351	Development and validation of microsatellite markers for an endangered dragonfly, <i>Libellula angelina</i> (Odonata: Libellulidae), with notes on population structures and genetic diversity. <i>International Journal of Odonatology</i> , 2020, 23, 93-102.	0.5	3

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8352	Geographical Genetic Variation and Sources of Korean <i>Aedes albopictus</i> (Diptera: Culicidae) Populations. <i>Journal of Medical Entomology</i> , 2020, 57, 1057-1068.	0.9	9
8353	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
8354	Population-specific signatures of intra-individual mitochondrial DNA heteroplasmy and their potential evolutionary advantages. <i>Scientific Reports</i> , 2020, 10, 211.	1.6	14
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8356	Genome-wide SNPs resolve spatiotemporal patterns of connectivity within striped marlin ( <i>Kajikia</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.5	23
8357	Genetic diversity and population structure of feral rapeseed ( <i>Brassica napus</i> L.) in Japan. <i>PLoS ONE</i> , 2020, 15, e0227990.	1.1	25
8358	Ice-age persistence and genetic isolation of the disjunct distribution of larch in Alaska. <i>Ecology and Evolution</i> , 2020, 10, 1692-1702.	0.8	4
8359	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
8360	Multiple decades of stocking has resulted in limited hatchery introgression in wild brook trout () Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4.	1.5	13
8361	Morphometric and genetic characterizations of blue swimming crab <i>Portunus segnis</i> , (Forsk., 1775) along the Iranian coasts of the Persian Gulf and Oman Sea. <i>Regional Studies in Marine Science</i> , 2020, 34, 101091.	0.4	7
8362	Major Histocompatibility Complex Class II (DRB3) Genetic Diversity in Spanish Morucha and Colombian Normande Cattle Compared to Taurine and Zebu Populations. <i>Frontiers in Genetics</i> , 2020, 10, 1293.	1.1	16
8363	Large-scale hybridization of Japanese populations of <i>Hinamoroko</i> , <i>Aphyocypris chinensis</i> , with <i>A. kikuchii</i> introduced from Taiwan. <i>Ichthyological Research</i> , 2020, 67, 361-374.	0.5	13
8364	Maize genetic diversity in traditionally cultivated polycultures in an isolated rural community in Mexico: implications for management and sustainability. <i>Plant Ecology and Diversity</i> , 2020, 13, 15-28.	1.0	4
8365	Phylogeography of the striped field mouse, <i>Apodemus agrarius</i> (Rodentia: Muridae), throughout its distribution range in the Palaearctic region. <i>Mammalian Biology</i> , 2020, 100, 19-31.	0.8	7
8366	Population Structure and Genetic Connectivity of Squat Lobsters ( <i>Munida</i> Leach, 1820) Associated With Vulnerable Marine Ecosystems in the Southwest Pacific Ocean. <i>Frontiers in Marine Science</i> , 2020, 6, .	1.2	7
8367	Genetic polymorphism of 20 autosomal short tandem repeats (STRs) in Himachal Pradesh population, India. <i>International Journal of Legal Medicine</i> , 2020, 134, 1663-1666.	1.2	0
8368	Climate shapes population variation in dogwhelk predation on foundational mussels. <i>Oecologia</i> , 2020, 192, 553-564.	0.9	10
8369	Genome-wide population structure and genetic diversity of Japanese whiting ( <i>Sillago japonica</i> ) inferred from genotyping-by-sequencing (GBS): Implications for fisheries management. <i>Fisheries Research</i> , 2020, 225, 105501.	0.9	13

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8371	SINE Retrotransposon variation drives Ecotypic disparity in natural populations of <i>Coilia nasus</i> . <i>Mobile DNA</i> , 2020, 11, 4.	1.3	8
8372	Joint selection for two malaria resistance mutations in a south-west Colombian population. <i>Infection, Genetics and Evolution</i> , 2020, 80, 104188.	1.0	1
8373	Patterns of Genomic Divergence and Signals of Selection in Sympatric and Allopatric Northeastern Pacific and Sea of Cortez Populations of the Sargo ( <i>Anisotremus davidsonii</i> ) and Longjaw Mudsucker ( <i>Gillichthys mirabilis</i> ). <i>Journal of Heredity</i> , 2020, 111, 57-69.	1.0	5
8374	Applying genomic data in wildlife monitoring: Development guidelines for genotyping degraded samples with reduced single nucleotide polymorphism panels. <i>Molecular Ecology Resources</i> , 2020, 20, 662-680.	2.2	64
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8376	Genetic analysis of male Hungarian Conquerors: European and Asian paternal lineages of the conquering Hungarian tribes. <i>Archaeological and Anthropological Sciences</i> , 2020, 12, 1.	0.7	23
8377	Development and application of a nonbinary SNP-based microhaplotype panel for paternity testing involving close relatives. <i>Forensic Science International: Genetics</i> , 2020, 46, 102255.	1.6	48
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8381	Population genetics of the banded coral shrimp, <i>Stenopus hispidus</i> (), in the Indonesian archipelago. <i>Journal of Experimental Marine Biology and Ecology</i> , 2020, 525, 151325.	0.7	7
8382	Molecular genetic diversity and differentiation of Nile tilapia ( <i>Oreochromis niloticus</i> , L. 1758) in East African natural and stocked populations. <i>BMC Evolutionary Biology</i> , 2020, 20, 16.	3.2	31
8383	Paths for colonization or exodus? New insights from the brown bear ( <i>Ursus arctos</i> ) population of the Cantabrian Mountains. <i>PLoS ONE</i> , 2020, 15, e0227302.	1.1	8
8384	Understanding Historical Demographic Processes to Inform Contemporary Conservation of an Arid Zone Specialist: The Yellow-Footed Rock-Wallaby. <i>Genes</i> , 2020, 11, 154.	1.0	2
8385	Development of a Core Collection of Six-Rowed Hulless Barley from the Qinghai-Tibetan Plateau. <i>Plant Molecular Biology Reporter</i> , 2020, 38, 305-313.	1.0	4
8386	Multi-targeted management of upland game birds at the agroecosystem interface in midwestern North America. <i>PLoS ONE</i> , 2020, 15, e0230735.	1.1	9
8387	No decline of genetic diversity in elongate loach ( <i>Leptobotia elongata</i> ) with a tendency to form population structure in the upper Yangtze River. <i>Global Ecology and Conservation</i> , 2020, 23, e01072.	1.0	7

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8389	A genome-wide analysis of DNA methylation identifies a novel association signal for Lp(a) concentrations in the LPA promoter. <i>PLoS ONE</i> , 2020, 15, e0232073.	1.1	8
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8391	Population structure, landscape genomics, and genetic signatures of adaptation to exotic disease pressure in <i>Cornus florida</i> . Insights from GWAS and GBS data. <i>Journal of Systematics and Evolution</i> , 2020, 58, 546-570.	1.6	13
8392	Rapid Genetic Divergence of an Invasive Species, <i>Spartina alterniflora</i> , in China. <i>Frontiers in Genetics</i> , 2020, 11, 284.	1.1	23
8393	Genetic Assessment of a Black Rockfish, <i>Sebastes schlegelii</i> , Stock Enhancement Program in Lido Bay, China Based on Mitochondrial and Nuclear DNA Analysis. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	7
8394	Comparison of Behavior and Genetic Structure in Populations of Family and Kenneled Beagles. <i>Frontiers in Veterinary Science</i> , 2020, 7, 183.	0.9	8
8395	Comparative genetic analysis of grayling ( <i>Thymallus</i> spp. Salmonidae) across the paleohydrologically dynamic river drainages of the Altai-Sayan mountain region. <i>Hydrobiologia</i> , 2020, 847, 2823-2844.	1.0	6
8396	Adaptive genetic diversity and evidence of population genetic structure in the endangered Sierra Madre Sparrow ( <i>Xenospiza baileyi</i> ). <i>PLoS ONE</i> , 2020, 15, e0232282.	1.1	4
8397	Loss of Mitochondrial Genetic Diversity in Overexploited Mediterranean Swordfish ( <i>Xiphias gladius</i> ), Tj ETQq1 1 0.784314 rgBT /Overl	0.7	7
8398	Potential of rutabaga ( <i>Brassica napus</i> var. <i>napobrassica</i> ) gene pool for use in the breeding of <i>B. napus canola</i> . <i>Crop Science</i> , 2020, 60, 157-171.	0.8	7
8399	BRCA1 and VDR gene polymorphisms are associated with prostate cancer risk in Mexican men. <i>Molecular Carcinogenesis</i> , 2020, 59, 629-639.	1.3	2
8400	Variability of the mitochondrial CO1 gene in native and invasive populations of <i>Harmonia axyridis</i> Pall. comparative analysis. <i>PLoS ONE</i> , 2020, 15, e0231009.	1.1	7
8401	Development of Single Nucleotide Polymorphism (SNP) Markers for Analysis of Population Structure and Invasion Pathway in the Coconut Leaf Beetle <i>Brontispa longissima</i> (Gestro) Using Restriction Site-Associated DNA (RAD) Genotyping in Southern China. <i>Insects</i> , 2020, 11, 230.	1.0	5
8402	Rediscovery of a presumed extinct species, <i>Salvelinus profundus</i> , after reâ€“oligotrophication. <i>Ecology</i> , 2020, 101, e03065.	1.5	2
8403	Genetic structure and forensic characteristics of the Kyrgyz population from Kizilsu Kirghiz autonomous prefecture based on autosomal DIPs. <i>International Journal of Legal Medicine</i> , 2022, 136, 539-541.	1.2	3
8404	Revisiting the genetic background and phylogenetic structure of five Sino-Tibetan-speaking populations: insights from autosomal InDels. <i>Molecular Genetics and Genomics</i> , 2020, 295, 969-979.	1.0	9
8405	Population genetics of the wolverine in Finland: the road to recovery?. <i>Conservation Genetics</i> , 2020, 21, 481-499.	0.8	12

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8406	Panmictic population genetic structure of northern British Columbia mountain goats ( <i>Oreamnos</i> ) Tj ETQq0 0 0 rgBT /Overlock 9 10 Tf 50	0.8	9
8407	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 /Overlock 1.0	1.0	1
8408	Isolation and characterization of microsatellite loci in <i>Astronium graveolens</i> (Anacardiaceae) and cross amplification in related species. <i>Molecular Biology Reports</i> , 2020, 47, 4003-4007.	1.0	3
8409	Genetic differentiation of <i>Mutator</i> insertion polymorphisms and association with agronomic traits in waxy and common maize. <i>Genes and Genomics</i> , 2020, 42, 631-638.	0.5	2
8410	Population Genetics of <i>Narcissus</i> Species Reveals High Diversity and Multiple Introductions into Kashmir. <i>Agricultural Research</i> , 2020, 9, 536-542.	0.9	1
8411	Comprehensive assessment of association between HLA polymorphisms and acute leukemia in Iranian population. <i>Gene Reports</i> , 2020, 19, 100674.	0.4	1
8412	Weak population structure and recent demographic expansion of the monogenean parasite <i>Kapentagyrus</i> spp. infecting clupeid fishes of Lake Tanganyika, East Africa. <i>International Journal for Parasitology</i> , 2020, 50, 471-486.	1.3	20
8413	Genetic consequences of being a dwarf: do evolutionary changes in life-history traits influence gene flow patterns in populations of the world's smallest goldenrod?. <i>Annals of Botany</i> , 2020, 126, 163-177.	1.4	3
8414	Low genetic divergence and variation in coastal dune populations of the widespread terrestrial orchid <i>Epipactis helleborine</i> . <i>Botanical Journal of the Linnean Society</i> , 2020, 193, 419-430.	0.8	7
8415	High genomic diversity in the bank vole at the northern apex of a range expansion: The role of multiple colonizations and end-glacial refugia. <i>Molecular Ecology</i> , 2020, 29, 1730-1744.	2.0	27
8416	Hemoplasmas Are Endemic and Cause Asymptomatic Infection in the Endangered Darwin's Fox ( <i>Lycalopex fulvipes</i> ). <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	16
8417	Conservation Genomic Analysis of the Croatian Indigenous Black Slavonian and Turopolje Pig Breeds. <i>Frontiers in Genetics</i> , 2020, 11, 261.	1.1	17
8418	Molecular Identification of the "Facciuta Della Valnerina" Local Goat Population Reared in the Umbria Region, Italy. <i>Animals</i> , 2020, 10, 601.	1.0	7
8419	Genetic patterns reveal northward range expansion and cryptic diversity in Nalbant's spined loach, <i>Cobitis nalbanti sensu lato</i> (Teleostei: Cypriniformes: Cobitidae). <i>Systematics and Biodiversity</i> , 2020, 18, 1-11.	0.5	3
8420	Morphological variation associated with trophic niche expansion within a lake population of a benthic fish. <i>PLoS ONE</i> , 2020, 15, e0232114.	1.1	6
8421	Effects of Temperature Treatments on Cytosine-Methylation Profiles of Diploid and Autotetraploid Plants of the Alpine Species <i>Ranunculus kuepferi</i> (Ranunculaceae). <i>Frontiers in Plant Science</i> , 2020, 11, 435.	1.7	15
8422	Patterns of Genetic Diversity in Highly Invasive Species: Cogongrass ( <i>Imperata cylindrica</i> ) Expansion in the Invaded Range of the Southern United States (US). <i>Plants</i> , 2020, 9, 423.	1.6	13
8423	Microsatellite Genotyping Corroborated Loss of Genetic Diversity in <i>Clarias batrachus</i> as a Result of Lack of Regulatory Reforms in Aquaculture. <i>Biochemical Genetics</i> , 2020, 58, 595-616.	0.8	2



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8425	Molecular Variation of the Phytopathogenic Fungus <i>Sporisorium reilianum</i> in Valle del Mezquital, Hidalgo. Frontiers in Ecology and Evolution, 2020, 8, .	1.1	6
8426	Insights into the genetic characteristics and population structures of Chinese two Tibetan groups using 35 insertion/deletion polymorphic loci. Molecular Genetics and Genomics, 2020, 295, 957-968.	1.0	7
8427	HLA class II genotyping of admixed Brazilian patients with type 1 diabetes according to self-reported color/race in a nationwide study. Scientific Reports, 2020, 10, 6628.	1.6	14
8428	Invalidation of taxa within the silvery wooly monkey ( <i>Lagothrix lagothricha poeppigii</i> , Atelidae,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 508	0.7	1
8429	Toward a preliminary assessment of the diversity and origin of Cyprinid fish genus <i>Carassius</i> in Iran. Journal of Applied Ichthyology, 2020, 36, 422-430.	0.3	6
8430	How many species of angulate tortoises occur in Southern Africa? (Testudines: Testudinidae:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502	0.7	6
8431	Iconic, threatened, but largely unknown: Biogeography of the Macaronesian dragon trees ( <i>Dracaena</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 504	0.4	14
8432	DNA Barcoding Silver Butter Catfish ( <i>Schilbe intermedius</i> ) Reveals Patterns of Mitochondrial Genetic Diversity Across African River Systems. Scientific Reports, 2020, 10, 7097.	1.6	8
8433	Influence of past climate change on phylogeography and demographic history of narwhals, <i>Monodon monoceros</i> . Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20192964.	1.2	39
8434	Multilocus phylogeny and systematics of Iberian endemic <i>Squalius</i> (Actinopterygii, Leuciscidae). Zoologica Scripta, 2020, 49, 440-457.	0.7	5
8435	Investigation of genetic diversity and stock structure of <i>Aristeus alcocki</i> Ramadan, 1938 (Decapoda:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 502	0.9	2
8436	Exploring the genetic base of the soybean germplasm from Africa, America and Asia as well as mining of beneficial allele for flowering and seed weight. 3 Biotech, 2020, 10, 195.	1.1	4
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8439	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. BMC Genetics, 2020, 21, 43.	2.7	5
8440	HLA-G14bp ins/del polymorphism and post-transplant weight gain in kidney transplantation: potential implications beyond tolerance. BMC Nephrology, 2020, 21, 109.	0.8	4
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8443	Mitochondrial genomes from Bronze Age Poland reveal genetic continuity from the Late Neolithic and additional genetic affinities with the steppe populations. <i>American Journal of Physical Anthropology</i> , 2020, 172, 176-188.	2.1	12
8444	Genetic variation in an ephemeral mudflat species: The role of the soil seed bank and dispersal in river and secondary anthropogenic habitats. <i>Ecology and Evolution</i> , 2020, 10, 3620-3635.	0.8	1
8445	Geography and spawning season drive genetic divergence among populations of the hard coral <i>Acropora tenuis</i> from Indonesia and Western Australia. <i>Coral Reefs</i> , 2020, 39, 989-999.	0.9	11
8446	A ddRAD-based population genetics and phylogenetics of an endangered freshwater fish from Japan. <i>Conservation Genetics</i> , 2020, 21, 641-652.	0.8	7
8447	Genetic characterization and molecular fingerprint of traditional Umbrian tomato ( <i>Solanum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf Resources and Crop Evolution, 2020, 67, 1807-1820.	0.8	15
8448	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
8449	Genetic structure and gene flow among populations of <i>Encholirium magalhaesii</i> , a rocky grassland fields bromeliad. <i>Revista Brasileira De Botanica</i> , 2020, 43, 283-290.	0.5	4
8450	Mitochondrial DNA (hypervariable region I) diversity in Basrah population "Iraq. <i>Genomics</i> , 2020, 112, 3560-3564.	1.3	3
8451	Analysis of forensic genetic parameters of 22 autosomal STR markers (PowerPlex® Fusion System) in a population sample from Bosnia and Herzegovina. <i>Annals of Human Biology</i> , 2020, 47, 273-283.	0.4	5
8452	The protected tree <i>Dimorphandra wilsonii</i> (Fabaceae) is a population of inter-specific hybrids: recommendations for conservation in the Brazilian Cerrado/Atlantic Forest ecotone. <i>Annals of Botany</i> , 2020, 126, 191-203.	1.4	9
8453	Allopolyploid Speciation Accompanied by Gene Flow in a Tree Fern. <i>Molecular Biology and Evolution</i> , 2020, 37, 2487-2502.	3.5	17
8454	Fine-scale genetic structuring in a group of living lizard, the gidgee skink ( <i>Egernia stokesii</i> ). <i>Austral Ecology</i> , 2020, 45, 435-443.	0.7	3
8455	Phylogeographic parallelism: Concordant patterns in closely related species illuminate underlying mechanisms in the historically glaciated Tasmanian landscape. <i>Journal of Biogeography</i> , 2020, 47, 1674-1686.	1.4	5
8456	Multiple late-Pleistocene colonisation events of the Antarctic pearlwort <i>Colobanthus quitensis</i> (Caryophyllaceae) reveal the recent arrival of native Antarctic vascular flora. <i>Journal of Biogeography</i> , 2020, 47, 1663-1673.	1.4	24
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8458	Fungal Evolution in Anthropogenic Environments: <i>Botrytis cinerea</i> Populations Infecting Small Fruit Hosts in the Pacific Northwest Rapidly Adapt to Human-Induced Selection Pressures. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	9
8459	Genetic diversity and differentiation of populations of <i>Chlorops oryzae</i> (Diptera, Chloropidae). <i>BMC Ecology</i> , 2020, 20, 22.	3.0	10

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8460	Identification of NUDT15 gene variants in Amazonian Amerindians and admixed individuals from northern Brazil. PLoS ONE, 2020, 15, e0231651.	1.1	18
8461	Multilocus sequence typing of Enterocytozoon bieneusi in crab-eating macaques (Macaca) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.0	2
8462	Plasmodium vivax HAP2/GCS1 gene exhibits limited genetic diversity among parasite isolates from the Greater Mekong Subregion. Parasites and Vectors, 2020, 13, 175.	1.0	1
8463	Development of 19 universal microsatellite loci for three closely related <i>Ficus</i> species (Moraceae) by high-throughput sequencing. Genes and Genetic Systems, 2020, 95, 21-27.	0.2	3
8464	Low mtDNA diversity in a highly differentiated population of spinner dolphins (Stenella longirostris) from the Fernando de Noronha Archipelago, Brazil. PLoS ONE, 2020, 15, e0230660.	1.1	6
8465	Genetic Analysis by nuSSR Markers of Silver Birch (Betula pendula Roth) Populations in Their Southern European Distribution Range. Frontiers in Plant Science, 2020, 11, 310.	1.7	13
8466	Close genetic relationship between central Thai and Mon people in Thailand revealed by autosomal microsatellites. International Journal of Legal Medicine, 2021, 135, 445-448.	1.2	6
8467	Islands within islands: genetic structuring at small spatial scales has implications for long-term persistence of a threatened species. Animal Conservation, 2021, 24, 95-107.	1.5	5
8468	Combined genotype and phenotype analyses reveal patterns of genomic adaptation to local environments in the subtropical oak <i>Quercus acutissima</i>. Journal of Systematics and Evolution, 2021, 59, 541-556.	1.6	19
8469	Evolutionary history of the reef fish <i>Anisotremus interruptus</i> (Perciformes: Haemulidae) throughout the Tropical Eastern Pacific. Journal of Zoological Systematics and Evolutionary Research, 2021, 59, 148-162.	0.6	6
8470	Post-glacial establishment of locally adapted fish populations over a steep salinity gradient. Journal of Evolutionary Biology, 2021, 34, 138-156.	0.8	28
8471	Genetic and morphological differences between yellowtail kingfish (Seriola lalandi) from the Bohai Sea, China and the Southern Ocean, Australia. Aquaculture and Fisheries, 2021, 6, 260-266.	1.2	4
8472	Genetic diversity of 17 autosomal STR loci in Meizhou Hakka population. International Journal of Legal Medicine, 2021, 135, 443-444.	1.2	4
8473	Molecular and paleoclimatic data uncover the impact of an ancient bottleneck on the demographic history and contemporary genetic structure of endangered Pinus uliginosa. Journal of Systematics and Evolution, 2021, 59, 596-610.	1.6	8
8474	Phylogeographic study of the West Australian freshwater mussel, Westralunio carteri, uncovers evolutionarily significant units that raise new conservation concerns. Hydrobiologia, 2021, 848, 2951-2964.	1.0	12
8475	Molecular identification and population differentiation of Aurelia spp. ephyrae in sea cucumber aquaculture ponds of northern China. Journal of Oceanology and Limnology, 2021, 39, 989-996.	0.6	2
8476	Comparative population genetics of Amblyomma maculatum and Amblyomma americanum in the mid-Atlantic United States. Ticks and Tick-borne Diseases, 2021, 12, 101600.	1.1	4
8477	Regional-scale aquifer hydrogeology as a driver of phylogeographic structure in the Neotropical catfish Rhamdia guatemalensis (Siluriformes: Heptapteridae) from cenotes of the Yucatán Peninsula, Mexico. Freshwater Biology, 2021, 66, 332-348.	1.2	5

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8478	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
8479	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
8480	Insights into the aridification history of Central Asian Mountains and international conservation strategy from the endangered wild apple tree. <i>Journal of Biogeography</i> , 2021, 48, 332-344.	1.4	11
8481	Historical and contemporary factors affect the genetic diversity and structure of <i>Laguncularia racemosa</i> (L.) Gaertn, along the western Atlantic coast. <i>Estuarine, Coastal and Shelf Science</i> , 2021, 249, 107055.	0.9	4
8482	Genetic epidemiology of lymphatic filariasis in American Samoa after mass drug administration. <i>International Journal for Parasitology</i> , 2021, 51, 137-147.	1.3	2
8483	Population genomics of selectively neutral genetic structure and herbicide resistance in <i>Alopecurus myosuroides</i> populations of UK. <i>Pest Management Science</i> , 2021, 77, 1520-1529.	1.7	16
8484	Variability analyses of the maternal lineage of horses and donkeys. <i>Gene</i> , 2021, 769, 145231.	1.0	3
8485	Genomic Architecture of Rapid Parallel Adaptation to Fresh Water in a Wild Fish. <i>Molecular Biology and Evolution</i> , 2021, 38, 1317-1329.	3.5	17
8486	Going against the flow: Barriers to gene flow impact patterns of connectivity in cryptic coral reef gobies throughout the western Atlantic. <i>Journal of Biogeography</i> , 2021, 48, 427-439.	1.4	16
8487	An assessment of the seascape genetic structure and hydrodynamic connectivity for subtropical seagrass restoration. <i>Restoration Ecology</i> , 2021, 29, .	1.4	10
8488	Recent hybrid speciation at the origin of the narrow endemic <i>Pulmonaria helvetica</i> . <i>Annals of Botany</i> , 2021, 127, 21-31.	1.4	12
8489	Genetic diversity of <i>Borrelia burgdorferi</i> sensu stricto: Novel strains from Mexican wild rodents. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 1263-1274.	1.3	2
8490	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
8491	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
8492	A generalized framework for AMOVA with multiple hierarchies and ploidies. <i>Integrative Zoology</i> , 2021, 16, 33-52.	1.3	9
8493	Maternal origins, population structure and demographic history of ten Chinese indigenous goat breeds from Yunnan. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 108-121.	0.8	2
8494	Patagonian glacial effects on the endemic Green-backed Firecrown, <i>Sebanoides sebanoides</i> (Aves). <i>Journal of Ornithology</i> , 2021, 162, 289-301.	0.5	6
8495	Balancing selection versus allele and supertype turnover in MHC class II genes in guppies. <i>Heredity</i> , 2021, 126, 548-560.	1.2	9

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8496	Genetic analysis in two species of <i>Loxa Amyot &amp; Serville 1843</i> (Pentatomidae) collected in Iguaçu National Park (Foz Do Iguaçu, Paraná, Brazil). <i>International Journal of Tropical Insect Science</i> , 2021, 41, 759-764.	0.4	1
8497	Association of a polymorphism in exon 3 of the IGF1R gene with growth, body size, slaughter and meat quality traits in Colored Polish Merino sheep. <i>Meat Science</i> , 2021, 172, 108314.	2.7	6
8498	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
8499	Origin of non-native <i>Xylosandrus germanus</i> , an invasive pest ambrosia beetle in Europe and North America. <i>Journal of Pest Science</i> , 2021, 94, 553-562.	1.9	19
8500	Genetic structure in Orkney island mice: isolation promotes morphological diversification. <i>Heredity</i> , 2021, 126, 266-278.	1.2	6
8501	Mitogenomics and the genetic differentiation of contemporary <i>Balaena mysticetus</i> (Cetacea) from Svalbard. <i>Zoological Journal of the Linnean Society</i> , 2021, 191, 1192-1203.	1.0	5
8502	Genetic diversity in natural populations of the endangered Neotropical orchid <i>Telipogon peruvianus</i> . <i>Plant Species Biology</i> , 2021, 36, 6-16.	0.6	7
8503	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
8504	New taxonomic and evolutionary insights relevant to the cat flea, <i>Ctenocephalides felis</i> : A geographic perspective. <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 106990.	1.2	16
8505	Study on the polymorphisms of HLA-ABCDQB1DRB1 alleles and haplotypes in Hubei Han population of China. <i>International Journal of Immunogenetics</i> , 2021, 48, 8-15.	0.8	2
8506	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
8507	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
8508	Forensic application and genetic diversity of 21 autosomal STR loci in five major population groups of Pakistan. <i>International Journal of Legal Medicine</i> , 2021, 135, 775-777.	1.2	4
8509	Global phylogeography and invasion history of the spotted lanternfly revealed by mitochondrial phylogenomics. <i>Evolutionary Applications</i> , 2021, 14, 915-930.	1.5	31
8510	A Y-chromosomal survey of Ecuador's multi-ethnic population reveals new insights into the tri-partite population structure and supports an early Holocene age of the rare Native American founder lineage C3-MPB373. <i>Forensic Science International: Genetics</i> , 2021, 51, 102427.	1.6	1
8511	Genome-wide assessment of diversity and differentiation between original and modern Brown cattle populations. <i>Animal Genetics</i> , 2021, 52, 21-31.	0.6	20
8512	Genomic insights into the origin of trans-Mediterranean disjunct distributions. <i>Journal of Biogeography</i> , 2021, 48, 440-452.	1.4	6
8513	Population genetic structure and classification of cultivated and wild pea ( <i>Pisum</i> sp.) based on morphological traits and SSR markers. <i>Journal of Systematics and Evolution</i> , 2021, , .	1.6	3

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8514	Lost at sea: determining geographic origins of illegally traded green sea turtles ( <i>Chelonia mydas</i> ) rescued on Hainan Island, China. <i>Wildlife Research</i> , 2021, 48, 55.	0.7	10
8515	Integrated conservation of important plant taxa through the improvement of the original plant micro-reserve (PMR) approach: The intensive PMR monitoring case of <i>Ophrys kotschyi</i> . <i>Journal of Environmental Management</i> , 2021, 280, 111731.	3.8	3
8516	Comparative phylogeography between parasitic sucking lice and their host the Namaqua rock mouse, <i>Micaelamys namaquensis</i> (Rodentia: Muridae). <i>Zoological Journal of the Linnean Society</i> , 2021, 192, 1017-1028.	1.0	3
8517	Selection in the Finnhorse, a native all-around horse breed. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 188-203.	0.8	4
8518	Genetic diversity and life-history traits of bonefish <i>Albula</i> spp. from the Red Sea. <i>Journal of Fish Biology</i> , 2021, 98, 855-864.	0.7	4
8519	Population genetic structure underlying the geographic variation in beetle structural colour with multiple transition zones. <i>Molecular Ecology</i> , 2021, 30, 670-684.	2.0	7
8520	Relationship between genetic risk and stock enhancement of the silver carp ( <i>Hypophthalmichthys</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	0.9	14
8521	Genome-wide SNPs reveal complex fine scale population structure in the California market squid fishery ( <i>Doryteuthis opalescens</i> ). <i>Conservation Genetics</i> , 2021, 22, 97-110.	0.8	12
8522	Allelic diversity and forensic estimations of the Beijing Hans: Comparative data on sequence-based and length-based STRs. <i>Forensic Science International: Genetics</i> , 2021, 51, 102424.	1.6	7
8523	Autosomal genetics and Y-chromosome haplogroup L1b-M317 reveal Mount Lebanon Maronites as a persistently non-emigrating population. <i>European Journal of Human Genetics</i> , 2021, 29, 581-592.	1.4	3
8524	HLA-DPB1 and HLA-C alleles are associated with leprosy in a Brazilian population. <i>Human Immunology</i> , 2021, 82, 11-18.	1.2	5
8525	Genetic diversity and structure of the hedgehogs <i>Erinaceus europaeus</i> and <i>Erinaceus roumanicus</i> : evidence for ongoing hybridization in Eastern Europe. <i>Biological Journal of the Linnean Society</i> , 2021, 132, 174-195.	0.7	11
8526	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
8527	Phylogenomics resolves the invasion history of <i>Acacia auriculiformis</i> in Florida. <i>Journal of Biogeography</i> , 2021, 48, 453-464.	1.4	12
8528	Genetic diversity of <i>Rhinogobius delicatus</i> (Perciformes: Gobiidae): origins of the freshwater fish in East Taiwan. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2021, 32, 12-19.	0.7	5
8529	<i>Dictyota cyanoloma</i> (Dictyotales, Phaeophyceae), a Newly Introduced Brown Algal Species in California. <i>Journal of Phycology</i> , 2021, 57, 370-378.	1.0	3
8530	Genetic analyses of the parasitic nematode, <i>Parelaphostrongylus tenuis</i> , in Missouri and Kentucky reveal unexpected levels of diversity and population differentiation. <i>Parasitology</i> , 2021, 148, 31-41.	0.7	2
8531	Mitochondrial COI based genetic diversity and phylogeographic structure of whitefly <i>Bemisia tabaci</i> (Gennadius) on cotton in India. <i>International Journal of Tropical Insect Science</i> , 2021, 41, 1543-1554.	0.4	5



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8532	Genetic diversity and population structure of <i>Acanthopagrus schlegelii</i> inferred from mtDNA sequences. <i>Regional Studies in Marine Science</i> , 2021, 41, 101532.	0.4	4
8533	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
8534	Oceanic dispersal barriers in a holoplanktonic gastropod. <i>Journal of Evolutionary Biology</i> , 2021, 34, 224-240.	0.8	16
8535	The story of endurance: Biogeography and the evolutionary history of four Holarctic butterflies with different habitat requirements. <i>Journal of Biogeography</i> , 2021, 48, 590-602.	1.4	6
8536	Phylogeography of a widespread Palearctic forest bird species: The White-backed Woodpecker (Aves). <i>Tj ETQq00.0 rgBT /Overlock 1</i>	0.7	6
8537	Conservation genetics of yellow-bellied toads ( <i>Bombina variegata</i> ): a matter of geographical scale and isolation. <i>Conservation Genetics</i> , 2021, 22, 83-96.	0.8	4
8538	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
8539	Evaluation of a custom GeneReadâ„¢ massively parallel sequencing assay with 210 ancestry informative SNPs using the Ion S5â„¢ and MiSeq platforms. <i>Forensic Science International: Genetics</i> , 2021, 50, 102411.	1.6	7
8540	Genetic variation and demographic history analysis of <i>Pestalotiopsis</i> , <i>Pseudopestalotiopsis</i> , and <i>Neopestalotiopsis</i> fungi associated with tea ( <i>Camellia sinensis</i> ) inferred from the internal transcribed spacer region of the nuclear ribosomal DNA. <i>Plant Pathology</i> , 2021, 70, 699-711.	1.2	3
8541	Genetic diversity of the cardiopulmonary canid nematode <i>Angiostrongylus vasorum</i> within and between rural and urban fox populations. <i>Infection, Genetics and Evolution</i> , 2021, 87, 104618.	1.0	5
8542	Genetic diversity and population structure of Pacific herring <i>Clupea pallasii</i> in the Northeast Asia inferred from mtDNA marker. <i>Ecological Genetics and Genomics</i> , 2021, 18, 100076.	0.3	2
8543	Population genetic data of 22 autosomal STR loci for the Mong people in Vietnam. <i>Legal Medicine</i> , 2021, 48, 101825.	0.6	2
8544	Wing geometry and genetic analyses reveal contrasting spatial structures between male and female <i>Aedes aegypti</i> (L.) (Diptera: Culicidae) populations in metropolitan Manila, Philippines. <i>Infection, Genetics and Evolution</i> , 2021, 87, 104676.	1.0	8
8545	Genome-wide analysis reveals the patterns of genetic diversity and population structure of 8 Italian local chicken breeds. <i>Poultry Science</i> , 2021, 100, 441-451.	1.5	18
8546	Mitochondrial DNA reveals genetically structured haplogroups of Bali sardinella ( <i>Sardinella lemuru</i> ) in Philippine waters. <i>Regional Studies in Marine Science</i> , 2021, 41, 101588.	0.4	4
8547	Candidate gene association of gene expression data in sugarcane contrasting for sucrose content. <i>Genomics</i> , 2021, 113, 229-237.	1.3	9
8548	Molecular systematics and phylogeography of a widespread Neotropical avian lineage: evidence for cryptic speciation with protracted gene flow throughout the Late Quaternary. <i>Biological Journal of the Linnean Society</i> , 2021, 132, 431-450.	0.7	5
8549	The combinatorial diversity of KIR and HLA class I allotypes in Peninsular Malaysia. <i>Immunology</i> , 2021, 162, 389-404.	2.0	12

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8550	Identifying multiple geographically restricted phylogeographic lineages of Moggel (Cyprinidae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74	0.5	6
8551	Population genetics of cold-water coral associated Pleustidae (Crustacea, Amphipoda) reveals cryptic diversity and recent expansion off Iceland. <i>Marine Ecology</i> , 2021, 42, .	0.4	7
8552	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
8553	Life-stage-dependent supergene haplotype frequencies and metapopulation neutral genetic patterns of Atlantic cod, <i>Gadus morhua</i> , from Canada's Northern cod stock region and adjacent areas. <i>Journal of Fish Biology</i> , 2021, 98, 817-828.	0.7	4
8554	Population genetic structure and species delimitation in the <i>Cryptanthus zonatus</i> complex (Bromeliaceae). <i>Botanical Journal of the Linnean Society</i> , 2021, 196, 123-140.	0.8	3
8555	Development and characterization of novel microsatellite markers for a dominant parasitoid <i>Stethynium empoasca</i> (Hymenoptera: Mymaridae) in tea plantations using high-throughput sequencing. <i>Applied Entomology and Zoology</i> , 2021, 56, 41-50.	0.6	2
8556	Genetic diversity and structure of <i>Taxus baccata</i> from the Cantabrian-Atlantic area in northern Spain: A guide for conservation and management actions. <i>Forest Ecology and Management</i> , 2021, 482, 118844.	1.4	8
8557	Phylogeography, genetic diversity and population structure of the freshwater stingray, <i>Paratrygon aiereba</i> (Müller & Henle, 1841) (Myliobatiformes: Potamotrygonidae) in the Colombian Amazon and Orinoco basins. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2021, 32, 20-33.	0.7	4
8558	Mitochondrial phylogeography reveals high haplotype diversity and unique genetic lineage in Indian dugongs ( <i>Dugong dugon</i> ). <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2021, 31, 818-829.	0.9	11
8559	Genetic Diversity and Population Structure of Endangered Indian Catfish, <i>Clarias magur</i> as Revealed by mtDNA D-loop Marker. <i>Turkish Journal of Fisheries and Aquatic Sciences</i> , 2021, 21, 9-18.	0.4	6
8560	Post-release genetic assessment of two congeneric weed biological control agents. <i>Biological Control</i> , 2021, 152, 104462.	1.4	1
8561	Assessment of association between HLA alleles and acquired aplastic anemia in Iranian population. <i>Ecological Genetics and Genomics</i> , 2021, 18, 100075.	0.3	0
8562	Genetic variation of 20 autosomal STR loci in the Han nationality in Central Yunnan, Southwest China. <i>Legal Medicine</i> , 2021, 48, 101807.	0.6	2
8563	Molecular characterization revealed <i>Fasciola</i> specimens in Ecuador are all <i>Fasciola hepatica</i> , none at all of <i>Fasciola gigantica</i> or parthenogenic <i>Fasciola</i> species. <i>Parasitology International</i> , 2021, 80, 102215.	0.6	9
8564	Mitochondrial DNA in <i>Ixodus ricinus</i> (Acari: Ixodidae) on birds reflects ticks' transportation routes to Lista, Norway. <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101553.	1.1	0
8565	Genetic differentiation among populations of the blackfin goodea ( <i>Goodea atripinnis</i> ) (Cyprinodontiformes: Goodeidae): implications for its evolutionary history. <i>Journal of Fish Biology</i> , 2021, 98, 1253-1266.	0.7	4
8566	Systematics, distribution, and sexual compatibility of six <i>Scytosiphon</i> species (Scytosiphonaceae, Phaeophyceae) from Japan and the description of four new species. <i>Journal of Phycology</i> , 2021, 57, 416-434.	1.0	7
8567	Simple sequence repeat-based mini-core collection for white Guinea yam ( <i>Dioscorea rotundata</i> ) germplasm. <i>Crop Science</i> , 2021, 61, 1268-1279.	0.8	12

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8568	Does the genetic diversity among pubescent white oaks in southern Italy, Sicily and Sardinia islands support the current taxonomic classification?. European Journal of Forest Research, 2021, 140, 355-371.	1.1	20
8569	A large wild salmon stock shows genetic and life history differentiation within, but not between, rivers. Conservation Genetics, 2021, 22, 35-51.	0.8	8
8570	Genetic structure of <i>Tricholoma matsutake</i> in Japan: conservation of genetic resources of domestic "matsutake" mushrooms. Journal of Forest Research, 2021, 26, 62-67.	0.7	1
8571	Recurrent hybridization underlies the evolution of novelty in <i>Gentiana</i> (Gentianaceae) in the Qinghai-Tibetan Plateau. AoB PLANTS, 2021, 13, plaa068.	1.2	14
8572	Intraspecific variation in landform engineering across a restored salt marsh shoreline. Evolutionary Applications, 2021, 14, 685-697.	1.5	10
8573	Cross-species transmission of retroviruses among domestic and wild felids in human-occupied landscapes in Chile. Evolutionary Applications, 2021, 14, 1070-1082.	1.5	13
8574	Genetic, morphological, and niche variation in the widely hybridizing <i>Rhus integrifolia</i> " <i>Rhus ovata</i> species complex. Plant Species Biology, 2021, 36, 17-35.	0.6	1
8575	Newly discovered cichlid fish biodiversity threatened by hybridization with non-native species. Molecular Ecology, 2021, 30, 895-911.	2.0	24
8576	Haplotype data and forensic evaluation of 23 Y-STR and 12 X-STR loci in eight ethnic groups from Eritrea. International Journal of Legal Medicine, 2021, 135, 449-453.	1.2	8
8577	Variation in genes implicated in B-cell development and antibody production affects susceptibility to pemphigus. Immunology, 2021, 162, 58-67.	2.0	7
8578	Tiny treefrogs in the Pleistocene: Phylogeography of <i>Dendropsophus oliveirai</i> in the Atlantic Forest and associated enclaves in northeastern Brazil. Journal of Zoological Systematics and Evolutionary Research, 2021, 59, 179-194.	0.6	5
8579	A paleogenetic perspective of the Sabana de Bogotá (Northern South America) population history over the Holocene (9000-550 cal BP). Quaternary International, 2021, 578, 73-86.	0.7	7
8580	Anthropogenic and natural barriers affect genetic connectivity in an Alpine butterfly. Molecular Ecology, 2021, 30, 114-130.	2.0	19
8581	No genetic signature of glacial refugia in current European fallow deer ( <i>Dama dama</i> L., 1758) populations: a comment on Baker et al. (2017). Mammalian Biology, 2021, 101, 305-312.	0.8	5
8582	Molecular diversity and genetic structure of wild rice accessions ( <i>Oryza rufipogon</i> Griff.) in Guangdong Province, China, as revealed by SNP markers. Genetic Resources and Crop Evolution, 2021, 68, 969-978.	0.8	3
8583	Late Quaternary Environmental and Human Impacts on the Mitochondrial DNA Diversity of Four Commensal Rodents in Myanmar. Journal of Mammalian Evolution, 2021, 28, 497-509.	1.0	4
8584	Subdividing Y-chromosome haplogroup R1a1 reveals Norse Viking dispersal lineages in Britain. European Journal of Human Genetics, 2021, 29, 512-523.	1.4	9
8585	Detecting no natural hybridization and predicting range overlap in <i>Saccharina angustata</i> and <i>Saccharina japonica</i> . Journal of Applied Phycology, 2021, 33, 693-702.	1.5	3

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8586	Investigation of free-living honey bee colonies in Ireland. <i>Journal of Apicultural Research</i> , 2021, 60, 229-240.	0.7	16
8587	Weak connectivity and population cohesiveness in rudderfish <i>Kyphosus sandwicensis</i> (Teleostei: Kyphosidae) inhabiting remote oceanic islands. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2021, 31, 356-366.	0.9	4
8588	Structuration of multilocus genotypes associated with insecticide resistance of the peach potato aphid, <scp><i>Myzus persicae</i></scp> (Sulzer), in potato fields in southern Belgium. <i>Pest Management Science</i> , 2021, 77, 482-491.	1.7	11
8589	Mining Favorable Alleles for Rice Coleoptile Elongation Length Sensitivity to Exogenous Gibberellin Under Submergence Condition. <i>Journal of Plant Growth Regulation</i> , 2021, 40, 1422-1439.	2.8	3
8590	Genetic Characterization of the Giant Liver Fluke, <i>Fascioloides magna</i> (Platyhelminthes: Fasciolidae) From the Adirondack Region of Northern New York. <i>Acta Parasitologica</i> , 2021, 66, 259-263.	0.4	3
8591	Globalâ€scale genetic structure of a cosmopolitan coldâ€water coral species. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2021, 31, 1-14.	0.9	7
8592	New Distribution and Molecular Diversity of the Reniform Nematode <i>Rotylenchulus macrosoma</i> (Nematoda: Rotylenchulinae) in Europe. <i>Phytopathology</i> , 2021, 111, 720-730.	1.1	4
8593	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
8594	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
8595	Phylogeographical and cytogeographical history of <i>Artemisia herba-alba</i> (Asteraceae) in the Iberian Peninsula and North Africa: mirrored intricate patterns on both sides of the Mediterranean Sea. <i>Botanical Journal of the Linnean Society</i> , 2021, 195, 588-605.	0.8	2
8596	Genetic Diversity and Mating Type Distribution of <i>Pseudocercospora fijiensis</i> on Banana in Uganda and Tanzania. <i>Phytopathology</i> , 2021, 111, 741-750.	1.1	4
8597	Genotyping-by-sequencing to determine the genetic structure of a Tibetan medicinal plant <i>Swertia musotii</i> Franch.. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 469-484.	0.8	3
8598	Phylogeny and phylogeography of <i>Arenaria</i> section <i>Pseudomoehringia</i> . <i>Journal of Systematics and Evolution</i> , 2021, 59, 298-315.	1.6	0
8599	Complex phylogeographic patterns in the intertidal goby <i>Chaenogobius annularis</i> around Kyushu Island as a boundary zone of three different seas. <i>Ichthyological Research</i> , 2021, 68, 86-100.	0.5	8
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8713	A study of genomic diversity in populations of Maharashtra, India, inferred from 20 autosomal STR markers. <i>BMC Research Notes</i> , 2021, 14, 69.	0.6	3
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8730	Genetic population structure of the Blackspot seabream ( <i>Pagellus bogaraveo</i> ): contribution of mtDNA control region to fisheries management. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2021, 32, 115-119.	0.7	3
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8732	Contrasting patterns of population structure in commercially fished sawsharks from southern Australian waters. <i>Reviews in Fish Biology and Fisheries</i> , 2021, 31, 359-379.	2.4	2

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8734	Complex evolution in <i>Aphis gossypii</i> group (Hemiptera: Aphididae), evidence of primary host shift and hybridization between sympatric species. <i>PLoS ONE</i> , 2021, 16, e0245604.	1.1	0
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8746	Population structure of two morphotypes of <i>Sideroxylon mascatense</i> (A.DC.) T.D.Penn. in Oman. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 1299-1308.	0.8	1
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8794	Genetic assessment of BoLA-DRB3 polymorphisms by comparing Bangladesh, Ethiopian, and Korean cattle. <i>Journal of Animal Science and Technology</i> , 2021, 63, 248-261.	0.8	3
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8808	Phylogeography and genetic diversity of the widespread katydid <i>Ducetia japonica</i> (Thunberg,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.8	1
8809	Spatial genetic patterns of the medicinal and edible shrub <i>Lycium ruthenicum</i> (Solanaceae) in arid Xinjiang, China. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	2
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8818	Cystic echinococcosis in sheep and goats of Lebanon. <i>Parasitology</i> , 2021, 148, 871-878.	0.7	13
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8836	Genetic diversity and population structure of cutlassfish ( <i>Lepturacanthus savala</i> ) along the coast of mainland China, as inferred by mitochondrial and microsatellite DNA markers. <i>Regional Studies in Marine Science</i> , 2021, 43, 101702.	0.4	13
8837	Ancient Xinjiang mitogenomes reveal intense admixture with high genetic diversity. <i>Science Advances</i> , 2021, 7, .	4.7	16
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8841	Molecular characteristics and taxonomic status of morphologically similar barnacles ( <i>Amphibalanus</i> ) assessed using the cytochrome c oxidase 1 gene. <i>Biodiversitas</i> , 2021, 22, .	0.2	0
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8843	Demography of swordfish (<sc><i>Xiphias gladius</i></sc> Linneus) populations from the coasts of Turkey, based on mitochondrial <sc>DNA</sc> and microsatellites. <i>Journal of Fish Biology</i> , 2021, 99, 37-48.	0.7	4

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8847	Evolutionary history of the oriental firebellied toad ( <i>Bombina orientalis</i> ) in Northeast China. Ecology and Evolution, 2021, 11, 4232-4242.	0.8	4
8849	Phylogeography and genetic structure of a subarctic-alpine shrub species, <i>Alnus alnobetula</i> (Ehrh.) K. Koch s. l., inferred from chloroplast DNA markers. Tree Genetics and Genomes, 2021, 17, 1.	0.6	4
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8851	Signatures of local adaptation to climate in natural populations of sweet chestnut ( <i>Castanea sativa</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.8	17
8852	Phylogeography of sika deer ( <i>Cervus nippon</i> ) inferred from mitochondrial cytochrome-b gene and microsatellite DNA. Gene, 2021, 772, 145375.	1.0	7
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8862	Study of 17 X-STRs in Native American and Mestizo populations of Central America for forensic and population purposes. International Journal of Legal Medicine, 2021, 135, 1773-1776.	1.2	4
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8866	Single nucleotide polymorphisms of leptin gene in five Ethiopian indigenous cattle breeds and the Korean Hanwoo breed. <i>Tropical Animal Health and Production</i> , 2021, 53, 202.	0.5	2
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8884	Comparative phylogeographic analysis suggests a shared history among eastern North American boreal forest birds. <i>Auk</i> , 2021, 138, .	0.7	9
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8889	Application of DNA barcodes and spatial analysis in conservation genetics and modeling of Iranian <i>Salicornia</i> genetic resources. <i>PLoS ONE</i> , 2021, 16, e0241162.	1.1	3
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8901	Genetic load has potential in large populations but is realized in small inbred populations. <i>Evolutionary Applications</i> , 2021, 14, 1540-1557.	1.5	58

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8903	<i>Gymnotus paraguensis</i> , a Good Example of Phenotypic Plasticity in the Pantanal Biome, Brazil. <i>Zebrafish</i> , 2021, 18, 162-173.	0.5	1
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8918	Genetic characteristics of the amphidromous fish Ayu <i>Plecoglossus altivelis altivelis</i> (Osmeriformes:). <i>Tj ETQq1 1 0.784314 rgBT /Overl</i> <i>Genetica</i> , 2021, 149, 117-128.	0.5	5
8919	Phylogeographic structure and historical demography of tarakihi ( <i>Nemadactylus macropterus</i> ) and king tarakihi ( <i>Nemadactylus</i> n.sp.) in New Zealand. <i>New Zealand Journal of Marine and Freshwater Research</i> , 2022, 56, 247-271.	0.8	8
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8948	Genetic composition of queen conch ( <i>Lobatus gigas</i> ) population on Pedro Bank, Jamaica and its use in fisheries management. <i>PLoS ONE</i> , 2021, 16, e0245703.	1.1	4
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8955	Deep divergence between island populations in lichenized fungi. <i>Scientific Reports</i> , 2021, 11, 7428.	1.6	4
8956	Demographic changes and loss of genetic diversity in two insular populations of bobcats ( <i>Lynx</i> ) Tj ETQq1 1 0.784314 rgBT / Overlock 10	1.0	6
8957	Cytochrome b gene based population study of <i>Tenuulosa ilisha</i> (Hamilton) in the Brahmaputra river system of India. <i>Asian Journal of Agriculture and Biology</i> , 0, , .	1.4	2
8958	Phylogeography of <i>Mytilisepta virgata</i> (Mytilidae: Bivalvia) in the northwestern Pacific: Cryptic mitochondrial lineages and mito-nuclear discordance. <i>Molecular Phylogenetics and Evolution</i> , 2021, 157, 107037.	1.2	11

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8960	Establishment of <i>Culex modestus</i> in Belgium and a Glance into the Virome of Belgian Mosquito Species. <i>MSphere</i> , 2021, 6, .	1.3	19
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8974	Rapid Parallel Adaptation to Anthropogenic Heavy Metal Pollution. <i>Molecular Biology and Evolution</i> , 2021, 38, 3724-3736.	3.5	19
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8976	CARACTERIZACIÓN GENÉTICA DE LA POBLACIÓN DE <i>Heliconius sara</i> (Nymphalidae) EN LA ISLA GORGONA, COLOMBIA. <i>Acta Biologica Colombiana</i> , 2021, 26, 374-384.	0.1	0



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8979	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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8981	Genetic Variation in the Prion Protein Gene (PRNP) of Two Tunisian Goat Populations. <i>Animals</i> , 2021, 11, 1635.	1.0	3
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8990	Genetic variation in a radish ( <i>Raphanus sativus</i> L.) geodiversity collection. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 163-171.	0.8	5
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8995	Brine chemistry matters: Isolation by environment and by distance explain population genetic structure of <i>Artemia franciscana</i> in saline lakes. <i>Freshwater Biology</i> , 2021, 66, 1546-1559.	1.2	15

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8997	Genetic diversity and phylogenetic relationships of Malayan tapir ( <i>Tapirus indicus</i> ) populations in the Malay Peninsula based on mitochondrial DNA control region. <i>Biodiversity and Conservation</i> , 2021, 30, 2433-2449.	1.2	1
8998	Genetic divergence between isolated populations of the North Island New Zealand Rifleman () Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667 fragmentation. <i>Ecology and Evolution</i> , 2021, 11, 5998-6014.	0.8	1
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9012	Genetic diversity and structure analysis of Croatian garlic collection assessed by SSR markers. <i>Folia Horticulturae</i> , 2021, 33, 157-171.	0.6	4
9013	Global population genetic structure of the sequential hermaphrodite, dusky grouper ( <i>Epinephelus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 0,9	0.9	

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9014	A novel interpretation of speciation, hybridization, and genetic population structure of the stone crabs <i>Menippe mercenaria</i> (Say, 1817) and <i>M. adina</i> Williams & Felder, 1986 (Decapoda: Brachyura). <i>Tj ETQq0 0 0 rgBT /Overlo</i>	0.4	0
9015	ddRAD sequencing: an emerging technology added to the biosecurity toolbox for tracing the origin of brown marmorated stink bug, <i>Halyomorpha halys</i> (Hemiptera: Pentatomidae). <i>BMC Genomics</i> , 2021, 22, 355.	1.2	6
9016	Europe as a bridgehead in the worldwide invasion history of grapevine downy mildew, <i>Plasmopara viticola</i> . <i>Current Biology</i> , 2021, 31, 2155-2166.e4.	1.8	36
9017	Effector Avr4 in <i>Phytophthora infestans</i> Escapes Host Immunity Mainly Through Early Termination. <i>Frontiers in Microbiology</i> , 2021, 12, 646062.	1.5	3
9019	Clear phylogeographic pattern and genetic structure of wild boar <i>Sus scrofa</i> population in Central and Eastern Europe. <i>Scientific Reports</i> , 2021, 11, 9680.	1.6	11
9020	Studying genetic population structure to shed light on the demographic explosion of the rare species <i>Barbitistes vicetinus</i> (Orthoptera, Tettigoniidae). <i>PLoS ONE</i> , 2021, 16, e0250507.	1.1	3
9021	Association of LCT -13910C>T polymorphism and hip fracture in a cohort of older adult population from Northern Spain. <i>Gene</i> , 2021, 783, 145560.	1.0	1
9022	Genetic differentiation and signatures of local adaptation revealed by RADseq for a highly dispersive mud crab <i>Scylla olivacea</i> (Herbst, 1796) in the Sulu Sea. <i>Ecology and Evolution</i> , 2021, 11, 7951-7969.	0.8	4
9023	Genetic characteristics of Korean Jeju Black cattle with high density single nucleotide polymorphisms. <i>Animal Bioscience</i> , 2021, 34, 789-800.	0.8	5
9024	Population discrimination of the French grunt, <i>Haemulon flavolineatum</i> (Desmarest, 1823) between the Campeche Bank and the Mexican Caribbean Sea, inferred by microsatellite loci. <i>Regional Studies in Marine Science</i> , 2021, 44, 101749.	0.4	1
9025	Dynamic landscapes in northwestern North America structured populations of wolverines ( <i>Gulo</i> ) <i>Tj ETQq0 0 0 rgBT /Overlock</i>	0.6	7
9026	Analysis of Skin Pigmentation and Genetic Ancestry in Three Subpopulations from Pakistan: Punjabi, Pashtun, and Baloch. <i>Genes</i> , 2021, 12, 733.	1.0	2
9027	Pleistocene climate fluctuations as the major driver of genetic diversity and distribution patterns of the Caspian green lizard, <i>Lacerta strigata</i> Eichwald, 1831. <i>Ecology and Evolution</i> , 2021, 11, 6927-6940.	0.8	12
9028	The DNA history of a lonely oak: <i>Quercus humboldtii</i> phylogeography in the Colombian Andes. <i>Ecology and Evolution</i> , 2021, 11, 6814-6828.	0.8	9
9029	Genetic signature of the natural gene pool of <i>Tilia cordata</i> Mill. in Lithuania: Compound evolutionary and anthropogenic effects. <i>Ecology and Evolution</i> , 2021, 11, 6260-6275.	0.8	6
9030	Historic range dynamics in Kaiser's mountain newt ( <i>Neurergus kaiseri</i> ): Insights from phylogeographic analyses and species distribution modeling. <i>Ecology and Evolution</i> , 2021, 11, 7622-7633.	0.8	14
9031	High-Resolution Characterization of KIR Genes in a Large North American Cohort Reveals Novel Details of Structural and Sequence Diversity. <i>Frontiers in Immunology</i> , 2021, 12, 674778.	2.2	21
9032	Phylogeography of <i>Otaria flavescens</i> (Carnivora: Pinnipedia): unravelling genetic connectivity at the southernmost limit of its distribution. <i>Biological Journal of the Linnean Society</i> , 2021, 134, 11-27.	0.7	3

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9033	An analysis of the demographic history of the risk allele R4810K in <i>RNF213</i> of moyamoya disease. <i>Annals of Human Genetics</i> , 2021, 85, 166-177.	0.3	3
9034	Genomic polymorphism in tribal population of Tripura: Signifying their closer affinity with the Nepalese and Tibetan populations. <i>Annals of Human Biology</i> , 2021, 48, 360-368.	0.4	0
9035	The Y-STR landscape of coastal southeastern Han: Forensic characteristics, haplotype analyses, mutation rates, and population genetics. <i>Electrophoresis</i> , 2021, 42, 1578-1593.	1.3	15
9036	How co-distribution of two related azaleas ( <i>Rhododendron</i> ) developed in the Japanese archipelago: insights from evolutionary and demographic analyses. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	0
9037	Exploring the genetic structure of <i>Parastrigea diovadena</i> Dubois and Macko, 1972 (Digenea: Strigeidae), an endoparasite of the white ibis, <i>Eudocimus albus</i> , from the Neotropical region of Mexico. <i>Parasitology Research</i> , 2021, 120, 2065-2075.	0.6	4
9038	Heterozygous Trees Rebound the Fastest after Felling by Beavers to Positively Affect Arthropod Community Diversity. <i>Forests</i> , 2021, 12, 694.	0.9	3
9039	Genetic structure of urban and non-urban populations differs between two common parid species. <i>Scientific Reports</i> , 2021, 11, 10428.	1.6	4
9040	Shedding Light on the Dark Ages: Sketching Potential Trade Relationships in Early Medieval Romania through Mitochondrial DNA Analysis of Sheep Remains. <i>Diversity</i> , 2021, 13, 208.	0.7	1
9041	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
9042	Identification and characterization of microsatellite markers for population genetic studies of <i>Panstrongylus megistus</i> (Burmeister, 1835) (Triatominae: Reduviidae). <i>Parasites and Vectors</i> , 2021, 14, 273.	1.0	3
9044	Processes that drive the population structuring of <i>Jenynsia lineata</i> (Cyprinodontiformes). <i>Journal of Herpetology</i> , 2021, 55, 104-114.	0.8	6
9045	Overexploitation and anthropogenic disturbances threaten the genetic diversity of an economically important neotropical palm. <i>Biodiversity and Conservation</i> , 2021, 30, 2395-2413.	1.2	7
9046	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
9047	The interaction of resource use and gene flow on the phenotypic divergence of benthic and pelagic morphs of Icelandic Arctic charr ( <i>Salvelinus alpinus</i> ). <i>Ecology and Evolution</i> , 2021, 11, 7315-7334.	0.8	12
9048	Population genetics of estuary and reservoir populations of Harris mud crabs, <i>Rhithropanopeus harrisi</i> , in Texas and Oklahoma. <i>Biological Invasions</i> , 2021, 23, 1.	1.2	1
9049	Estuary-Level Genomic Variation Confirms Demographic and Life History Differences among Black Drum Populations in Texas. <i>North American Journal of Fisheries Management</i> , 2021, 41, 1040-1052.	0.5	1
9050	Global changes explain the long-term demographic trend of the Eurasian common lizard (Squamata). <i>Journal of Herpetology</i> , 2021, 55, 115-125.	0.9	1
9051	Reliable wolf-dog hybrid detection in Europe using a reduced SNP panel developed for non-invasively collected samples. <i>BMC Genomics</i> , 2021, 22, 473.	1.2	13

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9052	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
9053	Fine-scale genetic structure of the freshwater snail <i>Promenetus exacuus</i> in the New York State region: the influences of historical colonization, habitat connectivity and dispersal ability. <i>Journal of Molluscan Studies</i> , 2021, 87, .	0.4	1
9054	Population genomics of the Eastern Rock Lobster, <i>Sagmariasus verreauxi</i> , during spawning stock recovery from over-exploitation. <i>ICES Journal of Marine Science</i> , 2021, 78, 2448-2459.	1.2	2
9055	Dispersal ability, habitat characteristics, and sea-surface circulation shape population structure of <i>Cingula trifasciata</i> (Gastropoda: Rissoidae) in the remote Azores Archipelago. <i>Bmc Ecology and Evolution</i> , 2021, 21, 128.	0.7	5
9056	Population genetic structure of <i>Bactrocera dorsalis</i> based on <i>cox1</i> sequences from Bangladesh and neighboring countries. <i>Journal of Asia-Pacific Entomology</i> , 2021, 24, 182-190.	0.4	0
9057	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
9058	Genetic Analysis of a Newly Established Deer Population Expanding in the Sasebo Area in Nagasaki Prefecture, Japan Reveals No Evidence of Genetic Disturbance by Formosan Sika Deer. <i>Mammal Study</i> , 2021, 46, .	0.2	2
9059	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
9060	Molecular characterization and phylogeography of Mediterranean picarels ( <i>Spicara flexuosa</i> , S.) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 42</i> <i>Marine Science</i> , 2021, 45, 101836.	0.4	4
9061	Isolation and reconnection: Demographic history and multiple contact zones of the green odorous frog ( <i>Odorrana margaretae</i> ) around the Sichuan Basin. <i>Molecular Ecology</i> , 2021, 30, 4103-4117.	2.0	7
9062	Transborder Gene Flow between Canada and the USA and Fine-Scale Population Structure of Atlantic Cod in the Broader Gulf of Maine Region. <i>Transactions of the American Fisheries Society</i> , 2021, 150, 560-577.	0.6	1
9063	Trophic-based diversification in benthivorous charrs ( <i>Salvelinus</i> ) dwelling littoral zones of Northern lakes. <i>Hydrobiologia</i> , 2021, 848, 4115-4133.	1.0	2
9064	Mutational analysis of SARS-CoV-2 ORF8 during six months of COVID-19 pandemic. <i>Gene Reports</i> , 2021, 23, 101024.	0.4	32
9065	Genetic differentiation of indigenous ( <i>Quercus robur</i> L.) and late flushing oak stands ( <i>Q. robur</i> L.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 42</i> <i>Forest Research</i> , 2021, 140, 1179-1194.	1.1	6
9066	Vocal phenotype of male rutting roars and genetic markers delineate East European red deer ( <i>Cervus</i> ) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 42</i>	0.8	3
9067	Comparative analysis of the superoxide dismutase gene family in <i>Cetartiodactyla</i> . <i>Journal of Evolutionary Biology</i> , 2021, 34, 1046-1060.	0.8	2
9068	Historical Demographic Processes Dominate Genetic Variation in Ancient Atlantic Cod Mitogenomes. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	9
9069	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

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9070	Low genetic diversity in the endangered marine alga <i>Silvetia siliquosa</i> (Ochrophyta: Fucaceae) and the implication to conservation. <i>Journal of Oceanology and Limnology</i> , 2022, 40, 216-225.	0.6	4
9071	Systematics and phylogeography of the Brazilian Atlantic Forest endemic harvestmen <i>Neosadocus Mello-Leitão</i> , 1926 (Arachnida: Opiliones: Gonyleptidae). <i>PLoS ONE</i> , 2021, 16, e0249746.	1.1	3
9072	Spatial and Temporal Genetic Diversity and Population Structure of <i>Hemileia vastatrix</i> from Peruvian Coffee Plantations. <i>Plant Pathology Journal</i> , 2021, 37, 280-290.	0.7	4
9073	Genetic differentiation and restricted gene flow in rice landraces from Yunnan, China: effects of isolation-by-distance and isolation-by-environment. <i>Rice</i> , 2021, 14, 54.	1.7	8
9074	The European species of <i>Ribes</i> subg. <i>Ribes</i> : population genetic testing of classical systematics. <i>Plant Systematics and Evolution</i> , 2021, 307, 1.	0.3	0
9075	Phylogeographic genetic variation of <i>Indoplanorbis exustus</i> (Deshayes, 1834) (Gastropoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10 16 1.5	1.5	9
9076	Coastal dunefields maintain pre-Holocene genetic structure in a rocky shore red alga. <i>Journal of Phycology</i> , 2021, 57, 1542-1553.	1.0	2
9078	Investigating genetic diversity in admixed populations from Ecuador. <i>American Journal of Physical Anthropology</i> , 2021, 176, 109-119.	2.1	5
9079	Genetic Diversity of <i>Kalopanax septemlobus</i> (Thunb.) Koidz. at the Northern Edge of the Range according to Chloroplast DNA Sequencing Data. <i>Russian Journal of Genetics</i> , 2021, 57, 745-749.	0.2	1
9080	High genetic differentiation in the endemic and endangered freshwater fish <i>Achondrostoma salmantinum</i> Doadrio and Elvira, 2007 from Spain, as revealed by mitochondrial and SNP markers. <i>Conservation Genetics</i> , 2021, 22, 585-600.	0.8	5
9081	Higher population genetic diversity within the algal symbiont <i>Durusdinium</i> in <i>Pocillopora verrucosa</i> from Mexican Pacific reefs correlates with higher resistance to bleaching after the El Niño 2015-16 event. <i>Marine Ecology</i> , 2021, 42, e12667.	0.4	2
9083	First Evidence of Presence of <i>Varroa underwoodi</i> Mites on Native <i>Apis cerana</i> Colonies in Primorsky Territory of Russia Based on COX1 Gene. <i>Journal of Apicultural Science</i> , 2021, 65, 177-187.	0.1	1
9084	Genetic diversity and transmission patterns of <i>Echinococcus granulosus sensu stricto</i> among domestic ungulates of Sardinia, Italy. <i>Parasitology Research</i> , 2021, 120, 2533-2542.	0.6	11
9085	High-Level Gene Flow Restricts Genetic Differentiation in Dairy Cattle Populations in Thailand: Insights from Large-Scale Mt D-Loop Sequencing. <i>Animals</i> , 2021, 11, 1680.	1.0	6
9086	Genetic conservation strategies of endemic plants from edaphic habitat islands: The case of <i>Jacobaea auricula</i> (Asteraceae). <i>Journal for Nature Conservation</i> , 2021, 61, 126004.	0.8	8
9087	<i>Acartia arbruta</i> (previously <i>A. tonsa</i> ) in British Columbia: a bioindicator of climate-driven ecosystem variability in the northeast Pacific Ocean. <i>Journal of Plankton Research</i> , 2021, 43, 546-564.	0.8	0
9088	Microsatellite variation in <i>Helicoverpa gelotopoeon</i> (Lepidoptera: Noctuidae) populations from Argentina. <i>Agricultural and Forest Entomology</i> , 2021, 23, 536.	0.7	3
9089	HLA diversity in the Russian population assessed by next generation sequencing. <i>Medical Immunology (Russia)</i> , 2021, 23, 509-522.	0.1	5



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9090	Genotyping of Two Mediterranean Trout Populations in Central-Southern Italy for Conservation Purposes Using a Rainbow-Trout-Derived SNP Array. <i>Animals</i> , 2021, 11, 1803.	1.0	7
9091	Genetic polymorphisms of 16 X-STR loci in the Hani population from Southwest China. <i>Forensic Sciences Research</i> , 2022, 7, 196-201.	0.9	3
9092	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
9093	Maternal genetic structure in ancient Shandong between 9500 and 1800 years ago. <i>Science Bulletin</i> , 2021, 66, 1129-1135.	4.3	10
9094	Molecular genotyping of <i>Candida albicans</i> isolated from different sites may trace the etiological infection routes: Observation in China. <i>Mycoses</i> , 2021, 64, 841-850.	1.8	2
9095	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
9096	Allelic losses and gains during translocations of a high conservation value fish, <i>Coregonus lavaretus</i> . <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2021, 31, 2575-2585.	0.9	3
9097	Assessing effects of chronic heavy metal exposure through a multibiomarker approach: the case of <i>Liomys irroratus</i> (Rodentia: Heteromyidae). <i>Environmental Science and Pollution Research</i> , 2021, 28, 55373-55387.	2.7	0
9098	Phylogeography, Population Structure, and Historical Demography of Black Drum in North America. <i>North American Journal of Fisheries Management</i> , 2021, 41, 1020-1039.	0.5	2
9099	Genetic and functional leaf trait diversity throughout the distribution of two Cerrado tree species: Testing the centre-periphery hypothesis. <i>Journal of Biogeography</i> , 2021, 48, 2258-2274.	1.4	2
9100	Genetic diversity and gene flow amongst admixed populations of <i>Ganoderma boninense</i> , causal agent of basal stem rot in African oil palm ( <i>Elaeis guineensis</i> Jacq.) in Sarawak (Malaysia), Peninsular Malaysia, and Sumatra (Indonesia). <i>Mycologia</i> , 2021, 113, 1-16.	0.8	7
9101	Different population size change and migration histories created genetic diversity of three oaks in Tokai region, central Japan. <i>Journal of Plant Research</i> , 2021, 134, 933-946.	1.2	5
9102	The last refugia for a polar relict pollinator: isolates of <i>Bombus glacialis</i> on Novaya Zemlya and Wrangel Island indicate its broader former range in the Pleistocene. <i>Polar Biology</i> , 2021, 44, 1691-1709.	0.5	9
9103	Surviving in southern refugia: the case of <i>Veronica aragonensis</i> , a rare endemic from the Iberian Peninsula. <i>Alpine Botany</i> , 2021, 131, 161-175.	1.1	4
9104	Wildlife conservation in a fragmented landscape: the Eurasian red squirrel on the Isle of Wight. <i>Conservation Genetics</i> , 2021, 22, 571-583.	0.8	4
9106	Global phylogeography of the smooth hammerhead shark: Glacial refugia and historical migration patterns. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2021, 31, 2348-2368.	0.9	6
9107	Genetic structure of <i>Turbinaria peltata</i> in the northern South China Sea suggest insufficient genetic adaptability of relatively high-latitude scleractinian corals to environment stress. <i>Science of the Total Environment</i> , 2021, 775, 145775.	3.9	9
9108	Annual climatic fluctuations and short-term genetic variation in the eastern spadefoot toad. <i>Scientific Reports</i> , 2021, 11, 13514.	1.6	3

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9109	Genetic diversity and population structure of <i>Robinia pseudoacacia</i> from six improved variety bases in China as revealed by simple sequence repeat markers. <i>Journal of Forestry Research</i> , 2022, 33, 611-621.	1.7	10
9110	On the origin and diversification of Podolian cattle breeds: testing scenarios of European colonization using genome-wide SNP data. <i>Genetics Selection Evolution</i> , 2021, 53, 48.	1.2	18
9111	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
9112	Cryopreservation and post-thaw genetic integrity of <i>Viola stagnina</i> Kit., an endangered species of wet habitats – A useful tool in ex situ conservation. <i>Scientia Horticulturae</i> , 2021, 284, 110056.	1.7	4
9113	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
9114	Morphological and molecular discordance in the taxonomic rearrangement of the <i>Marmosops pinheiroi</i> complex (Marsupialia: Didelphidae). <i>Systematics and Biodiversity</i> , 2021, 19, 770-781.	0.5	6
9116	Muskrats as a bellwether of a drying delta. <i>Communications Biology</i> , 2021, 4, 750.	2.0	5
9117	Genetic differentiation in Eurasian Woodcock ( <i>Scolopax rusticola</i> ) from the Azores. <i>Ibis</i> , 2022, 164, 313-319.	1.0	1
9118	Matrilineal diversity and population history of Norwegians. <i>American Journal of Physical Anthropology</i> , 2021, 176, 120-133.	2.1	3
9119	Herded and hunted goat genomes from the dawn of domestication in the Zagros Mountains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	32
9120	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
9121	Integrative taxonomy of the seasonally polyphenic scorpionfly <i>Panorpa liui</i> Hua, 1997 (Mecoptera: Tj ETQq1 1 0.784314 rgBT / Overlock 10 TFS	0.7	1
9122	A Study of Hybridization Between <i>Marmota baibacina</i> and <i>M. sibirica</i> in Their Secondary Contact Zone in Mongolian Altai. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	5
9123	New genetic evidences for distinct populations of the common minke whale ( <i>Balaenoptera</i> ) Tj ETQq1 1 0.784314 rgBT / Overlock 10 TFS	0.5	4
9124	Spatial Genetic Structure of the Sika Deer ( <i>Cervus nippon</i> ) Population on Yakushima: Significant Genetic Differentiation on a Small Island. <i>Mammal Study</i> , 2021, 46, .	0.2	0
9125	Genetic Structure of the Pacific Herring <i>Clupea pallasii</i> Valenciennes, 1847 on a Macrogeographic Scale. <i>Russian Journal of Genetics</i> , 2021, 57, 697-710.	0.2	0
9126	Distribution and Diversity of <i>Beauveria</i> in Boreal Forests of Northern European Russia. <i>Microorganisms</i> , 2021, 9, 1409.	1.6	3
9127	Hybridization and introgression in sympatric and allopatric populations of four oak species. <i>BMC Plant Biology</i> , 2021, 21, 266.	1.6	8

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9129	Uniparental genetic markers in Native Americans: A summary of all available data from ancient and contemporary populations. <i>American Journal of Physical Anthropology</i> , 2021, 176, 445-458.	2.1	5
9130	Urban landscapes increase dispersal, gene flow, and pathogen transmission potential in banded mongoose ( <i>Mungos mungo</i> ) in northern Botswana. <i>Ecology and Evolution</i> , 2021, 11, 9227-9240.	0.8	4
9131	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
9132	Genome-wide diversity analysis for signatures of selection of <i>Bos indicus</i> adaptability under extreme agro-climatic conditions of temperate and tropical ecosystems. <i>Animal Gene</i> , 2021, 20, 200115.	0.2	9
9133	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
9134	An evaluation of molecular characterization and population structure of Uttarakhand, India. <i>Gene Reports</i> , 2021, 23, 101076.	0.4	2
9135	Population genetics and species distribution modeling highlight conservation needs of the endemic trout from the Northern Sierra Madre Occidental. <i>Conservation Genetics</i> , 2021, 22, 629-643.	0.8	2
9136	Integration of genetic structure into conservation of an endangered, endemic lizard, <i>Ceratophora aspera</i> : A case study from Sri Lanka. <i>Biotropica</i> , 2021, 53, 1301-1315.	0.8	1
9137	Genetic diversity of the endangered Japanese golden eagle at neutral and functional loci. <i>Ecological Research</i> , 2021, 36, 815-829.	0.7	2
9138	Underlying microevolutionary processes parallel macroevolutionary patterns in ancient neotropical mountains. <i>Journal of Biogeography</i> , 2021, 48, 2312-2327.	1.4	8
9139	Spatial genetic patterns of <i>Octopus vulgaris</i> Mediterranean populations support the hypothesis of a transitional zone across the Siculo-Tunisian Strait. <i>Hydrobiologia</i> , 2021, 848, 4225-4240.	1.0	0
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9141	Evolutionary history of the calcareous sponge <i>Clathrina aurea</i> : genetic connectivity in the Western Atlantic and intriguing occurrence in the Eastern Pacific. <i>Marine Biology</i> , 2021, 168, 1.	0.7	1
9142	Genomic data support multiple introductions and explosive demographic expansions in a highly invasive aquatic insect. <i>Molecular Ecology</i> , 2021, 30, 4189-4203.	2.0	8
9143	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
9144	How natural selection shapes genetic differentiation in the MHC region: A case study with Native Americans. <i>Human Immunology</i> , 2021, 82, 523-531.	1.2	10
9145	Genetic diversity and population structure analysis of <i>Lateolabrax maculatus</i> from Chinese coastal waters using polymorphic microsatellite markers. <i>Scientific Reports</i> , 2021, 11, 15260.	1.6	5
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9148	Genetic structure and diversity of the mustard hill coral <i>Porites astreoides</i> along the Florida Keys reef tract. <i>Marine Biodiversity</i> , 2021, 51, 1.	0.3	4
9149	Phylogeography and demographic history of Thai <i>Pediculus humanus capitis</i> (Phthiraptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667 To 104825.	1.0	4
9151	Complex population structure of the Atlantic puffin revealed by whole genome analyses. <i>Communications Biology</i> , 2021, 4, 922.	2.0	14
9152	Genetic Structure of the <i>Goniopora lobata</i> and <i>G. djiboutiensis</i> Species Complex Is Better Explained by Oceanography Than by Morphological Characteristics. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	2
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9158	Geographic origin of <i>Explanatum explanatum</i> (Creplin, 1847) Fukui, 1929 detected from domestic water buffaloes in Sri Lanka. <i>Infection, Genetics and Evolution</i> , 2021, 91, 104806.	1.0	0
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9160	Balancing selection, genetic drift, and human-mediated introgression interplay to shape MHC (functional) diversity in Mediterranean brown trout. <i>Ecology and Evolution</i> , 2021, 11, 10026-10041.	0.8	6
9161	Drivers of species and genetic diversity within forest metacommunities across agricultural landscapes of different permeability. <i>Landscape Ecology</i> , 2021, 36, 3269-3286.	1.9	3
9162	Phylogeographic reconstructions can be biased by ancestral shared alleles: The case of the polymorphic lichen <i>Bryoria fuscescens</i> in Europe and North Africa. <i>Molecular Ecology</i> , 2021, 30, 4845-4865.	2.0	2
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9164	Addressing alpine plant phylogeography using integrative distributional, demographic and coalescent modeling. <i>Alpine Botany</i> , 2022, 132, 5-19.	1.1	6
9165	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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9174	Human Cystic Echinococcosis in Lebanon: A Retrospective Study and Molecular Epidemiology. <i>Acta Parasitologica</i> , 2022, 67, 186-195.	0.4	8
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9187	Influence of voltine ecotype and geographic distance on genetic and haplotype variation in the Asian corn borer. Ecology and Evolution, 2021, 11, 10244-10257.	0.8	3
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9238	Phylogeography of high Andean killifishes <i>Orestias</i> (Teleostei: Cyprinodontidae) in Caquena and Lauca sub-basins of the Altiplano (Chile): mitochondrial and nuclear analysis of an endangered fish. <i>PeerJ</i> , 2021, 9, e11917.	0.9	3
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9270	The Possibility of Regenerating a Pine Stand through Natural Regeneration. <i>Forests</i> , 2021, 12, 1055.	0.9	10
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9414	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
9415	Novel Expressed Sequence Tag-Derived and Other Genomic Simple Sequence Repeat Markers Revealed Genetic Diversity in Ethiopian Finger Millet Landrace Populations and Cultivars. <i>Frontiers in Plant Science</i> , 2021, 12, 735610.	1.7	4
9416	Ancestry analysis using autosomal SNPs in northern South America, reveals interpretation differences between an AIM panel and an identification panel. <i>Forensic Science International</i> , 2021, 326, 110934.	1.3	1
9417	Evolution of inbreeding: a gaze into five Italian beef cattle breeds history. <i>PeerJ</i> , 2021, 9, e12049.	0.9	4
9418	Diversification and biogeography of <i>Dawkinsia</i> (Teleostei: Cyprinidae) in the Western Ghats-Sri Lanka biodiversity hotspot. <i>Organisms Diversity and Evolution</i> , 2021, 21, 795-820.	0.7	8
9419	Small localized breeding populations in a widely distributed coastal shark species. <i>Conservation Genetics</i> , 2022, 23, 51-61.	0.8	1
9420	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
9421	The Quest for Genes Involved in Adaptation to Climate Change in Ruminant Livestock. <i>Animals</i> , 2021, 11, 2833.	1.0	18
9422	Population genetics of Bull Trout ( <i>Salvelinus confluentus</i> ) in the upper Athabasca River basin. <i>Ecology and Evolution</i> , 2021, 11, 14509-14520.	0.8	1
9423	Phylogeography of the East Asian grassland plant, <i>Viola orientalis</i> (Violaceae), inferred from plastid and nuclear restriction site-associated DNA sequencing data. <i>Journal of Plant Research</i> , 2021, 134, 1181-1198.	1.2	7
9424	Genetic imprints of <i>Brosimum alicastrum</i> Sw. in Mexico. <i>American Journal of Botany</i> , 2021, 108, 1793-1807.	0.8	3
9425	Structure of African Populations of <i>Pyricularia oryzae</i> from Rice. <i>Phytopathology</i> , 2021, 111, 1428-1437.	1.1	9



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9426	Unrestricted gene flow between two subspecies of translocated brushtail possums ( <i>Trichosurus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 7	1.2	1
9427	Genetic diversity and phylogeography of urban hedgehogs ( <i>Erinaceus europaeus</i> ) around Helsinki, Finland, revealed by mitochondrial DNA and microsatellite analyses. <i>Mammal Research</i> , 2022, 67, 99-107.	0.6	2
9428	Landscape Features Fail to Explain Spatial Genetic Structure in Whiteâ€Tailed Deer Across Ohio, USA. <i>Journal of Wildlife Management</i> , 2021, 85, 1669-1684.	0.7	4
9429	Development of microsatellite markers and evaluation of genetic diversity of the Amazonian ornamental fish <i>Pterophyllum scalare</i> . <i>Aquaculture International</i> , 2021, 29, 2435-2449.	1.1	4
9430	Development and preliminary application of novel genomewide SSR markers for genetic diversity analysis of an economically important bio-control agent <i>Platygaster robiniae</i> (Hymenoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 577	1.2	1
9431	Revealing the coexistence of differentiation and communication in an endemic hare, <i>Lepus yarkandensis</i> (Mammalia, Leporidae) using specific-length amplified fragment sequencing. <i>Frontiers in Zoology</i> , 2021, 18, 50.	0.9	2
9432	<i>Liolophura</i> species discrimination with geographical distribution patterns and their divergence and expansion history on the northwestern Pacific coast. <i>Scientific Reports</i> , 2021, 11, 17602.	1.6	7
9433	Diversidad genÃ©tica en poblaciones de <i>Pinus remota</i> (Pinaceae) del Noreste de MÃ©xico: evidencias de declinamiento demogrÃ¡fico histÃ³rico. <i>Acta Botanica Mexicana</i> , 2021, , e1890.	0.1	0
9434	Population Genetics for Inferring Introduction Sources of the Oriental Fruit Fly, <i>Bactrocera dorsalis</i> : A Test for Quarantine Use in Korea. <i>Insects</i> , 2021, 12, 851.	1.0	5
9435	Races of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> identified from the coastal areas of Turkey. <i>Canadian Journal of Plant Pathology</i> , 2021, 43, S323-S332.	0.8	8
9436	Twenty-Seven Y-Chromosome Short Tandem Repeats Analysis of Italian Mummies of the 16th and 18th Centuries: An Interdisciplinary Research. <i>Frontiers in Genetics</i> , 2021, 12, 720640.	1.1	2
9437	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
9438	Genetic diversity and expression profile of <i>Plasmodium falciparum</i> Pf34 gene supports its immunogenicity. <i>Current Research in Translational Medicine</i> , 2021, 69, 103308.	1.2	1
9439	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
9440	Population structure and pattern of geographic differentiation of Colorado Potato Beetle, <i>Leptinotarsa decemlineata</i> (Coleoptera: Chrysomelidae) in Turkey. <i>Pest Management Science</i> , 2021, , .	1.7	6
9441	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
9442	Genomic characterization of the nucleus for conservation of the Chino Santandereano breed using SNP markers. <i>Tropical Animal Health and Production</i> , 2021, 53, 492.	0.5	0
9443	Population genetic structure of the pen shell <i>Atrina pectinata sensu lato</i> (Bivalvia: Pinnidae) throughout East Asia. <i>Regional Studies in Marine Science</i> , 2021, 48, 102024.	0.4	1

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9444	Genetic structure of allopatric populations of <i>Lutzomyia longipalpis</i> sensu lato in Brazil. <i>Acta Tropica</i> , 2021, 222, 106031.	0.9	7
9445	Availability of HLA-allele-matched unrelated donors and registry size: Estimation from haplotype frequency in the Italian population. <i>Human Immunology</i> , 2021, 82, 758-766.	1.2	3
9446	Comparative population genetic structure of two ixodid tick species ( <i>Acari:Ixodidae</i> ) ( <i>Ixodes ovatus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 104999.	1.0	4
9447	Population Genetic Structure of the Invasive Spotted Alfalfa Aphid <i>Therioaphis trifolii</i> (Hemiptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 Evolution, 2021, 9, .	1.1	1
9448	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
9449	Specialist versus generalist parasites: the interactions between host diversity, environment and geographic barriers in avian malaria. <i>International Journal for Parasitology</i> , 2021, 51, 899-911.	1.3	9
9450	Genome-wide DNA arrays profiling unravels the genetic structure of Iranian sheep and pattern of admixture with worldwide coarse-wool sheep breeds. <i>Genomics</i> , 2021, 113, 3501-3511.	1.3	2
9451	Population and forensic analysis of 9 non-CODIS markers in Slovak population. <i>Legal Medicine</i> , 2021, 53, 101953.	0.6	0
9452	Genetic structure of the pink shrimp <i>Penaeus</i> ( <i>Farfantepenaeus</i> ) <i>notialis</i> (PÃ©rez-Farfante, 1967) (Decapoda: Penaeidae) in the Colombian Caribbean. <i>Fisheries Research</i> , 2021, 243, 106052.	0.9	9
9453	Evolutionary analysis of the anti-viral STAT2 gene of primates and rodents: Signature of different stages of an arms race. <i>Infection, Genetics and Evolution</i> , 2021, 95, 105030.	1.0	1
9454	Genetic structure of olive ridley sea turtles ( <i>Lepidochelys olivacea</i> ) in Ghana, West Africa. <i>Journal of Experimental Marine Biology and Ecology</i> , 2021, 544, 151614.	0.7	1
9455	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
9456	Genetic structure and connectivity among <i>Aedes aegypti</i> populations within Madurai city in Southern India. <i>Infection, Genetics and Evolution</i> , 2021, 95, 105031.	1.0	5
9457	Genetic pattern fluctuations in wild swimming crab populations, under the influence of continuous mass stock enhancement. <i>Fisheries Research</i> , 2021, 243, 106075.	0.9	7
9458	Biogeographically marginal: Source of evolutionary novelties and future potential. <i>Forest Ecology and Management</i> , 2021, 499, 119596.	1.4	0
9459	Does the transport of larvae throughout the south Atlantic support the genetic and morphometric diversity of the Sally Lightfoot Crabs <i>Grapsus grapsus</i> (Linnaeus, 1758) and <i>Grapsus adscensionis</i> (Osbeck, 1765) (Decapoda: Grapsidae) among the oceanic islands?. <i>Journal of Marine Systems</i> , 2021, 223, 103614.	0.9	12
9460	Forensic genetic polymorphisms of 16 X-STR loci in the Yunnan Miao population and their relationship to other Chinese groups. <i>Legal Medicine</i> , 2021, 53, 101961.	0.6	4
9461	BCISEQ-500RS sequencing of a 448-plex SNP panel for forensic individual identification and kinship analysis. <i>Forensic Science International: Genetics</i> , 2021, 55, 102580.	1.6	14

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9462	Sequential colonization of oceanic archipelagos led to a species-level radiation in the common chaffinch complex (Aves: <i>Fringilla coelebs</i> ). <i>Molecular Phylogenetics and Evolution</i> , 2021, 164, 107291.	1.2	19
9463	Population structure and the influence of microenvironment and genetic similarity on individual growth at Alaskan white spruce treelines. <i>Science of the Total Environment</i> , 2021, 798, 149267.	3.9	8
9464	Genetic diversity of Huaya India ( <i>Melicoccus oliviformis</i> Kunth), a neglected Neotropical fruit crop. <i>Scientia Horticulturae</i> , 2021, 290, 110535.	1.7	0
9465	Genetic lineage of the Amami islanders inferred from classical genetic markers. <i>Meta Gene</i> , 2021, 30, 100956.	0.3	1
9466	Spatio-temporal patterns of genetic variation of the silverside <i>Odontesthes regia</i> in the highly productive Humboldt Current System. <i>Fisheries Research</i> , 2021, 244, 106127.	0.9	3
9467	Genetic characterization of Kiddi shrimp, <i>Parapenaeopsis styliifera</i> (H. Milne Edwards, 1837) along the Indian coast using microsatellite markers. <i>Fisheries Research</i> , 2021, 244, 106128.	0.9	2
9468	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
9469	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
9470	Phylogeographic and demographic modeling analyses of the multiple origins of the rheophytic goldenrod <i>Solidago yokusaiana</i> Makino. <i>Heredity</i> , 2021, 126, 831-845.	1.2	2
9471	Genetic Diversity of <i>Bubalus bubalis</i> in Germany and Global Relations of Its Genetic Background. <i>Frontiers in Genetics</i> , 2020, 11, 610353.	1.1	7
9472	Population genetics of the endangered catfish <i>Pseudoplatystoma magdaleniatum</i> (Siluriformes: Tj ETQq0 0 0 rgBT /Overlock, 10 Tf 50 3	0.5	2
9473	Variability of the rs333 in Polish patients with lupus erythematosus. <i>Postepy Dermatologii i Alergologii</i> , 2021, 38, 131-136.	0.4	0
9474	The most important fishery resource in the Amazon, the migratory catfish <i>Brachyplatystoma vaillantii</i> (Siluriformes: Pimelodidae), is composed by an unique and genetically diverse population in the Solimões-Amazonas River System. <i>Neotropical Ichthyology</i> , 2021, 19, .	0.5	4
9475	Genetic diversity and population structure of Tarek ( <i>Alburnus tarichi</i> ), an endemic species to the Lake Van basin, Turkey. <i>Aquatic Living Resources</i> , 2021, 34, 3.	0.5	0
9476	Development of microsatellite loci and population genetics of the catfish <i>Pimelodus yuma</i> (Siluriformes: Pimelodidae). <i>Neotropical Ichthyology</i> , 2021, 19, .	0.5	4
9477	Genome-wide analysis clarifies the population genetic structure of wild gilthead sea bream ( <i>Sparus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock, 13	1.1	13
9478	Geological and Pleistocene glaciations explain the demography and disjunct distribution of red panda ( <i>A. fulgens</i> ) in eastern Himalayas. <i>Scientific Reports</i> , 2021, 11, 65.	1.6	7
9479	Reevaluation of Serum Arylesterase Activity in Neurodevelopmental Disorders. <i>Antioxidants</i> , 2021, 10, 164.	2.2	5

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9480	The ghosts of propagation past: haplotype information clarifies the relative influence of stocking history and phylogeographic processes on contemporary population structure of walleye ( <i>Sander</i> ) Tj ETQq0 0 0.08BT /Overlock 10 Tf		
9481	Genetic diversity of two populations of the tufted puffin <i>Fratercula cirrhata</i> (Pallas,) Tj ETQq1 1 0.784314 rgBT /Overlock 0,2		
9482	Evaluation of microhaplotypes in forensic kinship analysis from a Swedish population perspective. International Journal of Legal Medicine, 2021, 135, 1151-1160.	1.2	16
9483	Molecular identification and temporal genetic differentiation of <i>Cyprinus carpio</i> (Cypriniformes:) Tj ETQq1 1 0.784314 rgBT /Overlock 0,4		
9484	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. Marine Ecology, 2021, 42, .	0.4	3
9485	Population genetics and forensic utility of 23 autosomal PowerPlex Fusion 6C STR loci in the Kuwaiti population. Scientific Reports, 2021, 11, 1865.	1.6	6
9486	Signatures of Post-Glacial Genetic Isolation and Human-Driven Migration in the Dothistroma Needle Blight Pathogen in Western Canada. Phytopathology, 2021, 111, 116-127.	1.1	15
9487	Generalizations of genetic conservation principles in islands are not always likely: a case study from a Neotropical insular cactus. Botanical Journal of the Linnean Society, 2022, 199, 210-227.	0.8	3
9488	Association of whole mtDNA, an NADPH G11914A variant, and haplogroups with high physical performance in an elite military troop. Brazilian Journal of Medical and Biological Research, 2021, 54, e10317.	0.7	0
9491	Temporal evaluation of a woodrat (genus <i>Neotoma</i> ) hybrid zone based on genotypic and georeferenced data. Journal of Mammalogy, 2021, 102, 541-557.	0.6	3
9492	Genetic Diversity Assessment of <i>Cucurbita</i> Genetic Resources in Japan by Nuclear and Organelle DNA Markers. Horticulture Journal, 2021, 90, .	0.3	0
9493	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. Marine and Freshwater Research, 2021, 72, 131.	0.7	0
9494	Spatial Genetic Structure and Demographic History of the Wild Boar in the Qinling Mountains, China. Animals, 2021, 11, 346.	1.0	6
9495	Exploitation of a novel slowly mutating Y-STRs set and evaluation of slowly mutating Y-STRs plus Y-SNPs typing strategy in forensic genetics and evolutionary research. Electrophoresis, 2021, 42, 774-785.	1.3	10
9496	Cryptic speciation in the Warbling Vireo ( <i>Vireo gilvus</i> ). Auk, 2021, 138, .	0.7	4
9497	Restoration of transborder connectivity for Fennoscandian brown bears ( <i>Ursus arctos</i> ). Biological Conservation, 2021, 253, 108936.	1.9	7
9499	Comparative seascape genetics of co-distributed intertidal snails <i>Monodonta</i> spp. in the Japanese and Ryukyu archipelagoes. Marine Ecology - Progress Series, 2021, 657, 135-146.	0.9	6
9500	Genetic study in <i>Aedes (Stegomyia) aegypti</i> (Linnaeus, 1762) from Londrina (Paraná State, Brazil): an approach to population structure and pyrethroid resistance. Revista Brasileira De Entomologia, 2021, 65, .	0.1	0

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9501	Under the radar: genetic assessment of Rio Grande Shiner ( <i>Notropis jemezanus</i> ) and Speckled Chub ( <i>Macrhybopsis aestivalis</i> ), two Rio Grande basin endemic cyprinids that have experienced recent range contractions. <i>Conservation Genetics</i> , 2021, 22, 187-204.	0.8	2
9502	Morphological and genetic variation in natural populations of <i>Quercus vulcanica</i> and <i>Q. frainetto</i> . <i>Plant Systematics and Evolution</i> , 2021, 307, 1.	0.3	10
9503	Genetic homogeneity coupled with morphometric variability suggests high phenotypic plasticity in the sea louse <i>Caligus rogercresseyi</i> (Boxshall and Bravo, 2000), infecting farmed salmon ( <i>Salmo</i> )	0.0	0
9504	Genetic Connectivity of the West Indian Manatee in the Southern Range and Limited Evidence of Hybridization With Amazonian Manatees. <i>Frontiers in Marine Science</i> , 2021, 7, .	1.2	15
9505	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
9506	Identification and sequencing of 59 highly polymorphic microhaplotypes for analysis of DNA mixtures. <i>International Journal of Legal Medicine</i> , 2021, 135, 1137-1149.	1.2	15
9507	<i>Pseudoperonospora humuli</i> might be an introduced species in Central Europe with low genetic diversity but high distribution potential. <i>European Journal of Plant Pathology</i> , 2021, 159, 903-915.	0.8	3
9508	Deep genetic structure of a ground-herb along contrasting environments of seasonally dry understories in Amazonia and Cerrado as revealed from targeted genomic sequencing. <i>Botanical Journal of the Linnean Society</i> , 2022, 199, 196-209.	0.8	3
9509	Balancing selection and recombination as evolutionary forces caused population genetic variations in golden pheasant MHC class I genes. <i>BMC Evolutionary Biology</i> , 2016, 16, .	3.2	1
9511	Morphological and molecular characterization of freshwater prawn of genus <i>Macrobrachium</i> in the coastal area of Cameroon. <i>Ecology and Evolution</i> , 2019, 9, 14217-14233.	0.8	10
9512	Identification and population genetic comparison of three ascidian species based on mtDNA sequences. <i>Ecology and Evolution</i> , 2020, 10, 3758-3768.	0.8	4
9513	Phylogeny and biogeography of the Japanese rhinoceros beetle, <i>Trypoxylus dichotomus</i> (Coleoptera:)	0.8	11
9514	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
9515	Diversification Processes in Lizards and Snakes from the Middle São Francisco River Dune Region, Brazil. <i>Fascinating Life Sciences</i> , 2020, , 713-740.	0.5	6
9516	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
9518	Comparative Genetic Diversity, Population Structure, and Adaptations of Walleye and Yellow Perch Across North America. , 2015, , 643-689.		16
9519	Statistical Softwares Used in Evaluation of Forensic DNA Typing. , 2020, , 105-134.		1
9520	Population differentiation across small distances in a coral reef-associated vermetid ( <i>Ceraesignum</i> )	0.9	3

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9521	Genetic variation of introduced red oak ( <i>Quercus rubra</i> ) stands in Germany compared to North American populations. <i>European Journal of Forest Research</i> , 2020, 139, 321-331.	1.1	7
9522	Population genetic characterization of the black-veined white, <i>Aporia crataegi</i> (Lepidoptera: Pieridae), using novel microsatellite markers and mitochondrial DNA gene sequences. <i>Conservation Genetics</i> , 2020, 21, 359-371.	0.8	9
9523	Effect of host resistance on genetic structure of core and accessory chromosomes in Irish <i>Zymoseptoria tritici</i> populations. <i>European Journal of Plant Pathology</i> , 2018, 150, 139-148.	0.8	15
9524	A new morph of <i>Telmatochromis temporalis</i> (Cichlidae; Cichliformes) from Lake Tanganyika. <i>Hydrobiologia</i> , 2021, 848, 3655-3665.	1.0	2
9525	Morphological description and population structure of an ophiuroid species from cobalt-rich crust seamounts in the Northwest Pacific: Implications for marine protection under deep-sea mining. <i>Acta Oceanologica Sinica</i> , 2021, 40, 79-89.	0.4	6
9526	Geographically well-distributed citizen science data reveals range-wide variation in the chipping sparrow's simple song. <i>Animal Behaviour</i> , 2020, 161, 63-76.	0.8	23
9527	Analysis of genetic variation and inbreeding among three lines of hatchery-reared <i>Crassostrea virginica</i> broodstock. <i>Aquaculture</i> , 2020, 527, 735452.	1.7	17
9528	Genetic diversity and population structure of <i>Zymoseptoria tritici</i> in Ethiopia as revealed by microsatellite markers. <i>Fungal Genetics and Biology</i> , 2020, 141, 103413.	0.9	15
9529	Genetic characterization of Guinea-Bissau using a 12 X-chromosomal STR system: Inferences from a multiethnic population. <i>Forensic Science International: Genetics</i> , 2017, 31, 89-94.	1.6	15
9530	Forensic parameters and genetic structure based on Y-chromosome short tandem repeats in Lesotho populations. <i>Forensic Science International: Genetics Supplement Series</i> , 2019, 7, 414-415.	0.1	3
9531	Forensic characteristics of Tibeto-Burman-speaking Tibetans revealed by 50 InDels. <i>Forensic Science International: Genetics Supplement Series</i> , 2019, 7, 758-759.	0.1	1
9532	Estimation of optimal donor number in Bone Marrow Donor Registry: Hong Kong's experience. <i>Human Immunology</i> , 2017, 78, 610-613.	1.2	8
9533	Recognizing peripheral ecosystems in marine protected areas: A case study of golden jellyfish lakes in Raja Ampat, Indonesia. <i>Marine Pollution Bulletin</i> , 2020, 151, 110700.	2.3	5
9534	Molecular and morphological signatures for extreme environmental adaptability of the invasive mussel <i>Brachidontes pharaonis</i> (Fischer, 1870). <i>Molecular and Cellular Probes</i> , 2020, 53, 101594.	0.9	1
9535	Population genetics of two chromatic morphs of the Chagas disease vector <i>Rhodnius pallescens</i> Barber, 1932 in Panamá. <i>Infection, Genetics and Evolution</i> , 2020, 84, 104369.	1.0	2
9536	Pinpointing cryptic borders: Fine-scale phylogeography and genetic landscape analysis of the <i>Hormogaster elisae</i> complex (Oligochaeta, Hormogastridae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 112, 185-193.	1.2	24
9537	Trans-oceanic genomic divergence of Atlantic cod ecotypes is associated with large inversions. <i>Heredity</i> , 2017, 119, 418-428.	1.2	108
9538	Ancestry and demography and descendants of Iron Age nomads of the Eurasian Steppe. , 0, .		1



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9539	Mitochondrial ancestry of medieval individuals carelessly interred in a multiple burial from southeastern Romania. <i>Scientific Reports</i> , 2019, 9, 961.	1.6	2
9540	Global phylogeography and genetic diversity of the long-finned pilot whale <i>Globicephala melas</i> , with new data from the southeastern Pacific. <i>Scientific Reports</i> , 2020, 10, 1769.	1.6	7
9541	Molecular species boundaries in the phreaticidean genus <i>Amphisopus</i> (Isopoda : <i>Amphisopidae</i> ) and evidence for a new freshwater isopod species from Western Australia. <i>Invertebrate Systematics</i> , 2013, 27, 173.	0.5	4
9542	Lack of genetic differentiation observed in Pacific bluefin tuna ( <i>Thunnus orientalis</i> ) from Taiwanese and New Zealand waters using mitochondrial and nuclear DNA markers. <i>Marine and Freshwater Research</i> , 2012, 63, 198.	0.7	10
9543	Cryptic diversity of the spotted scat <i>Scatophagus argus</i> (Perciformes: <i>Scatophagidae</i> ) in the South China Sea: pre- or post-production isolation. <i>Marine and Freshwater Research</i> , 2020, 71, 1640.	0.7	15
9544	Limited sex bias in the fine-scale spatial genetic structure of the eastern grey kangaroo and its relationship to habitat. <i>Australian Journal of Zoology</i> , 2017, 65, 33.	0.6	3
9545	Phylogeography and population genetic structure of an exotic invasive brine shrimp, <i>Artemia</i> Leach, 1819 (Crustacea : <i>Anostraca</i> ), in Australia. <i>Australian Journal of Zoology</i> , 2018, 66, 307.	0.6	17
9546	Historical Influences of Volcanism and Glaciation in Shaping Mitochondrial DNA Variation and Distribution in Yellowstone Cutthroat Trout across Its Native Range. <i>Transactions of the American Fisheries Society</i> , 2011, 140, 91-107.	0.6	10
9547	Distribution, body size, genetic structure and conservation of <i>Siphlaenigma janae</i> (Insecta:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422 To	0.6	4
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9789	Biogeography and Genetic Structure in Populations of a Widespread Lichen ( <i>Parmelina tiliacea</i> , Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 4	1.1	12
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9812	Evaluation of Genetic Diversity and Development of a Core Collection of Wild Rice ( <i>Oryza rufipogon</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.1	68
9813	Integrating Paleodistribution Models and Phylogeography in the Grass-Cutting Ant <i>Acromyrmex striatus</i> (Hymenoptera: Formicidae) in Southern Lowlands of South America. PLoS ONE, 2016, 11, e0146734.	1.1	17



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9839	Genetic Diversity and Structure among Isolated Populations of the Endangered Gees Golden Langur in Assam, India. PLoS ONE, 2016, 11, e0161866.	1.1	11
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9841	Striking Phenotypic Variation yet Low Genetic Differentiation in Sympatric Lake Trout ( <i>Salvelinus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlode	1.1	16
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9856	Between the Balkans and the Baltic: Phylogeography of a Common Vole Mitochondrial DNA Lineage Limited to Central Europe. PLoS ONE, 2016, 11, e0168621.	1.1	26
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9862	Genetic structure and distribution of <i>Parisotoma notabilis</i> (Collembola) in Europe: Cryptic diversity, split of lineages and colonization patterns. PLoS ONE, 2017, 12, e0170909.	1.1	16
9863	Genes encoding two <i>Theileria parva</i> antigens recognized by CD8+ T-cells exhibit sequence diversity in South Sudanese cattle populations but the majority of alleles are similar to the Muguga component of the live vaccine cocktail. PLoS ONE, 2017, 12, e0171426.	1.1	14
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9866	Extensive genetic differentiation detected within a model marsupial, the tammar wallaby ( <i>Notamacropus eugenii</i> ). PLoS ONE, 2017, 12, e0172777.	1.1	6
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9871	Taming the late Quaternary phylogeography of the Eurasiatic wild ass through ancient and modern DNA. PLoS ONE, 2017, 12, e0174216.	1.1	40
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9873	The role of the Strait of Gibraltar in shaping the genetic structure of the Mediterranean Grenadier, <i>Coryphaenoides mediterraneus</i> , between the Atlantic and Mediterranean Sea. PLoS ONE, 2017, 12, e0174988.	1.1	6
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9876	Rapid expansion of the invasive oyster <i>Crassostrea gigas</i> at its northern distribution limit in Europe: Naturally dispersed or introduced?. PLoS ONE, 2017, 12, e0177481.	1.1	29
9877	Genetic structuring, dispersal and taxonomy of the high-alpine populations of the <i>Geranium arabicum</i> /kilimandscharicum complex in tropical eastern Africa. PLoS ONE, 2017, 12, e0178208.	1.1	4
9878	Peripatric speciation in an endemic Macaronesian plant after recent divergence from a widespread relative. PLoS ONE, 2017, 12, e0178459.	1.1	8
9879	Ancient female philopatry, asymmetric male gene flow, and synchronous population expansion support the influence of climatic oscillations on the evolution of South American sea lion ( <i>Otaria</i> ) Tj ETQq1 1 0.784314 rgBT 49verlock I	1.1	14
9880	Mitochondrial DNA markers reveal high genetic diversity and strong genetic differentiation in populations of <i>Dendrolimus kikuchii</i> Matsumura (Lepidoptera: Lasiocampidae). PLoS ONE, 2017, 12, e0179706.	1.1	19
9881	Genetic diversity and stock identification of small abalone ( <i>Haliotis diversicolor</i> ) in Taiwan and Japan. PLoS ONE, 2017, 12, e0179818.	1.1	12
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9887	Population genetics of Southern Hemisphere tope shark ( <i>Galeorhinus galeus</i> ): Intercontinental divergence and constrained gene flow at different geographical scales. PLoS ONE, 2017, 12, e0184481.	1.1	22
9888	Converting quadratic entropy to diversity: Both animals and alleles are diverse, but some are more diverse than others. PLoS ONE, 2017, 12, e0185499.	1.1	48
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9892	Pleistocene climatic oscillations in Neotropical open areas: Refuge isolation in the rodent <i>Oxymycterus nasutus</i> endemic to grasslands. PLoS ONE, 2017, 12, e0187329.	1.1	21
9893	Phylogeography of the Central American lancehead <i>Bothrops asper</i> (SERPENTES: VIPERIDAE). PLoS ONE, 2017, 12, e0187969.	1.1	36
9894	The disjunct pattern of the Neotropical harvestman <i>Discocyrtus dilatatus</i> (Gonyleptidae) explained by climate-driven range shifts in the Quaternary: Paleodistributional and molecular evidence. PLoS ONE, 2017, 12, e0187983.	1.1	11
9895	Genome-wide association study and genetic diversity analysis on nitrogen use efficiency in a Central European winter wheat ( <i>Triticum aestivum</i> L.) collection. PLoS ONE, 2017, 12, e0189265.	1.1	70
9896	High genetic structure and low mitochondrial diversity in bottlenose dolphins of the Archipelago of Bocas del Toro, Panama: A population at risk?. PLoS ONE, 2017, 12, e0189370.	1.1	18
9897	Phylogeography and population diversity of <i>Simulium hirtipupa</i> Lutz (Diptera: Simuliidae) based on mitochondrial COI sequences. PLoS ONE, 2017, 12, e0190091.	1.1	7
9898	Phylogeography of screaming hairy armadillo <i>Chaetophractus vellerosus</i> : Successive disjunctions and extinctions due to cyclical climatic changes in southern South America. PLoS ONE, 2018, 13, e0190944.	1.1	5
9899	Comparative analysis of genetic diversity and differentiation of cauliflower ( <i>Brassica oleracea</i> var.) Tj ETQq1 1 0.784314 rgBT/Overlook	1.1	29
9900	Divergence in male sexual odor signal and genetics across populations of the red mason bee, <i>Osmia bicornis</i> , in Europe. PLoS ONE, 2018, 13, e0193153.	1.1	7
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9908	Reconstructing the population history of the sandy beach amphipod <i>Haustorioides japonicus</i> using the calibration of demographic transition (CDT) approach. PLoS ONE, 2019, 14, e0223624.	1.1	4
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9911	Fingerprinting of hatchery haplotypes and acquisition of genetic information by whole-mitogenome sequencing of masu salmon, <i>Oncorhynchus masou masou</i> , in the Kase River system, Japan. PLoS ONE, 2020, 15, e0240823.	1.1	3
9912	Time-lapse sentinel surveillance of SARS-CoV-2 spread in India. PLoS ONE, 2020, 15, e0241172.	1.1	3
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9915	Association of PARP1-specific polymorphisms and haplotypes with non-small cell lung cancer subtypes. PLoS ONE, 2020, 15, e0243509.	1.1	6
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9918	Fragmentation-related patterns of genetic differentiation in pedunculate oak (<i>Quercus) Tj ETQqO 0 0 rgBT /Overlock 10 Tf 50 18	0.5	18
9919	Impact of Habitat Damage on <i>Wikstroemia ganpi</i> (Siebold & Zucc.) Maxim. Genetic Diversity and Structure. Journal of Agriculture & Life Science, 2018, 52, 33-44.	0.1	2
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9921	Tracing imprints of past climatic fluctuations and heterogeneous topography in <i>Cynips quercusfolii</i> (Hymenoptera: Cynipidae) in Turkey. European Journal of Entomology, 0, 116, 141-157.	1.2	2



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9935	Genetic variability of blood groups in southern Brazil. <i>Genetics and Molecular Biology</i> , 2020, 43, e20180327.	0.6	2
9936	Global phylogeography of the critically endangered hawksbill turtle ( <i>Eretmochelys imbricata</i> ). <i>Genetics and Molecular Biology</i> , 2020, 43, e20190264.	0.6	12
9937	Microsatellite loci development for three catfish species from northwestern South America. <i>Neotropical Ichthyology</i> , 2020, 18, .	0.5	4
9938	Genetic differentiation through dispersal and isolation in two freshwater fish species from coastal basins of Northeastern Brazil. <i>Neotropical Ichthyology</i> , 2020, 18, .	0.5	2
9939	Diversidade genÄ©tica de <i>Xylella fastidiosa</i> em regiÄ°es produtoras de citros na Bahia. <i>Pesquisa Agropecuaria Brasileira</i> , 2014, 49, 26-33.	0.9	1

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9941	Deep genetic divergence in the Southern kingcroaker <i>Menticirrhus americanus</i> in its southernmost distribution. <i>Brazilian Journal of Oceanography</i> , 2017, 65, 515-519.	0.6	2
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9949	Phylogeographic Analysis of Mudpuppies ( <i>Necturus maculosus</i> ). <i>Journal of Herpetology</i> , 2020, 54, 78.	0.2	2
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9951	Conservation Genetics of the Endangered Yellow Lampmussel ( <i>Lampsilis cariosa</i> ). <i>American Midland Naturalist</i> , 2019, 181, 271.	0.2	2
9952	Phylogeography of <i>Sesamia nonagrioides</i> (Lepidoptera: Noctuidae) in Iran inferred from mitochondrial DNA. <i>Acta Zoologica Academiae Scientiarum Hungaricae</i> , 2015, 61, 341-359.	0.1	6
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9957	Holarctic phylogeographic structure of Eurasian wigeon ( <i>Mareca penelope</i> ). <i>Vavilovskii Zhurnal Genetiki i Selektcii</i> , 2019, 23, 362-369.	0.4	1

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9960	Population Structure of Two Flightless Weevils of Genus <i>Scepticus</i> Roelofs (Coleoptera,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662 Td (C	0.3	2
9961	Population Structure, Admixture, and Migration Patterns of Japanese Sika Deer ( <i>Cervus nippon</i> ) Inhabiting Toyama Prefecture in Japan. <i>Zoological Science</i> , 2019, 36, 128.	0.3	4
9963	Genetic Diversity and Population Structure Analysis of Bigleaf Hydrangea Using Genotyping-by-sequencing. <i>Journal of the American Society for Horticultural Science</i> , 2019, 144, 257-263.	0.5	7
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9971	Genetic differentiation among sexually compatible relatives of <i>Brassica napus</i> L.. <i>Genetika</i> , 2013, 45, 309-327.	0.1	15
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9976	Detecting Sex-Biased Gene Flow in African-americans Through the Analysis of Intra- and Inter-Population Variation at Mitochondrial DNA and Y- Chromosome Microsatellites. <i>Balkan Journal of Medical Genetics</i> , 2012, 15, 7-34.	0.5	5

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9978	Development of novel <i>Quercus rubra</i> chloroplast genome CAPS markers for haplotype identification. <i>Silvae Genetica</i> , 2020, 69, 78-85.	0.4	5
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9981	Genetic Diversity of <i>Lilium auratum</i> var. <i>platyphyllum</i> ; Endemic to the Izu Archipelago and its Relationship to a Nearby Population of <i>L. auratum</i> var. <i>auratum</i> ; by Morphological and SSR Analysis. <i>Horticulture Journal</i> , 2017, 86, 379-388.	0.3	6
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9987	Mitochondrial DNA Analyses of Invasive Raccoons ( <i>Procyon lotor</i> ) in the Boso Peninsula, Japan. <i>Mammal Study</i> , 2020, 45, 71.	0.2	6
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10005	Genetic stock composition of loggerhead turtles <i>Caretta caretta</i> bycaught in the pelagic waters of the North Atlantic. Endangered Species Research, 2013, 22, 73-84.	1.2	16
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10012	Documentation of a New Zealand blue whale population based on multiple lines of evidence. Endangered Species Research, 2018, 36, 27-40.	1.2	38
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10015	Found: a missing breeding ground for endangered western North Pacific humpback whales in the Mariana Archipelago. <i>Endangered Species Research</i> , 2020, 41, 91-103.	1.2	19
10016	Long-term stocking practices threaten the original genetic diversity of the southernmost European populations of Atlantic salmon <i>Salmo salar</i> . <i>Endangered Species Research</i> , 2020, 41, 303-317.	1.2	12
10017	Searching for humpback whales in a historical whaling hotspot of the Coral Sea, South Pacific. <i>Endangered Species Research</i> , 2020, 42, 67-82.	1.2	5
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10020	Loggerhead turtles nesting in Libya: an important management unit for the Mediterranean stock. <i>Marine Ecology - Progress Series</i> , 2012, 450, 207-218.	0.9	28
10021	Searching for common threads in threadfins: phylogeography of Australian polynemids in space and time. <i>Marine Ecology - Progress Series</i> , 2012, 449, 263-276.	0.9	20
10022	Differential invading potential among cryptic species of a Lessepsian bioinvader, the blotchfin dragonet <i>Callionymus filamentosus</i> . <i>Marine Ecology - Progress Series</i> , 2012, 450, 159-166.	0.9	4
10023	Phylogeography of the bivalve <i>Tegillarca granosa</i> in coastal China: implications for management and conservation. <i>Marine Ecology - Progress Series</i> , 2012, 452, 119-130.	0.9	11
10024	Population genetics of Australian white sharks reveals fine-scale spatial structure, transoceanic dispersal events and low effective population sizes. <i>Marine Ecology - Progress Series</i> , 2012, 455, 229-244.	0.9	100
10025	Genetic structure of European flounder <i>Platichthys flesus</i> : effects of both the southern limit of the species' range and chemical stress. <i>Marine Ecology - Progress Series</i> , 2013, 472, 257-273.	0.9	19
10026	Settling-depth vs. genotype and size vs. genotype correlations at the Pan I locus in 0-group Atlantic cod <i>Gadus morhua</i> . <i>Marine Ecology - Progress Series</i> , 2012, 468, 267-278.	0.9	29
10027	Pronounced genetic structure in a highly mobile coral reef fish, <i>Caesio cuning</i> , in the Coral Triangle. <i>Marine Ecology - Progress Series</i> , 2013, 480, 185-197.	0.9	27
10028	Dispersal barriers and stochastic reproductive success do not explain small-scale genetic structure in a broadcast spawning marine mussel. <i>Marine Ecology - Progress Series</i> , 2013, 482, 133-140.	0.9	3
10029	Life history matters: comparisons of population structuring in sympatric octopus species that differ in the presence of a pelagic larval stage. <i>Marine Ecology - Progress Series</i> , 2013, 486, 203-212.	0.9	17
10030	Strong maternal fidelity and natal philopatry shape genetic structure in North Pacific humpback whales. <i>Marine Ecology - Progress Series</i> , 2013, 494, 291-306.	0.9	151
10031	Genetic structure among spawning aggregations of the gulf coney <i>Hyporthodus acanthistius</i> . <i>Marine Ecology - Progress Series</i> , 2014, 499, 193-201.	0.9	8



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10032	Genetic structure of <i>Carcinus maenas</i> in southeast Australia. <i>Marine Ecology - Progress Series</i> , 2014, 500, 139-147.	0.9	7
10033	Life history traits of <i>Lepetodrilus nux</i> in the Okinawa Trough, based upon gametogenesis, shell size, and genetic variability. <i>Marine Ecology - Progress Series</i> , 2014, 505, 119-130.	0.9	18
10034	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
10035	The most vagile host as the main determinant of population connectivity in marine macroparasites. <i>Marine Ecology - Progress Series</i> , 2015, 520, 85-99.	0.9	23
10036	Genetic population structure of four hydrothermal vent shrimp species ( <i>Alvinocarididae</i> ) in the Okinawa Trough, Northwest Pacific. <i>Marine Ecology - Progress Series</i> , 2015, 529, 159-169.	0.9	25
10037	On-shelf larval retention limits population connectivity in a coastal broadcast spawner. <i>Marine Ecology - Progress Series</i> , 2015, 532, 1-12.	0.9	40
10038	Metapopulation structure informs conservation management in a heavily exploited coastal shark ( <i>Mustelus henlei</i> ). <i>Marine Ecology - Progress Series</i> , 2015, 533, 191-203.	0.9	26
10039	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
10040	Long-finned pilot whale population diversity and structure in Atlantic waters assessed through biogeochemical and genetic markers. <i>Marine Ecology - Progress Series</i> , 2015, 536, 243-257.	0.9	9
10041	Passive dispersal against an ocean current. <i>Marine Ecology - Progress Series</i> , 2015, 539, 153-163.	0.9	17
10042	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
10043	Genetic and phenotypic diversity in the wedgefish <i>Rhynchobatus australiae</i> , a threatened ray of high value in the shark fin trade. <i>Marine Ecology - Progress Series</i> , 2016, 548, 165-180.	0.9	21
10044	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
10045	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
10046	Trans-Tasman genetic connectivity in the intertidal air-breathing slug <i>Onchidella nigricans</i> . <i>Marine Ecology - Progress Series</i> , 2016, 562, 93-100.	0.9	8
10047	Population genetic structure in European lobsters: implications for connectivity, diversity and hatchery stocking. <i>Marine Ecology - Progress Series</i> , 2017, 563, 123-137.	0.9	22
10048	Dispersal of green turtles from Africa's largest rookery assessed through genetic markers. <i>Marine Ecology - Progress Series</i> , 2017, 569, 215-225.	0.9	17
10049	Lack of genetic introgression between wild and selectively bred Sydney rock oysters <i>Saccostrea glomerata</i> . <i>Marine Ecology - Progress Series</i> , 2017, 570, 127-139.	0.9	16

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10050	Origin and route of establishment of the invasive Pacific oyster <i>Crassostrea gigas</i> in Scandinavia. <i>Marine Ecology - Progress Series</i> , 2017, 575, 95-105.	0.9	7
10051	Rookery contributions, movements and conservation needs of hawksbill turtles at foraging grounds in the eastern Pacific Ocean. <i>Marine Ecology - Progress Series</i> , 2018, 586, 203-216.	0.9	18
10052	A global estimate of genetic and geographic differentiation in macromedusae—implications for identifying the causes of jellyfish blooms. <i>Marine Ecology - Progress Series</i> , 2018, 591, 199-216.	0.9	16
10053	Complex genetic structure revealed in the circum-Antarctic broadcast spawning sea urchin <i>Sterechinus neumayeri</i> . <i>Marine Ecology - Progress Series</i> , 2018, 601, 153-166.	0.9	5
10054	Stock composition of green turtles <i>Chelonia mydas</i> foraging in the Ryukyu Archipelago differs with size class. <i>Marine Ecology - Progress Series</i> , 2018, 600, 151-163.	0.9	14
10055	Mixed stock analyses indicate population-scale connectivity effects of active dispersal by surface-pelagic green turtles. <i>Marine Ecology - Progress Series</i> , 2018, 601, 215-226.	0.9	14
10056	Low genetic connectivity in a fouling amphipod among man-made structures in the southern North Sea. <i>Marine Ecology - Progress Series</i> , 2019, 615, 133-142.	0.9	6
10057	Exceptionally high natal homing precision in hawksbill sea turtles to insular rookeries of the Caribbean. <i>Marine Ecology - Progress Series</i> , 2019, 620, 155-171.	0.9	15
10058	Green turtle mitochondrial microsatellites indicate finer-scale natal homing to isolated islands than to continental nesting sites. <i>Marine Ecology - Progress Series</i> , 2020, 643, 159-171.	0.9	15
10059	Population Genetics of European Anchovy ( <i>Engraulis encrasicolus</i> L.) in the Seas of Turkey Based on Microsatellite DNA. <i>Frontiers in Marine Science</i> , 0, 1, .	1.2	1
10060	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
10061	Climate-Driven Range Shifts of Brown Seaweed <i>Sargassum horneri</i> in the Northwest Pacific. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	7
10062	Linking Scales of Life-History Variation With Population Structure in Atlantic Cod. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	3
10063	Characterizing Y-STRs in the Evaluation of Population Differentiation Using the Mean of Allele Frequency Difference between Populations. <i>Genes</i> , 2020, 11, 566.	1.0	2
10064	Population Structure of the Greenhouse Whitefly, <i>Trialeurodes vaporariorum</i> (Westwood), an Invasive Species from the Americas, 60 Years after Invading China. <i>International Journal of Molecular Sciences</i> , 2014, 15, 13514-13528.	1.8	11
10065	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
10066	Tracing the Invasion and Expansion Characteristics of the Flatid Planthopper, <i>Metcalfa pruinosa</i> (Hemiptera: Flatidae), in Korea Using Mitochondrial DNA Sequences. <i>Insects</i> , 2021, 12, 4.	1.0	5
10067	The origin and dispersal pathway of the spotted sea hare <i>Aplysia dactylomela</i> (Mollusca: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.6	30

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10068	Population ecology and genetics of the invasive lionfish in Puerto Rico. <i>Aquatic Invasions</i> , 2014, 9, 227-237.	0.6	26
10069	Analyses with newly developed microsatellite markers elucidate the spread dynamics of <i>Tricellaria inopinata</i> dâ€™Hondt and Occhipinti-Ambrogi, 1985 - a recently established bryozoan along the New England seashore. <i>Aquatic Invasions</i> , 2015, 10, 135-145.	0.6	3
10070	Genetic evidence of successful establishment of the Nile perch ( <i>Lates spp. L.</i> ) in East African lakes and implications for management. <i>Management of Biological Invasions</i> , 2012, 3, 77-88.	0.5	5
10073	Phylogeography of the <I> <i>Phrynocephalus vlangalii</i> </I> Species Complex in the Upper Reaches of the Yellow River Inferred from mtDNA <I>ND4-tRNA</I><SUP>LEU</SUP> Segments. <i>Asian Herpetological Research</i> , 2012, 3, 52-68.	0.2	8
10074	Phylogeography of the North Pacific lightfish &lt;i>Maurolicus japonicus&lt;/i>. <i>Plankton and Benthos Research</i> , 2018, 13, 180-184.	0.2	4
10075	Genetic diversity and population structure of a vestimentiferan annelid <i>Lamellibrachia satsuma</i> in Japanese and northern Mariana waters. <i>Plankton and Benthos Research</i> , 2012, 7, 146-150.	0.2	6
10076	Delineation of seed collection zones based on environmental and genetic characteristics for <i>Quercus suber</i> L. in Sardinia, Italy. <i>IForest</i> , 2018, 11, 651-659.	0.5	9
10077	Phylogeography, species delimitation and population structure of a Western Australian short-range endemic mite harvestman (Arachnida: Opiliones: Pettalidae: Karripurcellia). <i>Evolutionary Systematics</i> , 2018, 2, 81-87.	0.2	8
10078	Assessment of the ecological structure of <i>Posidonia oceanica</i> (L.) Delile on the northern coast of Lazio, Italy (central Tyrrhenian, Mediterranean). <i>Italian Botanist</i> , 0, 9, 1-19.	0.0	12
10079	Can metabarcoding resolve intraspecific genetic diversity changes to environmental stressors? A test case using river macrozoobenthos. <i>Metabarcoding and Metagenomics</i> , 0, 4, .	0.0	18
10080	Increasing confidence for discerning species and population compositions from metabarcoding assays of environmental samples: case studies of fishes in the Laurentian Great Lakes and Wabash River. <i>Metabarcoding and Metagenomics</i> , 0, 4, .	0.0	5
10081	Microsatellite based genetic diversity of the widespread epiphytic lichen <i>Usnea subfloridana</i> (Parmeliaceae, Ascomycota) in Estonia: comparison of populations from the mainland and an island. <i>MycoKeys</i> , 2019, 58, 27-45.	0.8	2
10082	Natural habitats uncovered? â€“ Genetic structure of known and newly found localities of the endangered bitterling <i>Pseudorhodeus tanago</i> (Cyprinidae). <i>Nature Conservation</i> , 0, 17, 19-33.	0.0	7
10083	Evidence for geographic substructuring of mtDNA variation in the East European Hermit beetle ( <i>Osmoderma barnabita</i> ). <i>Nature Conservation</i> , 0, 19, 171-189.	0.0	12
10084	Colonization of Brazil by the cattle egret ( <i>Bubulcus ibis</i> ) revealed by mitochondrial DNA. <i>NeoBiota</i> , 0, 21, 49-63.	1.0	9
10085	Unravelling the origin and introduction pattern of the tropical species <i>Paracaprella pusilla</i> Mayer, 1890 (Crustacea, Amphipoda, Caprellidae) in temperate European waters: first molecular insights from a spatial and temporal perspective. <i>NeoBiota</i> , 0, 47, 43-80.	1.0	7
10086	Cryptic diversity and mtDNA phylogeography of the invasive demon shrimp, <i>Dikerogammarus haemobaphes</i> (Eichwald, 1841), in Europe. <i>NeoBiota</i> , 0, 57, 53-86.	1.0	26
10087	First insights into the molecular population structure and origins of the invasive Chinese sleeper, <i>Perccottus glenii</i> , in Europe. <i>NeoBiota</i> , 0, 57, 87-107.	1.0	5

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10088	Geographically structured genetic diversity in the cave beetle <i>Darlingtonia kentuckensis</i> Valentine, 1952 (Coleoptera, Carabidae, Trechini, Trechina). <i>Subterranean Biology</i> , 0, 34, 1-23.	5.0	9
10089	Gene flow and genetic structure of <i>Bactrocera carambolae</i> (Diptera, Tephritidae) among geographical differences and sister species, <i>B. dorsalis</i> , inferred from microsatellite DNA data. <i>ZooKeys</i> , 2015, 540, 239-272.	0.5	16
10090	Mitochondrial genotyping of an endangered bitterling <i>Acheilognathus typus</i> (Cyprinidae). <i>ZooKeys</i> , 2016, 623, 131-141.	0.5	6
10091	Taxonomic reassessment of two subspecies of Chinese skink in Taiwan based on morphological and molecular investigations (Squamata, Scincidae). <i>ZooKeys</i> , 2017, 687, 131-148.	0.5	7
10092	<i>Cecidonius pampeanus</i> , gen. et sp. n.: an overlooked and rare, new gall-inducing micromoth associated with <i>Schinus</i> in southern Brazil (Lepidoptera, Cecidosidae). <i>ZooKeys</i> , 2017, 695, 37-74.	0.5	17
10093	Phylogeography and population structure of <i>- grypotus</i> (Richardson, 1846) as revealed by mitochondrial control region sequences. <i>ZooKeys</i> , 2017, 705, 143-158.	0.5	4
10094	Genetic structure of <i>Octopus minor</i> around Chinese waters as indicated by nuclear DNA variations (Mollusca, Cephalopoda). <i>ZooKeys</i> , 2018, 775, 1-14.	0.5	6
10095	Population genetic structure of Marbled Rockfish, <i>Sebastiscus marmoratus</i> (Cuvier, 1829), in the northwestern Pacific Ocean. <i>ZooKeys</i> , 2019, 830, 127-144.	0.5	7
10096	Molecular evidence for cryptic species in the common slug eating snake <i>Duberria lutrix lutrix</i> (Squamata, Lamprophiidae) from South Africa. <i>ZooKeys</i> , 2019, 838, 133-154.	0.5	6
10097	Population structure of <i>Aphyocypris normalis</i> : phylogeography and systematics. <i>ZooKeys</i> , 2019, 872, 77-90.	0.5	11
10098	Genetic diversity and population structure of <i>Terapon jarbua</i> (Forsk., 1775) (Teleostei, Terapontidae) in Malaysian waters. <i>ZooKeys</i> , 2020, 911, 139-160.	0.5	19
10099	Habitat requirements affect genetic variation in three species of mayfly (Ephemeroptera, Baetidae) from South Africa. <i>ZooKeys</i> , 2020, 936, 1-24.	0.5	4
10100	Population genetics and diversity structure of an invasive earthworm in tropical and temperate pastures from Veracruz, Mexico. <i>ZooKeys</i> , 2020, 941, 49-69.	0.5	1
10101	Mitochondrial DNA control region variability of wild boar <i>Sus scrofa</i> with various external phenotypes in Turkey. <i>Turkish Journal of Zoology</i> , 2016, 40, 957-971.	0.4	1
10102	Isolation and Identification of <i>Bacillus megaterium</i> Bacteriophages via AFLP Technique. <i>Current Research in Bacteriology</i> , 2015, 8, 77-89.	0.1	7
10103	Phylogeny and Evolutionary Analysis of Goat Breeds in Jordan Based on DNA Sequencing. <i>Pakistan Journal of Biological Sciences</i> , 2012, 15, 850-853.	0.2	2
10104	Insights into the Genetic Population Structure of Black-Backed Jackal and Caracal in South Africa. <i>African Journal of Wildlife Research</i> , 2019, 49, .	0.2	5
10106	Loss of genetic variability in a hatchery strain of Senegalese sole ( <i>Solea senegalensis</i> ) revealed by sequence data of the mitochondrial DNA control region and microsatellite markers. <i>Scientia Marina</i> , 2012, 76, 225-235.	0.3	4

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10108	Range-Wide and Regional Patterns of Population Structure and Genetic Diversity in the Gopher Tortoise. <i>Journal of Fish and Wildlife Management</i> , 2017, 8, 497-512.	0.4	11
10109	Eight Novel Microsatellite Loci Developed from Vernal Pool Fairy Shrimp. <i>Journal of Fish and Wildlife Management</i> , 2013, 4, 134-138.	0.4	3
10110	Biogeographic origins of the viviparous sea snake assemblage (Elapidae) of the Indian Ocean. <i>Ceylon Journal of Science</i> , 2017, 46, 101.	0.1	5
10111	Using high-resolution human leukocyte antigen typing of 11,423 randomized unrelated individuals to determine allelic varieties, deduce probable human leukocyte antigen haplotypes, and observe linkage disequilibria between human leukocyte antigen-B and-C and human leukocyte antigen-DRB1 and-DQB1 alleles in the Taiwanese Chinese population. <i>Tzu Chi Medical Journal</i> , 2017, 29, 84.	0.4	8
10112	HLA Class II (DRB1 and DQB1) Polymorphism in Omanis. <i>Journal of Transplantation Technologies &amp; Research</i> , 2014, 04, .	0.1	2
10113	Monitoring Climate Change Impact on the Genetic Population Structure: The Case of the Fivebeard Rockling ( <i>Ciliata Mustela</i> , Linnaeus, 1758) In Its Southern Limit of Distribution. <i>Journal of Phylogenetics &amp; Evolutionary Biology</i> , 2014, 02, .	0.2	3
10114	Genetic Structure and Effective Population Size through Time: A Tale on Two Coastal Marine Species with Contrasting Life-History Patterns. <i>Journal of Phylogenetics &amp; Evolutionary Biology</i> , 2015, 03, .	0.2	3
10115	Molecular Phylogeny Inferred from the Concatenated Genes of Two Neotropical Catfish Species and Implications for Conservation. <i>Journal of Phylogenetics &amp; Evolutionary Biology</i> , 2017, 05, .	0.2	2
10116	Mitochondrial DNA-HVR1 Variation Reveals Genetic Heterogeneity in Thai-Isan Peoples from the Lower Region of Northeastern Thailand. <i>Advances in Anthropology</i> , 2014, 04, 7-12.	0.1	4
10117	Intraspecific Relationships and Variation of Two <i>Lefua</i> Species ( <i>Balitoridae</i> , <i>Cypriniformes</i> ) in the Tokai Region, Honshu, Japan. <i>Journal of Water Resource and Protection</i> , 2017, 09, 238-253.	0.3	4
10118	Patterns of Genetic Diversity of the White-Nosed Coati Reveals Phylogeographically Structured Subpopulations in Mexico. <i>Natural Resources</i> , 2017, 08, 31-53.	0.2	3
10119	Microsatellite-Based Genetic Structure and Differentiation of Goldfish ( <i>Carassius auratus</i> ) with Sarcoma. <i>Open Journal of Animal Sciences</i> , 2015, 05, 36-43.	0.2	3
10120	Genetic diversity and population structure of <i>Prochilodus costatus</i> and <i>Prochilodus argenteus</i> preceding dam construction in the Paraopeba River, S#227;o Francisco River Basin, Minas Gerais, Brazil. <i>Open Journal of Genetics</i> , 2012, 02, 121-130.	0.1	12
10121	Genetic Variability and Reproduction Structure of <i>Corbicula japonica</i> in Major Fishing Brackish Lakes in Japan. <i>Open Journal of Marine Science</i> , 2014, 04, 174-184.	0.3	4
10122	Dispersal Ability and Genetic Structure in Mytilid Mussels of Whale-Fall Communities. <i>Open Journal of Marine Science</i> , 2015, 05, 295-305.	0.3	2
10123	First isolation and characterization of genomic SSR markers for the giant red shrimp <i>Aristaeomorpha foliacea</i> (Risso, 1827). <i>Genetics and Molecular Research</i> , 2012, 11, 2745-2748.	0.3	1
10124	Short Communication Y-STR haplotype diversity and population data for Central Brazil: implications for environmental forensics and paternity testing. <i>Genetics and Molecular Research</i> , 2014, 13, 3404-3410.	0.3	4

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10125	Polymorphic microsatellite markers for the rare and endangered cactus <i>Uebelmannia pectinifera</i> (Cactaceae) and its congeneric species. <i>Genetics and Molecular Research</i> , 2014, 13, 10359-10366.	0.3	3
10126	Genetic relatedness between Ardi, Black Bedouin and Damascus goat breeds. <i>Genetics and Molecular Research</i> , 2014, 13, 4654-4665.	0.3	8
10127	Genetic structure and diversity in natural and stocked populations of the mandarin fish ( <i>Siniperca</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	0.3	8
10128	Variability of Cutaneous Leishmaniasis Lesions Is Not Associated with Genetic Diversity of <i>Leishmania tropica</i> in Khyber Pakhtunkhwa Province of Pakistan. <i>American Journal of Tropical Medicine and Hygiene</i> , 2017, 97, 1489-1497.	0.6	4
10129	Lack of Geospatial Population Structure Yet Significant Linkage Disequilibrium in the Reservoir of <i>Plasmodium falciparum</i> in Bongo District, Ghana. <i>American Journal of Tropical Medicine and Hygiene</i> , 2017, 97, 1180-1189.	0.6	12
10130	Genetic Differentiation of <i>Glossina pallidipes</i> Tsetse Flies in Southern Kenya. <i>American Journal of Tropical Medicine and Hygiene</i> , 2018, 99, 945-953.	0.6	8
10131	Multiple Novel Mutations in <i>Plasmodium falciparum</i> Chloroquine Resistance Transporter Gene during Implementation of Artemisinin Combination Therapy in Thailand. <i>American Journal of Tropical Medicine and Hygiene</i> , 2018, 99, 987-994.	0.6	8
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10133	Linguistic, geographic and genetic isolation: a collaborative study of Italian populations. <i>Journal of Anthropological Sciences</i> , 2014, 92, 201-31.	0.4	43
10134	Mitochondrial <i>cox1</i> and <i>cob</i> sequence diversities in <i>Gelidium vagum</i> (Gelidiales, Rhodophyta) in Korea. <i>Algae</i> , 2014, 29, 15-25.	0.9	10
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10136	Population structure and phylogenetic analysis of laboratory rabbits in Taiwan based on microsatellite markers. <i>World Rabbit Science</i> , 2018, 26, 57.	0.1	3
10137	Effect of the &lt;i>IGF-I&lt;/i> gene polymorphism on growth, body size, carcass and meat quality traits in Coloured Polish Merino sheep. <i>Archives Animal Breeding</i> , 2017, 60, 161-173.	0.5	15
10138	Identification of genomic regions and candidate genes of functional importance for gastrointestinal parasite resistance traits in Djallonké sheep of Burkina Faso. <i>Archives Animal Breeding</i> , 2019, 62, 313-323.	0.5	12
10139	Lack of association between IRF6 polymorphisms and nonsyndromic oral clefts in South Indian population. <i>Dentistry 3000</i> , 2013, 1, 25-29.	0.1	4
10140	Variations in the Regulatory Region of Alpha S1-Casein Milk Protein Gene among Tropically Adapted Indian Native (<i>Bos Indicus</i>) Cattle. <i>ISRN Biotechnology</i> , 2013, 2013, 1-10.	1.9	8
10141	Short communication. Mitochondrial DNA diversity of the founder populations of the Asturcãn pony. <i>Spanish Journal of Agricultural Research</i> , 2013, 11, 702.	0.3	1
10142	Saffron ( <i>Crocus sativus</i> L.), a monomorphic or polymorphic species?. <i>Spanish Journal of Agricultural Research</i> , 2014, 12, 753.	0.3	15



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10144	Genetic relationships between local Brazilian goat breeds based on mtDNA D-loop region similarity. Spanish Journal of Agricultural Research, 2020, 17, e0407.	0.3	1
10145	Conservation of <i>Primula farinosa</i> in Poland with respect to the genetic structure of populations. Acta Societatis Botanicorum Poloniae, 2018, 87, .	0.8	3
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10150	Mitochondrial DNA variation and phylogeography of native Mongolian goats. Asian-Australasian Journal of Animal Sciences, 2020, 33, 902-912.	2.4	8
10151	Genetic diversity and population structure of indigenous chicken of Bangladesh using microsatellite markers. Asian-Australasian Journal of Animal Sciences, 2020, 33, 1732-1740.	2.4	6
10152	Genetic Diversity of mtDNA D-loop Polymorphisms in Laotian Native Fowl Populations. Asian-Australasian Journal of Animal Sciences, 2014, 27, 19-23.	2.4	25
10153	The Anatolian Diagonal and Paleoclimatic Changes Shaped the Phylogeography of <i>Cynips quercus</i> (Hymenoptera, Cynipidae). Annales Zoologici Fennici, 2019, 56, 65.	0.2	6
10154	Interspecific and Intraspecific Genetic Diversity of <i>Thunnus</i> Species. , 0, , .		3
10156	HLA-A, HLA-B, HLA-DRB1 Polymorphisms and Risk of Cervical Squamous Epithelial Cell Carcinoma: A Population Study in China. Asian Pacific Journal of Cancer Prevention, 2013, 14, 4427-4433.	0.5	13
10157	Association of Leptin Receptor Lys109Arg and Gln223Arg Polymorphisms with Increased Risk of Clear Cell Renal Cell Carcinoma. Asian Pacific Journal of Cancer Prevention, 2014, 15, 4211-4215.	0.5	14
10158	An enigmatic group of arctic island caribou and the potential implications for conservation of biodiversity. Rangifer, 2014, 34, 73.	0.6	7
10159	Nuclear microsatellites reveal population genetic structuring and fine-scale pattern of hybridization in the Japanese mantis shrimp<i>Oratosquilla oratoria</i>. PeerJ, 2020, 8, e10270.	0.9	9
10160	Genetic diversity, population structure, and effective population size in two yellow bat species in south Texas. PeerJ, 2020, 8, e10348.	0.9	6
10161	From promise to practice: pairing non-invasive sampling with genomics in conservation. PeerJ, 2015, 3, e1106.	0.9	158

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10162	Environmental influences on the Indo-Pacific octocoral <i>Isis hippuris</i> Linnaeus 1758 (Alcyonacea: Tj ETQq0.0 rgBT /Qverlock 1	0.9	11
10163	Lack of genetic structure in greylag goose ( <i>Anser anser</i> ) populations along the European Atlantic flyway. PeerJ, 2015, 3, e1161.	0.9	15
10164	Population subdivision of the surf clam <i>Macra chinensis</i> in the East China Sea: Changjiang River outflow is not the sole driver. PeerJ, 2015, 3, e1240.	0.9	17
10165	Historical and current introgression in a Mesoamerican hummingbird species complex: a biogeographic perspective. PeerJ, 2016, 4, e1556.	0.9	22
10166	Genetic diversity in migratory bats: Results from RADseq data for three tree bat species at an Ohio windfarm. PeerJ, 2016, 4, e1647.	0.9	33
10167	Unequal contribution of native South African phylogeographic lineages to the invasion of the African clawed frog, <i>Xenopus laevis</i> , in Europe. PeerJ, 2016, 4, e1659.	0.9	26
10168	Mind the gaps: investigating the cause of the current range disjunction in the Cape Platanna, <i>Xenopus gilli</i> (Anura: Pipidae). PeerJ, 2013, 1, e166.	0.9	13
10169	Broad-scale sampling of primary freshwater fish populations reveals the role of intrinsic traits, inter-basin connectivity, drainage area and latitude on shaping contemporary patterns of genetic diversity. PeerJ, 2016, 4, e1694.	0.9	16
10170	Characterization of SSR genomic abundance and identification of SSR markers for population genetics in Chinese jujube ( <i>Ziziphus jujuba</i> Mill.). PeerJ, 2016, 4, e1735.	0.9	13
10171	Association of <i>NOD1</i> , <i>CXCL16</i> , <i>STAT6</i> and <i>TLR4</i> gene polymorphisms with Malaysian patients with Crohn's disease. PeerJ, 2016, 4, e1843.	0.9	14
10172	Evaluating the adaptive potential of the European eel: is the immunogenetic status recovering?. PeerJ, 2016, 4, e1868.	0.9	1
10173	Fine scale patterns of genetic partitioning in the rediscovered African crocodile, <i>Crocodylus suchus</i> (Saint-Hilaire 1807). PeerJ, 2016, 4, e1901.	0.9	15
10174	Incorporation of an invasive plant into a native insect herbivore food web. PeerJ, 2016, 4, e1954.	0.9	32
10175	Genetic structure of the crown-of-thorns seastar in the Pacific Ocean, with focus on Guam. PeerJ, 2016, 4, e1970.	0.9	12
10176	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
10177	Microsatellite loci in the tiger shark and cross-species amplification using pyrosequencing technology. PeerJ, 2016, 4, e2205.	0.9	6
10178	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
10179	Characterization, development and multiplexing of microsatellite markers in three commercially exploited reef fish and their application for stock identification. PeerJ, 2016, 4, e2418.	0.9	4

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10180	Highly divergent mussel lineages in isolated Indonesian marine lakes. PeerJ, 2016, 4, e2496.	0.9	20
10181	Mitochondrial DNA hyperdiversity and its potential causes in the marine periwinkle <i>Melarhaphe neritoides</i> (Mollusca: Gastropoda). PeerJ, 2016, 4, e2549.	0.9	15
10182	Phylogeography of <i>Arenaria balearica</i> L. (Caryophyllaceae): evolutionary history of a disjunct endemic from the Western Mediterranean continental islands. PeerJ, 2016, 4, e2618.	0.9	9
10183	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
10184	Asymmetrical dispersal and putative isolation-by-distance of an intertidal blennioid across the Atlantic-Mediterranean divide. PeerJ, 2017, 5, e3195.	0.9	5
10185	Getting off to a good start? Genetic evaluation of the <i>ex situ</i> conservation project of the Critically Endangered Montseny brook newt ( <i>Calotriton arnoldi</i> ). PeerJ, 2017, 5, e3447.	0.9	8
10186	Characterisation of microsatellite and SNP markers from Miseq and genotyping-by-sequencing data among parapatric <i>Urophora cardui</i> (Tephritidae) populations. PeerJ, 2017, 5, e3582.	0.9	3
10187	Simulations indicate that scores of lionfish ( <i>Pterois volitans</i> ) colonized the Atlantic Ocean. PeerJ, 2017, 5, e3996.	0.9	8
10188	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
10189	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
10190	Population genetic structure of Patagonian toothfish ( <i>Dissostichus eleginoides</i> ) in the Southeast Pacific and Southwest Atlantic Ocean. PeerJ, 2018, 6, e4173.	0.9	19
10191	Genetic analysis of the Hungarian draft horse population using partial mitochondrial DNA D-loop sequencing. PeerJ, 2018, 6, e4198.	0.9	8
10192	Geographic variation in the advertisement calls of <i>Hyla eximia</i> and its possible explanations. PeerJ, 2014, 2, e420.	0.9	6
10193	Strong genetic differentiation in tropical seagrass <i>Enhalus acoroides</i> (Hydrocharitaceae) at the Indo-Malay Archipelago revealed by microsatellite DNA. PeerJ, 2018, 6, e4315.	0.9	10
10194	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
10195	Phylogeographic structure in three North American tent caterpillar species (Lepidoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 e4479.	0.9	16
10196	Effects of landscape features on population genetic variation of a tropical stream fish, Stone lapping minnow, <i>Garra cambodgiensis</i> , in the upper Nan River drainage basin, northern Thailand. PeerJ, 2018, 6, e4487.	0.9	5
10197	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

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10198	Genetic divergence and fine scale population structure of the common bottlenose dolphin ( <i>Tursiops</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 20	0.9	20
10199	Patterns of genetic structuring at the northern limits of the Australian smelt ( <i>Retropinna</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 3	0.9	3
10200	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
10201	Genetic differentiation, local adaptation and phenotypic plasticity in fragmented populations of a rare forest herb. PeerJ, 2018, 6, e4929.	0.9	18
10202	Adaptive genetic variation at three loci in South African vervet monkeys ( <i>Chlorocebus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 Tf 5	0.9	5
10203	Weak population structure in the ant <i>Formica fusca</i> . PeerJ, 2018, 6, e5024.	0.9	11
10204	Divergence by depth in an oceanic fish. PeerJ, 2014, 2, e525.	0.9	21
10205	Historical connections among river basins and climatic changes explain the biogeographic history of a water rat. PeerJ, 2018, 6, e5333.	0.9	6
10206	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
10207	Phylogeography of <i>Swertia perennis</i> in Europe based on cpDNA markers. PeerJ, 2018, 6, e5512.	0.9	6
10208	Natural history and molecular evolution of demersal Mediterranean sharks and skates inferred by comparative phylogeographic and demographic analyses. PeerJ, 2018, 6, e5560.	0.9	14
10209	Population genetics of the main population of brown bears in southwest Asia. PeerJ, 2018, 6, e5660.	0.9	39
10210	Genetic population structure of the pelagic mollusk <i>Limacina helicina</i> in the Kara Sea. PeerJ, 2018, 6, e5709.	0.9	6
10211	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
10212	Species diversity of drifting fish eggs in the Yangtze River using molecular identification. PeerJ, 2018, 6, e5807.	0.9	18
10213	Genetic evidence supports a distinct lineage of American crocodile ( <i>Crocodylus acutus</i> ) in the Greater Antilles. PeerJ, 2018, 6, e5836.	0.9	13
10214	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
10215	Genetic and phenotypic differentiation of lumpfish ( <i>Cyclopterus lumpus</i> ) across the North Atlantic: implications for conservation and aquaculture. PeerJ, 2018, 6, e5974.	0.9	25

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10216	Genetic assessment of a bighorn sheep population expansion in the Silver Bell Mountains, Arizona. PeerJ, 2018, 6, e5978.	0.9	2
10217	Local persistence of Mann's soft-haired mouse <i>Abrothrix manni</i> (Rodentia, Sigmodontinae) during Quaternary glaciations in southern Chile. PeerJ, 2018, 6, e6130.	0.9	6
10218	Genetic diversity and its conservation implications of <i>Vitex rotundifolia</i> (Lamiaceae) populations in East Asia. PeerJ, 2019, 7, e6194.	0.9	14
10219	Intraspecific divergences and phylogeography of <i>Panzerina lanata</i> (Lamiaceae) in northwest China. PeerJ, 2019, 7, e6264.	0.9	10
10220	Climate change and conservation in a warm North American desert: effect in shrubby plants. PeerJ, 2019, 7, e6572.	0.9	2
10221	Evidence of cryptic lineages within a small South American crocodilian: the Schneider's dwarf caiman <i>Paleosuchus trigonatus</i> (Alligatoridae: Caimaninae). PeerJ, 2019, 7, e6580.	0.9	31
10222	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
10223	Boto ( <i>Inia geoffrensis</i> ) "Cetacea: Iniidae) aggregations in two provisioning sites in the lower Negro River, Amazonas, Brazil: are they related?. PeerJ, 2019, 7, e6692.	0.9	7
10224	Introgressive hybridization in a Spiny-Tailed Iguana, <i>Ctenosaura pectinata</i> , and its implications for taxonomy and conservation. PeerJ, 2019, 7, e6744.	0.9	4
10225	Forensic characteristics and population genetics of Chinese Kazakh ethnic minority with an efficient STR panel. PeerJ, 2019, 7, e6802.	0.9	1
10226	Population expansions shared among coexisting bacterial lineages are revealed by genetic evidence. PeerJ, 2014, 2, e696.	0.9	14
10227	Maternal ancestry analyses of red tilapia strains based on D-loop sequences of seven tilapia populations. PeerJ, 2019, 7, e7007.	0.9	16
10228	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
10229	The role of dispersal for shaping phylogeographical structure of flightless beetles from the Andes. PeerJ, 2019, 7, e7226.	0.9	5
10230	RAD genotyping reveals fine-scale population structure and provides evidence for adaptive divergence in a commercially important fish from the northwestern Pacific Ocean. PeerJ, 2019, 7, e7242.	0.9	13
10231	Integrating phylogeographic and ecological niche approaches to delimiting cryptic lineages in the blue "green damselfish" ( <i>Chromis viridis</i> ). PeerJ, 2019, 7, e7384.	0.9	8
10232	Population genetic structure of Texas horned lizards: implications for reintroduction and captive breeding. PeerJ, 2019, 7, e7746.	0.9	5
10233	Population genetics and historical demographic inferences of the blue crab <i>Callinectes sapidus</i> in the US based on microsatellites. PeerJ, 2019, 7, e7780.	0.9	17

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10234	The distribution and mitochondrial genotype of the hydroid <i>Aglaophenia latecarinata</i> is correlated with its pelagic <i>Sargassum</i> substrate type in the tropical and subtropical western Atlantic Ocean. PeerJ, 2019, 7, e7814.	0.9	12
10235	Evaluation of variation within the barcode region of Cytochrome c 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
10236	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
10237	Phylogeography of the rare and endangered lycophyte <i>Isoetes yunguiensis</i> . PeerJ, 2020, 8, e8270.	0.9	5
10238	Genetic diversity and population structure of two subspecies of western honey bees ( <i>Apis mellifera</i> L.) in the Republic of South Africa as revealed by microsatellite genotyping. PeerJ, 2020, 8, e8280.	0.9	6
10239	Genetic structure is stronger across human-impacted habitats than among islands in the coral <i>Porites lobata</i> . PeerJ, 2020, 8, e8550.	0.9	17
10240	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
10241	Phylogeography of the widespread Caribbean spiny orb weaver <i>Gasteracantha cancriformis</i> . PeerJ, 2020, 8, e8976.	0.9	15
10242	Time matters: genetic composition and evaluation of effective population size in temperate coastal fish species. PeerJ, 2020, 8, e9098.	0.9	7
10243	Phylogeographic structure and northward range expansion in the barnacle <i>Chthamalus fragilis</i> . PeerJ, 2015, 3, e926.	0.9	11
10244	Genetic variation of the Chilean endemic long-haired mouse <i>Abrothrix longipilis</i> (Rodentia, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	0.9	12
10245	Ancient globetrotters' connectivity and putative native ranges of two cosmopolitan biofouling amphipods. PeerJ, 2020, 8, e9613.	0.9	14
10246	Recent population expansion of longtail tuna <i>Thunnus tonggol</i> (Bleeker, 1851) inferred from the mitochondrial DNA markers. PeerJ, 2020, 8, e9679.	0.9	5
10247	Population genomics reveals a mismatch between management and biological units in green abalone ( <i>Haliotis fulgens</i> ). PeerJ, 2020, 8, e9722.	0.9	12
10248	Population structure of three <i>Psammomys</i> species in the Iberian Peninsula. PeerJ, 2015, 3, e994.	0.9	3
10249	Population Genetic Structure of the Bumblebee, <i>Bombus ignitus</i> (Hymenoptera: Apidae), Based on Mitochondrial COI Gene and Nuclear Ribosomal ITS2 Sequences. International Journal of Industrial Entomology, 2013, 27, 142-158.	0.1	5
10250	ATPase 8/6 Gene Based Genetic Diversity Assessment of Snakehead Murrel, <i>Channa striata</i> (Perciformes, Tj ETQq0 0 0 rgBT /Overlock 10	0.4	4
10252	Phylogenetic analysis of Myanmar indigenous chickens using mitochondrial D-loop sequence reveals their characteristics as a genetic resource. Animal Science Journal, 2021, 92, e13647.	0.6	3



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10253	Patchily distributed but not necessarily isolated populations of <i>Deuterocohnia meziana</i> : a threatened bromeliad from rock outcrops. Botanical Journal of the Linnean Society, 2022, 199, 312-330.	0.8	3
10254	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
10257	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
10258	Diversidad G�netica de poblaciones de guan�bana ( <i>Annona muricata</i> L.) en Nayarit, M�xico mediante marcadores SSR y SRAP.. Acta Biologica Colombiana, 2021, 27, .	0.1	0
10259	Population data for 15 autosomal STR loci in Orang Asli subgroups of Peninsular Malaysia. International Journal of Legal Medicine, 2021, , 1.	1.2	3
10261	Species��landscape interactions drive divergent population trajectories in four forest��dependent Afromontane forest songbird species within a biodiversity hotspot in South Africa. Evolutionary Applications, 2021, 14, 2680-2697.	1.5	1
10262	Haplogroup Distribution of 309 Thais from Admixed Populations across the Country by HVI and HVII Sanger-Type Sequencing. Diversity, 2021, 13, 496.	0.7	1
10263	Remarkably Low <i>KIR</i> and <i>HLA</i> Diversity in Amerindians Reveals Signatures of Strong Purifying Selection Shaping the Centromeric <i>KIR</i> Region. Molecular Biology and Evolution, 2022, 39, .	3.5	8
10264	Cryptic diversity and phylogeography of the <i>Rhabdophis nuchalis</i> group (Squamata: Colubridae). Molecular Phylogenetics and Evolution, 2022, 166, 107325.	1.2	4
10265	Phylogenetics and Evolution of Potato Virus V: Another Potyvirus that Originated in the Andes. Plant Disease, 2022, 106, 691-700.	0.7	8
10266	A Preliminary Assessment of the Potential Health and Genetic Impacts of Releasing Confiscated Passerines Into the Wild: A Reduced-Risk Approach. Frontiers in Veterinary Science, 2021, 8, 679049.	0.9	4
10267	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
10268	Genome-wide development and application of miRNA-SSR markers in <i>Melilotus</i> genus. Physiology and Molecular Biology of Plants, 2021, 27, 2269-2282.	1.4	3
10269	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
10270	High genetic diversity and low structure in an endemic long-lived tree, <i>Yucca capensis</i> (Asparagaceae). Plant Biology, 2022, 24, 185-191.	1.8	3
10271	Evaluation of a custom QIAseq targeted DNA panel with 164 ancestry informative markers sequenced with the Illumina MiSeq. Scientific Reports, 2021, 11, 21040.	1.6	3
10272	Insights Into the Genetic Diversity of Nordic Red Clover ( <i>Trifolium pratense</i> ) Revealed by SeqSNP-Based Genic Markers. Frontiers in Plant Science, 2021, 12, 748750.	1.7	11
10273	Moderating effect of ppar�� on the association of c-reactive protein and ischemic stroke in patients younger than 60. Gene, 2022, 809, 146029.	1.0	2

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10274	Isolation and characterization of microsatellites markers in <i>Centaureum grandiflorum</i> ssp. <i>boissieri</i> . <i>Molecular Biology Reports</i> , 2021, 48, 8249-8253.	1.0	1
10275	Genetic differentiation and gene flow of the Amazonian catfish <i>Pseudoplatystoma punctifer</i> across the Madeira River rapids prior to the construction of hydroelectric dams. <i>Hydrobiologia</i> , 2022, 849, 29-46.	1.0	2
10276	Genetic Diversity and Population Structure of the Asian Tiger Mosquito ( <i>Aedes albopictus</i> ) in Vietnam: Evidence for Genetic Differentiation by Climate Region. <i>Genes</i> , 2021, 12, 1579.	1.0	11
10277	Population genomics provides insights into the population structure and temperature-driven adaptation of <i>Collichthys lucidus</i> . <i>BMC Genomics</i> , 2021, 22, 729.	1.2	3
10278	Hidden Diversity Revealed in the Freshwater Snails, <i>Bythinella</i> and <i>Pseudamnicola</i> , in the Island of Crete. <i>Integrative Zoology</i> , 2021, , .	1.3	0
10279	Population genetic structure of <i>Gymnospermium scipetarum</i> subsp. <i>eddae</i> (Berberidaceae), an endangered forest endemic from the Southern Apennines (Italy). <i>Plant Biosystems</i> , 0, , 1-17.	0.8	1
10280	A novel set of short microhaplotypes based on non-binary SNPs for forensic challenging samples. <i>International Journal of Legal Medicine</i> , 2022, 136, 43-53.	1.2	6
10282	Genetic Variability of Tree Junipers of Section <i>Sabina</i> : Data from Dagestan, Armenia, and Crimea. <i>Russian Journal of Genetics</i> , 2021, 57, 1223-1228.	0.2	2
10283	Genetic Evaluation of Black Sea Bream ( <i>Acanthopagrus schlegelii</i> ) Stock Enhancement in the South China Sea Based on Microsatellite DNA Markers. <i>Fishes</i> , 2021, 6, 47.	0.7	6
10285	Genetic polymorphisms of 16 X-STR loci analyzed in the Han population of Yunnan Province, Southwest China. <i>Legal Medicine</i> , 2022, 54, 101974.	0.6	1
10286	Understanding how an amphicarpic species with a mixed mating system responds to fire: a population genetic approach. <i>AoB PLANTS</i> , 2021, 13, plab067.	1.2	0
10287	Susceptibility of Field-Collected <i>Nyssorhynchus darlingi</i> to <i>Plasmodium</i> spp. in Western Amazonian Brazil. <i>Genes</i> , 2021, 12, 1693.	1.0	0
10288	Population genetics meets phylogenetics: new insights into the relationships among members of the genus <i>Euthynnus</i> (family Scombridae). <i>Hydrobiologia</i> , 2022, 849, 47-62.	1.0	5
10289	Genetic Diversity and Variation in Mitochondrial COI Gene in Wild and Hatchery Populations of <i>Saxidomus purpuratus</i> . <i>Biochemical Genetics</i> , 2021, , 1.	0.8	0
10290	Bee Trypanosomatids: First Steps in the Analysis of the Genetic Variation and Population Structure of <i>Lotmaria passim</i> , <i>Crithidia bombi</i> and <i>Crithidia mellificae</i> . <i>Microbial Ecology</i> , 2022, 84, 856-867.	1.4	5
10291	Phylogeography of cicadas on continental and oceanic islands in the northwestern Pacific region. <i>Journal of Biogeography</i> , 2021, 48, 3060-3071.	1.4	4
10292	Another Piece of the Puzzle: <i>Echinococcus oligarthrus</i> Recorded in Jaguarundis ( <i>Herpailurus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102 T	0.8	2
10293	Genetic variation and reproductive patterns in wetland mosses suggest efficient initial colonization of disturbed sites. <i>Ecology and Evolution</i> , 2021, 11, 15846-15859.	0.8	5

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10295	The influence of chalk grasslands on butterfly phenology and ecology. <i>Ecology and Evolution</i> , 2021, 11, 14521-14539.	0.8	0
10296	The mitochondrial DNA control region sequences from the Chinese sui population of southwestern China. <i>Annals of Human Biology</i> , 2021, 48, 635-640.	0.4	4
10297	Phylogeography and Taxonomic Revision of the Pen Shell <i>Atrina pectinata</i> Species Complex in the South China Sea. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	1
10298	Landscape and climatic features drive genetic differentiation processes in a South American coastal plant. <i>Bmc Ecology and Evolution</i> , 2021, 21, 196.	0.7	6
10299	Seasonal migration patterns and the maintenance of evolutionary diversity in a cryptic bird radiation. <i>Molecular Ecology</i> , 2021, , .	2.0	5
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10761	Comparative Phylogeography and Phylogeny of Pennah Croakers (Teleostei: Sciaenidae) in Southeast Asian Waters. <i>Genes</i> , 2021, 12, 1926.	1.0	1
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10833	Strong spatial structuring of clonal genetic diversity within blackthorn ( <i>Prunus spinosa</i> ) hedgerows and woodlands. <i>Tree Genetics and Genomes</i> , 2022, 18, 1.	0.6	1
10834	Genetic Variation in ATXN3 (Ataxin-3) 3'UTR: Insights into the Downstream Regulatory Elements of the Causative Gene of Machado-Joseph Disease/Spinocerebellar Ataxia Type 3. <i>Cerebellum</i> , 2023, 22, 37-45.	1.4	4
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10852	Population genetic structure of <i>Sitobion miscanthi</i> in China. <i>Journal of Integrative Agriculture</i> , 2022, 21, 178-187.	1.7	4
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10872	Biogeography and Biodiversity of the Intertidal Barnacle <i>Tetraclita</i> Species in the Gulf of Thailand and Andaman Sea – Influences of Oceanographic Currents and Pleistocene Glaciations. Frontiers in Marine Science, 2022, 8, .	1.2	6
10873	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. Insects, 2022, 13, 123.	1.0	1



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10877	Intraspecific genetic consequences of Pleistocene climate change on <i>Lupinus microphyllus</i> (Fabaceae) in the Andes. <i>Alpine Botany</i> , 0, , 1.	1.1	2
10878	Differentiation of Cold Tolerance in an Artificial Population of a Mangrove Species, <i>Kandelia obovata</i> , Is Associated With Geographic Origins. <i>Frontiers in Plant Science</i> , 2021, 12, 695746.	1.7	9
10879	Genetic diversity of meat quality related genes in Argentinean pigs. <i>Veterinary and Animal Science</i> , 2022, 15, 100237.	0.6	2
10880	RELATIONSHIP BETWEEN GENETIC AND ENVIRONMENTAL CHARACTERISTICS OF LITHUANIAN POPULATIONS OF PURPLE LOOSESTRIFE ( <i>LYTHRUM SALICARIA</i> ). <i>Journal of Environmental Engineering and Landscape Management</i> , 2022, 30, 81-93.	0.4	6
10881	Analysis of mitochondrial <i>cyt b</i> haplogroup frequencies in the population of the slab burial mortuary culture of Mongolia (ca. 1100–300 BCE). <i>American Journal of Biological Anthropology</i> , 2022, 177, 644-657.	0.6	1
10882	<i>Magnolia tamaulipana</i> : Genetic Evaluation Shows High Vulnerability in a Narrow Distribution. <i>International Journal of Plant Sciences</i> , 2022, 183, 154-167.	0.6	4
10883	Human leucocyte antigens profiling in Malay female patients with systemic lupus erythematosus: are we the same or different?. <i>Lupus Science and Medicine</i> , 2022, 9, e000554.	1.1	3
10884	Strong Philopatry, Isolation by Distance, and Local Habitat Have Promoted Genetic Structure in Heermann's Gull. <i>Diversity</i> , 2022, 14, 108.	0.7	3
10885	Local adaptation and migratory habits balance spatial genetic structure between continental and insular chestnut tiger butterflies in East Asia. <i>Molecular Ecology</i> , 2022, 31, 1864-1878.	2.0	1
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10887	Genetic diversity of Sesame ( <i>Sesamum indicum</i> L) using high throughput diversity array technology. <i>Journal of Crop Science and Biotechnology</i> , 2022, 25, 359-371.	0.7	4
10888	Forensic features and genetic structure revealed by 47 Individual Identification InDels in the Shaanxi Han population. <i>Legal Medicine</i> , 2022, 56, 102030.	0.6	0
10889	Lack of Genetic Structure Among Populations of Striped Flea Beetle <i>Phyllotreta striolata</i> (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 T	1.1	0
10890	<i>COI</i> gene-based mitochondrial DNA variation of horseshoe crab ( <i>Tachypleus gigas</i> ) reveals high genetic variation and occurrence of distinct populations in the Bay of Bengal, India, and its comparison with other populations. <i>Marine Ecology</i> , 2022, 43, .	0.4	1
10891	Genetic diversity, gene flow and hybridization in fan-shaped sponges ( <i>Phakellia</i> spp.) in the North-East Atlantic deep sea. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2022, 181, 103685.	0.6	6
10892	Two new pseudocryptic species in the medium-sized common European land snails, <i>Fruticicola</i> Held, 1838; as a result of phylogeographic analysis of <i>Fruticicola fruticum</i> (O. F. Mäÿll, 1774) (Gastropoda: Tj ETQq1 1 0.7843 14 rgBT /Ov	0.7	1

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10898	Long evolutionary history of an emerging fungal pathogen of diverse tree species in eastern Asia, Australia and the Pacific Islands. <i>Molecular Ecology</i> , 2022, 31, 2013-2031.	2.0	3
10899	Genetic connectivity in <i>Sparisoma aurofrenatum</i> (redband parrotfish): an unexpected journey. <i>Hydrobiologia</i> , 2022, 849, 1727.	1.0	4
10900	Mitochondrial DNA variation of <i>Drosophila obscura</i> (Diptera: Drosophilidae) across Europe. <i>European Journal of Entomology</i> , 0, 119, 99-110.	1.2	0
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10904	Genetic polymorphism of 27 Y-STR loci in Kazakh populations from Northern Kazakhstan. <i>Annals of Human Biology</i> , 2022, 49, 87-89.	0.4	6
10905	New Insight into the human genetic diversity in North African populations by genotyping of <i>DRD3</i> , <i>CSMD1</i> and <i>NRG1</i> genes. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2022, 10, e1871.	0.6	2
10906	Single Nucleotide Polymorphism Detection for Peach Gummosis Disease Resistance by Genome-Wide Association Study. <i>Frontiers in Plant Science</i> , 2021, 12, 763618.	1.7	4
10907	Genetic Diversity and Population Structure of Doum Palm ( <i>Hyphaene compressa</i> ) Using Genotyping by Sequencing. <i>Frontiers in Genetics</i> , 2022, 13, 762202.	1.1	0
10908	Mitochondrial DNA (CA) <sub>n</sub> dinucleotide repeat variations in Sinhalese and Vedda populations in Sri Lanka. <i>Genetica</i> , 2022, 150, 145-150.	0.5	2
10909	Discordant phylogeographic patterns between the tortoise tick <i>Hyalomma aegyptium</i> and their <i>Testudo graeca</i> hosts. <i>Ticks and Tick-borne Diseases</i> , 2022, 13, 101924.	1.1	0
10910	<i>Phytophthora capsici</i> Populations Are Structured by Host, Geography, and Fluopicolide Sensitivity. <i>Phytopathology</i> , 2022, 112, 1559-1567.	1.1	3
10911	Genetic Identification of Closely Related Endangered <i>Rhododendron</i> Species from East Asia. <i>Russian Journal of Genetics</i> , 2022, 58, 116-121.	0.2	1

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10915	Further Evidence of Population Admixture in the Serbian Honey Bee Population. Insects, 2022, 13, 180.	1.0	4
10917	Satellitome comparison of two oedipodine grasshoppers highlights the contingent nature of satellite DNA evolution. BMC Biology, 2022, 20, 36.	1.7	29
10919	Comparative population genomics in Tabebuia alliance shows evidence of adaptation in Neotropical tree species. Heredity, 2022, 128, 141-153.	1.2	1
10921	A contribution to the knowledge of the taxonomy of the subgenus Abrothrix (Angelomys) (Rodentia,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 T	0.5	2
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10923	Population data and phylogenetic structure of 19 STR loci in Chinese Hui ethnic group residing in Yunnan province of China. Legal Medicine, 2022, 56, 102044.	0.6	3
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10930	Genomic consequences of colonisation, migration and genetic drift in barn owl insular populations of the eastern Mediterranean. Molecular Ecology, 2022, 31, 1375-1388.	2.0	5
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10932	Independent evolution of intermediate bill widths in a seabird clade. Molecular Genetics and Genomics, 2022, 297, 183-198.	1.0	6

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10937	Genetic Diversity of the Symbiotic Fungus <i>Epichloa festucae</i> in Naturally Occurring Host Grass Populations. <i>Frontiers in Microbiology</i> , 2021, 12, 756991.	1.5	3
10938	Mitochondrial signatures revealed panmixia in <i>Lutjanus argentimaculatus</i> (Forssk 1775). <i>Journal of Genetics</i> , 2018, 97, 179-187.	0.4	1
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10946	Admixture and selection patterns across the European distribution of Scots pine, <i>Pinus sylvestris</i> (Pinaceae). <i>Botanical Journal of the Linnean Society</i> , 2022, 200, 416-432.	0.8	5
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10949	Population structuration and chromosomal features homogeneity in <i>Parodon nasus</i> (Characiformes). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf Ichthyology</i> , 2022, 20, .	0.5	2
10950	Cytochrome c oxidase subunit 1 gene reveals species composition and phylogenetic relationships of <i>Oesophagostomum</i> spp. infecting pigs in northeastern Brazil. <i>Brazilian Journal of Veterinary Parasitology</i> , 2022, 31, e018421.	0.2	2
10951	Molecular data reveal a complex population genetic structure for <i>Psalidodon scabripinnis</i> (Teleostei). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i>	0.6	2
10952	Little Sharks in a Big World: Mitochondrial DNA Reveals Small-scale Population Structure in the California Horn Shark ( <i>Heterodontus francisci</i> ). <i>Journal of Heredity</i> , 2022, 113, 298-310.	1.0	3
10953	Prevalence of Antifungal Resistance, Genetic Basis of Acquired Azole and Echinocandin Resistance, and Genotyping of <i>Candida krusei</i> Recovered from an International Collection. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, AAC0185621.	1.4	4
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10956	Phylogeography and Genetic Structure of the Swimming Crabs <i>Portunus sanguinolentus</i> (Herbst, 1783) in East Asia. <i>Journal of Marine Science and Engineering</i> , 2022, 10, 281.	1.2	1
10957	Hematodinium sp. infection does not drive collateral disease contraction in a crustacean host. <i>ELife</i> , 2022, 11, .	2.8	7
10958	Population differentiation of the endangered salt-marsh snail <i>Ellobium chinense</i> in Japan (Gastropoda: Ellobiidae). <i>Plankton and Benthos Research</i> , 2022, 17, 66-75.	0.2	1
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10961	Population Genetic Structure and Biodiversity Conservation of a Relict and Medicinal Subshrub <i>Capparis spinosa</i> in Arid Central Asia. <i>Diversity</i> , 2022, 14, 146.	0.7	6
10962	Consequences of the Last Glacial Period on the Genetic Diversity of Southeast Asians. <i>Genes</i> , 2022, 13, 384.	1.0	3
10963	Genetic diversity of <i>Plasmodium falciparum</i> AMA-1 antigen from the Northeast Indian state of Tripura and comparison with global sequences: implications for vaccine development. <i>Malaria Journal</i> , 2022, 21, 62.	0.8	3
10965	Potential drivers of samango monkey ( <i>Cercopithecus albogularis</i> ) population subdivision in a highly fragmented mountain landscape in northern South Africa. <i>Primates</i> , 2022, , 1.	0.7	1
10966	Resilience to Historical Human Manipulations in the Genomic Variation of Italian Wild Boar Populations. <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	6
10967	Genetic differentiation and evolutionary history of two medicinal gentians ( <i>Gentiana stipitata</i> Edgew.) and Aromatic Plants, 2022, , 100375.	0.9	2
10968	Evolutionary history and colonization patterns of the wing dimorphic grasshopper <i>Dichroplus vittatus</i> in two Argentinean biomes. <i>Scientific Reports</i> , 2022, 12, 2920.	1.6	1
10969	A genetic assessment of the population structure and demographic history of <i>Odontamblyopus lacepedii</i> (Perciformes, Amblyopinae) from the northwestern Pacific. <i>ZooKeys</i> , 2022, 1088, 1-15.	0.5	4
10970	The species of <i>Oxytropis</i> DC. of section <i>Gloecephala</i> Bunge (Fabaceae) from Northeast Asia: genetic diversity and relationships based on sequencing of the intergenic spacers of cpDNA and ITS nrDNA. <i>Genetica</i> , 2022, 150, 117-128.	0.5	3
10971	Population genetic structure of the malaria vector <i>Anopheles fluviatilis</i> species T (Diptera: Tj ETQq1 1 0.784314 rgBT /Overlock	0.7	0
10972	Can DNA help trace the local trade of pangolins? Conservation genetics of white-bellied pangolins from the Dahomey Gap (West Africa). <i>Bmc Ecology and Evolution</i> , 2022, 22, 16.	0.7	8
10973	Phylogeography of the Kura Barbel <i>Barbus cyri</i> De Filippi as Inferred from mtDNA Data. <i>Inland Water Biology</i> , 2022, 15, 11-22.	0.2	4

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10994	Genetic variation in lowland and mountain populations of <i>Tofieldia calyculata</i> and their ability to survive within low levels of genetic diversity. <i>Conservation Genetics</i> , 2022, 23, 605-622.	0.8	2
10995	Molecular testing of the São Francisco River as an ecological filter for the Brazilian large-eyed stingray <i>Hypanus marianae</i> (Dasyatidae, Myliobatiformes). <i>Hydrobiologia</i> , 0, , 1.	1.0	1
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10997	Molecular Phylogeny and Historical Biogeography of <i>Petroleuciscus</i> (Teleostei: Leuciscidae) Species in Turkey. <i>Journal of Anatolian Environmental and Animal Sciences</i> , 0, , .	0.2	1
10998	The Clam <i>Cyclina sinensis</i> (Gmelin) Phylogeography Study with 28S rRNA Gene and Potential of Nuclear rRNA Genes in Genetic Assessments of Molluscs. <i>Journal of Ocean University of China</i> , 2022, 21, 395-399.	0.6	0
10999	Multilocus phylogeography of the endemic and endangered angular angelshark ( <i>Squatina</i> ) Tj ETQq1 1 0.784314 rgBT <sub>1</sub> /Overlock 10 Tf50	1.0	1
11000	Genetic diversity and population structure of <i>Androctonus crassicauda</i> (Scorpiones: Buthidae) in different ecogeographical regions of Saudi Arabia and Iran. <i>Zoology in the Middle East</i> , 0, , 1-9.	0.2	6
11001	Spatial analysis of genetic variation in a natural population of the dark forest bee ( <i>Apis mellifera</i> ) Tj ETQq1 1 0.784314 rgBT <sub>1</sub> /Overlock 0.7 0	0.7	0
11002	Genetic diversity and phylogenetic analyses of ixodid ticks infesting cattle in northeast Thailand: the discovery of <i>Rhipicephalus microplus</i> clade C and the rarely detected <i>R. haemaphysaloides</i> . <i>Experimental and Applied Acarology</i> , 2022, 86, 535-548.	0.7	6
11003	A genomic perspective on the conservation status of the endangered Nashville crayfish ( <i>Faxonius</i> ) Tj ETQq1 1 0.784314 rgBT <sub>2</sub> /Overlock 0.8	0.8	2
11004	Genome-wide analysis suggests multiple domestication events of Chinese local pigs. <i>Animal Genetics</i> , 2022, 53, 293-306.	0.6	5
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11006	Multispecies colour polymorphisms associated with contrasting microhabitats in two Mediterranean wrasse radiations. <i>Journal of Evolutionary Biology</i> , 2022, 35, 633-647.	0.8	3
11007	Genomic Screening to Identify Food Trees Potentially Dispersed by Precolonial Indigenous Peoples. <i>Genes</i> , 2022, 13, 476.	1.0	5
11008	Extremely high diversity and endemism of chlorotypes in <i>Wikstroemia monnula</i> Hance (Thymelaeaceae) shed light on the effects of habitat heterogeneity on intraspecific differentiation in southeast China. <i>Journal of Systematics and Evolution</i> , 2023, 61, 399-413.	1.6	2
11009	Neutral and Selective Processes Shape MHC Diversity in Roe Deer in Slovenia. <i>Animals</i> , 2022, 12, 723.	1.0	5
11010	Do Genetic Drift and Gene Flow Affect the Geographic Distribution of Female Plants in Gynodioecious <i>Lobelia siphilitica</i> ?. <i>Plants</i> , 2022, 11, 825.	1.6	2
11011	Genetic monitoring of the Critically Endangered Araripe Manakin reveals low diversity and declining effective population size. <i>Condor</i> , 0, , .	0.7	1

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11016	Deep Genomic Divergence and Phenotypic Admixture of the Treefrog <i>Dendropsophus elegans</i> (Hylidae). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Evolution</i> , 2022, 10, .	1.1	4
11017	Genetic diversity and population structure of <i>Salix alba</i> across river systems in Turkey and their importance in conservation management. <i>Plant Ecology and Diversity</i> , 2021, 14, 293-304.	1.0	2
11018	Genetic variation of the giant water bug <i>Lethocerus indicus</i> (Lepeletier and Serville, 1825) (Hemiptera: Belostomatidae) collected from natural habitats in northeastern Thailand. <i>Aquatic Insects</i> , 0, , 1-12.	0.6	0
11019	Long-maintained social ecological systems and genetic diversity in coexisting insects: A case of the straw-thatched roof nesting solitary wasp <i>Symmorphus apiciornatus</i> (Hymenoptera: Vespidae). <i>Tj ETQq1 1 0 3 78431 0 rgBT /Overlock 10 Tf 50</i>	1.1	0
11020	Genetic diversity and differentiation of <i>Pealius mori</i> Takahashi (Hemiptera: Aleyrodidae) in Yunnan, China. <i>International Journal of Tropical Insect Science</i> , 2022, 42, 1123-1135.	0.4	0
11021	Haplotype analysis of the mitochondrial DNA <i>d-loop</i> region reveals the maternal origin and historical dynamics among the indigenous goat populations in east and west of the Democratic Republic of Congo. <i>Ecology and Evolution</i> , 2022, 12, e8713.	0.8	2
11022	Limited gene flow and pronounced population genetic structure of Eastern Massasauga ( <i>Sistrurus</i> ). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	1.1	0
11023	Linkage disequilibrium and population structure in a core collection of <i>Brassica napus</i> (L.). <i>PLoS ONE</i> , 2022, 17, e0250310.	1.1	9
11024	Glacial Expansion or Interglacial Expansion? Contrasting Demographic Models of Four Cold-Adapted Fir Species in North America and East Asia. <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	1
11025	Establishment, Genetic Diversity, and Habitat Suitability of <i>Aedes albopictus</i> Populations from Ecuador. <i>Insects</i> , 2022, 13, 305.	1.0	5
11027	Landscape genetics of the tropical willow <i>Salix humboldtiana</i> : influence of climate, salinity, and orography in an altitudinal gradient. <i>American Journal of Botany</i> , 2022, 109, 456-469.	0.8	3
11028	Immunogenetic profile of MIC (A, B) HLA loci linked to MHC antigenic complex in Russians of the Chelyabinsk Region. <i>Medical Immunology (Russia)</i> , 2022, 24, 41-52.	0.1	0
11029	Quaternary geomorphological and climatic changes associated with the diversification of Iberian freshwater fishes: The case of the genus <i>Cobitis</i> (Cypriniformes, Cobitidae). <i>Ecology and Evolution</i> , 2022, 12, e8635.	0.8	4
11030	Does the Kuroshio Current transport planktonic larvae of the hydrothermal-vent crab <i>Xenograpsus</i> ? Takeda & Kurata, 1977 (Decapoda: Brachyura: Grapsoidea?). <i>Journal of Crustacean Biology</i> , 2022, 42, .	0.3	0

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11031	Conservation Genetics of Mediterranean Brown Trout in Central Italy (Latium): A Multi-Marker Approach. <i>Water</i> (Switzerland), 2022, 14, 937.	1.2	10
11032	Convergent selection of a WD40 protein that enhances grain yield in maize and rice. <i>Science</i> , 2022, 375, eabg7985.	6.0	110
11033	Strong Population Genetic Structure of <i>Phrynocephalus versicolor</i> in Mongolia. <i>Herpetologica</i> , 2022, 78, .	0.2	0
11034	Phylogeography of the widespread New Zealand tree lancewood/horoeka ( <i>Pseudopanax</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.8	3
11035	Genetic and morphological variation of <i>Vespa velutina nigrithorax</i> which is an invasive species in a mountainous area. <i>Scientific Reports</i> , 2022, 12, 4737.	1.6	2
11036	Genetic evidence of stable northward extension of <i>Pinus thunbergii</i> Parl. forests in the Democratic People's Republic of Korea. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 2105-2114.	0.8	4
11037	Current Genetic Status of Nagaremon-charr, a Threatened Morphotype of <i>Salvelinus leucomaenis</i> in the Ane River, Lake Biwa System, Central Japan, With Comments on Its Conservation. <i>Zoological Science</i> , 2022, 39, .	0.3	2
11038	Rangewide Population Structure of the Clearnose Skate. <i>Transactions of the American Fisheries Society</i> , 0, , .	0.6	0
11039	Reduced genetic diversity associated with the northern expansion of an amphibian species with high habitat specialization, <i>Ascaphus truei</i> , resolved using two types of genetic markers. <i>Ecology and Evolution</i> , 2022, 12, e8716.	0.8	0
11040	Molecular phylogenetic and morphometric analysis of population structure and demography of endangered threadfin fish <i>Eleutheronema</i> from Indo-Pacific waters. <i>Scientific Reports</i> , 2022, 12, 3455.	1.6	4
11041	Population genetic analysis reveals secondary contact between <i>Eriocheir sinensis</i> and <i>E. japonica</i> in South Korea. <i>Genes and Genomics</i> , 2022, , 1.	0.5	1
11042	Reproductive homing and fine-scaled genetic structuring of anadromous Baltic Sea perch ( <i>Perca</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.0	4
11043	Are Roma People Descended from the Punjab Region of Pakistan: A Y-Chromosomal Perspective. <i>Genes</i> , 2022, 13, 532.	1.0	2
11044	Deep genome-wide phylogeographic structure indicates cryptic diversity in the Middle Spotted Woodpecker ( <i>Dendrocoptes medius</i> ). <i>Ibis</i> , 2022, 164, 719-734.	1.0	0
11045	Phylogeography of the parasitic mite <i>Laelaps agilis</i> in Western Palearctic shows lineages lacking host specificity but possessing different demographic histories. <i>BMC Zoology</i> , 2022, 7, .	0.3	8
11046	Influence of anthropogenic pressure on the genetic diversity and chromosomal instability of an endangered forest-specialist anuran. <i>Hydrobiologia</i> , 0, , 1.	1.0	0
11047	Riverscape Genomics Clarifies Neutral and Adaptive Evolution in an Amazonian Characin Fish ( <i>Triportheus albus</i> ). <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	2
11048	Mitogenomic phylogenetics and population genetics of several taxa of agouties ( <i>Dasyprocta</i> sp.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.6	1

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11049	Gone With the Water: The Loss of Genetic Variability in Black and Gold Howler Monkeys ( <i>Alouatta</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	0
11050	Population Genetics Reveals That the Western Tianshan Mountains Populations of <i>Agrilus mali</i> (Coleoptera: Buprestidae) May Have Not been Recently Introduced. <i>Frontiers in Genetics</i> , 2022, 13, 857866.	1.1	2
11051	Ancient <scp>DNA</scp> analysis reveals temporal and geographical patterns of mitochondrial diversity in <scp>pre-Hispanic</scp> populations from Central Argentina. <i>American Journal of Human Biology</i> , 2022, 34, e23733.	0.8	2
11052	Patterns of genetic variation on wild pig (<i>Sus scrofa</i>) populations over a complete range of the species in Argentina. <i>Mammalia</i> , 2022, 86, 359-372.	0.3	5
11053	Circum-Saharan Prehistory through the Lens of mtDNA Diversity. <i>Genes</i> , 2022, 13, 533.	1.0	5
11055	Limited genetic diversity and high differentiation in <i>Angelica dahurica</i> resulted from domestication: insights to breeding and conservation. <i>BMC Plant Biology</i> , 2022, 22, 141.	1.6	12
11056	Invasion history of <i>Orosanga japonica</i> (Melichar, 1898) (Hemiptera: Ricaniidae) in Turkey, comparisons with other Ricaniidae family members using molecular tools and modeling of potential global distribution. <i>Turkiye Entomoloji Dergisi</i> , 2022, 46, 99-114.	0.1	1
11057	Genetic Connectivity and Diversity of a Protected, Habitat-Forming Species: Evidence Demonstrating the Need for Wider Environmental Protection and Integration of the Marine Protected Area Network. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	2
11058	Seamounts and oceanic currents drive the population structure of <i>Octopus insularis</i> in the Southwest Tropical Atlantic. <i>Aquatic Ecology</i> , 2022, 56, 1143-1155.	0.7	2
11059	Phylogeographical Analyses of a Relict Fern of Palaeotropical Flora ( <i>Vandenboschia speciosa</i> ): Distribution and Diversity Model in Relation to the Geological and Climate Events of the Late Miocene and Early Pliocene. <i>Plants</i> , 2022, 11, 839.	1.6	1
11060	Taxonomic re-appraisal for toothfish (<scp><i>Dissostichus</i></scp>: <i>Nototothenioidea&lt;/scp&gt; across the &lt;scp&gt;Antarctic Polar Front&lt;/scp&gt; using genomic and morphological studies. <i>Journal of Fish Biology</i>, 2022, 100, 1158-1170.</i>	0.7	10
11061	Ancient mitochondrial genomes recovered from small vertebrate bones through minimally destructive DNA extraction: Phylogeography of the New Zealand gecko genus <i>Hoplodactylus</i>. <i>Molecular Ecology</i> , 2023, 32, 2964-2984.	2.0	7
11062	The architecture of assisted colonisation in sea turtles: building new populations in a biodiversity crisis. <i>Nature Communications</i> , 2022, 13, 1580.	5.8	6
11063	Genetic differentiation between Czech and Norwegian raspberry populations: new options for breeding. <i>Euphytica</i> , 2022, 218, 1.	0.6	1
11064	Selection and localised genetic structure in the threatened Manauense Harlequin Frog ( <i>Bufonidae</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.8	0
11065	Phylogeographic structure and population demography of the leopard mandarin fish ( <i>Siniperca</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.4	1
11066	Assessment of genotyping markers in the molecular characterization of a population of clinical isolates of <i>Fusarium</i> in Colombia. <i>Biomedica</i> , 2022, 42, 18-30.	0.3	1
11067	DNA barcoding and population genetic structure of the red palm weevil, <i>Rhynchophorus ferrugineus</i> (Coleoptera: Curculionidae) in Egypt based on mtDNA sequencing. <i>Biologia (Poland)</i> , 2022, 77, 1017-1025.	0.8	4

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11068	Phylogeography of the endangered orchids <i>Cypripedium japonicum</i> and <i>Cypripedium formosanum</i> in East Asia: Deep divergence at intra- and interspecific levels. <i>Taxon</i> , 2022, 71, 733-757.	0.4	4
11069	Molecular diversity of exotic durian ( <i>Durio</i> spp.) germplasm: a case study of Kalimantan, Indonesia. <i>Journal of Genetic Engineering and Biotechnology</i> , 2022, 20, 39.	1.5	7
11070	Intraspecific evolution of sexually dimorphic characters in a female diving beetle can be promoted by demographic history and temperature. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 1003-1015.	1.1	1
11071	Population Genetic Analysis of the Threatened Plant <i>Leavenworthia exigua</i> var. <i>laciniata</i> (Brassicaceae) Reveals Virtually No Genetic Diversity and a Unique Mating System. <i>Frontiers in Conservation Science</i> , 2022, 3, .	0.9	1
11072	Sociogenetic structure, reproductive strategies and queen replacement in the erratic ant ( <i>Tapinoma erraticum</i> ). <i>Biological Journal of the Linnean Society</i> , 0, .	0.7	0
11073	Challenging ancient DNA results about putative HLA protection or susceptibility to <i>Yersinia pestis</i> . <i>Molecular Biology and Evolution</i> , 2022, .	3.5	1
11074	Historical connections between Atlantic Forest and Amazonia drove genetic and ecological diversity in <i>Lithobates palmipes</i> (Anura, Ranidae). <i>Systematics and Biodiversity</i> , 2022, 20, 1-19.	0.5	3
11075	Maintenance of Genetic Diversity of Black Sea Bream despite Unmonitored and Large-Scale Hatchery Releases. <i>Biology</i> , 2022, 11, 554.	1.3	3
11076	Signatures of selection and drivers for novel mutation on transmission-blocking vaccine candidate Pfs25 gene in western Kenya. <i>PLoS ONE</i> , 2022, 17, e0266394.	1.1	2
11077	Subtle limits to connectivity revealed by outlier loci within two divergent metapopulations of the deep-sea hydrothermal gastropod <i>Ifremeria nautiliei</i> . <i>Molecular Ecology</i> , 2022, 31, 2796-2813.	2.0	7
11078	Genetic insights into the range expansion of the cattle egret (Pelecaniformes: Ardeidae) in Brazil and population differentiation between the native and colonized areas. <i>Biological Journal of the Linnean Society</i> , 0, .	0.7	0
11079	Molecular epidemiology of <i>Ascaris</i> species recovered from humans and pigs in Cameroon. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2022, 116, 949-958.	0.7	0
11080	Microevolution of <i>Pieris</i> butterfly genes involved in host plant adaptation along a host plant community cline. <i>Molecular Ecology</i> , 2022, 31, 3083-3097.	2.0	3
11081	Use of Investigator 24plex GO! To analyse allele frequencies of 21 autosomal STRs in the population of Veracruz state, Mexico. <i>Annals of Human Biology</i> , 2022, 49, 164-169.	0.4	1
11082	Incidence of Coffee Leaf Rust in Vietnam, Possible Original Sources and Subsequent Pathways of Migration. <i>Frontiers in Plant Science</i> , 2022, 13, 872877.	1.7	5
11083	Population genetic structure and dispersal of <i>Pinus occidentalis</i> in the Dominican Republic by chloroplastic SSR, with implications for its conservation, management, and reforestation. <i>Canadian Journal of Forest Research</i> , 2022, 52, 553-560.	0.8	0
11084	Molecular insights into the population structure and haplotype network of <i>Theileria annulata</i> based on the small-subunit ribosomal RNA (18S rRNA) gene. <i>Infection, Genetics and Evolution</i> , 2022, 99, 105252.	1.0	10
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11087	Ilbâ€RADâ€sequencing coupled with random forest classification indicates regional population structuring and sexâ€specific differentiation in salmon lice ( <i>Lepeophtheirus salmonis</i> ). Ecology and Evolution, 2022, 12, e8809.	0.8	2
11088	Assessing the Speciation of <i>Lutjanus campechanus</i> and <i>Lutjanus purpureus</i> through Otolith Shape and Genetic Analyses. Fishes, 2022, 7, 85.	0.7	2
11089	An evaluation of the genetic connectivity and temporal stability of the blue and red shrimp <i>Aristeus antennatus</i> : a case study of spawning femalesâ€™ grounds in the Western Mediterranean Sea. Hydrobiologia, 2022, 849, 2043-2055.	1.0	2
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11091	Genetic Analysis Reveals a Distinct Lineage of Hog Deer ( <i>Axis porcinus</i> ) in Kratie Province, Cambodia. Journal of Heredity, 2022, 113, 444-452.	1.0	0
11092	Multiple genetic analyses for Chinese Hunan Han population via 46 A-STRs. Annals of Human Biology, 2022, , 1-26.	0.4	0
11093	Genetic analyses reveal regional structure and demographic expansion of the predominant tea pest <i>Empoasca onukii</i> (Hemiptera: Cicadellidae) in China. Pest Management Science, 2022, 78, 2838-2850.	1.7	6
11094	Comparison of genetic diversity and population structure of eight <i>Macrobrachium nipponense</i> populations in China based on D-loop sequences. Aquaculture Reports, 2022, 23, 101086.	0.7	6
11095	Characterization of Genetic Diversity and Variation in Pathogenicity of the Rice False Smut Pathogen <i>Ustilaginoidea virens</i> from a Single Source. Plant Disease, 2022, 106, 2648-2655.	0.7	4
11096	Pollinator sharing, copollination, and speciation by host shifting among six closely related dioecious fig species. Communications Biology, 2022, 5, 284.	2.0	11
11097	Unraveling the population structure of the sugarcane borer, <i>Diatraea saccharalis</i> , in Argentina. Entomologia Experimentalis Et Applicata, 0, , .	0.7	2
11098	Dissecting a Geographical Colourful Tapestry: Phylogeography of the Colour Polymorphic Spider <i>Gasteracantha cancriformis</i> . Journal of Zoological Systematics and Evolutionary Research, 2022, 2022, 1-11.	0.6	4
11099	Genomic insights into the genotypeâ€environment mismatch and conservation units of a Qinghaiâ€Tibet Plateau endemic cypress under climate change. Evolutionary Applications, 2022, 15, 919-933.	1.5	7
11100	The right tool for the right question: contrasting biogeographic patterns in the notothenioid fish <i>Harpagifer</i> spp. along the Magellan Province. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, 20212738.	1.2	4
11101	Genetic population structure defines wild boar as an urban exploiter species in Barcelona, Spain. Science of the Total Environment, 2022, 833, 155126.	3.9	7
11102	Post-Austronesian migrational wave of West Polynesians to Micronesia. Gene, 2022, 823, 146357.	1.0	1
11103	Regional-scale genetic differentiation of the stony coral <i>Desmophyllum dianthus</i> in the southwest Pacific Ocean is consistent with regional-scale physico-chemical oceanography. Deep-Sea Research Part I: Oceanographic Research Papers, 2022, 183, 103739.	0.6	2



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11105	Genome-wide SNPs reveal the fine-scale population structure of <i>Laodelphax striatellus</i> in China using double-digest restriction site-associated DNA sequencing. <i>Genomics</i> , 2022, 114, 110329.	1.3	2
11106	Large-scale survey for canine vector-borne parasites in free-ranging dogs and foxes from six diverse bioclimatic regions of Chile. <i>Veterinary Parasitology: Regional Studies and Reports</i> , 2022, 30, 100721.	0.3	6
11107	Population genetic structure of the elephant tick <i>Amblyomma tholloni</i> from different elephant populations in Kenya. <i>Ticks and Tick-borne Diseases</i> , 2022, 13, 101935.	1.1	2
11108	Molecular data confirm <i>Triatoma pallidipennis</i> Stål, 1872 (Hemiptera: Reduviidae: Triatominae) as a novel cryptic species complex. <i>Acta Tropica</i> , 2022, 229, 106382.	0.9	9
11109	Genetic diversity and growth-related traits in <i>Penaeus vannamei</i> after ten years without introducing new stocks into Cuba. <i>Aquaculture</i> , 2022, 554, 738097.	1.7	2
11110	Screening and selection of 21 novel microhaplotype markers for ancestry inference in ten Chinese subpopulations. <i>Forensic Science International: Genetics</i> , 2022, 58, 102687.	1.6	12
11111	Distribution of HLA-A, -C, -B, -DRB1, and -DQB1 polymorphisms in the Korean minority in Kazakhstan, and relatedness to neighboring and distant populations. <i>Gene</i> , 2022, 823, 146386.	1.0	2
11112	The tangled evolutionary history of a long-debated Mesoamerican taxon: The Velazquez Woodpecker ( <i>Melanerpes santacruzi</i> , Aves: Picidae). <i>Molecular Phylogenetics and Evolution</i> , 2022, 170, 107445.	1.2	2
11113	Mosaic or melting pot: The use of monogeneans as a biological tag and magnifying glass to discriminate introduced populations of Nile tilapia in sub-Saharan Africa. <i>Genomics</i> , 2022, 114, 110328.	1.3	13
11114	Genetic variation of 17 autosomal STR loci in the Lahu population from Yunnan and phylogenetic structure exploration among 28 populations. <i>Legal Medicine</i> , 2022, 56, 102050.	0.6	1
11115	The uplift of the Hengduan Mountains contributed to the speciation of three <i>Rhododendron</i> species. <i>Global Ecology and Conservation</i> , 2022, 35, e02085.	1.0	3
11116	Population genetic characterization of the endangered dung beetle <i>Copris tripartitus</i> (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.4	3
11117	Fingerprinting, structure, and genetic relationships among selected accessions of blue honeysuckle ( <i>Lonicera caerulea</i> L.) from European collections. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2022, 34, e00721.	2.1	3
11118	Molecular analyses confirm the coexistence of <i>Fasciola gigantica</i> and parthenogenetic <i>Fasciola</i> in the Philippines. <i>Parasitology International</i> , 2022, 88, 102562.	0.6	3
11119	Application of machine learning for ancestry inference using multi-InDel markers. <i>Forensic Science International: Genetics</i> , 2022, 59, 102702.	1.6	3
11120	Updated connectivity assessment for the scalloped hammerhead ( <i>Sphyrna lewini</i> ) in Pacific and Indian Oceans using a multi-marker genetic approach. <i>Fisheries Research</i> , 2022, 251, 106305.	0.9	6
11121	Characterization of simple sequence repeat loci for <i>Peltigera membranacea</i> (lichenized) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.5	0

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11124	Genetic diversity and selective sweeps in historical and modern Canadian spring wheat cultivars using the 90K SNP array. <i>Scientific Reports</i> , 2021, 11, 23773.	1.6	10
11125	River Reorganization Affects Populations of Dwarf Cichlid Species ( <i>Apistogramma</i> Genus) in the Lower Negro River, Brazil. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	1
11126	Fish out of water: Genomic insights into persistence of rainbowfish populations in the desert. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 171-183.	1.1	10
11127	Demographic history and genetic diversity of wild African harlequin quail ( <i>Coturnix delegorguei</i> )	0.8	2
11128	Damming shapes genetic patterns and may affect the persistence of freshwater fish populations. <i>Freshwater Biology</i> , 2022, 67, 603-618.	1.2	8
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11131	Cryptic niche differentiation of novel sediment ecotypes of <i>Ruegeria pomeroyi</i> correlates with nitrate respiration. <i>Environmental Microbiology</i> , 2022, 24, 390-403.	1.8	5
11132	Contrasting genetic responses to habitat fragmentation for two Lycaenid butterfly species. <i>Insect Conservation and Diversity</i> , 2022, 15, 337-347.	1.4	0
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11136	Genetic diversity analysis of cattle genetic groups of Kerala state using microsatellite data. <i>Animal Biotechnology</i> , 2021, , 1-9.	0.7	0
11137	Scanning electron microscopy of <i>Quilonia renniei</i> from Asian elephants revealing variation in coronal leaflet number. <i>Parasitology</i> , 2022, 149, 529-533.	0.7	0
11138	Dual Host and Pathogen RNA-Seq Analysis Unravels Chicken Genes Potentially Involved in Resistance to Highly Pathogenic Avian Influenza Virus Infection. <i>Frontiers in Immunology</i> , 2021, 12, 800188.	2.2	7
11139	Comparative analysis of genetic diversity in Norway spruce ( <i>Picea abies</i> ) clonal seed orchards and seed stands. <i>Notulae Botanicae Horti Agrobotanici Cluj-Napoca</i> , 2021, 49, 12575.	0.5	1
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11141	DNA barcodes evidence the contact zone of eastern and western caddisfly lineages in the Western Carpathians. <i>Scientific Reports</i> , 2021, 11, 24020.	1.6	2

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11142	It takes two to tango – Phylogeography, taxonomy and hybridization in grass snakes and dice snakes (Serpentes: Natricidae: <i>Natrix natrix</i> , <i>N. tessellata</i> ). <i>Vertebrate Zoology</i> , 0, 71, 813-834.	2.0	16
11143	Ancient DNA reveals the maternal genetic history of East Asian domestic pigs. <i>Journal of Genetics and Genomics</i> , 2022, 49, 537-546.	1.7	4
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11146	Genetic diversity and structure of captive gentoo penguin populations in Japan. <i>Zoo Biology</i> , 2021, , .	0.5	0
11147	Insights Into the Environmental Impact on Genetic Structure and Larval Dispersal of Crown-of-Thorns Starfish in the South China Sea. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	5
11148	Genetic Diversity of the Surubim-Do-Iguaçu, a Giant Catfish Species Threatened with Extinction: Recommendations for Species Conservation. <i>Diversity</i> , 2022, 14, 16.	0.7	1
11149	Homogenized Phylogeographic Structure across the Indo-Burma Ranges of a Large Monoecious Fig, <i>Ficus altissima</i> Blume. <i>Diversity</i> , 2021, 13, 654.	0.7	5
11150	From Settlers to Subspecies: Genetic Differentiation in Commerson's Dolphins Between South America and the Kerguelen Islands. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	1
11151	<i>Juniperus excelsa</i> s. str. in crimea – differentiation and history inferred from genetic and morphological markers. <i>Folia Forestalia Polonica, Series A</i> , 2021, 63, 276-288.	0.1	1
11152	Divergencia genética en musarañas (Mammalia: Soricidae) de los bosques húmedos de montaña al norte del Neotrópico. <i>Revista Mexicana De Biodiversidad</i> , 2021, 92, 923781.	0.4	5
11154	Population genomics indicates microrefuges and riverine barriers for a southern South American grassland nightshade. <i>Journal of Biogeography</i> , 2022, 49, 51-65.	1.4	7
11156	Genomic analysis of red snapper, <i>Lutjanus campechanus</i> , population structure in the U.S. Atlantic and Gulf of Mexico. <i>ICES Journal of Marine Science</i> , 2022, 79, 12-21.	1.2	5
11157	Population Data of D6S1043, Penta D and Penta E Loci in Calabria (South of Italy). <i>Journal of Basic &amp; Applied Sciences</i> , 0, 16, 74-78.	0.0	1
11158	The role of sex-biased dispersion in promoting mitonuclear discordance in <i>Partamona helleri</i> (Hymenoptera: Apidae: Meliponini). <i>Biological Journal of the Linnean Society</i> , 2022, 136, 423-435.	0.7	2
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11785	Polygenic analysis of genetic susceptibility to essential hypertension. <i>Arterial Hypertension (Russian)</i> Tj ETQq1 1 0.784314 rgBT /Overlock 0.1	0.1	0
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11791	RADseq Data Suggest Occasional Hybridization between <i>Microcebus murinus</i> and <i>M. ravelobensis</i> in Northwestern Madagascar. <i>Genes</i> , 2022, 13, 913.	1.0	1
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11803	Characterization, Selection, and Trans-Species Polymorphism in the MHC Class II of Heermannâ€™s Gull ( <i>Charadriiformes</i> ). <i>Genes</i> , 2022, 13, 917.	1.0	0
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11808	HLA Genotypes and Type 1 Diabetes and Its Relationship to Reported Race/Skin Color in Their Relatives: A Brazilian Multicenter Study. <i>Genes</i> , 2022, 13, 972.	1.0	1

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11810	Population and Landscape Genetics Provide Insights Into Species Conservation of Two Evergreen Oaks in Qinghaiâ€Tibet Plateau and Adjacent Regions. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	1
11811	Something Fishy about Siamese Fighting Fish ( <i>Betta splendens</i> ) Sex: Polygenic Sex Determination or a Newly Emerged Sex-Determining Region?. <i>Cells</i> , 2022, 11, 1764.	1.8	9
11812	Short Communication: Assessment of cogongrass ( <i>Imperata cylindrica</i> (L.) P.Beauv.) genetic variation in Java, Indonesia using <i>atpB-rbcL</i> and <i>trnL-F</i> intergenic spacer. <i>Biodiversitas</i> , 2022, 23, .	0.2	1
11813	Worldwide phylogeography of roughâ€toothed dolphins ( <i>Steno bredanensis</i> ) provides evidence for subspecies delimitation. <i>Marine Mammal Science</i> , 2022, 38, 1371-1397.	0.9	5
11814	Molecular detection of <i>Metastrongylus salmi</i> eggs from pigs in low-resource communities in the state of PiauÃ; northeastern Brazil. <i>Journal of Veterinary Diagnostic Investigation</i> , 0, , 104063872210921.	0.5	2
11815	Disassociation of social and sexual partner relationships in a gibbon population with stable oneâ€male twoâ€female groups. <i>American Journal of Primatology</i> , 2022, 84, .	0.8	2
11816	Forensic Efficiency Estimation of a Homemade Six-Color Fluorescence Multiplex Panel and In-Depth Anatomy of the Population Genetic Architecture in Two Tibetan Groups. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
11817	Genetic Structure of Native Blue Honeysuckle Populations in the Western and Eastern Eurasian Ranges. <i>Plants</i> , 2022, 11, 1480.	1.6	4
11818	Genetic Diversity of <i>Rhanterium eppaposum</i> Oliv. Populations in Kuwait as Revealed by GBS. <i>Plants</i> , 2022, 11, 1435.	1.6	4
11819	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
11821	Evolution of an Apomixis-Specific Allele Class in Supernumerary Chromatin of Apomictic <i>Boechera</i> . <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	3
11822	EST-Microsatellite Types and Structural Scenarios in European Hake Fisheries. <i>Animals</i> , 2022, 12, 1462.	1.0	2
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11824	Extremely Low mtDNA Diversity and High Genetic Differentiation Reveal the Precarious Genetic Status of Dugongs in New Caledonia, South Pacific. <i>Journal of Heredity</i> , 2022, 113, 516-524.	1.0	6
11825	Identification of new stock [ <i>Matthiola incana</i> (L.) R. Br.] cultivars with high fertility through morphological and molecular markers. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 2719-2730.	0.8	3
11826	Development and characterization of microsatellite markers, genetic diversity and population structure analysis in <i>Sapota</i> ( <i>Manilkara zapota</i> (L.) P. Royen). <i>Genetic Resources and Crop Evolution</i> , 0, , .	0.8	0
11827	Hybridization and low genetic diversity in the endangered Alabama redâ€bellied turtle ( <i>Pseudemys</i> ) TJ ETQq1 1 0.784314 4gBT /Overl	0.8	0

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11836	Temporal dynamics of mildly deleterious nonsynonymous substitutions in mitochondrial gene sequences in rodents and moles. <i>Genes and Genetic Systems</i> , 2022, 97, 111-121.	0.2	2
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11838	The first evidence for genetic differentiation of a non-native false mussel <i>Mytilopsis sallei</i> (R��cluz, 1849) in southern Thailand.. <i>Molluscan Research</i> , 2022, 42, 110-114.	0.2	2
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11840	Dramatic impact of future climate change on the genetic diversity and distribution of ecologically relevant Western Mediterranean <i>Carex</i> (Cyperaceae). <i>PeerJ</i> , 0, 10, e13464.	0.9	2
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11843	Cold��adaptive evolution at the reproductive stage in <i>Gengjaponica</i> subspecies reveals the role of <i>OsMAPK3</i> and <i>OsLEA9</i> . <i>Plant Journal</i> , 2022, 111, 1032-1051.	2.8	13
11844	Genetic differentiation that is exceptionally high and unexpectedly sensitive to geographic distance in the absence of gene flow: Insights from the genus <i>Eranthis</i> in East Asian regions. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	1
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11846	Genetic diversity and population structure of <i>Caryopteris mongholica</i> revealed by reduced representation sequencing. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
11847	Cultural transmission of traditional songs in the Ryukyu Archipelago. <i>PLoS ONE</i> , 2022, 17, e0270354.	1.1	0
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11849	Diversity and metabolomic characterization of <i>Penicillium expansum</i> isolated from apples grown in Argentina and Spain. <i>Fungal Biology</i> , 2022, 126, 547-555.	1.1	5
11850	Combining phylogeography and landscape genetics reveals genetic variation and distribution patterns of <i>Stipa breviflora</i> populations. <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2022, 293, 152102.	0.6	1
11851	Legacy of supervolcanic eruptions on population genetic structure of brown kiwi. <i>Current Biology</i> , 2022, 32, 3389-3397.e8.	1.8	3
11852	Genetic diversity, gene flow, and differentiation among wild, semiwild, and landrace chile pepper ( <i>Capsicum annuum</i> ) populations in Oaxaca, Mexico. <i>American Journal of Botany</i> , 2022, 109, 1157-1176.	0.8	14
11853	SNP Genotyping Characterizes the Genome Composition of the New Baisary Fat-Tailed Sheep Breed. <i>Animals</i> , 2022, 12, 1468.	1.0	3



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11858	Genetic diversity and demography of <i>Bufo japonicus</i> and <i>B. torrenticola</i> (Amphibia: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.9	5
11859	From <i>STRs</i> to <i>SNPs</i> via <i>ddRAD</i> seq: Geographic assignment of confiscated tortoises at reduced costs. <i>Evolutionary Applications</i> , 2022, 15, 1344-1359.	1.5	2
11860	Genetic Diversity and Structure of Persian Walnut ( <i>Juglans regia</i> L.) in Pakistan: Implications for Conservation. <i>Plants</i> , 2022, 11, 1652.	1.6	12
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11862	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
11863	Genetic structure of American bullfrog populations in Brazil. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
11864	Genetic diversity analysis of <i>Camellia fascicularis</i> H. T. Chang based on SSR markers. <i>Journal of Applied Research on Medicinal and Aromatic Plants</i> , 2022, 31, 100404.	0.9	0
11865	High levels of inbreeding with spatial and host-associated structure in lice of an endangered freshwater seal. <i>Molecular Ecology</i> , 2022, 31, 4593-4606.	2.0	10
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11869	DNA Identification and Diversity of the Vector Mosquitoes <i>Culex pipiens</i> s.s. and <i>Culex torrentium</i> in Belgium (Diptera: Culicidae). <i>Diversity</i> , 2022, 14, 486.	0.7	4
11870	Mitochondrial Lineage Diversity and Phylogeography of <i>Daphnia</i> ( <i>Daphnia</i> ) (Crustacea: Cladocera) in North-East Russia. <i>Water (Switzerland)</i> , 2022, 14, 1946.	1.2	1
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11874	Population Genetic Structure of the Bean Leaf Beetle <i>Ootheca mutabilis</i> (Coleoptera: Chrysomelidae) in Uganda. <i>Insects</i> , 2022, 13, 543.	1.0	2
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11876	Helena's Many Daughters: More Mitogenome Diversity behind the Most Common West Eurasian mtDNA Control Region Haplotype in an Extended Italian Population Sample. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6725.	1.8	3
11877	Tracking population genetic signatures of local extinction with herbarium specimens. <i>Annals of Botany</i> , 2022, 129, 857-868.	1.4	8
11878	Genetics, Morphometrics and Health Characterization of Green Turtle Foraging Grounds in Mainland and Insular Chile. <i>Animals</i> , 2022, 12, 1473.	1.0	1
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11880	An efficient ancestry informative SNPs panel for further discriminating East Asian populations. <i>Electrophoresis</i> , 2022, 43, 1774-1783.	1.3	2
11881	Asymmetric character displacement in mixed oak stands. <i>New Phytologist</i> , 2022, 236, 1212-1224.	3.5	9
11882	Filogeografía de <i>Tigridia durangensis</i> (Tigridieae: Iridaceae), una especie endémica de la Zona de Transición Mexicana. <i>Botanical Sciences</i> , 2022, 100, 1040-1057.	0.3	1
11883	Forensic efficacy evaluation and genetic structure exploration of the Yunnan Miao group by a multiplex InDel panel. <i>Electrophoresis</i> , 2022, 43, 1765-1773.	1.3	4
11884	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
11885	Effects of Late Pleistocene Climatic Fluctuations on the Phylogeographic and Demographic History of Japanese Scud (Decapoda: Scudidae). <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	0
11886	Spatial Variation of <i>Acanthophlebia cruentata</i> (Ephemeroptera), a Mayfly Endemic to the North Island of Aotearoa, New Zealand. <i>Insects</i> , 2022, 13, 567.	1.0	0
11887	Population structure of blackfin tuna ( <i>Thunnus atlanticus</i> ) in the western Atlantic Ocean inferred from microsatellite loci. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
11888	Significant genetic structure in <i>Macrobathra</i> moths feeding on <i>Acacia auriculiformis</i> – implications for prioritising biological control agents. <i>Biological Control</i> , 2022, 172, 104969.	1.4	1
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11890	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

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11891	Development and validation of a low-density SNP panel for paternity and kinship analysis and evaluation of genetic variability and structure of commercial Pacific white shrimp ( <i>Litopenaeus</i> ) Tj ETQq0 0 0 rgBT /Overlock 30 Tf 50 73		
11892	Evidence of mitochondrial capture in Australian glass shrimp ( <i>Paratya australiensis</i> ) in south-eastern Queensland. <i>Marine and Freshwater Research</i> , 2022, , .	0.7	0
11893	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
11894	Mitochondrial diversity and population structure of grass carp (<i>Ctenopharyngodon idella</i>) in the Pearl River after anthropogenic release. <i>Knowledge and Management of Aquatic Ecosystems</i> , 2022, , 14.	0.5	1
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11897	Identification of confiscated pangolin for conservation purposes through molecular approach. <i>Journal of Threatened Taxa</i> , 2022, 14, 21127-21139.	0.1	1
11898	Phylogeography of the economic seaweeds <i>Chondrus</i> (Gigartinales.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 7 6 2022, 37, 135-147.	0.9	6
11899	Türkçe Mezopotamya Dikenli Yaban Balık (Mastacembelus mastacembelus) (Teleostei:) Tj ETQq0 0 0 rgBT /Overlock 0.2 0 Muğendislik Bilimleri Dergisi, 2022, 3, 34-39.	0.2	0
11900	Red Junglefowl Resource Management Guide: Bioresource Reintroduction for Sustainable Food Security in Thailand. <i>Sustainability</i> , 2022, 14, 7895.	1.6	5
11901	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
11902	Morphological variation and reproductive isolation in the <i>Hetaerina americana</i> species complex. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
11903	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
11904	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
11905	The Diversity of <i>Melia azedarach</i> L. from China Based on Transcriptome-Developed SSR Marker. <i>Forests</i> , 2022, 13, 1011.	0.9	5
11906	Conservation genomics of urban populations of Streamside Salamander ( <i>Ambystoma barbouri</i> ). <i>PLoS ONE</i> , 2022, 17, e0260178.	1.1	2
11907	Phylogeography of <i>Tridentiger bifasciatus</i> (Gobiidae) in the Northwestern Pacific. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	0
11908	Genetic Stock Structure and Differentiation of Green Turtle, <i>Chelonia mydas</i> , Rookeries on St. Croix, US Virgin Islands. <i>Chelonian Conservation and Biology</i> , 2022, 21, .	0.1	0

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11912	Extended population genetic analysis of 12 X-STRs “ Exemplified using a Norwegian population sample. <i>Forensic Science International: Genetics</i> , 2022, 60, 102745.	1.6	3
11914	Identifying cryptic species of <i>Planococcus</i> infesting vineyards to improve control efforts. <i>Journal of Pest Science</i> , 0, , .	1.9	0
11915	Phylogeographical Analysis of the Freshwater Gudgeon <i>Huigobio chenhshienensis</i> (Cypriniformes:) Tj ETQq1 1 0.784314 rgBT /Overloc	1.1	4
11916	Genome-wide SNPs reveal fine-scale genetic structure in ornate spiny lobster <i>Panulirus ornatus</i> throughout Indo-West Pacific Ocean. <i>ICES Journal of Marine Science</i> , 2022, 79, 1931-1941.	1.2	5
11917	Consequences of introgression and gene flow on the genetic structure and diversity of Lima bean ( <i>Phaseolus lunatus</i> L.) in its Mesoamerican diversity area. <i>PeerJ</i> , 0, 10, e13690.	0.9	5
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11919	Integrative Phylogeography Reveals Conservation Priorities for the Giant Anteater <i>Myrmecophaga tridactyla</i> in Brazil. <i>Diversity</i> , 2022, 14, 542.	0.7	2
11920	Estimation of allele and haplotype frequencies for 23 YSTR markers of Iraqi populations in Baghdad. <i>Asia-Pacific Journal of Molecular Biology and Biotechnology</i> , 0, , 11-22.	0.2	1
11921	Microsatellite Characteristics of Silver Carp ( <i>Hypophthalmichthys molitrix</i> ) Genome and Genetic Diversity Analysis in Four Cultured Populations. <i>Genes</i> , 2022, 13, 1267.	1.0	1
11922	Population genetic structure and demographic history of <i>Rhodeus atremius suigensis</i> , an endangered bitterling in Japan. <i>Conservation Genetics</i> , 0, , .	0.8	0
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11925	Mitochondrial DNA diversity and the population genetic structure of contemporary roe deer ( <i>Capreolus capreolus</i> ) in Europe. <i>Mammalian Biology</i> , 0, , .	0.8	0
11926	HLA-B*46 associates with rapid HIV disease progression in Asian cohorts and prominent differences in NK cell phenotype. <i>Cell Host and Microbe</i> , 2022, 30, 1173-1185.e8.	5.1	5
11927	New Zealand endemic open-habitat specialist, the Black-fronted Tern ( <i>Chlidonias albobristatus</i> ) experienced population expansion during Pleistocene glaciation and recent decline. <i>Ibis</i> , 0, , .	1.0	0

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11929	Genetic diversity of <i>Diaphorina citri</i> (Hemiptera: Liviidae) unravels phylogeographic structure and invasion history of eastern African populations. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	4
11930	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
11931	Differentiation and Temperature Adaptation of <i>Pampus Echinogaster</i> Based on Genome-Wide SNPs. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1
11932	<i>ddRAD-Seq</i> reveals evolutionary insights into population differentiation and the cryptic phylogeography of <i>Hyporhamphus intermedius</i> in Mainland China. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	1
11933	The Population Structure of a Globe Artichoke Worldwide Collection, as Revealed by Molecular and Phenotypic Analyzes. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
11934	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
11935	Mitochondrial diversity and inter-specific phylogeny among dolphins of the genus <i>Stenella</i> in the Southwest Atlantic Ocean. <i>PLoS ONE</i> , 2022, 17, e0270690.	1.1	3
11936	Susceptibility and Severity of COVID-19 Are Both Associated With Lower Overall Viral Peptide Binding Repertoire of HLA Class I Molecules, Especially in Younger People. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	7
11937	Resurrection of dormant zooplankton grazers reveals multiple evolutionary responses to toxic cyanobacteria. <i>Limnology and Oceanography</i> , 2022, 67, 2000-2011.	1.6	3
11938	Genetic Diversity of Fish in Aquaculture and of Common Carp ( <i>Cyprinus carpio</i> ) in Traditional Rice-Fish Coculture. <i>Agriculture (Switzerland)</i> , 2022, 12, 997.	1.4	5
11939	The minnow <i>Phoxinus phoxinus</i> (Leuciscidae) shifts the Adriatic-Black Sea basin divide in the north-western Dinaric Karst region. <i>Ecohydrology</i> , 2022, 15, .	1.1	2
11940	Population Genetic Differentiation and Structure of <i>Maruca vitrata</i> (Lepidoptera: Crambidae) in India. <i>Diversity</i> , 2022, 14, 546.	0.7	2
11941	Dynamics of natural infection of white grub larvae by <i>Beauveria</i> and <i>Metarhizium</i> in maize crops from Mexico. <i>Biocontrol Science and Technology</i> , 2022, 32, 1177-1193.	0.5	1
11942	Evidence for Genetic Hybridization between Released and Wild Game Birds: Phylogeography and Genetic Structure of Chukar Partridge, <i>Alectoris chukar</i> , in Turkey. <i>Diversity</i> , 2022, 14, 571.	0.7	1
11943	Molecular evidence for introgressive hybridization in New Zealand masked gulls. <i>Ibis</i> , 2023, 165, 248-269.	1.0	0
11944	Genetic diversity and population structure of critically endangered <i>Dactylorhiza hatagirea</i> (D. Don) Soo from North-Western Himalayas and implications for conservation. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
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11957	Molecular genetic differentiation of native populations of Mediterranean blue mussels, <i>Mytilus galloprovincialis</i> Lamarck, 1819, and the relationship with environmental variables. , 2022, 89, 755-784.		7
11958	Morphogenetic diversity of the selected hatchery populations of an Indian major carp ( <i>Labeo rohita</i> .) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 10 9.2 1	0.2	1
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12073	Palaeoclimatic changes resulted in range expansion and subsequent divergence in brown fur seals, <i>Arctocephalus pusillus</i>. <i>Biology Letters</i> , 2022, 18, .	1.0	0
12074	Wolbachia infection and genetic diversity of Italian populations of <i>Philaenus spumarius</i> , the main vector of <i>Xylella fastidiosa</i> in Europe. <i>PLoS ONE</i> , 2022, 17, e0272028.	1.1	5
12075	Genetic variability of indigenous ( <i>Quercus robur</i> L.) and late flushing oak ( <i>Quercus robur</i> L. subsp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 <i>Journal of Forest Research</i> , 2022, 141, 1073-1088.	1.1	1
12076	Genetic pattern and demographic history of cutlassfish ( <i>Trichiurus nanhaiensis</i> ) in South China Sea by the influence of Pleistocene climatic oscillations. <i>Scientific Reports</i> , 2022, 12, .	1.6	2



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12078	Effect of landscape features on the genetic structure of forest duikers (Cephalophinae) in Moukalaba forest, Gabon. <i>Mammalian Biology</i> , 2022, 102, 1879-1888.	0.8	1
12079	Memories, museum artefacts and excavations in resolving the history of maternal lineages in the Finnhorse. <i>Animal Genetics</i> , 0, , .	0.6	1
12080	Decades of Miscomputation in Genomic Clades and Distances. <i>International Journal on Computational Science &amp; Applications</i> , 2022, 112, 1-15.	0.4	0
12081	Global phylogeography of ridley sea turtles ( <i>Lepidochelys</i> spp.): evolution, demography, connectivity, and conservation. <i>Conservation Genetics</i> , 2022, 23, 995-1010.	0.8	7
12082	Distribution of <i>Diaphanosoma</i> (Diplostraca: Sididae) genus in Central Europe – morphological and molecular approach. , 2022, 89, 1115-1128.		2
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12085	Tierra Del Fuego: What Is Left from the Precolonial Male Lineages?. <i>Genes</i> , 2022, 13, 1712.	1.0	1
12086	Patterns of DNA barcode diversity in butterfly species (Lepidoptera) introduced to the Nearctic. <i>European Journal of Entomology</i> , 0, 119, 379-387.	1.2	2
12087	Lack of a genetic cline and temporal genetic stability in an introduced barnacle along the Pacific coast of Japan. <i>PeerJ</i> , 0, 10, e14073.	0.9	0
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12089	Population Genetic Data of 30 Insertion-Deletion Markers in the Polish Population. <i>Genes</i> , 2022, 13, 1683.	1.0	0
12090	Phylogeographic structure of common sage ( <i>Salvia officinalis</i> L.) reveals microrefugia throughout the Balkans and colonizations of the Apennines. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
12091	Systematic selections and forensic application evaluations of 111 individual identification SNPs in the Chinese Inner Mongolia Manchu group. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
12092	Intraspecific differentiation of <i>Allium canadense</i> var. <i>canadense</i> (Amaryllidaceae) across the North American Coastal Plain. <i>Plant Species Biology</i> , 0, , .	0.6	0
12093	Origin of the Bunun Indigenous People of Taiwan, a Review of Published Material Using Y-Chromosome and Mitochondrial DNA Gene Systems. <i>Dna</i> , 2022, 2, 185-201.	0.4	1
12096	Migratory behaviour of Brown planthopper, Nilaparvata lugens (Stål) (Hemiptera: Delphacidae), in India as inferred from genetic diversity and reverse trajectory analysis. <i>3 Biotech</i> , 2022, 12, .	1.1	2

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12098	Genome-derived Microsatellite Markers in <i>Lippia origanoides</i> from Colombia. <i>Journal of Herbs, Spices and Medicinal Plants</i> , 0, , 1-18.	0.5	0
12099	Sequence diversity of the uniparentally transmitted portions of the genome in the resident population of Catalonia. <i>Forensic Science International: Genetics</i> , 2022, 61, 102783.	1.6	1
12100	Aneuploidy promotes intraspecific diversification of the endemic East Asian herb <i>Lycoris aurea</i> complex. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
12102	Genetic structure and differentiation from early bronze age in the mediterranean island of sicily: Insights from ancient mitochondrial genomes. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
12103	Structured Populations of Critically Endangered Yellow Water Lily ( <i>Nuphar shimadai</i> Hayata,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	1.8	1
12105	Genomic analyses of fairy and fulmar prions (Procellariidae: <i>Pachyptila</i> spp.) reveals parallel evolution of bill morphology, and multiple species. <i>PLoS ONE</i> , 2022, 17, e0275102.	1.1	1
12107	Holocene climate changes explain the spatial pattern in genetic diversity in populations of <i>Cyperus papyrus</i> from Southeast Africa wetlands. <i>Heredity</i> , 0, , .	1.2	0
12108	Genetic structure and recent population demographic history of Taihangshan macaque ( <i>Macaca</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.3	1
12109	Cryptic diversity and population genetic structure of the mantis shrimp <i>Oratosquilla oratoria</i> in South Korea. <i>Genes and Genomics</i> , 2022, 44, 1343-1352.	0.5	1
12110	Genetic decline and recovery of a demographically rebuilt fishery species. <i>Molecular Ecology</i> , 2022, 31, 5684-5698.	2.0	4
12111	Gene flow between wild trees and cultivated varieties shapes the genetic structure of sweet chestnut ( <i>Castanea sativa</i> Mill.) populations. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
12112	Genetic Differentiation Among Populations of <i>Octopus minor</i> Based on Simple Sequence Repeats Mined from Transcriptome Data. <i>Journal of Ocean University of China</i> , 2022, 21, 1265-1272.	0.6	0
12113	Genetic origin of donkeys in Brazil. <i>Tropical Animal Health and Production</i> , 2022, 54, .	0.5	0
12114	Variation in genetics, morphology, and recruitment of the invasive barnacle <i>Amphibalanus eburneus</i> (Gould, 1841) in the southern Korean peninsula. <i>PeerJ</i> , 0, 10, e14002.	0.9	0
12115	Insights into breeding history, hotspot regions of selection, and untapped allelic diversity for bread wheat breeding. <i>Plant Journal</i> , 2022, 112, 897-918.	2.8	3
12116	Plio-Pleistocene climatic change drives allopatric speciation and population divergence within the <i>Scrophularia incisa</i> complex (Scrophulariaceae) of desert and steppe subshrubs in Northwest China. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
12117	Genetic signature of blind reintroductions of Iberian ibex ( <i>Capra pyrenaica</i> ) in Catalonia, Northeast Spain. <i>PLoS ONE</i> , 2022, 17, e0269873.	1.1	3

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12119	Frequency and parameters of linkage disequilibrium of the two-locus <i>HLA-B-MICA</i> haplotypes in russians from chelyabinsk region. <i>Russian Journal of Immunology: RJl: Official Journal of Russian Society of Immunology</i> , 2022, 25, 139-146.	0.2	0
12120	Mitochondrial D-loop sequences and haplotypes diversity in Egyptian rabbit breeds. <i>World Rabbit Science</i> , 2022, 30, 201-207.	0.1	1
12121	An integrative insight into the diversity, distribution, and biogeography of the freshwater endemic clade of the <i>Ponticola syman group</i> (Teleostei: Gobiidae) in the Caucasus biodiversity hotspot. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	5
12122	Population Genetics of the Blueberry Gall Midge, <i>Dasineura oxycoccana</i> (Diptera: Cecidomyiidae), on Blueberry and Cranberry and Testing Invasion Scenarios. <i>Insects</i> , 2022, 13, 880.	1.0	0
12123	Assessment of connectivity patterns of the marbled crab <i>Pachygrapsus marmoratus</i> in the Adriatic and Ionian seas through combination of genetic data and Lagrangian simulations. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1
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12127	Using genetic tools to inform conservation of fragmented populations of Asian elephants () Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422 T	1.3	0
12128	Quaternary Environmental Changes Shaped Mitochondrial DNA Diversity in the Large Japanese Wood Mouse <i>Apodemus speciosus</i> in Hokkaido, Japan. <i>Mammal Study</i> , 2022, 47, .	0.2	2
12129	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
12130	Evaluation of genetic diversity of Himalayan balsam ( <i>Impatiens glandulifera</i> Royle) populations using microsatellites. <i>Zemdirbyste</i> , 2022, 109, 259-268.	0.3	1
12131	Multiple <i>Doris</i> â€œ <i>kerghuelensis</i> â€•(Nudibranchia) species span the Antarctic Polar Front. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	0
12132	Linked selection, differential introgression and recombination rate variation promote heterogeneous divergence in a pair of yellow croakers. <i>Molecular Ecology</i> , 2022, 31, 5729-5744.	2.0	8
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12135	High levels of genetic diversity and population structure in the Mediterranean seagrass <i>Posidonia oceanica</i> at its easternmost distribution limit. <i>ICES Journal of Marine Science</i> , 2022, 79, 2286-2297.	1.2	3
12136	Diversity and Genetic Structure of Scarlet Plume ( <i>Euphorbia fulgens</i> ), an Endemic Plant of Mexico. <i>Plants</i> , 2022, 11, 2542.	1.6	0

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12139	Genetic diversity and population structure of sorghum [ <i>Sorghum bicolor</i> (L.) Moench] in Ethiopia as revealed by microsatellite markers. <i>Acta Agriculturae Scandinavica - Section B Soil and Plant Science</i> , 2022, 72, 873-884.	0.3	3
12140	Demographic resilience of brook trout populations subjected to experimental size-selective harvesting. <i>Evolutionary Applications</i> , 2022, 15, 1792-1805.	1.5	0
12141	Population structure and demographic history of the gastropod <i>Thaisella chocolata</i> (Duclos,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Evolution, 2022, 12, .	0.8	1
12143	Trans-Arctic vicariance in <i>Strongylocentrotus</i> sea urchins. <i>PeerJ</i> , 0, 10, e13930.	0.9	1
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12146	Evaluation of genetic polymorphisms at 21 autosomal STR loci in Ramgharia Sikh population of Punjab, India. <i>Annals of Human Biology</i> , 0, , 1-6.	0.4	1
12147	Genetic diversity and population structure of the antimalarial plant <i>Cryptolepis sanguinolenta</i> in Ghana. <i>Frontiers in Conservation Science</i> , 0, 3, .	0.9	0
12149	The genetic characteristics of <i>Sarcoptes scabiei</i> from Chinese serow ( <i>Capricornis milneedwardsii</i> ) and goral ( <i>Naemorhedus goral arnouxiensis</i> ) compared with other mites from different hosts and geographic locations using ITS2 and cox1 sequences. <i>Parasitology Research</i> , 2022, 121, 3611-3618.	0.6	1
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12151	Connectivity and divergence of symbiotic bacteria of deep-sea hydrothermal vent mussels in relation to the structure and dynamics of mid-ocean ridges. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
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12153	Drug resistance and population structure of <i>Plasmodium falciparum</i> and <i>Plasmodium vivax</i> in the Peruvian Amazon. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
12154	Allele frequencies of 31 autosomal short tandem repeat (auSTR) loci obtained using the Precision ID GlobalFiler <sup>®</sup> , <sup>®</sup> NGS STR Panel v2 in 322 individuals from the Japanese population. <i>Legal Medicine</i> , 2022, 59, 102151.	0.6	0
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12156	Dispersal direction of Malaysian <i>Fasciola gigantica</i> from neighboring southeast Asian countries inferred using mitochondrial DNA analysis. <i>Infection, Genetics and Evolution</i> , 2022, 105, 105373.	1.0	1

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12158	Population genetic structure analysis of big head croaker ( <i>Lateolabrax japonicus</i> ) based on mitochondrial <i>cytb</i> and <i>COI</i> gene sequences. <i>Journal of Fishery Sciences of China</i> , 2021, 28, 1-10.	0.2	1
12159	Breeding system and geospatial variation shape the population genetics of <i>Triodanis perfoliata</i> . <i>Ecology and Evolution</i> , 2022, 12, .	0.8	1
12160	Genetic Diversity and Population Structure of <i>Hemiculter leucisculus</i> (Basilesky, 1855) in Xinjiang Tarim River. <i>Genes</i> , 2022, 13, 1790.	1.0	2
12161	Comparative phylogeography of two commensal rat species ( <i>Rattus tanezumi</i> and <i>Rattus</i> ) based on mitochondrial <i>cytb</i> and <i>COI</i> data. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	2
12162	Current Genetic Structure Analysis of Leopard Cats Reveals a Weak Disparity Trend in Subpopulations in Beijing, China. <i>Biology</i> , 2022, 11, 1478.	1.3	0
12163	Probing for depthâ€‘gradient diversification in the riverineâ€‘spawning Dolly Varden: Insights from a recently discovered ecomorph assemblage. <i>Ecology of Freshwater Fish</i> , 2023, 32, 322-335.	0.7	1
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12167	Remarkably low host specificity in the bat fly <i>Penicillidia fulvida</i> (Diptera: Nycteribiidae) as assessed by mitochondrial COI and nuclear 28S sequence data. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	2
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12169	Zavot cattle genetic characterization using microsatellites. <i>Tropical Animal Health and Production</i> , 2022, 54, .	0.5	4
12170	A comprehensive GlobalFilerâ„¢ autosomal STR reference dataset for Southern African.. <i>Forensic Science International: Genetics Supplement Series</i> , 2022, , .	0.1	0
12171	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
12172	Genetic diversity in the transmission-blocking vaccine candidate <i>Plasmodium vivax</i> gametocyte protein Pvs230 from the Chinaâ€‘Myanmar border area and central Myanmar. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	1
12173	Larval Retention and Homing Behaviour Shape the Genetic Structure of the Bullet Tuna ( <i>Auxis rochei</i> ) in the Mediterranean Sea. <i>Fishes</i> , 2022, 7, 300.	0.7	3
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12176	Genetic ancestry in Afro-descendants from the Andes and Pacific Coast regions of Ecuador. <i>Forensic Science International: Genetics Supplement Series</i> , 2022, , .	0.1	1
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12178	Evidence for high gene flow, nonrandom mating, and genetic bottlenecks of <i>Ganoderma boninense</i> infecting oil palm ( <i>Elaeis guineensis</i> Jacq.) plantations in Malaysia and Indonesia. <i>Mycologia</i> , 2022, 114, 947-963.	0.8	1
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12182	The paternal genetic legacy of Hungarian-speaking Răzărz (Hungary) and Váh valley (Slovakia) populations. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
12183	Genetic and population diversity of <i>Toxocara cati</i> (Schränk, 1788) Brumpt, 1927, on the basis of the internal transcribed spacer (ITS) region. <i>Parasitology Research</i> , 2022, 121, 3477-3493.	0.6	3
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12188	Diploid chromosome-level reference genome and population genomic analyses provide insights into Gypenoside biosynthesis and demographic evolution of <i>Gynostemma pentaphyllum</i> (Cucurbitaceae). <i>Horticulture Research</i> , 2023, 10, .	2.9	3
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12192	Development and forensic efficiency evaluations of a novel multiplex amplification panel of 17 Multi-InDel loci on the X chromosome. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	0
12193	The paternal heritage of self-declared Ecuadorian indigenous people. <i>Forensic Science International: Genetics Supplement Series</i> , 2022, , .	0.1	0
12194	Molecular and morphological evaluation of the bonnethead shark complex <i>Sphyrna tiburo</i> (Carcharhiniformes: Sphyrnidae). <i>Environmental Biology of Fishes</i> , 2022, 105, 1643-1658.	0.4	3
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12197	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
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12199	Genetic Diversity and Population Structure of the Giant Mottled Eel, <i>Anguilla marmorata</i> Quoy & Gaimard, 1824 in Central Vietnam. <i>Fishes</i> , 2022, 7, 286.	0.7	1
12200	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
12201	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
12202	Co-introduction of <i>Doliciriopectanum lacustre</i> , a monogenean gill parasite of the invasive Nile perch <i>Lates niloticus</i> : intraspecific diversification and mitonuclear discordance in native versus introduced areas. <i>International Journal for Parasitology</i> , 2022, 52, 775-786.	1.3	3
12203	Assessment of Genetic Diversity, Gene Flow and Demographic History of Frigate Tuna ( <i>Auxis thazard</i> ) Populations in Tanzanian Marine Waters Using Mitochondrial DNA Control Region. <i>Asian Journal of Fisheries and Aquatic Research</i> , 0, , 9-20.	0.0	0
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12205	Genetic Diversity and Population Structure of an Arctic Tertiary Relict Tree Endemic to China ( <i>Sassafras tzumu</i> ) Revealed by Novel Nuclear Microsatellite (nSSR) Markers. <i>Plants</i> , 2022, 11, 2706.	1.6	1
12206	Genetic Diversity and Population Genetic Structure of <i>Aedes albopictus</i> in the Yangtze River Basin, China. <i>Genes</i> , 2022, 13, 1950.	1.0	2
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12210	Genetic population structure of cisco, <i>Coregonus artedii</i> , in the Laurentian Great Lakes. <i>Journal of Great Lakes Research</i> , 2022, , .	0.8	0
12211	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
12212	The Evolution and Global Spatiotemporal Dynamics of Senecavirus A. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	1
12213	Detection of Genetic Patterns in Endangered Marine Species Is Affected by Small Sample Sizes. <i>Animals</i> , 2022, 12, 2763.	1.0	2

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12237	Variaci3n gen3tica en dos genes candidatos contra par3sitos gastrointestinales en Ovinos de Pelo Colombiano. Revista MVZ Cordoba, 2022, 27, e2747.	0.2	0
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12273	The genetic structure and connectivity in two sympatric rodent species with different life histories are similarly affected by land use disturbances. <i>Conservation Genetics</i> , 0, , .	0.8	0
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12284	The development of multiplex STR panels for the identification of bald eagles ( <i>Haliaeetus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 0.3 0	0.3	0
12285	Estimaci3n de heredabilidad y correlaciones gen3ticas en caracteres morfol3gicos y fisiol3gicos para una poblaci3n de <i>Zamia obliqua</i> A.Br. (Zamiaceae: Cycadales). <i>Actualidades Biol3gicas</i> , 2017, 36, 137-148.	0.1	1
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12294	Phylogeographic Diversity Analysis of <i>Bipolaris sorokiniana</i> (Sacc.) Shoemaker Causing Spot Blotch Disease in Wheat and Barley. Genes, 2022, 13, 2206.	1.0	5
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12303	Genetic dynamics of a 11-year ex situ managed <i>Itasenpara</i> bitterling population. Conservation Genetics, 0, , .	0.8	0
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12306	Deep ecomorphological and genetic divergence in Steller's Jays ( <i>Cyanocitta stelleri</i> , Aves:) Tj ETQq1 1 0.784314 rgBT <sub>3</sub> /Overlock 0,8	0.8	0



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12307	Genetic variation of <i>Sparicotyle chrysophrii</i> (Monogenea: Microcotylidae) from the gilthead sea bream <i>Sparus aurata</i> (Teleostei: Sparidae) in the Mediterranean Sea. <i>Parasitology Research</i> , 2023, 122, 157-165.	0.6	1
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12313	Incorporating distance metrics and temporal trends to refine mixed stock analysis. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
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12328	Three mitochondrial lineages and no Atlantic-Mediterranean barrier for the bogue Boops boops across its widespread distribution. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
12329	Low genetic diversity in a widespread whistling alien: A comparison of <i>Eleutherodactylus johnstonei</i> Barbour, 1914 (Eleutherodactylidae) and congeners in native and introduced ranges. <i>NeoBiota</i> , 0, 79, 31-50.	1.0	1
12330	Weak genetic structure, shared nonbreeding areas, and extensive movement in a declining waterbird. <i>Condor</i> , 2023, 125, .	0.7	1
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12332	Spatially explicit assessment of genetic variation to inform conservation effort for an endangered Mediterranean conifer, <i>Cedrus atlantica</i> . <i>Ecology and Evolution</i> , 2022, 12, .	0.8	0
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12355	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
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#	ARTICLE	IF	CITATIONS
12480	Genetic Diversity and Fine-Scale Genetic Structure of <i>Spodoptera litura</i> Fabricius (Lepidoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74	1.0	0
12481	Chloroplast DNA reveals genetic population structure in <i>Sinomenium acutum</i> in subtropical China. Chinese Herbal Medicines, 2023, , .	1.2	0
12482	Single nucleotide variants in microRNA biosynthesis genes in Mexican individuals. Frontiers in Genetics, 0, 14, .	1.1	0
12483	Genetic variation and demographic history of Sudan desert sheep reveal two diversified lineages. BMC Genomics, 2023, 24, .	1.2	3
12484	The Relationship between Cadmium-Related Gene Sequence Variations in Rice and Cadmium Accumulation. Agronomy, 2023, 13, 800.	1.3	1
12485	Seascape Genomics and Phylogeography of the Sailfish (<i>Istiophorus platypterus</i>). Genome Biology and Evolution, 2023, 15, .	1.1	4
12486	Dental pattern diversity in a military population and its usefulness for assessing the degree of certainty in dental identification. Forensic Science International, 2023, 345, 111609.	1.3	0
12487	Multilocus approach reveals distinct evolutionary units of the South American apapa <i>Pellona flavipinnis</i> (Valenciennes, 1837) (Clupeiformes, Pristigasteridae). Journal of Fish Biology, 0, , .	0.7	0
12488	Despite Shared Geography, <i>Campylobacter</i> Isolated from Surface Water Are Genetically Distinct from <i>Campylobacter</i> Isolated from Chickens. Microbiology Spectrum, 2023, 11, .	1.2	1
12489	Restricted connectivity for cobia <scp> <i>Rachycentron canadum</i> </scp> (Perciformes: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 74	0.9	0
12490	An MPS-Based 50plex Microhaplotype Assay for Forensic DNA Analysis. Genes, 2023, 14, 865.	1.0	1
12491	Genetic markers associated with divergent selection against the parasite <i>Marteilia cochillia</i> in common cockle ( <i>Cerastoderma edule</i> ) using transcriptomics and population genomics data. Frontiers in Marine Science, 0, 10, .	1.2	2
12492	The development of the novel 22 X- indel multiplex system for forensic genetics. Legal Medicine, 2023, 62, 102224.	0.6	2
12493	Population structure and genetic diversity of tobacco mild green mosaic virus variants in Western Anatolia of Turkey. Physiological and Molecular Plant Pathology, 2023, 125, 102008.	1.3	2
12494	Genetic diversity and natural selection of rif gene (PF3D7_1254800) in the <i>Plasmodium falciparum</i> global populations. Molecular and Biochemical Parasitology, 2023, 254, 111558.	0.5	1
12495	Population genetic characteristics of the bumble bee <i>Bombus ardens ardens</i> (Hymenoptera: Apidae) in South Korea using novel microsatellite markers. Journal of Asia-Pacific Entomology, 2023, 26, 102071.	0.4	1
12496	Observations on a Reemerging Epizootic of the Sea Scallop, <i>Placopecten magellanicus</i> , Resource. Journal of Shellfish Research, 2023, 42, .	0.3	1
12497	Body color selection of domesticated carp ( <i>Cyprinus carpio</i> ) in traditional agricultural systems: Insight provided by growth performance, nutritional quality, and genetic diversity. Aquaculture, 2023, 572, 739528.	1.7	2

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12498	Sequence-based allelic variations and frequencies for 22 autosomal STR loci in the Lebanese population. <i>Forensic Science International: Genetics</i> , 2023, 65, 102872.	1.6	2
12499	Geography and past climate changes have shaped the evolution of a widespread lizard in arid Central Asia. <i>Molecular Phylogenetics and Evolution</i> , 2023, 184, 107781.	1.2	3
12500	Genetic population structure in Norway lobster ( <i>Nephrops norvegicus</i> ): management regime under panmixia. <i>ICES Journal of Marine Science</i> , 0, , .	1.2	0
12501	Small population of the largest water strider after the late Pleistocene and the implications for its conservation. <i>Gene</i> , 2023, 859, 147219.	1.0	0
12502	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
12503	Limited population genetic variation but pronounced seascape genetic structuring in populations of the Mediterranean mussel ( <i>Mytilus galloprovincialis</i> ) from the eastern Adriatic Sea. <i>Ecology and Evolution</i> , 2023, 13, .	0.8	1
12504	Genetic connectivity in Twospot flounder ( <i>Bothus robinsi</i> ) across the Gulf of Mexico, inferred with single nucleotide polymorphisms from larvae and adults. <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	0
12505	Tracing the origin of Oriental beech stands across Western Europe and reporting hybridization with European beech “ Implications for assisted gene flow. <i>Forest Ecology and Management</i> , 2023, 531, 120801.	1.4	9
12506	Phylogeography and genetic diversity of the <i>Scapholeberis kingii</i> species complex (Cladocera:) Tj ETQq0 0 0 rgBT /Qverlock 10 Tf 50 422	1.2	0
12507	Genetic diversity of <i>Contracaecum 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
12508	Untangling the <i>Hymenaea stigonocarpa</i> complex (Fabaceae) using population genetics and morphology. <i>Botanical Journal of the Linnean Society</i> , 0, , .	0.8	0
12509	Spatio-temporal genetic structure of the striped field mouse ( <i>Apodemus agrarius</i> ) populations inhabiting national parks in South Korea: Implications for conservation and management of protected areas. <i>Frontiers in Ecology and Evolution</i> , 0, 11, .	1.1	1
12510	Genetic Structure and Phylogeography of Commercial <i>Mytilus unguiculatus</i> in China Based on Mitochondrial COI and Cytb Sequences. <i>Fishes</i> , 2023, 8, 89.	0.7	4
12511	Study of sockeye salmon <i>Oncorhynchus nerka</i> (Walbaum, 1792) microsatellite variability in Bolshaya River. The Researches of the Aquatic Biological Resources of Kamchatka and of the North-west Part of the Pacific Ocean, 2023, , 68-78.	0.3	0
12512	Mitochondrial DNA diversity and genetic structure of striped dolphin <i>Stenella coeruleoalba</i> in the Northern Ionian Sea. <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	0
12513	The Search of Association of HLA Class I and Class II Alleles with COVID-19 Mortality in the Russian Cohort. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3068.	1.8	1
12514	Genetic diversity analysis of severely infesting invasive thrips, <i>Thrips parvispinus</i> (Karny) in chilli ( <i>Capsicum annuum</i> L.) in India. <i>Phytoparasitica</i> , 2023, 51, 227-239.	0.6	2
12515	Mitochondrial diversity and genetic structure of common carp ( <i>Cyprinus carpio</i> ) in <sc>Pearl River and Nanduijiang River</sc>. <i>Journal of Fish Biology</i> , 2023, 102, 1109-1120.	0.7	1

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12517	Genotypic detection of barriers to rat dispersal: <i>Rattus rattus</i> behind a peninsula predator-proof fence. <i>Biological Invasions</i> , 0, , .	1.2	0
12518	Discovering novel clues of natural selection on four worldwide goat breeds. <i>Scientific Reports</i> , 2023, 13, .	1.6	2
12519	Forest health in the Anthropocene: the emergence of a novel tree disease is associated with poplar cultivation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2023, 378, .	1.8	2
12520	Evaluating the Potential Fitness Effects of Chinook Salmon ( <i>Oncorhynchus tshawytscha</i> ) Aquaculture Using Non-Invasive Population Genomic Analyses of MHC Nucleotide Substitution Spectra. <i>Animals</i> , 2023, 13, 593.	1.0	0
12521	Conservation at the edge: connectivity and opportunities from non-protected coral reefs close to a National Park in the Colombian Caribbean. <i>Biodiversity and Conservation</i> , 2023, 32, 1493-1522.	1.2	0
12522	Genetic Monitoring of the Last Captive Population of Greater Mouse-Deer on the Thai Mainland and Prediction of Habitat Suitability before Reintroduction. <i>Sustainability</i> , 2023, 15, 3112.	1.6	0
12523	<scp>DRD4</scp> allele frequencies in greylag geese vary between urban and rural sites. <i>Ecology and Evolution</i> , 2023, 13, .	0.8	0
12525	Retrospective analysis of <i>Plasmodium vivax</i> genomes from a pre-elimination China inland population in the 2010s. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
12526	Cryptic diversity in a gastrointestinal acanthocephalan of New World primates from Costa Rica. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
12527	Genetic Diversity of <i>Oxytropis</i> Species from the Center of the Genus Origin: Insight from Molecular Studies. <i>Diversity</i> , 2023, 15, 244.	0.7	1
12529	Phylogeography and Genetic Diversity of Duck Mussel <i>Anodonta anatina</i> (Bivalvia: Unionidae) in Eurasia. <i>Diversity</i> , 2023, 15, 260.	0.7	3
12530	Genetic population structure of <i>Pseudoplatystoma corruscans</i> (Siluriformes: Pimelodidae) and evidence of temporal variation in structure. <i>Journal of Fish Biology</i> , 2023, 102, 1040-1048.	0.7	0
12531	Phylogeography of the Altai weasel (Carnivora: Mustelidae: <i>Mustela altaica</i>) based on an analysis of mitochondrial control-region haplotypes. <i>Biological Journal of the Linnean Society</i> , 2023, 138, 274-281.	0.7	1
12532	Phylogenomic analyses reveal incongruences between divergence times and fossil records of freshwater snails in East Asia. <i>Molecular Phylogenetics and Evolution</i> , 2023, 182, 107728.	1.2	0
12533	Population genetic structure of a recent insect invasion: a gall midge, <i>Asynapta groverae</i> (Diptera: Tj ETQq0 0 0 rgBTj/Overlock 10 Tf 50	1.6	0
12534	Gene flow with the help of sea turtles: phylogeography of the epibiont barnacle<i>Chelonibia testudinaria</i> (Linnaeus, 1758) (Crustacea: Cirripedia: Chelonibiidae) from the Persian Gulf. <i>Journal of Crustacean Biology</i> , 2023, 43, .	0.3	0
12535	Antifungal alternation can be beneficial for durability but at the cost of generalist resistance. <i>Communications Biology</i> , 2023, 6, .	2.0	0
12537	Deciphering local adaptation of native Indian cattle ( <i>Bos indicus</i> ) breeds using landscape genomics and in-silico prediction of deleterious SNP effects on protein structure and function. <i>3 Biotech</i> , 2023, 13, .	1.1	1



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12538	Genetic differences among the Interior Highlands walleye ( <i>Sander vitreus</i> ) with mitochondrial and nuclear markers indicate the need for updated stocking practices. <i>Conservation Genetics</i> , 0, , .	0.8	0
12539	Multiple genetic lineages of anadromous migratory Mekong catfish <i>Pangasius krempfi</i> revealed by mtDNA control region and cytochrome <i>b</i> . <i>Ecology and Evolution</i> , 2023, 13, .	0.8	1
12540	Cross-Hemispheric Genetic Diversity and Spatial Genetic Structure of <i>Callinectes sapidus</i> Reovirus 1 (CsRV1). <i>Viruses</i> , 2023, 15, 563.	1.5	1
12541	Single nucleotide polymorphisms within exon four of the prolactin gene and their effect on milk traits in cattle populations of Ethiopia. <i>Animal Biotechnology</i> , 2023, 34, 4634-4644.	0.7	0
12542	Phylogeography of the Plateau Pika ( <i>Ochotona curzoniae</i> ) in Response to the Uplift of the Qinghai-Tibet Plateau. <i>Diversity</i> , 2023, 15, 307.	0.7	0
12544	Non-synonymous variation and protein structure of candidate genes associated with selection in farm and wild populations of turbot ( <i>Scophthalmus maximus</i> ). <i>Scientific Reports</i> , 2023, 13, .	1.6	0
12545	The genomic and epigenetic footprint of local adaptation to variable climates in kiwifruit. <i>Horticulture Research</i> , 2023, 10, .	2.9	3
12546	Genetic Diversity Analysis of Banana Cultivars ( <i>Musa</i> sp.) in Saudi Arabia Based on AFLP Marker. <i>Current Issues in Molecular Biology</i> , 2023, 45, 1810-1819.	1.0	2
12547	Genetic structure of the Japanese Robin ( <i>Larvivora akahige</i> ) endemic to East Asian islands. <i>Ibis</i> , 2023, 165, 875-889.	1.0	0
12549	Commercial sharks under scrutiny: Baseline genetic distinctiveness supports structured populations of small-spotted catsharks in the Mediterranean Sea. <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	5
12550	Weak range-wide population structure in the blackfin tuna ( <i>Thunnus atlanticus</i> ) revealed by analysis of genome-wide SNPs. <i>ICES Journal of Marine Science</i> , 0, , .	1.2	0
12551	Low genetic diversity among introduced axis deer: comments on the genetic paradox and invasive species. <i>Journal of Mammalogy</i> , 2023, 104, 603-618.	0.6	1
12553	Genetic diversity and population structure of the invasive populations of goldfish <i>Carassius auratus</i> complex in Tibet. <i>Biological Invasions</i> , 0, , .	1.2	0
12554	Population structure and evolutionary history of the greater cane rat ( <i>Thryonomys swinderianus</i> ) from the Guinean Forests of West Africa. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	1
12555	Genetic Variation versus Morphological Variability in European Peatland Violets ( <i>Viola epipsila</i> V.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.3	0
12557	Genetic Adaptation of Siberian Larch ( <i>Larix sibirica</i> Ledeb.) to High Altitudes. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4530.	1.8	4
12558	Phylogeography of <i>Aphyocypris normalis</i> Nichols and Pope, 1927 at Hainan Island and adjacent areas based on mitochondrial DNA data. <i>PLoS ONE</i> , 2023, 18, e0282460.	1.1	3
12559	Population genomics reveals differences in genetic structure between two endemic arboreal rodent species in threatened cloud forest habitat. <i>Mammal Research</i> , 2023, 68, 223-235.	0.6	0

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12560	Investigating an Unknown Biodiversity: Evidence of Distinct Lineages of the Endemic Chola Guitarfish <i>Pseudobatos percellens</i> Walbaum, 1792 in the Western Atlantic Ocean. <i>Diversity</i> , 2023, 15, 344.	0.7	1
12561	Genetically isolated population of the coastal species with high dispersal potential: the case of the sentinel crab <i>Macrophthalmus japonicus</i> (Brachyura: Macrophthalmidae) in Japan. <i>Plankton and Benthos Research</i> , 2023, 18, 13-20.	0.2	1
12562	VARIABILITY OF PDYN AND OPRK1 GENES IN FOUR ARGENTINIAN POPULATIONS AND ITS GENETIC ASSOCIATION WITH CLINICAL VARIABLES RELATED TO ACUTE POSTSURGICAL PAIN. <i>BAG: Journal of Basic and Applied Genetics</i> , 2022, 33, 7-18.	0.1	0
12563	Applications of X-Chromosome Short Tandem Repeats for Human Identification: A Review. <i>Journal of Tropical Life Science</i> , 2023, 13, 193-218.	0.1	2
12564	<i>RRS1</i> shapes robust root system to enhance drought resistance in rice. <i>New Phytologist</i> , 2023, 238, 1146-1162.	3.5	9
12565	Verification of insertion-deletion markers (InDels) and microsatellites (STRs) as subsidiary tools for inferring Slavic population ancestry. <i>Archiwum Medycyny Sadowej I Kryminologii</i> , 2023, 72, 120-137.	0.3	0
12567	Genetic polymorphisms and population genetic analyses of 57 autosomal InDel loci in Hubei Tujia group. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0
12568	Genetic diversity and population structure of <i>Capitulum mitella</i> (Linnaeus, 1767) in Fujian (China) revealed by mtDNA COI sequences. <i>F1000Research</i> , 0, 12, 238.	0.8	0
12569	Geographic Genetic Structure of <i>Alectoris chukar</i> in TÃ¼rkiye: Post-LGM-Induced Hybridization and Human-Mediated Contaminations. <i>Biology</i> , 2023, 12, 401.	1.3	6
12570	Genetic variables, population features and reproductive success of <i>Gymnocalycium monvillei</i> (Cactaceae) along an altitudinal gradient. <i>Botanical Journal of the Linnean Society</i> , 2023, 202, 389-405.	0.8	2
12571	A genetic Study of the Ghanaian Population Using 15 Autosomal STR Loci. <i>Biochemical Genetics</i> , 0, , .	0.8	0
12572	Low genetic diversity and lack of genetic structure among populations of the sandfish <i>Holothuria (Metriatyla) scabra</i> on the Tanzanian coast. <i>Marine Biology Research</i> , 2022, 18, 611-619.	0.3	0
12573	Biological Investigation of the Endangered Northern Madtom in the North Channel St. Clair River. <i>North American Journal of Fisheries Management</i> , 2023, 43, 730-742.	0.5	1
12574	Diversity of Wolbachia infection and its influence on mitochondrial DNA variation in the diamondback moth, <i>Plutella xylostella</i> . <i>Molecular Phylogenetics and Evolution</i> , 2023, 182, 107751.	1.2	2
12575	Phylogeographic and Morphological Analysis of <i>Botrylloides niger</i> Herdman, 1886 from the Northeastern Mediterranean Sea. <i>Diversity</i> , 2023, 15, 367.	0.7	3
12576	Population genetics of zig-zag eel ( <i>Mastacembelus armatus</i> ) uncover gene flow between an isolated island and the mainland China. <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	1
12579	Late Quaternary history of Siberian stone pine as revealed by genetic and paleoecological data. <i>Tree Genetics and Genomes</i> , 2023, 19, .	0.6	1
12580	Mitochondrial, morphological and environmental data partially support current subspecies designation in <i>Amazilia yucatanensis</i> hummingbirds. <i>Biological Journal of the Linnean Society</i> , 2023, 138, 413-436.	0.7	1

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12581	Phylogenetic History and Phylogeographic Patterns of the European Wildcat ( <i>Felis silvestris</i> ) Populations. <i>Animals</i> , 2023, 13, 953.	1.0	1
12582	Genetic differentiation within species exhibiting widespread gene flow; phylogeography of the downstream-inhabiting species <i>Ephemera orientalis</i> (Insecta: Ephemeroptera). <i>Biological Journal of the Linnean Society</i> , 2023, 138, 351-364.	0.7	1
12583	Genetic Diversity and Population Structure of <i>Anopheles funestus</i> in Western Kenya Based on Mitochondrial DNA Marker COII. <i>Insects</i> , 2023, 14, 273.	1.0	2
12584	Analysis of sequence diversity in <i>Plasmodium falciparum</i> glutamic acid-rich protein (PfGARP), an asexual blood stage vaccine candidate. <i>Scientific Reports</i> , 2023, 13, .	1.6	2
12585	Intraspecific genetic diversity of the fish-infecting microsporidian parasite <i>Pseudokababata alburnus</i> (Microsporidia). <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
12586	New Approach to the Systematics of the Section <i>Psammiris</i> (Iris, Iridaceae): What Does Chloroplast DNA Sequence Tell Us?. <i>Plants</i> , 2023, 12, 1254.	1.6	1
12587	Genetic Diversity and Phylogeography of a Turf-Forming Cosmopolitan Marine Alga, <i>Gelidium crinale</i> (Gelidiales, Rhodo-Phyta). <i>International Journal of Molecular Sciences</i> , 2023, 24, 5263.	1.8	0
12588	Genetic diversity and population structure of a Peruvian cattle herd using SNP data. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	1
12592	Aflatoxin contamination of maize and groundnut in Burundi: Distribution of contamination, identification of causal agents and potential biocontrol genotypes of <i>Aspergillus flavus</i> . <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
12593	Geographic isolation and environmental heterogeneity contribute to genetic differentiation in <i>Cephalotaxus oliveri</i> . <i>Ecology and Evolution</i> , 2023, 13, .	0.8	4
12594	HV1 mtDNA Reveals the High Genetic Diversity and the Ancient Origin of Vietnamese Dogs. <i>Animals</i> , 2023, 13, 1036.	1.0	0
12595	New record of <i>Halymenia malaysiana</i> (Halymeniaceae, Rhodophyta) from Viet Nam, and its genetic diversity in the western Pacific. <i>Botanica Marina</i> , 2023, 66, 113-123.	0.6	2
12596	Genetic Diversity and Insights into the Distribution of Brown Howler Monkeys ( <i>Alouatta guariba</i> ) Tj ETQq0 0 0 rgBT/Qverlock 10 Tf 50 2	0.9	1
12598	Historical Landscape Evolution Shaped the Phylogeography and Population History of the Cyprinid Fishes of <i>Acrossocheilus</i> (Cypriniformes: Cyprinidae) According to Mitochondrial DNA in Zhejiang Province, China. <i>Diversity</i> , 2023, 15, 425.	0.7	1
12599	Fine-scale spatial distribution of deltamethrin resistance and population structure of <i>Anopheles funestus</i> and <i>Anopheles arabiensis</i> populations in Southern Mozambique. <i>Malaria Journal</i> , 2023, 22, .	0.8	2
12600	Population Genetics of Chilean Jack Mackerel, <i>Trachurus murphyi</i> Nichols, 1920, (Pisces, Carangidae), in Waters of the South Pacific Ocean. <i>Fishes</i> , 2023, 8, 162.	0.7	0
12602	Genetic Evidence for Indo-Western Pacific Olive Ridley Sea Turtles in Mexican Waters. <i>Diversity</i> , 2023, 15, 430.	0.7	1
12603	Genetics as a novel tool in mining impact assessment and biomonitoring of critically endangered western chimpanzees in the Nimba Mountains, Guinea. <i>Conservation Science and Practice</i> , 2023, 5, .	0.9	2

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12606	Maternal genetic history of ancient Tibetans over the past 4000 years. <i>Journal of Genetics and Genomics</i> , 2023, 50, 765-775.	1.7	4
12607	Life-history characteristics and historical factors are important to explain regional variation in reproductive traits and genetic diversity in perennial mosses. <i>Annals of Botany</i> , 2023, 132, 29-42.	1.4	3
12608	Virulence and Genetic Types of <i>Blumeria graminis</i> f. sp. <i>hordei</i> in Tibet and Surrounding Areas. <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 363.	1.5	3
12609	New insights into the diversity of cryptobenthic <i>Cirripectes</i> blennies in the Mascarene Archipelago sampled using Autonomous Reef Monitoring Structures (ARMS). <i>Ecology and Evolution</i> , 2023, 13, .	0.8	1
12610	Genetic Diversity in Oilseed and Vegetable Mustard ( <i>Brassica juncea</i> L.) Accessions Revealed by Nuclear and Mitochondrial Molecular Markers. <i>Agronomy</i> , 2023, 13, 919.	1.3	2
12611	Marine Pollutant Tributyltin Affects DNA Methylation and Fitness of Banded Murex ( <i>Hexaplex</i> ) Tj ETQq1 1 0.784314 ggBT /Overlock 10 T	1.6	1
12613	Different waves of postglacial recolonisation and genomic structure of bank vole populations in NE Poland. <i>Heredity</i> , 2023, 130, 269-277.	1.2	1
12614	Genetic Diversity of Dengue Vector <i>Aedes albopictus</i> Collected from South Korea, Japan, and Laos. <i>Insects</i> , 2023, 14, 297.	1.0	0
12615	<i>Aspidistra daibuensis</i> var. <i>longkiauensis</i> , a new variety of <i>Aspidistra</i> (Asparagaceae) from Taiwan, identified through morphological and genetic analyses. <i>PhytoKeys</i> , 0, 222, 129-151.	0.4	0
12616	Genome Scan of Rice Landrace Populations Collected Across Time Revealed Climate Changesâ€™ Selective Footprints in the Genes Network Regulating Flowering Time. <i>Rice</i> , 2023, 16, .	1.7	3
12617	Phylogeographic analysis revealed allopatric distribution pattern and biogeographic processes of the widespread pale chub <i>Opsariichthys acutipinnis-evolans</i> complex (Teleostei: Cyprinidae) in southeastern China. <i>Frontiers in Ecology and Evolution</i> , 0, 11, .	1.1	1
12618	Analysis of genetic diversity and population structure of <i>Babesia gibsoni</i> . <i>Frontiers in Veterinary Science</i> , 0, 10, .	0.9	2
12619	An HLA map of the world: A comparison of HLA frequencies in 200 worldwide populations reveals diverse patterns for class I and class II. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	12
12620	Landscape genetics of the Southern Flying Squirrel ( <i>Glaucomys volans</i> ) in the northeastern United States. <i>Journal of Mammalogy</i> , 0, , .	0.6	0
12621	To all the gar I loved before: range-wide population genetic structure in Alligator gar. <i>Conservation Genetics</i> , 0, , .	0.8	1
12622	Peeping into Mitochondrial Diversity of Andaman Goats: Unveils Possibility of Maritime Transport with Diversified Geographic Signaling. <i>Genes</i> , 2023, 14, 784.	1.0	0
12623	Genetic footprints of a rapid and large-scale range expansion: the case of cyclic common vole in Spain. <i>Heredity</i> , 2023, 130, 381-393.	1.2	2
12624	Climatic oscillation promoted diversification of spinous assassin bugs during Pleistocene glaciation. <i>Evolutionary Applications</i> , 2023, 16, 880-894.	1.5	2

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12625	Update on the genetic diversity and population structure of <i>Echinococcus granulosus</i> in Gansu Province, Tibet Autonomous Region, and Xinjiang Uygur Autonomous Region, Western China, inferred from mitochondrial <i>cox1</i> , <i>nad1</i> , and <i>nad5</i> sequences. <i>Parasitology Research</i> , 2023, 122, 1107-1126.	0.6	0
12627	Geographic isolation and long-distance gene flow influence the genetic structure of the blue fan palm <i>Brahea armata</i> (Arecaceae). <i>Journal of Plant Research</i> , 2023, 136, 277-290.	1.2	0
12628	A 37ÂK SNP array for the management and conservation of Golden Eagles ( <i>Aquila chrysaetos</i> ). <i>Conservation Genetics</i> , 0, , .	0.8	0
12629	Possible species discrimination of a blotched nerite <i>Nerita albicilla</i> with their distribution pattern and demographic history in the Indo-Pacific. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
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12633	âfÿâf^â,³âf³âf%âf^â,¢DNA D-loop é~âÿÿâšâ,^â³Y æÿ“è%â²â½“&lt;l&gt;ZFY&lt;l&gt; é²â¼ââ,ç”~â,âÿ âf ©â,²â,¹âœæ¥â,¹ââ,®âf¥â		
12634	Population Genetic Structure of a Rare Butterfly in a Fragmented South Florida Ecosystem. <i>Insects</i> , 2023, 14, 321.	1.0	0
12635	Wild papaya shows evidence of gene flow from domesticated Maradol papaya in Mexico. <i>Genetic Resources and Crop Evolution</i> , 0, , .	0.8	0
12636	A rangeâ€wide postglacial history of Swiss stone pine based on molecular markers and palaeoecological evidence. <i>Journal of Biogeography</i> , 2023, 50, 1049-1062.	1.4	3
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