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1639	Evolution of mimicry patterns in Metriorrhynchus (Coleoptera: Lycidae): the history of dispersal and speciation in southeast Asia. 2010 , 64, 39-52	38
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1633	Nuclear and mitochondrial sequence data reveal and conceal different demographic histories and population genetic processes in Caribbean reef fishes. 2010 , 64, 3380-97	58
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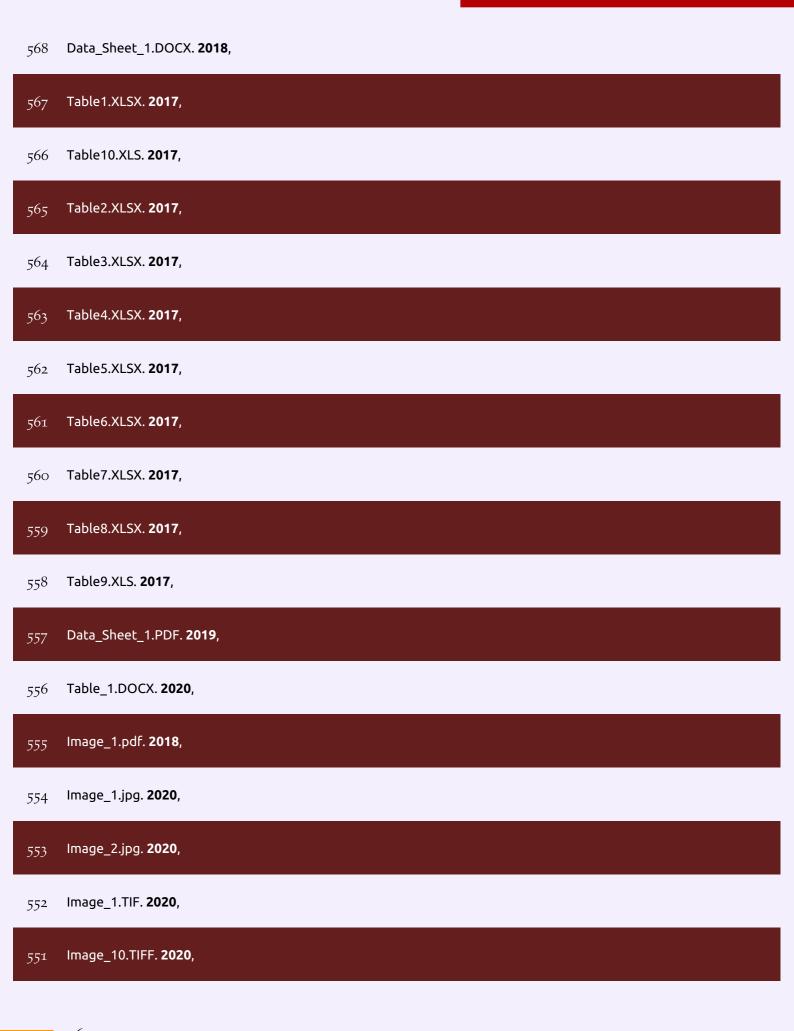
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282	Species Diversity of Cordyceps -Like Fungi in the Tiankeng Karst Region of China.	O
281	Influenza A(H11N2) Virus Detection in Fecal Samples from Adlie (Pygoscelis adeliae) and Chinstrap (Pygoscelis antarcticus) Penguins, Penguin Island, Antarctica.	O

280	Understanding the spatio-temporal dynamics of Anadenanthera colubrina var. cebil in the biogeographical context of Neotropical seasonally dry forest. 2022 , 295, 152149	0
279	Death by massive air sac fluke (Trematoda: Bothriogaster variolaris) infection in a free-ranging snail kite (Rostrhamus sociabilis). 2022 , 19, 155-160	О
278	Resolving the deep phylogeny: Implications for early adaptive radiation, cryptic, and present-day ecological diversity of Papuan microhylid frogs. 2022 , 177, 107618	0
277	Investigations on white spot disease reveal high genetic diversity of the fish parasite, Ichthyophthirius multifiliis (Fouquet, 1876) in China. 2023 , 562, 738804	О
276	Testing Phylogenetic Stability with Variable Taxon Sampling. 2022, 167-188	0
275	Integrative taxonomy reveals a new species of Cyphocharax (Characiformes: Curimatidae) from the Upper Paraßa do Sul River basin, Brazil. 2022 , 20,	О
274	Reconstruction of State-Dependent Diversification: Integrating Phenotypic Traits into Molecular Phylogenies. 2022 , 305-326	0
273	Emergence and Molecular Characterization of an Avian Hepatitis E Virus From Donglan Black Chicken in Southern China. 9,	O
272	New insights into the genetic variability of Fasciola hepatica (Trematoda) in Algeria and relationships with other geographic regions revealed by mitochondrial DNA. 2022 , 59, 152-164	O
271	Molecular archaeology of human cognitive traits. 2022 , 40, 111287	О
270	Emergence of a Reassortant 2.3.4.4b Highly Pathogenic H5N1 Avian Influenza Virus Containing H9N2 PA Gene in Burkina Faso, West Africa, in 2021. 2022 , 14, 1901	О
269	Africal oldest dinosaurs reveal early suppression of dinosaur distribution. 2022, 609, 313-319	2
268	Identification and estimation of sequence variation dynamics of Tomato Leaf curl Palampur virus and betasatellite complex infecting a new weed host. 2022 , 36, 609-619	0
267	Species differentiation in two closely related Neotropical rodents across a transition zone between ecoregions.	1
266	Biogeographic role of the Indonesian Seaway implicated by colonization history of purpleback flying squid, Sthenoteuthis oualaniensis (Lesson, 1830), in the Indo-Pacific Ocean. 9,	0
265	Discovery and Genomic Characterization of a Novel Henipavirus, Angavokely Virus, from Fruit Bats in Madagascar. 2022 , 96,	О
264	The Pyrenees as a cradle of plant diversity: phylogeny, phylogeography and niche modeling of Saxifraga longifolia.	0
263	Variation in Heat Shock Protein 40kDa relates to divergence in thermotolerance among cryptic rotifer species.	o

262	Evolutionary history of the Asplenium scolopendrium complex (Aspleniaceae), a relictual fern with a northern pan-temperate disjunct distribution. 2022 , 137, 183-199	O
261	Genomes From Historic DNA Unveil Massive Hidden Extinction and Terminal Endangerment in a Tropical Asian Songbird Radiation. 2022 , 39,	O
260	Evolutionary dynamics of dengue virus in India.	O
259	The Mitogenome Structure of Righteye Flounders (Pleuronectidae): Molecular Phylogeny and Systematics of the Family in East Asia. 2022 , 14, 805	O
258	The pet trade as a source of non-native decapods: the case of crayfish and shrimps in a thermal waterbody in Hungary. 2022 , 194,	О
257	Spatio-temporal spread and evolution of influenza A (H7N9) viruses. 13,	O
256	Biogeography of Zehneria (Cucurbitaceae) and a New Species from India. 2022 , 47, 738-747	O
255	Infectious bursal disease virus in Western Europe: the rise of reassortant strains as the dominant field threat. 1-31	1
254	Immunoglobulin heavy constant gamma gene evolution is modulated by both the divergent and birth-and-death evolutionary models.	O
253	Plio-Pleistocene climatic change drives allopatric speciation and population divergence within the Scrophularia incisa complex (Scrophulariaceae) of desert and steppe subshrubs in Northwest China. 13,	1
252	From southern Africa and beyond: historical biogeography of the Ledebouriinae (Scilloideae, Asparagaceae).	О
251	Taxonomical review of Prosymna angolensis Boulenger, 1915 (Elapoidea, Prosymnidae) with the description of two new species. 1121, 97-143	O
250	Genomic and geographic diversification of a great-speciator[[Rhipidura rufifrons].	O
249	Global transmission of HIV-1 subtype C and its impact on the circulation of B/C recombination strains in China. Publish Ahead of Print,	O
248	Global mosquito virome profiling and mosquito spatial diffusion pathways revealed by marker-viruses.	O
247	Characterization of the Complete Mitochondrial Genome of Eight Diurnal Hawkmoths (Lepidoptera: Sphingidae): New Insights into the Origin and Evolution of Diurnalism in Sphingids. 2022 , 13, 887	O
246	Integrative taxonomy of the stick insect genus. 2022 , 36, 849-873	О
245	Epidemiological and Genomic Characterisation of Middelburg and Sindbis Alphaviruses Identified in Horses with Febrile and Neurological Infections, South Africa (2014\(\bar{\pi}\)018). 2022 , 14, 2013	O

244	Early evolution and transmission of GII.P16-GII.2 norovirus in China.	1
243	Epidemiological and Phylogeographic Study of Equid Herpesviruses in Tunisia. 2022 , 11, 1016	O
242	Molecular and Morphological Investigations of Two Giant Diatom Cymbella Species from the Transbaikal Area (Russia, Siberia) with Comments on Their Distributions. 2022 , 11, 2445	О
241	Deep vicariance and frequent transoceanic dispersal shape the evolutionary history of a globally distributed fern family.	O
240	Prevalence of S. aureus and/or MRSA from seafood products from Indian seafood products. 2022 , 22,	O
239	Multigene phylogeny, phylogenetic network, and morphological characterizations reveal four new arthropod-associated Simplicillium species and their evolutional relationship. 13,	O
238	Phytest: Quality Control for Phylogenetic Analyses.	O
237	An advanced sequence clustering and designation workflow reveals the enzootic maintenance of a dominant West Nile virus subclade in Germany.	1
236	A DNA barcode library for katydids, cave crickets, and leaf-rolling crickets (Tettigoniidae, Rhaphidophoridae and Gryllacrididae) from Zhejiang Province, China. 1123, 147-171	0
235	Phylodynamics of a regional SARS-CoV-2 rapid spreading event in Colorado in late 2020. 2022 , 17, e0274050	O
234	Plastome phylogenomics and biogeography of the subfam. Polygonoideae (Polygonaceae). 13,	O
233	Systematics of Thraupis (Aves, Passeriformes) reveals an extensive hybrid zone between T. episcopus (Blue-gray Tanager) and T. sayaca (Sayaca Tanager). 2022 , 17, e0270892	O
232	Molecular characterization of pathogenic African trypanosomes in biting flies and camels in surra-endemic areas outside the tsetse fly belt in Kenya.	O
231	Phylogenomics provides insights into the evolution of cactophily and host plant shifts in Drosophila. 2022 , 107653	O
230	Phylogenetic Characterization of HIV-1 Sub-Subtype A1 in Karachi, Pakistan. 2022, 14, 2307	О
229	Species delimitation polyphasic approach reveals Meyerella similis sp. nov.: a new species of amall green balls within the Chlorella-clade (Trebouxiophyceae, Chlorophyta).	O
228	Molecular phylodynamics of fowl adenovirus serotype 11 and 8b from inclusion body hepatitis outbreaks.	О

226	GII.17[P17] and GII.8[P8] noroviruses showed different RdRp activities associated with their epidemic characteristics.	O
225	Ecological and evolutionary trends of body size in Pristimantis frogs, the world's most diverse vertebrate genus. 2022 , 12,	O
224	A New Species of Placoneis Mereschkowsky (Bacillariophyceae: Cymbellales) from Wet Soils in Southern Vietnam. 2022 , 43,	0
223	Wind-dispersed seeds blur phylogeographic breaks: The complex evolutionary history of Populus lasiocarpa around the Sichuan Basin. 2022 ,	О
222	Ancient homomorphy of molluscan sex chromosomes sustained by reversible sex-biased genes and sex determiner translocation.	O
221	Unrecognized species diversity and endemism in the cichlid genus Bujurquina (Teleostei: Cichlidae) together with a molecular phylogeny document large-scale transformation of the western Amazonian river network and reveal complex paleogeography of the Ecuadorian Amazon.	0
220	Phylogeography of Himalrandia lichiangensis from the dry-hot valleys in Southwest China. 13,	O
219	Vivaria calvasensis new genus and species of Araceae (Araceae: Aroidea: Spathicarpeae) from southern Ecuador. 2022 , 17, e0273867	Ο
218	Aphid BCR4 Structure and Activity Uncover a New Defensin Peptide Superfamily. 2022, 23, 12480	1
217	DNA Barcoding and Species Classification of Morchella. 2022 , 13, 1806	Ο
216	Insights into genetic differentiation and migration routes of rhesus macaques (Macaca mulatta) based on samples from almost all distribution areas.	Ο
215	Biogeography and eye size evolution of the ogre-faced spiders. 2022 , 12,	O
214	Molecular Evolution of Metallothioneins of Antarctic Fish: A Physiological Adaptation to Peculiar Seawater Chemical Characteristics. 2022 , 10, 1592	1
213	Evolutionary loss of shell pigmentation, pattern, and eye structure in deep-sea snails in the dysphotic zone.	O
212	Expectation-Maximization enables Phylogenetic Dating under a Categorical Rate Model.	0
211	The Impact of Model Misspecification on Phylogenetic Network Inference.	O
210	Phylogeography reveals a panmictic population of the Chilean nylon shrimp along its exploitation range in the southeast Pacific Ocean.	0
209	Integrative taxonomic analysis of new collections from the central Angolan highlands resolves the taxonomy of African pipistrelloid bats on a continental scale.	O

208	The Genetic Diversity and the Divergence Time in Extant Primitive Mayfly, Siphluriscus chinensis Ulmer, 1920 Using the Mitochondrial Genome. 2022 , 13, 1780	O
207	SOPHIE: Viral outbreak investigation and transmission history reconstruction in a joint phylogenetic and network theory framework. 2022 , 13, 844-856.e4	O
206	Phylogeography and genetic variation in Western Jacob's ladder (Polemonium occidentale) provide insights into the origin and conservation of rare species in the Great Lakes region.	0
205	The Evolution and Global Spatiotemporal Dynamics of Senecavirus A.	O
204	A new species of scops-owl (Aves, Strigiformes, Strigidae, Otus) from Prficipe Island (Gulf of Guinea, Africa) and novel insights into the systematic affinities within Otus. 1126, 1-54	O
203	Molecular phylogeny and divergence time estimates for native giant clams (Cardiidae: Tridacninae) in the Asia-Pacific: Evidence from mitochondrial genomes and nuclear 18S rRNA genes. 9,	O
202	Identification of a new circulating recombinant form of human immunodeficiency virus type 1, CRF124_cpx involving subtypes A, G, H, and CRF27_cpx in Angola. 13,	O
201	Overview of the epidemic history of Hepatitis C uncommon subtypes 2i and 4d in Tunisia and in the world. 2022 , 105, 105375	O
200	No cost but high performanceAn alternative open source solution for 3D-visualizations in morphology.	O
199	Next-Generation Sequencing of Four Mitochondrial Genomes of Dolichovespula (Hymenoptera: Vespidae) with a Phylogenetic Analysis and Divergence Time Estimation of Vespidae. 2022 , 12, 3004	O
198	Genetic variability in the Crocidura kegoensis (L. zaitsevi group (Mammalia, Eulipotyphla) and re-evaluation of C. zaitsevi from Vietnam.	O
197	Molecular and biometric data on Carabus (Macrothorax) morbillosus Fabricius, 1792 (Coleoptera, Carabidae) from Mid Mediterranean areas. 1127, 119-134	O
196	Cryptic and widespread: a recipe for taxonomic misidentification in a freshwater crab species (Decapoda: Potamonautidae: Potamonautes sidneyi) as evident from species delimitation methods.	O
195	Biogeography in the deep: Hierarchical population genomic structure of two beaked whale species. 2022 , 40, e02308	O
194	Morphology, molecular phylogeny, and species delimitation within microalgal genera Eubrownia, Spongiococcum, and Chlorococcum (Chlorophyceae, Chlorophyta). 2022 , 151, 396-409	O
193	Bayesian phylogenetics illuminate shallower relationships among Trans-Himalayan languages in the Tibet-Arunachal area. 2022 , 45, 171-210	O
192	Genetic and structural data on the SARS-CoV-2 Omicron BQ.1 variant reveal its low potential for epidemiological expansion.	1
191	Integrative approach clarifies the distinct taxonomic account of gryloblattids endemic to Hokkaido, Japan, with a description of two new species (Insecta, Grylloblattodea). 2022 ,	O

190	Phylogeny, biogeography, and character evolution in the genus Scilla's.l. and its close relatives Chionodoxa, Gemicia, Puschkinia, and Prospero (Asparagaceae). 2022 , 308,	0
189	Testing assertions of widespread introgressive hybridization in a clade of neotropical toads with low mate selectivity (Rhinella granulosa species group).	О
188	Plastid phylogenomic insights into relationships, divergence, and evolution of Apiales. 2022 , 256,	0
187	Redefinition of the Glyptonsternine genus Pareuchiloglanis (Teleostei: Sisoridae), with descriptions of three new genera.	О
186	Molecular assessment of Ulva (Ulvales, Chlorophyta) diversity in Vietnam including the new species U. vietnamensis.	0
185	Whole-genome sequencing analysis of wild house mice (<i>Mus musculus</i>) captured in Madagascar. 2022 ,	0
184	Evolutionary analyses of polymeric immunoglobulin receptor (pIgR) in the mammals reveals an outstanding mutation rate in the lagomorphs. 13,	0
183	Geographic factors and climatic fluctuation drive the genetic structure and demographic history of Cycas taiwaniana (Cycadaceae), an endemic endangered species to Hainan Island in China. 2022 , 12,	О
182	Characterizing a century of genetic diversity and contemporary antigenic diversity of N1 neuraminidase in IAV from North American swine.	1
181	Peripheral isolation and demographic stability are reflected in the genetic diversity of the populations of the Helmeted Manakin: a bird endemic to the gallery forests. 2022 , 94,	o
180	Macroevolutionary analyses point to a key role of hosts in diversification of the highly speciose eriophyoid mite superfamily. 2023 , 179, 107676	1
179	Abundance and trait-matching both shape interaction frequencies between plants and birds in seed-dispersal networks. 2023 , 66, 11-21	0
178	Monitoring of Avian Influenza Viruses and Paramyxoviruses in Ponds of Moscow and the Moscow Region. 2022 , 14, 2624	2
177	Neontological and paleontological congruence in the evolution of Podocarpaceae (coniferales) reproductive morphology. 10,	O
176	Ancestral area analyses reveal Pleistocene-influenced evolution in a clade of coastal plain endemic plants.	0
175	Spatial and temporal dynamic analysis of rabies: A review of current methodologies. 2022 , 17,	0
174	Interplay of Ecological Opportunities and Functional Traits Drives the Evolution and Diversification of Millettiod Legumes (Fabaceae). 2022 , 13, 2220	0
173	Phylogenetic relationships and divergence times of the poorly known genus Spalerosophis (Serpentes: Colubridae).	o

172	Re-emergence of cholera in Haiti linked to environmentalV. choleraeO1 Ogawa strains.	1
171	Unweaving a hard taxonomic knot in coral reef dwellers: integrative systematics reveals two parallel cryptic species complexes in harbled hrimps of the genus Saron Thallwitz 1891 (Caridea: Hippolytidae).	O
170	Assembly of 43 diverse human Y chromosomes reveals extensive complexity and variation.	0
169	Comparative chloroplast genomics provides insights into the genealogical relationships of endangered Tetraena mongolica and the chloroplast genome evolution of related Zygophyllaceae species. 13,	O
168	Mitochondrial DNA of Sardinian and North-West Italian Populations Revealed a New Piece in the Mosaic of Phylogeography and Phylogeny of Salariopsis fluviatilis (Blenniidae). 2022 , 12, 3403	1
167	Illusion of flight? Absence, evidence and the age of winged insects.	1
166	Macroevolution in axial morphospace: innovations accompanying the transition to marine environments in elapid snakes. 2022 , 9,	1
165	Mitochondrial DNA and Microsatellite Analyses Showed Panmixia between Temporal Samples in Endangered Anguilla japonica in the Pearl River Basin (China). 2022 , 12, 3380	О
164	Diversification and historical demography of Haloxylon ammodendron in relation to Pleistocene climatic oscillations in northwestern China. 10, e14476	0
163	A 2-million-year-old ecosystem in Greenland uncovered by environmental DNA. 2022 , 612, 283-291	O
162	Existence of biogeographic barriers for the long-term NeogeneQuaternary divergence and differentiation of Koenigia forrestii in the HimalayaHengduan Mountains.	0
161	Horizontal transmission of penicillin binding protein 1A caused a nationwide spread of Elactam resistance in pneumococci.	O
160	Commerson dolphin population structure: evidence for female phylopatry and male dispersal. 2022 , 12,	0
159	bayroot: Bayesian sampling of HIV-1 integration dates by root-to-tip regression.	O
158	Species diversity and distribution of genus Pampus (Pelagiaria: Stromateidae) based on global mitochondrial data. 9,	О
157	Origin and evolutionary history of Populus (Salicaceae): Further insights based on time divergence and biogeographic analysis. 13,	O
156	Production of Fluorescent Dissolved Organic Matter by Microalgae Strains from the Ob and Yenisei Gulfs (Siberia). 2022 , 11, 3361	О
155	Extensive reorganization of the chloroplast genome of Corydalis platycarpa: A comparative analysis of their organization and evolution with other Corydalis plastomes. 13,	0

154	Out of Madagascar, repeatedly: The phylogenetics and biogeography of Dombeyoideae (Malvaceae s.l.). 2022 , 107687	О
153	Host-Parasite Relationships of Quill Mites (Syringophilidae) and Parrots (Psittaciformes). 2023 , 15, 1	1
152	Genetic and Structural Data on the SARS-CoV-2 Omicron BQ.1 Variant Reveal Its Low Potential for Epidemiological Expansion. 2022 , 23, 15264	4
151	A new genome of an African weakly electric fish (Campylomormyrus compressirostris, Mormyridae) indicates rapid gene family evolution in Osteoglossomorpha.	O
150	Molecular Basis of the Toxigenic Vibrio cholerae O1 Serotype Switch from Ogawa to Inaba in Haiti.	0
149	A scalable model for simulating multi-round antibody evolution and benchmarking of clonal tree reconstruction methods. 13,	O
148	Phylogenetic relationships of sleeper gobies (Eleotridae: Gobiiformes: Gobioidei), with comments on the position of the miniature genus Microphilypnus. 2022 , 12,	О
147	Taxonomic, functional and phylogenetic diversity of forest mammals mainly associated with elevation range.	O
146	Molecular and cytogenetic evidence for sibling species in the Chagas disease vector Triatoma maculata.	O
145	Species delineation and genetic structure of two Chaerephon species (C. pusillus and C. leucogaster) on Madagascar and the Comoro archipelago. 2022 , 12,	O
144	Evolution and Introductions of Influenza A Virus H1N1 in a Farrow-to-Finish Farm in Guatemala.	О
143	The functional significance of residual yolk in lizards.	O
142	Population structure of mud flounder Paralichthys orbignyanus from the south-western Atlantic Ocean.	О
141	Paratype: a genotyping tool for Salmonella Paratyphi A reveals its global genomic diversity. 2022 , 13,	1
140	Genome-based comparison between the recombinant SARS-CoV-2 XBB and its parental lineages.	1
139	Herbarium Specimen Sequencing Allows Precise Datation of Xanthomonas citripv.citriDiversification History.	О
138	Cryptic Lineage and Genetic Structure of Acanthopagrus pacificus Populations in a Natural World Heritage Site Revealed by Population Genetic Analysis. 2022 , 14, 1117	0
137	DNA barcoding unveils a high diversity of caddisflies (Trichoptera) in the Mount Halimun Salak National Park (West Java; Indonesia). 10, e14182	О

136	Emergence and Evolutionary Response of Vibrio cholerae to Novel Bacteriophage, Democratic Republic of the Congo1. 2022 , 28, 2482-2490	Ο
135	New insights on patterns of genetic admixture and phylogeographic history in Iberian high mountain populations of midwife toads. 2022 , 17, e0277298	O
134	To explore strange new worlds I the diversification in Tremella caloplacae was linked to the adaptive radiation of the Teloschistaceae. 2022 , 107680	О
133	The episodic resurgence of highly pathogenic avian influenza H5 virus.	1
132	Ancient vicariance is reinforced by adaptive divergence in the southern beech: Contributions from geogenomics.	0
131	Species tree estimation under joint modeling of coalescence and duplication: Sample complexity of quartet methods. 2022 , 32,	О
130	Genomic analysis of hypoxia inducible factor alpha in ray-finned fishes reveals missing Ohnologs and evidence of widespread positive selection. 2022 , 12,	О
129	Island life accelerates geographic radiation in the white-eyes (Zosteropidae).	O
128	Molecular Characterization of Leishmania Species among Patients with Cutaneous Leishmaniasis in Asir Province, Saudi Arabia. 2022 , 11, 1472	1
127	The Delta variant wave in Tunisia: Genetic diversity, spatio-temporal distribution and evidence of the spread of a divergent AY.122 sub-lineage. 10,	O
126	Reconstructing the phylodynamic history and geographic spread of the CRF01_AE-predominant HIV-1 epidemic in the Philippines from PR/RT sequences sampled from 2008-2018.	Ο
125	Evolutionary Origin, Genetic Recombination, and Phylogeography of Porcine Kobuvirus. 2023 , 15, 240	Ο
124	Digging into the admixture strata of current-day Canary Islanders based on mitogenomes. 2023 , 26, 105907	0
123	Machine learning and metagenomics enhance surveillance of antimicrobial resistance in chicken production in China.	O
122	WestBast diversification model explains pattern phylogeography of the Band-tailed Manakin Pipra fasciicauda.	0
121	Cosmopolitan abyssal lineages? A systematic study of East Pacific deep-sea squat lobsters (Decapoda: Galatheoidea: Munidopsidae). 2023 , 37, 14	O
120	Phylogeny of Saxifraga section Saxifraga subsection Arachnoideae (Saxifragaceae) and the origin of low elevation shade-dwelling species. 2023 , 13,	0
119	A practical approach to Simulating Heterochronic Sequence Alignments.	О

118	Multidrug resistance plasmids underlie clonal expansions and international spread of Salmonella entericaserotype 4,[5],12,i:- ST34 in Southeast Asia.	0
117	Time-calibrated phylogenies reveal mediterranean and pre-mediterranean origin of the thermophilous vegetation of the Canary Islands.	O
116	Widespread and ongoing invasion by the ant Technomyrmex brunneus Forel in eastern Asia as elucidated by molecular data.	0
115	Diversity and distribution of mitochondrial DNA in non-Austronesian-speaking Taiwanese individuals. 2023 , 10,	O
114	Introgressive Descent and Hypersexuality Drive The Evolution Of Sexual Parasitism and Morphological Reduction In a Fungal Species Complex.	О
113	Evolutionary rate of SARS-CoV-2 increases during zoonotic infection of farmed mink.	1
112	Diversification in the mountains: Evolutionary history and molecular phylogeny of Anatolian rock lizards. 2023 , 180, 107675	0
111	A new bunting species in South China revealed by an integrative taxonomic investigation of the Emberiza godlewskii complex (Aves, Emberidae). 2023 , 180, 107697	Ο
110	Comparative Phylogeography in the Taiwan Iluzon Volcanic Belt Indicates Fast Diversification History of Pachyrhynchus Weevils (Coleoptera: Curculionidae). 2022 , 6,	0
109	Insights into HIV-1 Transmission Dynamics Using Routinely Collected Data in the Mid-Atlantic United States. 2023 , 15, 68	Ο
108	Out of the Qinghai-Tibetan plateau: Origin, evolution and historical biogeography of Morchella (both Elata and Esculenta clades). 13,	0
107	Variation in heat shock protein 40 kDa relates to divergence in thermotolerance among cryptic rotifer species. 2022 , 12,	O
106	Tracing the relationship among HIV-1 sub-subtype F1 strains: a phylodynamic perspective. 117,	О
105	Genetic Variation and Phylogeography of Lumbriculus variegatus (Annelida: Clitellata: Lumbriculidae) Based on Mitochondrial Genes. 2023 , 15, 158	O
104	Phylogenomics of trans-Andean tetras of the genus Hyphessobrycon Durbin 1908 (Stethaprioninae: Characidae) and colonization patterns of Middle America. 2023 , 18, e0279924	0
103	Toxic effect of copper on soil microalgae: experimental data and critical review.	Ο
102	Phylogeography as a Proxy for Population Connectivity for Spatial Modeling of Foot-and-Mouth Disease Outbreaks in Vietnam. 2023 , 15, 388	0
101	The dawn of relaxed phylogenetics. 2023 , 21, e3001998	O

100	Next-Generation Sequencing in the Study of Infectious Diseases. 2023 , 35-56	О
99	Plagued by a cryptic clock: insight and issues from the global phylogeny of Yersinia pestis. 2023 , 6,	O
98	Relationship between fruit phenotypes and domestication in hexaploid populations of birib[] (Annona mucosa) in Brazilian Amazonia. 11, e14659	O
97	Phylogenetics and phylogeography of Euphorbia canariensis reveal an extreme Canarian-Asian disjunction and limited inter-island colonization.	O
96	Genetic diversity and structure of Brycon henni in regulated and non-regulated water flow rivers of the Colombian Andes. 11,	О
95	Traditional taxonomy underestimates the number of species of Bokermannohyla (Amphibia: Anura: Hylidae) diverging in the mountains of southeastern Brazil since the Miocene. 2023 , 21,	O
94	Genetic evidence for widespread population size expansion in North American boreal birds prior to the Last Glacial Maximum. 2023 , 290,	1
93	Systematics of Ditaxinae and Related Lineages within the Subfamily Acalyphoideae (Euphorbiaceae) Based on Molecular Phylogenetics. 2023 , 12, 173	1
92	Climacocystaceae fam. nov. and Gloeoporellaceae fam. nov., two new families of Polyporales (Basidiomycota). 14,	О
91	Genetic diversity, phylogenetic and phylogeographic analyses of Oncideres impluviata (Germar, 1823) (Coleoptera: Cerambycidae) in Rio Grande do Sul state, Brazil. 2023 , 67,	O
90	New species of Rhyacoglanis (Siluriformes: Pseudopimelodidae) from the upper rio Tocantins basin. 2023 , 21,	О
89	Global expansion of a solitary-social tropical spitting spider shaped by multiple long-distance dispersals. 2023 , 2023,	O
88	Distimake vitifolius(Convolvulaceae): reclassification of a widespread species in view of phylogenetics and convergent pollen evolution.	О
87	Best practice for wildlife gut microbiome research: A comprehensive review of methodology for 16S rRNA gene investigations. 14,	O
86	Contrasting patterns of population structure of Bulwerl petrel (Bulweria bulwerii) between oceans revealed by statistical phylogeography. 2023 , 13,	О
85	Convergence of resistance and evolutionary responses inEscherichia coliandSalmonella entericaco-inhabiting chicken farms in China.	O
84	Cases of paternal inheritance and recombination of mictochondria in peas (Pisum L.).	О
83	Molecular phylogenetics and diversity of the Himalayan shrew (Soriculus nigrescens Gray, 1842) (Eulipotyphla, Soricidae) in Southwest China. 2023 , 5263, 061-078	O

82	H10Nx avian influenza viruses detected in wild birds in China pose potential threat to mammals. 2023 , 16, 100515	О
81	Is it inappropriate to ask for your age? Evaluating parameter impact on tree dating in a challenging clade (Macroscelidea). 2023 , 183, 107756	O
80	Systematics of the Stripetail Darter, Etheostoma kennicotti (Putnam), and the Distinctiveness of the Upper Cumberland Endemic Etheostoma cumberlandicum Jordan and Swain. 2023 , 111,	О
79	Interspecific sociality alters the colonization and extinction rates of birds on subtropical reservoir islands. 2023 , 378,	1
78	Molecular phylogenetics shed light on polyploid speciation in gorses (Ulex, Fabaceae: Genisteae) and on the origin of the invasive Ulex europaeus.	O
77	Still Many to Be Named: An Integrative Analysis of the Genus Dendronotus (Gastropoda: Nudibranchia) in the North Pacific Revealed Seven New Species. 2023 , 15, 162	O
76	Allopatric mosaics in the Indo-West Pacific crab subfamily Chlorodiellinae reveal correlated patterns of sympatry, genetic divergence, and genitalic disparity. 2023 , 181, 107710	0
75	Sequence analysis of SARS-CoV-2 Delta variant isolated from Makassar, South Sulawesi, Indonesia. 2023 , 9, e13382	O
74	Deciphering complex reticulate evolution of AsianBuddleja(Scrophulariaceae): insights into the taxonomy and speciation of polyploid taxa in the Sino-Himalayan region.	0
73	Novel Deletion in Exon 7 of Betaine Aldehyde Dehydrogenase 2 (BADH2). 2023 , 30, 104-112	O
72	Investigations on SARS-CoV-2 and other coronaviruses in mink farms in France at the end of the first year of COVID-19 pandemic.	O
71	Global population genetic structure and lineage differentiation of the stable fly, Stomoxys calcitrans.	O
70	The possible region of the Late Miocene split of the sandfly subgenus Transphlebotomus Artemiev and the early late Neogene to late Quaternary dispersal of the ancestor of Phlebotomus mascittii Grassi.	О
69	New Incidets into Blackid and Mitochandria Evolution in Wild Door (Disum L.) 2022, 15, 216	
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