Citation Report

List of articles citing

New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0

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738	Operculina and Neoassilina: A Revision of Recent Nummulitid Genera Based on Molecular and Morphological Data Reveals a New Genus.	0
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725	Phylogenetic Characterization of HIV-1 Sub-Subtype A1 in Karachi, Pakistan. **2022**, 14, 2307	0
724	Antiviral immune response reveals host-specific virus infections in natural ant populations.	0
723	Diversity of Genotyping Chlamydia Trachomatis Serovars in Urogenital Samples from Mexican Patients: A Molecular and Bioinformatic Characterization. **2023**, 127-135	0
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721	Chromosome-Level Assembly of Male Opsariichthys bidens Genome Provides Insights into the Regulation of the GnRH Signaling Pathway and Genome Evolution. **2022**, 11, 1500	0
720	Genomic evidence supports genetic convergence of a supergene controlling the distylous floral syndrome.	0
719	Reclassification of probioticLactobacillus acidophilusNCIMB 30184 asLactobacillus helveticusandLactobacillus caseiNCIMB 30185 asLacticaseibacillus paracasei.	0
718	A near-complete species-level phylogeny of uropeltid snakes harnessing historical museum collections as a DNA source. **2022**, 107651	0
717	Evolution of sperm morphology in a crustacean genus with fertilization inside an open brood pouch. 2,	0
716	One new species of Comesoma Bastian, 1865 (Nematoda: Araeolaimida: Comesomatidae) and redescription with molecular characterisation of Sphaerolaimus callisto Zograf, Pavlyuk, Trebukhova & Nguyen, 2020 (Nematoda: Monhysterida: Sphaerolaimidae) from the South China Sea. **2022**, 1-17	0
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713	Rapid evolution of an RNA virus to escape recognition by a rice NLR immune receptor.	1
712	Comparative and Phylogenetic Analysis of Chloroplast Genomes of Two Medicinal Species of Spatholobus.	0
711	A new edible species of <i>Gomphus</i> (<i>Gomphaceae</i>) from southwestern China. **2022**,	0
710	Strains of Bradyrhizobium barranii sp. nov. associated with legumes native to Canada are symbionts of soybeans and belong to different subspecies (subsp. barranii subsp. nov. and subsp. apii subsp. nov.) and symbiovars (sv. glycinearum and sv. septentrionale). **2022**, 72,	0
709	Evolution of LysM-RLK Gene Family in Wild and Cultivated Peanut Species. **2022**, 8, 1000	0

708	The identity ofArgyria lacteella(Fabricius, 1794) (Lepidoptera, Pyraloidea, Crambinae), synonyms, and related species using morphology and DNA capture in type specimens.	0
707	Hyporthodus griseofasciatus (Perciformes: Epinephelidae), a new species of deep-water grouper from the west coast of Australia.	0
706	Morphology, morphogenesis and molecular phylogeny of Lamtostyla granulifera sinensis subsp. nov. (Ciliophora, Hypotrichia) from a wetland in China. **2022**, 125938	0
705	Undescribed Diversity in a Widespread, Common Group of Asian Mud Snakes (Serpentes: Homalopsidae: Hypsiscopus). **2022**, 110,	0
704	Straw-Colored Fruit Bats (Eidolon helvum) and Their Bat Flies (Cyclopodia greefi) in Nigeria Host Viruses with Multifarious Modes of Transmission.	0
703	Cecinothofagus Nieves-Aldrey &amp; Liljeblad (Hymenoptera, Cynipidae) is likely an endoparasitoid of the gall-maker genus Aditrochus R�bsaamen (Hymenoptera, Pteromalidae). 93, 33-42	0
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701	Monogenoidean parasites of the nasal cavities of Bryconops melanurus (Characiformes: Iguanodectidae) of the coastal drainages of the Eastern Amazon, Brazil: Proposal of Guamacotyle forficata n. gen. n. sp. (Polyonchoinea: Dactylogyridae).	0
700	Preparation and Characterization of an Ancient Aminopeptidase Obtained from Ancestral Sequence Reconstruction for L-Carnosine Synthesis. **2022**, 27, 6620	0
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695	Phylogenomics reveals the relationships of butterflies and moths (Lepidoptera): providing the potential landscape using universal single copy orthologues.	0
694	The wtf meiotic driver gene family has unexpectedly persisted for over 100 million years. 11,	1
693	Prediction of a conserved pheromone receptor lineage from antennal transcriptomes of the pine sawyer genus Monochamus (Coleoptera: Cerambycidae).	0
692	Shedding Light on the Origin of Egyptian Sheep Breeds by Evolutionary Comparison of Mitochondrial D-Loop. **2022**, 12, 2738	0
691	Cladomorphus petropolisensis, a New Species of Stick Insect from the Atlantic Forest, Rio de Janeiro, Brazil. **2022**, 12, 2871	0

690	A fungal lytic polysaccharide monooxygenase is required for cell wall integrity, thermotolerance, and virulence of the fungal human pathogenCryptococcus neoformans.	0
689	Update: Assessing the evolutionary trajectory of the Apaporis caiman (Caiman crocodilus apaporiensis, Medem 1955) via mitochondrial molecular markers.	0
688	Hidden diversity of the genus Trinomys (Rodentia: Echimyidae): phylogenetic and populational structure analyses uncover putative new lineages.	0
687	Genome-scale analysis of Arabidopsis splicing-related protein kinase families reveals roles in abiotic stress adaptation. **2022**, 22,	0
686	Multilocus Phylogeography and Population Genetic Analyses of Opsariichthys hainanensis Reveal Pleistocene Isolation Followed by High Gene Flow around the Gulf of Tonkin. **2022**, 13, 1908	1
685	Diversity, Phylogenetic Relationships and Distribution of Marsh Frogs (the Pelophylax ridibundus complex) from Kazakhstan and Northwest China. **2022**, 14, 869	0
684	Brenneria tiliae sp. nov., isolated from symptomatic Tilia moltkei and Tilia europaea trees in the UK. **2022**, 72,	1
683	Expectation-Maximization enables Phylogenetic Dating under a Categorical Rate Model.	0
682	An insight into mitochondrial genomes of Trichoderma afroharzianum strains: a comparative and evolutionary analysis.	0
681	De novo genome assembly and annotation of Holothuria scabra (Jaeger, 1833) from nanopore sequencing reads.	0
680	Polyphasic evaluation and cytotoxic investigation of isolated cyanobacteria with an emphasis on potent activities of a Scytonema strain. 13,	0
679	A putative bifunctional CPD/ (6-4) photolyase from the cyanobacteria Synechococcus sp. PCC 7335 is encoded by a UV-B inducible operon: New insights into the evolution of photolyases. 13,	0
678	Common but Nonpersistent Acquisitions of Plant Viruses by Plant-Associated Fungi. **2022**, 14, 2279	2
677	Comparison Study on Wild and Cultivated Opuntia sp.: Chemical, Taxonomic, and Antioxidant Evaluations. **2022**, 12, 1755	1
676	Viral Small Terminase: A Divergent Structural Framework for a Conserved Biological Function. **2022** , 14, 2215	2
675	Genome sequence of the entomopathogenic Serratia entomophila isolate 626 and characterisation of the species specific itaconate degradation pathway. **2022**, 23,	0
674	Engineering indel and substitution variants of diverse and ancient enzymes using Graphical Representation of Ancestral Sequence Predictions (GRASP). **2022**, 18, e1010633	1
673	Probing the origin of prion protein misfolding via reconstruction of ancestral proteins.	0

672	SOPHIE: Viral outbreak investigation and transmission history reconstruction in a joint phylogenetic and network theory framework. **2022**, 13, 844-856.e4	0
671	Bioinformatics approaches for classification and investigation of the evolution of the Na/K-ATPase alpha-subunit. **2022**, 22,	0
670	Chara zhengzhouensis (Characeae, Charophyta), a New Freshwater Algal Species Described from North China. **2022**, 14, 864	0
669	Massive genome investigations reveal insights of prevalent introgression for environmental adaptation and triterpene biosynthesis in Ganoderma.	0
668	Coordinated adaptations define the ontogenetic shift from worm- to fish-hunting in a venomous cone snail.	0
667	Genomic Characterisation of Canis Familiaris Papillomavirus Type 24, a Novel Papillomavirus Associated with Extensive Pigmented Plaque Formation in a Pug Dog. **2022**, 14, 2357	0
666	Morphological and molecular diversity of monothalamids (Rhizaria, Foraminifera), including two new species and a new genus, from SW Greenland. **2022**, 125932	0
665	Molecular and morphological evidence reveals a new fern species of Hymenasplenium (Aspleniaceae) from south and southwestern China. 211, 93-106	0
664	Identification of RNA virus-derived RdRp sequences in publicly available transcriptomic datasets.	1
663	Tempo and Mode of Floristic Exchanges between Hainan Island and Mainland Asia: A Case Study of the Persea Group (Lauraceae). **2022**, 13, 1722	0
662	An Unwanted Association: The Threat to Papaya Crops by a Novel Potexvirus in Northwest Argentina. **2022**, 14, 2297	0
661	Identifikasi dan Kekerabatan Rhizobia Pohon Mangium dan Sengon Berdasarkan nodD1 dan nifH. **2022**, 27, 627-633	0
660	Complex statistical modelling for phylogenetic inference.	0
659	Characterization of novel of temperate phages of Staphylococcus aureus isolated from bovine milk. **2022**, 204,	0
658	Evolution of increased complexity and specificity at the dawn of form I Rubiscos. **2022**, 378, 155-160	2
657	Non-triplet genetic code inEuplotesciliates is a result of neutral evolution.	0
656	Recapitulating the life cycle of the global pathogenEntamoebain mice.	0
655	A New Species of the Genus Microhyla (Amphibia: Anura: Microhylidae) from the Dabie Mountains, China. **2022**, 12, 2894	1

654	Diversity of myxozoans parasitizing the catfish Rhamdia quelen (Siluriformes: Heptapteridae), in southeastern Brazil, based on morphological and molecular evidence. **2022**, 12,	0
653	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,	0
652	Morphological, Molecular and Metabolic Characterization of the Pigmented Fungus Subramaniula asteroids. **2022**, 8, 1149	0
651	Detection of beak and feather disease virus in india and its implications.	0
650	Complete Mitochondrial Genomes and Phylogenetic Positions of Two Longicorn Beetles, Anoplophora glabripennis and Demonax pseudonotabilis (Coleoptera: Cerambycidae). **2022**, 13, 1881	0
649	Increased cases of influenza C virus in children and adults in Austria, 2022.	0
648	MAST: Phylogenetic Inference with Mixtures Across Sites and Trees.	0
647	De novo assembly and characterization of the complete chloroplast genome of Elymus magellanicus (▯Desv.) ▯L▯e, 1984 (Poaceae, Pooideae). **2022**, 7, 1873-1875	0
646	Red fox (Vulpes vulpes) play an important role in the propagation of tick-borne pathogens. **2022**, 102076	1
645	Non-lactose fermenting Escherichia coli: Following in the footsteps of lactose fermenting E. coli high-risk clones. 13,	0
644	Chromosome-level genome assembly of the bar-headed goose (Anser indicus). **2022**, 9,	0
643	Analysis of Homologous Regions of Small RNAs MIR397 and MIR408 Reveals the Conservation of Microsynteny among Rice Crop-Wild Relatives. **2022**, 11, 3461	3
642	BACTERIAL NADQ (COG4111) IS A NUDIX-LIKE, ATP-RESPONSIVE REGULATOR OF NAD BIOSYNTHESIS. **2022**, 107917	0
641	The complete chloroplast genome sequence of the water fern Ceratopteris thalictroides (Pteridaceae). **2022**, 7, 1904-1906	0
640	Morphology and molecular phylogeny of Keronopsis koreana n. sp. (Ciliophora, Hypotricha), a new soil species from South Korea. **2022**, 125939	0
639	Biogeographical events, not cospeciation, might be the main drivers in the historical association between Noctiliostrebla species (Streblidae) and their bulldog bat hosts.	0
638	Late Pleistocene landscape changes and habitat specialization as promoters of population genomic divergence in Amazonian floodplain birds.	0
637	Genome mining reveals abiotic stress resistance genes in plant genomes acquired from microbes via HGT. 13,	0

636	Cryptic diversity of Oxythyrea flower chafers and its implication for conservation of non-forest biotopes in the Balkans.	0
635	Molecular characteristics of glutathione transferase gene family in a neglect medical Spirometra tapeworm. 9,	0
634	Molecular Detection and Phylogenetic Analyses of Diverse Bartonella Species in Bat Ectoparasites Collected from Yunnan Province, China. **2022**, 11, 1283	0
633	Complete genome analysis reveals evolutionary history and temporal dynamics of Marek’s disease virus. 13,	1
632	Complete mitochondrial genomes and updated divergence time of the two freshwater clupeids endemic to Lake Tanganyika (Africa) suggest intralacustrine speciation. **2022**, 22,	0
631	Molecular phylogeny of Columbellidae (Gastropoda: Neogastropoda). 10, e13996	0
630	Whole genome sequencing of the fast-swimming Southern bluefin tuna (Thunnus maccoyii). 13,	0
629	New genetic information and geographic distribution of charismatic carnivores: the olingos (Procyonidae: Bassaricyon) in Colombia.	0
628	Antigenic Characterization and Pandemic Risk Assessment of North American H1 Influenza A Viruses Circulating in Swine.	0
627	European and Mediterranean Myzocallidini Aphid Species: DNA Barcoding and Remarks on Ecology with Taxonomic Modifications in An Integrated Framework. **2022**, 13, 1006	0
626	Genome-wide association studies identify an association of transferrin binding protein B variation and invasive serogroup Y meningococcal disease in older adults.	0
625	First rhyncaphytoptine mite (Eriophyoidea, Diptilomiopidae) parasitizing American hazelnut (Corylus americana): molecular identification, confocal microscopy, and phylogenetic position.	1
624	Epidemiology of tick-borne pathogens of cattle and tick control practices in coastal Kenya. **2022**, 209, 105777	0
623	A preliminary study on the feasibility of industrialization for n-caproic acid recovery from food wastewater: From lab to pilot. **2022**, 366, 128154	0
622	The applications of machine learning in HIV neutralizing antibodies research：A systematic review. **2022**, 134, 102429	0
621	A partial duplication of an X-linked gene exclusive of a primate lineage (Macaca). **2023**, 851, 146997	0
620	Can avian flyways reflect dispersal barriers of clinostomid parasites? First evidence from the mitogenome of Clinostomum complanatum. **2023**, 851, 146952	0
619	The Soursop Genome (Annona muricata L., Annonaceae). **2022**, 149-174	0

618	Mitogenome of a monotypic genus, Oliotius Kottelat, 2013 (Cypriniformes: Cyprinidae): Genomic characterization and phylogenetic position. **2023**, 851, 147035	1
617	Concordance and Discordance in the Phylogenomics of the Wrasses and Parrotfishes (Teleostei: Labridae).	1
616	May Sulfonamide Inhibitors of Carbonic Anhydrases from Mammaliicoccus sciuri Prevent Antimicrobial Resistance Due to Gene Transfer to Other Harmful Staphylococci?. **2022**, 23, 13827	3
615	Is the Intergenic Region of Aedes aegypti Totivirus a Recombination Hotspot?. **2022**, 14, 2467	0
614	Well-known species, unexpected results: high genetic diversity in declining Vipera ursinii in central, eastern and southeastern Europe. **2022**, 1-17	0
613	Massive gene rearrangements of mitochondrial genomes and implications for the phylogeny of Trichoptera (Insecta).	2
612	Forensic Analysis of Novel SARS2r-CoV Identified in Game Animal Datasets in China Shows Evolutionary Relationship to Pangolin GX CoV Clade and Apparent Genetic Experimentation. **2022**, 2, 882-904	0
611	Co-circulation of alpha- and beta- coronaviruses in Pteropus vampyrus flying foxes from Indonesia.	0
610	Initiation of speciation across multiple dimensions in a rock-restricted, tropical lizard.	1
609	Viruses in sanctuary chimpanzees across Africa.	0
608	Morphospecies and molecular diversity of □lace corals□the genus Reteporella (Bryozoa: Cheilostomatida) in the central North Atlantic Azores Archipelago. **2022**, 22,	0
607	First detection of Chlamydia avium in healthy Amazon parrots (Amazona aestiva) in Argentina.	0
606	Comparative and pangenomic analysis of the genus Streptomyces. **2022**, 12,	0
605	The complete chloroplast genome of Primula odontocalyx, a heterostylous species. **2022**, 7, 1979-1982	0
604	Evaluation of tangential flow filtration coupled to long-read sequencing for ostreid herpesvirus type 1 genome assembly. **2022**, 8,	0
603	Meta-transcriptional Detection of Rickettsia canadensis from Ixodes persulcatus in China.	0
602	Eucorna sanarita (Schaus) (Riodinidae: Riodininae): Distribution, systematic position, and conservation of a threatened brazilian butterfly in the Atlantic Forest biodiversity hotspot.	0
601	Drug Resistance to Integrase Strand-Transfer Inhibitors among HIV-1-Infected Adults in Guangdong, China. **2022**, 11, 1321	0

600	Hidden Diversity within Tetralophozia filiformis (Marchantiophyta, Anastrophyllaceae) in East Asia. **2022**, 11, 3121	1
599	Distant genetic variants of Anaplasma phagocytophilum from Ixodes ricinus attached to people.	0
598	Analysis of R Genes Related to Blackcurrant Reversion Virus Resistance in the Comparative Transcriptome of Ribes nigrum cv. Aldoniai. **2022**, 11, 3137	1
597	New hosts for a snake's helminth: First report of intermediate and definitive hosts naturally infected by Ophidascaris arndti (Ascarididae) in the wild. **2022**,	0
596	Investigation of B-atp6-orfH79 distributing in Chinese populations of Oryza rufipogon and analysis of its chimeric structure.	0
595	Assessment of the Genetic Distinctiveness and Uniformity of Pre-Basic Seed Stocks of Italian Ryegrass Varieties. **2022**, 13, 2097	0
594	Reconstitution of an N-AChR from Brugia malayi an evolved change in acetylcholine receptor accessory protein requirements in filarial parasites. **2022**, 18, e1010962	0
593	Mitochondrial DNA variation of the caracal (Caracal caracal) in Iran and range-wide phylogeographic comparisons.	0
592	Transfer of Erwinia toletana and Erwinia iniecta to a novel genus Winslowiella gen. nov. as Winslowiella toletana comb. nov. and Winslowiella iniecta comb. nov. and description of Winslowiella arboricola sp. nov., isolated from bleeding cankers on broadleaf hosts. 13,	1
591	Complete Mitogenomes of Ticks Ixodes acutitarsus and Ixodes ovatus Parasitizing Giant Panda: Deep Insights into the Comparative Mitogenomic and Phylogenetic Relationship of Ixodidae Species. **2022**, 13, 2049	0
590	Near-shore island lizard fauna shaped by a combination of human-mediated and natural dispersal.	1
589	Genetic diversity of the tomato russet mite supporting oligophagy and evidencing widespread of an invasive haplotype.	0
588	Chromosome-level genome assembly reveals potential epigenetic mechanisms of the thermal tolerance in the oriental fruit fly, Bactrocera dorsalis. **2022**,	0
587	A New Species of Myxobolus (Cnidaria: Myxosporea: Myxobolidae) from the Fins of the Western Creek Chubsucker, Erimyzon claviformis (Cypriniformes: Catostomidae), from Arkansas. **2022**, 108,	0
586	Intra-Patient Evolution of HIV-2 Molecular Properties. **2022**, 14, 2447	0
585	Fungicolous Fungi on Pseudosclerotial Plates and Apothecia of Hymenoscyphus fraxineus and Their Biocontrol Potential. **2022**, 10, 2250	0
584	Ancestral APOBEC3B Nuclear Localization Is Maintained in Humans and Apes and Altered in Most Other Old World Primate Species.	0
583	Endo-parasitoid lifestyle promotes endogenization and domestication of dsDNA viruses.	0

582	Molecular phylogenetics and systematics of two enteric helminth parasites (Baylisascaris laevis and Diandrya vancouverensis) in the Vancouver Island marmot (Marmota vancouverensis). **2022**,	0
581	High prevalence of qnrVC variants in Vibrio spp. isolated from food samples in South China. **2022**, 127261	0
580	Evolutionary Trajectories of Avian Avulaviruses and Vaccines Compatibilities in Poultry. **2022**, 10, 1862	0
579	Phylogenomic and comparative genomic studies robustly demarcate two distinct clades of Pseudomonas aeruginosa strains: proposal to transfer the strains from an outlier clade to a novel species Pseudomonas paraeruginosa sp. nov.. **2022**, 72,	0
578	CrusTome: A transcriptome database resource for large-scale analyses across Crustacea.	0
577	Complete Mitochondrial Genome Analysis of Daphniopsis tibetana (Branchiopoda: Diplostraca): New Insights into the Taxonomy of the Genus and Its Phylogenetic Implications for Branchiopoda. **2022**, 21, 1622-1632	0
576	Genetic Diversity and Possible Origins of the Hepatitis B Virus in Siberian Natives. **2022**, 14, 2465	0
575	Prevalence, Infection Intensity and Molecular Diagnosis of Mixed Infections with Metastrongylus spp. (Metastrongylidae) in Wild Boars in Uzbekistan. **2022**, 11, 1316	0
574	Aim18p and Aim46p are CHI-domain-containing mitochondrial hemoproteins in Saccharomyces cerevisiae..	0
573	Genotyping-by-sequencing reveals range expansion of Adonis vernalis (Ranunculaceae) from Southeastern Europe into the zonal Euro-Siberian steppe. **2022**, 12,	0
572	Genetic Diversity and Characterization of Circular Replication (Rep)-Encoding Single-Stranded (CRESS) DNA Viruses.	1
571	Target enrichment of long open reading frames and ultraconserved elements to link microevolution and macroevolution in non-model organisms.	0
570	Introducing the Bacterial and Viral Bioinformatics Resource Center (BV-BRC): a resource combining PATRIC, IRD´and ViPR.	10
569	Genomic remnants of ancestral methanogenesis and hydrogenotrophy in Archaea drive anaerobic carbon cycling. **2022**, 8,	0
568	A massive bloom of Karenia species (Dinophyceae) off the Kamchatka coast, Russia, in the fall of 2020. **2022**, 120, 102337	2
567	MSClustering: A Cytoscape Tool for Multi-Level Clustering of Biological Networks. **2022**, 23, 14240	0
566	Aedes aegypti Totivirus identified in mosquitoes in the Brazilian Amazon region.	0
565	Molecular epidemiology of Ralstonia pseudosolanacearum phylotype I strains in the South West Indian Ocean region and their relatedness to African strains.	0

564	The complete mitochondrial genome of the terrestrial snail Monacha cartusiana (O.F. M�ler, 1774) (Gastropoda, Eupulmonata, Hygromiidae). 1130, 65-78	0
563	Genetic diversity in Babesia bovis from southern Africa and estimation of B. bovis infection levels in cattle using an optimised quantitative PCR assay. **2022**, 102084	0
562	Reaction Mechanism of Ancestral l-Lys �Oxidase from Caulobacter Species Studied by Biochemical, Structural, and Computational Analysis.	0
561	Characterizing a century of genetic diversity and contemporary antigenic diversity of N1 neuraminidase in IAV from North American swine.	1
560	Phlebovirus diversity in ticks from livestock in arid ecologies in Kenya. **2022**, 102087	0
559	No phylogenomic support for a Cenozoic origin of the �iving fossil�soetes.	1
558	Evolutionary and structural aspects of Solanaceae RNases T2. **2023**, 46,	0
557	Comparative´study between´molecular and´genetic´evolutionary´analysis´tools´using African SARS-CoV-2´variants. **2023**, 36, 101143	0
556	Ancient origin and conserved gene function in terpene pheromone and defense evolution of stink bugs and hemipteran insects. **2023**, 152, 103879	1
555	A MYB transcription factor containing fragment introgressed from Gossypium bickii confers pink flower on Gossypium hirsutum L.. **2023**, 192, 116121	0
554	Genomic organization and gene evolution of two warm temperature acclimation proteins (Wap65s) of Micropterus salmoides and their responses to temperature and bacterial/viral infections. **2023**, 227, 340-353	0
553	A new species of the genus Nebalia (Crustacea: Phyllocarida: Leptostraca) from hydrothermal vent fields of the submarine Piip Volcano (the southwestern Bering Sea) described through molecular and morphological analysis. **2023**, 207, 105237	0
552	Genome-wide evolutionary analysis of AUX/IAA gene family in wheat identifies a novel gene TaIAA15-1A regulating flowering time by interacting with ARF. **2023**, 227, 285-296	0
551	Bacterial diversity on stained glass windows. **2023**, 177, 105529	0
550	Neuronal expression of ndst3 in early zebrafish development is responsive to Wnt signaling manipulation. **2023**, 47, 119300	0
549	Dispersal limitation and host selection drive geo-specific and plant-specific differentiation of soil bacterial communities in the Tibetan alpine ecosystem. **2023**, 863, 160944	0
548	Prediction and verification of glycosyltransferase activity by bioinformatics analysis and protein engineering. **2023**, 4, 101905	0
547	Fungal Planet description sheets: 1436�477. **2022**,	0

546	Identification of stress-related characteristics of the <i>WRKY</i> gene family: A case study of <i>Dendrobium catenatum</i>. **2022**, 2, 1-15	0
545	Mitigation of Paddy Field Soil Methane Emissions by Betaproteobacterium <i>Azoarcus</i> Inoculation of Rice Seeds. **2022**, 37, n/a	0
544	Molecular revision of Rhagiini sensu lato (Coleoptera, Cerambycidae): Paraphyly, intricate evolution and novel taxonomy. **2022**, 30, 295-309	0
543	New Mitogenome Features of Philopotamidae (Insecta: Trichoptera) with Two New Species of Gunungiella. **2022**, 13, 1101	0
542	Activation of pheromone-sensitive olfactory neurons by plant volatiles in the moth Agrotis ipsilon does not occur at the level of the pheromone receptor protein. 10,	0
541	ddRADseq reveals the relationships of harakeke and wharariki (Phormium species, Asphodelaceae) and selected weaving cultivars in Aotearoa New Zealand.	0
540	Assessment of the phylogenetic relationships within the spondylidine branch of Spondylidinae (Coleoptera, Cerambycidae). **2022**, 1-31	0
539	Rouxiella badensis, a new bacterial pathogen of onion causing bulb rot. 13,	0
538	Tyroviruses are a new group of temperate phages that infect Bacillus species in soil environments worldwide. **2022**, 23,	1
537	Meta-analysis of Antarctic phylogeography reveals strong sampling bias and critical knowledge gaps. **2022**, 2022,	1
536	Genomic basis of the giga-chromosomes and giga-genome of tree peony Paeonia ostii. **2022**, 13,	0
535	ITS1 and cpb genetic polymorphisms in Algerian and Tunisian Leishmania infantum isolates from humans and dogs.	0
534	Recurrent co-domestication of PIF/Harbinger transposable element proteins in insects. **2022**, 13,	0
533	Apoptotic-like PCD inducing HRC gene when silenced enhances multiple disease resistance in plants. **2022**, 12,	0
532	WGDTree: a phylogenetic software tool to examine conditional probabilities of retention following whole genome duplication events. **2022**, 23,	0
531	Argopistes sexvittatus and Argopistes capensis (Chrysomelidae: Alticini): Mitogenomics and Phylogeny of Two Flea Beetles Affecting Olive Trees. **2022**, 13, 2195	0
530	Genetic and pathogenic diversity of Ralstonia solanacearum species complex strains isolated in Burkina Faso. **2023**, 171, 1-11	0
529	Leaf rolling in bread wheat (Triticum aestivum L.) is controlled by the upregulation of a pair of closely linked/duplicate zinc finger homeodomain class transcription factors during moisture stress conditions. 13,	0

528	Survivor bias drives overestimation of stability in reconstructed ancestral proteins.	0
527	The first genome sequence of Phomopsis vexans: a fungal pathogen causing Phomopsis blight in eggplant.	1
526	A high-quality genome assembly and annotation of Quercus acutissima Carruth. 13,	0
525	Adaptive duplication and genetic diversification of protein kinase R contribute to the specificity of bat-virus interactions. **2022**, 8,	1
524	Endozoicomonas-chlamydiae interactions in cell-associated microbial aggregates of the coralPocillopora acuta.	0
523	Changes in Bacterial Community Structure Across the Different Life Stages of Black Soldier Fly (Hermetia illucens).	0
522	Genetic diversity of Bartonella infection in residential and field rodents in Hebei, China. 13,	0
521	Deep ecomorphological and genetic divergence in Steller's Jays (Cyanocitta stelleri , Aves: Corvidae). **2022**, 12,	0
520	Freshwater Mussels Show Elevated Viral Richness and Intensity during a Mortality Event. **2022**, 14, 2603	2
519	Deciphering RNA G-quadruplex function during the early steps of HIV-1 infection. **2022**, 50, 12328-12343	0
518	Molecular identification of Trypanosoma cruzi in domestic animals in municipalities of the State of Rio Grande do Norte, Brazil.	0
517	Marine bacteroidetes use a conserved enzymatic cascade to digest diatom □mannan.	0
516	IMA genome-F17. **2022**, 13,	0
515	The phylogeography of some soil-feeding termites shaped by the Andes.	0
514	Haemosporidian parasites in the ash-breasted Sierra finch (Geospizopsis plebejus): insights from an Andean dry forest population. **2023**, 150, 115-128	0
513	Hemiurid Trematodes (Digenea: Hemiuridae) from Marine Fishes off the Coast of Rio de Janeiro, Brazil, with Novel Molecular Data. **2022**, 12, 3355	0
512	Comparative genomics reveals insight into the evolutionary origin of massively scrambled genomes. 11,	1
511	Transcriptome mining extends the host range of theFlaviviridaeto non-bilaterians.	0

510	The pan-genome of the emerging multidrug-resistant pathogen Corynebacterium striatum. **2023**, 23,	0
509	Is Borrelia burgdorferi Sensu Stricto in South America? First Molecular Evidence of Its Presence in Colombia. **2022**, 7, 428	0
508	A Compositional Heterogeneity Analysis of Mitochondrial Phylogenomics in Chalcidoidea Involving Two Newly Sequenced Mitogenomes of Eupelminae (Hymenoptera: Chalcidoidea). **2022**, 13, 2340	0
507	Geology, climate, and hydrochemistry shape the spatial patterns of multiple diversity facets and functional traits of fishes.	0
506	A high-quality reference genome for the fission yeastSchizosaccharomyces osmophilus.	0
505	Cyclitol metabolism is a central feature of Burkholderia leaf symbionts.	0
504	The endocytic TPLATE complex internalizes ubiquitinated plasma membrane cargo. **2022**, 8, 1467-1483	0
503	Circulation of Ngari Virus in Livestock, Kenya. **2022**, 7,	1
502	Integrative approach resolves the taxonomy of Eulaema cingulata (Hymenoptera, Apidae), an important pollinator in the Neotropics. 94, 247-269	0
501	Symbiotic Performance and Characterization of Pigeonpea (Cajanus cajan L. Millsp.) Rhizobia Occurring in South African Soils. **2023**, 13, 30	0
500	Phage Encounters Recorded in CRISPR Arrays in the Genus Oenococcus. **2023**, 15, 15	0
499	CherryML: Scalable Maximum Likelihood Estimation of Phylogenetic Models.	0
498	Revising the taxonomic placement of Laetiporus persicinus within the Laetiporaceae. 1-15	0
497	Isolation, antibacterial screening, and identification of bioactive cave dwelling bacteria in Fiji. 13,	0
496	Ancient Darwinian replicators nested within eubacterial genomes. 2200085	0
495	First record of Anatololacerta pelasgiana (Mertens, 1959) in mainland Greece: another new species in Athens. 35, 239-244	0
494	Varieties of Lettuce Forming Distinct Microbial Communities Inhabiting Roots and Rhizospheres with Various Responses to Osmotic Stress. **2022**, 8, 1174	1
493	Widespread, human-associated redondoviruses infect the commensal protozoan Entamoeba gingivalis. **2022**,	1

492	Genome-wide Identification and Expression Profile Analysis of Laccase Family Genes in theHypsizygus marmoreus.	0
491	Minute moss beetles in the Southern Hemisphere: Molecular phylogeny, historical biogeography and habitat shifts (Coleoptera: Hydraenidae).	0
490	Multiple introductions and recombination events underlie the emergence of a hyper-transmissible Cryptosporidium hominis subtype in the USA. **2022**,	0
489	Age-dependent nasal immune responses in non-hospitalized bronchiolitis children. 13,	0
488	Characterization of a novel botybirnavirus with a unique dsRNA infectingDidymella theifoliafrom tea plants.	0
487	Population Genetics of Anopheles pretoriensis in Grande Comore Island. **2023**, 14, 14	0
486	Fine-mapping and comparative genomic analysis reveal the gene composition at the S and Z self-incompatibility loci in grasses.	0
485	Isolation, Characterization, and Comparative Genomic Analysis of vB_Pd_C23, a Novel Bacteriophage of Pantoea dispersa. **2023**, 80,	0
484	Genomic Characterization of hox Genes in Senegalese Sole (Solea senegalensis, Kaup 1858): Clues to Evolutionary Path in Pleuronectiformes. **2022**, 12, 3586	0
483	The oriental armyworm genome yields insights into the long-distance migration of noctuid moths. **2022**, 41, 111843	1
482	Heterologous expression and functional characterization of Drosophila suzukii OR69a transcript variants unveiled response to kairomones and to a candidate pheromone.	0
481	Nutritional Profile and Ecological Interactions of Yeast Symbionts Associated with North American Spruce Beetle (Dendroctonus rufipennis).	0
480	Evidence linking APOBEC3B genesis and evolution of innate immune antagonism by gamma-herpesvirus ribonucleotide reductases. 11,	0
479	Rapid molecular diversification and homogenization of clustered major ampullate silk genes in Argiope garden spiders. **2022**, 18, e1010537	0
478	NSD1 gene evolves under episodic selection within primates and mutations of specific exons in humans cause Sotos syndrome. **2022**, 23,	0
477	Transcriptome mining extends the host range of the Flaviviridae to non-bilaterians.	0
476	Allopatric divergence of cooperators confers cheating resistance and limits effects of a defector mutation. **2022**, 22,	0
475	Analysis of multipartite bacterial genomes using alignment free and alignment-based pipelines. **2023**, 205,	1

474	Occurrence and Variability of the Efflux Pump Gene norA across the Staphylococcus Genus. **2022**, 23, 15306	0
473	Diversification and historical demography of Rhampholeon spectrum in West-Central Africa. **2022**, 17, e0277107	0
472	Evolutionary analyses and expression patterns of TCP genes in Ranunculales. 13,	1
471	Genetic characterization of Staphylococcus aureus isolated from Norway rats in Boston, Massachusetts.	0
470	Mitochondrial Genomes of the American Dog Tick (Dermacentor variabilis) Isolated from Horses in the Midwestern United States.	0
469	Identifying antibiotics based on structural differences in the conserved allostery from mitochondrial heme-copper oxidases. **2022**, 13,	0
468	Integration of mitogenomic and morphological data disentangles the systematics of Pollenia and establishes a revised phylogenetic hypothesis for the Polleniidae.	0
467	Morphological Characteristics and Phylogeny Reveal Six New Species in Russula Subgenus Russula (Russulaceae, Russulales) from Yanshan Mountains, North China. **2022**, 8, 1283	0
466	The genome of the king protea, Protea cynaroides.	0
465	Evolution and Diversity of TGF-Pathways are Linked with Novel Developmental and Behavioral Traits. **2022**, 39,	0
464	Elucidating the Interactome of G Protein-Coupled Receptors (GPCRs) and Receptor Activity-Modifying Proteins (RAMPs). PHARMREV-AR-2020-000180	1
463	Morphological Description and Phylogenetic Analyses of a New Species of Callistoctopus (Cephalopoda, Octopodidae) from China. **2022**, 14, 1083	0
462	First record of Mordellistena semiferruginea (Coleoptera: Mordellidae) in Italy and analysis of intraspecific variation in the COI gene. **2022**, 1-9	0
461	Halalkalirubrum. 1-10	0
460	Enhanced Arbovirus Surveillance with High-Throughput Metatranscriptomic Processing of Field-Collected Mosquitoes. **2022**, 14, 2759	0
459	Startle: a star homoplasy approach for CRISPR-Cas9 lineage tracing.	0
458	Muscle Regeneration in Holothurians without the Upregulation of Muscle Genes. **2022**, 23, 16037	0
457	Transposon-derived transcription factors across metazoans.	1

456	Genetic characterization of the zoonotic parasiteAncylostoma caninumin the central and eastern USA.	0
455	Comprehensive identification of bHLH transcription factors in Litsea cubeba reveals candidate gene involved in the monoterpene biosynthesis pathway. 13,	0
454	Codonoblepharonteae, a New Major Lineage among Orthotrichoideae (Orthotrichaceae, Bryophyta). **2022**, 11, 3557	0
453	Zygotic genome activation by the totipotency pioneer factor Nr5a2. **2022**, 378, 1305-1315	0
452	Olfactory Gene Families in Scopula subpunctaria and Candidates for Type-II Sex Pheromone Detection. **2022**, 23, 15775	0
451	Whole-genome analysis revealed the growth-promoting mechanism of endophytic bacterial strain Q2H1 in potato plants. 13,	0
450	Diversity and Ecology of Lobophora Species Associated with Coral Reef Systems in the Western Gulf of Thailand, including the Description of Two New Species. **2022**, 11, 3349	0
449	Faunimonas pinastri gen. nov., sp. nov., an endophyte from a pine tree of the family Pleomorphomonadaceae, class Alphaproteobacteria. **2022**, 72,	0
448	A remarkable troglomorphic ant,. **2022**, 36, 1118-1138	0
447	HCV-HIV Chronic Coinfection Prevalence in Amazon Region. **2022**, 11, 7284	0
446	Silencing of juvenile hormone epoxide hydrolase gene in Spodoptera litura (Lepidoptera: Noctuidae) by oral delivery of double-stranded RNA.	0
445	Intestinal gluconeogenesis: metabolic benefits make sense in the light of evolution.	0
444	CAULIFINDER: a pipeline for the automated detection and annotation of caulimovirid endogenous viral elements in plant genomes. **2022**, 13,	0
443	Host-microbiome metabolism of a plant toxin in bees. 11,	1
442	First chromosome scale genomes of ithomiine butterflies (Nymphalidae: Ithomiini): comparative models for mimicry genetic studies.	0
441	Evolution of monkeypox virus from 2017 to 2022: In the light of point mutations. 13,	1
440	Morphological and Molecular Characterizations of Three Species of the Genus Synura (Synurales, Chrysophyceae) from China. **2022**, 14, 1092	0
439	Full genome sequence of a novel iflavirus from the aster leafhopper Macrosteles fascifrons.	0

438	Dethiobacteria class. nov.. 1-3	0
437	African army ants at the forefront of virome surveillance in a remote tropical forest.	0
436	MtDNA Analysis of the Upper Yenisei Grayling (Thymallus svetovidovi) and the Mongolian Grayling (Thymallus brevirostris) and Clarification of Their Ranges. **2022**, 49, 721-726	0
435	Genomic characterization of viruses associated with the parasitoid Anagyrus vladimiri (Hymenoptera: Encyrtidae). **2022**, 103,	0
434	Molecular characterization of a novel Victorivirus (Gharbivirales: Totiviridae) infecting Metarhizium anisopliae.	0
433	Long-Term and Low-Level Envelope C2V3 Stimulation by Highly Diverse Virus Isolates Leads to Frequent Development of Broad and Elite Antibody Neutralization in HIV-1-Infected Individuals. **2022**, 10,	0
432	Metagenomic analysis reveals novel dietary-related viruses in the gut virome of marmosets hybrids (Callithrix jacchus x Callithrix penicillata), Brazil. **2022**, 199017	0
431	Incidence of cotton leaf curl Gezira virus and the associated alphasatellites and betasatellites in crops and ornamental plants in southern Iran.	0
430	An aphid symbiont confers protection against a specialized RNA virus, another increases vulnerability to the same pathogen.	0
429	Novel Divergent Members of the Kitrinoviricota Discovered through Metagenomics in the Intestinal Contents of Red-Backed Voles (Clethrionomys gapperi). **2023**, 24, 131	0
428	Molecular evolution of the ependymin-related gene epdl2 in African weakly electric fish.	0
427	Grassland ecosystem type drives AM fungal diversity and functional guild distribution in North American Grasslands.	0
426	House sparrows do not exhibit a preference for the scent of potential partners with different MHC-I diversity and genetic distances. **2022**, 17, e0278892	0
425	Survivors and colonizers: Contrasting biogeographic histories reconciled in the Antarctic freshwater copepod Boeckella poppei. 10,	0
424	Evolutionary analysis of endogenous intronic retroviruses in primates reveals an enrichment in transcription binding sites associated with key regulatory processes. 10, e14431	0
423	High-throughput profiling of drug interactions in Gram-positive bacteria.	0
422	Inclusion of rare taxa from Blattidae and Anaplectidae improves phylogenetic resolution in the cockroach superfamily Blattoidea. **2023**, 48, 23-39	0
421	Genomic characterization and molecular evolution of SARS-CoV-2 in Rio Grande do Sul State, Brazil.	0

420	Succession of the microbiota in the gut of reproductives of Macrotermes subhyalinus (Termitidae) at colony foundation gives insights into symbionts transmission. 10,	0
419	Genomics of the umorigenesclade of the familyRhizobiaceaeand description ofRhizobium rhododendrisp. nov..	0
418	Acanthopharynx Marine Nematodes (Nematoda, Chromadoria, Desmodoridae) Dwelling in Tropical Demosponges: Integrative Taxonomy with Description of a New Species. **2023**, 15, 48	0
417	Comparative Genomics and Phenotypic Characterization of Gluconacetobacter entanii, a Highly Acetic Acid-Tolerant Bacterium from Vinegars. **2023**, 12, 214	0
416	Genome-Wide Identification of the Odorant Receptor Gene Family and Revealing Key Genes Involved in Sexual Communication in Anoplophora glabripennis. **2023**, 24, 1625	0
415	Structural and evolutionary insights into astacin metallopeptidases. 9,	1
414	Management of genetic erosion: The (successful) case study of the pear (Pyrus communis L.) germplasm of the Lazio region (Italy). 13,	1
413	Cryptic, sibling or neither of the two? Integrative species delimitation of Psylliodes flea beetles with overlapping ranges.	0
412	Mosquito vector competence for dengue is modulated by insect-specific viruses. **2023**, 8, 135-149	0
411	Complete chloroplast genomes and comparative analysis of Ligustrum species. **2023**, 13,	0
410	Diversity of RNA viruses of three dominant tick species in North China. 9,	0
409	Dynamics of Microbial Community and Potential Microbial Pollutants in Shopping Malls.	0
408	A new species of jupati, genus Metachirus Burmeister 1854 (Didelphimorphia, Didelphidae) for the Brazilian Amazon. **2023**,	0
407	Transcriptomic analysis of seed development in Paysonia auriculata (Brassicaceae) identifies genes involved in hydroxy fatty acid biosynthesis. 13,	0
406	The complete chloroplast genome of Primula calliantha subsp. bryophila, an ornamental alpine plant from China. **2023**, 8, 4-6	0
405	Contrasting Phylogeographic Patterns of Mitochondrial and Genome-Wide Variation in the Groundwater Amphipod Crangonyx islandicus That Survived the Ice Age in Iceland. **2023**, 15, 88	0
404	Cohombrillo-associated virus: a novel virus infecting Ecballium elaterium plants. **2023**, 168,	0
403	Disclisioprocta edmondsii (Butler, 1882) comb. nov. (Lepidoptera, Geometridae, Larentiinae). 11,	0

402	Novel polyomaviruses identified in fecal samples from four carnivore species. **2023**, 168,	0
401	Cytospora paraplurivora sp. nov. isolated from orchards with fruit tree decline syndrome in Ontario, Canada. **2023**, 18, e0279490	0
400	Morphological Description and Molecular Analysis of Newly Recorded Asteroid, Henricia djakonovi Chichvarkhin, 2017 (Asteroidea: Spinulosida: Echinasteridae), from Dokdo Island, Korea. **2023**, 3, 46-54	0
399	Prediction and validation of novel SigB regulon members in Bacillus subtilis and regulon structure comparison to Bacillales members. **2023**, 23,	0
398	Heterogeneity in diagnostic characters across ecoregions: A case study with Botrynema (Hydrozoa: Trachylina: Halicreatidae). 9,	0
397	Inconsistency between morphological diversity and genetic structuring: proposal for one species of Undaria in Japan. **2023**,	0
396	Disruption of the standard kinetochore in holocentricCuscutaspecies.	0
395	Description of a new species of Scorpio´(Scorpiones: Scorpionidae) from Northwestern Algeria using morphological and molecular data.	0
394	Chromosome-level genome of black cutworm provides novel insights into polyphagy and seasonal migration in insects. **2023**, 21,	1
393	A chromosome-level genome assembly reveals that a bipartite gene cluster formed via an inverted duplication controls monoterpenoid biosynthesis in Japanese catnip. **2023**,	0
392	Identification of a TonB-Dependent Receptor Involved in Lanthanide Switch by the Characterization of Laboratory-Adapted Methylosinus trichosporium OB3b.	0
391	Phytophthora species cause sudden and severe decline of naturally regenerated European beech (Fagus sylvatica) seedlings.	0
390	Phylogenomics reveals patterns of ancient hybridization and differential diversification contributing to phylogenetic conflict inPopulusL. andSalixL.	0
389	Conformational exchange divergence along the evolutionary pathway of eosinophil-associated ribonucleases. **2023**,	0
388	Genomic characterization and assessment of pathogenic potential of Legionella spp. isolates from environmental monitoring. 13,	0
387	The African endemic species Nychiodes lyttha Prout, 1915 (Lepidoptera, Geometridae, Ennominae) belongs to the genus Aphilopota Warren, 1899. 46, 1-17	0
386	Reduced coenzyme Q synthesis confers non-target site resistance to the herbicide thaxtomin A. **2023**, 19, e1010423	0
385	Mechanisms of sex differentiation and sex reversal in hermaphrodite fish as revealed by the Epinephelus coioides genome.	0

384	Mitochondrial genome characteristics and phylogenetic analysis of the medicinal and edible plant Mesona chinensis Benth. 13,	0
383	Identification of Kazal Inhibitor Scaffolds with Identical Canonical Binding Loops and Their Effects on Binding Properties. **2023**, 62, 535-542	0
382	Biohydrogenation of 1,3-Butadiene to 1-Butene under Acetogenic Conditions by Acetobacterium wieringae.	0
381	Three New Species of Lactifluus (Basidiomycota, Russulaceae) from Guizhou Province, Southwest China. **2023**, 9, 122	0
380	First mitochondrial genome of subfamily Julodinae (Coleoptera, Buprestidae) with its phylogenetic implications. 1139, 165-182	0
379	Ammonium Uptake, Mediated by Ammonium Transporters, Mitigates Manganese Toxicity in Duckweed, Spirodela polyrhiza. **2023**, 12, 208	2
378	Integrating phylogenetics with intron positions illuminates the origin of the complex spliceosome.	0
377	Genome-wide assessment of the population structure and genetic diversity of four Portuguese native sheep breeds. 14,	0
376	Genomes of the human filarial parasitesMansonella perstansandMansonella ozzardi.	0
375	A single silk and multiple pollen-expressed PMEs at the Ga1 locus modulate maize unilateral cross-incompatibility.	0
374	Silencing of a Pectin Acetylesterase (PAE) Gene Highly Expressed in Tobacco Pistils Negatively Affects Pollen Tube Growth. **2023**, 12, 329	0
373	New Negombata species discovered: latrunculin mystery solved.	0
372	Comparative phyloproteomics identifies conserved plasmodesmal proteins.	0
371	Structural and functional analysis of a tandem repeat galacturonic acid-binding lectin from the sea hare Aplysia californica. **2023**, 132, 108513	0
370	Molecular analyses of pseudoscorpions in a subterranean biodiversity hotspot reveal cryptic diversity and microendemism. **2023**, 13,	0
369	Surface frustration re-patterning underlies the structural landscape and evolvability of fungal orphan candidate effectors.	0
368	Differential carbon utilization enables co-existence of recently speciated Campylobacteraceae in the cow rumen epithelial microbiome.	0
367	A Genome of Temperate Enterococcus Bacteriophage Placed in a Space of Pooled Viral Dark Matter Sequences. **2023**, 15, 216	0

366 A circovirus and cycloviruses identified in feces of bobcats (Lynx rufus) in California. **2023**, 168, o

365 Complete mitochondrial genome of the Spanish toothcarp, Aphanius iberus (Valenciennes, 1846) (Actinopterygii, Aphaniidae) and its phylogenetic position within the Cyprinodontiformes order. o

364 Differential Infectivity of Human Neural Cell Lines by a Dengue Virus Serotype-3 Genotype-III with a Distinct Nonstructural Protein 2A (NS2A) Amino Acid Substitution Isolated from the Cerebrospinal Fluid of a Dengue Encephalitis Patient. **2023**, 2023, 1-11 o

363 Legionella maioricensis sp. nov., a new species isolated from the hot water distribution systems of a hospital and a shopping center during routine sampling. **2023**, 73, o

362 A new Pipistrelle bat from the oceanic Island of Pr�cipe (Western Central Africa). o

361 Phylogenetic analysis of Prevotella copri from fecal and mucosal microbiota of IBS and IBD patients. **2023**, 16, 175628482211363 o

360 A chromosome-level genome assembly enables the identification of the follicule stimulating hormone receptor as the master sex-determining gene in the flatfish Solea senegalensis. o

359 Origin, evolution and systematics of the genus Poecilimon (Orthoptera: Tettigoniidae)�An outburst of diversification in the Aegean area. **2023**, 48, 198-220 o

358 Assessing the hidden diversity underlying consensus sequences of SARS-CoV-2 using VICOS, a novel bioinformatic pipeline for identification of mixed viral populations.. **2023**, 325, 199035 o

357 Four antimicrobial peptides of Asian gypsy moth respond to infection of its viral pathogen, nucleopolyhedrovirus (LdMNPV). **2023**, 190, 105335 o

356 The evolutionary journey of freshwater crabs of the genus Potamon (Decapoda: Brachyura: Potamidae). **2023**, 180, 107690 o

355 Comparative mitochondrial genomics and phylogenetics for species of the snakehead genus Channa Scopoli, 1777 (Perciformes: Channidae). **2023**, 857, 147186 o

354 Temporal pesticide dynamics alter specific eukaryotic taxa in a coastal transition zone. **2023**, 866, 161205 o

353 Gnawing pressure led to the expansion of JAZ genes in angiosperms. **2023**, 230, 123165 o

352 Ultraconserved elements-based phylogenomic systematics of the snake superfamily Elapoidea, with the description of a new Afro-Asian family. **2023**, 180, 107700 o

351 Taxonomic significance and evolution of homobaric and heterobaric leaves in Adesmia clade species (Leguminosae �Papilionoideae). **2023**, 58, 125714 o

350 Two new species of Anaptychia (Physciaceae) from western North America, with notes on the other species of section Protoanaptychia. **2022**, 125, o

349 Diversity and Taxonomy of Telipogon (Orchidaceae) in Colombia and Adjacent Areas. 109, o

348	Genomic Epidemiology of the SARS-CoV-2 Epidemic in Cyprus from November 2020 to October 2021: The Passage of Waves of Alpha and Delta Variants of Concern. **2023**, 15, 108	1
347	Plant age-dependent dynamics of annatto pigment (bixin) biosynthesis inBixa orellanaL..	0
346	Patterns of hybridization in a secondary contact zone between two passerine species, the common nightingale Luscinia megarhynchos and the thrush nightingale Luscinia luscinia.	0
345	Morphological and Genetic Characterization of Didelphonema longispiculata (Nematoda: Spiruroidea) in the Black-Eared Opossum Didelphis marsupialis. **2022**, 108,	0
344	Revisiting the Phylogenetic Relationship and Evolution of Gargarini with Mitochondrial Genome (Hemiptera: Membracidae: Centrotinae). **2023**, 24, 694	0
343	Parallel evolution of two AIM24 protein subfamilies and their conserved functions in ER stress tolerance in land plants. **2022**, 100513	0
342	Sabahia polypodii gen. et sp. nov. (Hemiptera: Cicadellidae: Evacantihinae) and its Phylogenetic Position within the Nirvanini Tribe. **2022**, 70, 151-162	0
341	Lifestyle switching and refugee availability are the main factors in the evolution and distribution of the genus Synurella Wrze�iowski, 1877 (Amphipoda: Crangonyctidae)´. **2022**, 31, 393-448	0
340	The Brazilian Amazonian rainforest harbors a high diversity of yeasts associated with rotting wood, including many candidates for new yeast species.	1
339	Postglacial adaptations enabled colonization and quasi-clonal dispersal of ammonia-oxidizing archaea in modern European large lakes. **2023**, 9,	1
338	Ticks (Acari: Ixodidae) and Tick-Borne Pathogens in Extensively Reared Cattle from Coastal Kenya.	0
337	Genome-scale metabolic reconstruction of 7,302 human microorganisms for personalized medicine.	1
336	Comparative analysis of mitochondrial genomes of two alpine medicinal plants of Gentiana (Gentianaceae). **2023**, 18, e0281134	0
335	Omicron Waves in Argentina: Dynamics of SARS-CoV-2 Lineages BA.1, BA.2 and the Emerging BA.2.12.1 and BA.4/BA.5. **2023**, 15, 312	1
334	Phylogenomics of trans-Andean tetras of the genus Hyphessobrycon Durbin 1908 (Stethaprioninae: Characidae) and colonization patterns of Middle America. **2023**, 18, e0279924	0
333	Northernmost record of the Chilean torpedo Tetronarce tremens from tropical coastal waters of the Mexican Pacific. **2023**, 103,	0
332	Genomic analysis of an ultrasmall freshwater green alga, Medakamo hakoo. **2023**, 6,	0
331	No loss of genetic divergence in Torymus sinensis following its release for Dryocosmus kuriphilus control in Europe.	0

330	Multiplepalsgene modules control a balance between immunity and development inCaenorhabditis elegans.	0
329	Vibrio sinus sp. nov., a marine bacterium isolated from coastal seawater. **2023**, 73,	0
328	Vibrio amylolyticus sp. nov. and Vibrio gelatinilyticus sp. nov., two marine bacteria isolated from surface seawater of Qingdao. **2023**, 73,	0
327	An integrated approach to explore the monophyletic status of the cosmopolitan genus Hexabathynella (Crustacea, Bathynellacea, Parabathynellidae): two new species from Rottnest Island (Wadjemup), Western Australia. **2023**, 21,	0
326	SCORPiOs, a Novel Method to Reconstruct Gene Phylogenies in the Context of a Known WGD Event. **2023**, 155-173	0
325	Evolutionary dynamics of glue gene copy number in Drosophila species.	0
324	Ancient loss of catalytic selenocysteine spurred convergent adaptation in a mammalian oxidoreductase.	0
323	Comparative Mitogenomic Analysis of Two Snake Eels Reveals Irregular Gene Rearrangement and Phylogenetic Implications of Ophichthidae. **2023**, 13, 362	0
322	Pleistocene dispersion supports a unique native diversity in the Colombian avocado germplasm.	0
321	Large-scale proteomic analysis of T. spiralis muscle-stage ESPs identifies a novel upstream motif for in silico prediction of secreted products. 2,	0
320	Interspecific introgression patterns reveal the origins of worldwide cultivated bananas in New Guinea.	0
319	New insights into the coevolutionary history of termites and their gut flagellates: Description of Retractinympha glossotermitis gen. nov. sp. nov. (Retractinymphidae fam. nov.). 11,	0
318	In-Depth Characterization of Full-Length Archived Viral Genomes after Nine Years of Posttreatment HIV Control.	0
317	Streamlined regulation of chloroplast development in the liverwortMarchantia polymorpha.	0
316	Prey-mimetism in cercariae of Apatemon (Digenea, Strigeidae) in freshwater in northern latitudes.	0
315	Aeromonas hydrophila ST251 and Aeromonas dhakensis are major emerging pathogens of striped catfish in Vietnam. 13,	0
314	Chlorophyll f production in two new subaerial cyanobacteria of the family Oculatellaceae.	0
313	HIV-PULSE: A long-read sequencing assay for high-throughput near full-length HIV-1 proviral genome characterization.	0

312	Whole-genome resequencing reveals recent divergence of geographic populations of the dung beetle Phelotrupes auratus with color variation. **2023**, 13,	0
311	Parallel duplication and loss of aquaporin-coding genes during the out of the sea transition as potential key drivers of animal terrestrialization.	0
310	Highly Dynamic Gene Family Evolution Suggests Changing Roles for PON Genes Within Metazoa.	0
309	Complete genome sequence of a novel mycovirus from Pleurotus citrinopileatus. **2023**, 168,	0
308	Stabilization of membrane topologies by proteinaceous remorin scaffolds. **2023**, 14,	2
307	New Caledonia's enigmatic terrestrial diving beetle Typhlodessus monteithi is a derived species of Paroster. **2023**, 52, 176-183	0
306	Minimal Antigenic Evolution after a Decade of Norovirus GII.4 Sydney_2012 Circulation in Humans.	0
305	A Zinc Finger Motif in the P1 N Terminus, Highly Conserved in a Subset of Potyviruses, Is Associated with the Host Range and Fitness of Telosma Mosaic Virus.	0
304	Canonical or noncanonical? Structural plasticity of serine protease-binding loops in Kunitz-STI protease inhibitors. **2023**, 32,	0
303	Investigation of B-atp6-orfH79 distributing in Chinese populations of Oryza rufipogon and analysis of its chimeric structure. **2023**, 23,	0
302	The complete mitochondrial genome of the Reef Manta Ray, Mobula alfredi, from Hawaii. **2023**, 8, 197-203	0
301	Molecular data confirm the presence of the Southern Crested Newt Triturus karelinii (Strauch, 1870) in Anatolia. **2023**, 69, 13-18	0
300	Morphology and molecular phylogeny of Chauhanellus Bychowsky & Nagibina, 1969 (Monogenoidea) parasitizing marine catfish (Ariidae) from the Atlantic coast of South America: a new species, supplementary taxonomic information and new insights. **2023**, 97,	0
299	The genus Microcotyle in Mediterranean scorpaenoids (Teleostei), including the description of Microcotyle merche n. sp. from Helicolenus dactylopterus (Delaroche, 1809). **2023**, 97,	0
298	Global expansion of a solitary-social tropical spitting spider shaped by multiple long-distance dispersals. **2023**, 2023,	0
297	Distant genetic variants of Anaplasma phagocytophilum from Ixodes ricinus attached to people. **2023**, 16,	0
296	High-resolution phylogenetic analysis reveals long-term microbial dynamics and microdiversity in phytoplankton microbiome.	0
295	Evidence for an early green/red photocycle that precedes the diversification of GAF domain photoreceptor cyanobacteriochromes.	0

294	Extensive crop‐wild hybridization during Brassica evolution and selection during the domestication and diversification of Brassica crops. **2023**, 223,	0
293	Mordellistena platypoda, a new species of tumbling flower beetle from the island of Ischia in Italy (Coleoptera, Mordellidae). 1148, 41-63	0
292	Understanding the Divergent Evolution and Epidemiology of H3N8 Influenza Viruses in Dogs and Horses.	0
291	Evolutionary History and Taxonomic Reclassification of the Critically Endangered Daggernose Shark, a Species Endemic to the Western Atlantic. **2023**, 2023, 1-16	0
290	Gossypium purpurascens genome provides insight into the origin and domestication of upland cotton. **2023**,	0
289	The alg-1 Gene Is Necessary for Orsay Virus Replication in Caenorhabditis elegans.	0
288	A new semi-slug of the genus Microparmarion from Brunei, discovered, described and DNA-barcoded on citizen-science 'taxon expeditions' (Gastropoda, Stylommatophora, Ariophantidae). 11,	0
287	Molecular detection and characterization of Anaplasma spp. in cattle and sable antelope from Lusaka and North-Western provinces of Zambia. **2023**, 39, 100847	0
286	An orphan protein drove the ecological expansion of nitrogen fixation.	0
285	The third symbiotic partner of the volcano lichenCladonia vulcaniSavicz drove adaptation to an extreme environment.	0
284	Genomes of the human filarial parasites Mansonella perstans and Mansonella ozzardi. 4,	0
283	Pseudobangia corderoi sp. nov. (Bangiales, Rhodophyta) from the Philippines. 1-7	0
282	Identification and management of tomato brown rugose fruit virus in greenhouses in Mexico. **2023**, 168,	0
281	A Transducing Bacteriophage Infecting Staphylococcus epidermidis Contributes to the Expansion of a Novel Siphovirus Genus and Implies the Genus Is Inappropriate for Phage Therapy.	0
280	RNAi-mediated knockdown of two orphan G-protein coupled receptors reduces fecundity in the yellow fever mosquitoAedes aegypti.	0
279	Different configurations of SARS-CoV-2 spike protein delivered by integrase-defective lentiviral vectors induce persistent functional immune responses, characterized by distinct immunogenicity profiles. 14,	0
278	Sequencing the genomes of LPP-1, the first isolated cyanophage, and its relative LPP-2 reveal different integration mechanisms in closely related phages. **2023**, 124, 102409	0
277	Chromosome-level genome of the bean bug Megacopta cribraria in native range, provides insights into adaptation and pest management. **2023**, 237, 123989	0

276	Genomic characterization and molecular evolution of SARS-CoV-2 in Rio Grande do Sul State, Brazil. **2023**, 582, 1-11	0
275	Origin and diversification of pheretimoid megascolecid earthworms in the Japanese Archipelago as revealed by mitogenomic phylogenetics. **2023**, 182, 107735	0
274	Soft rot disease of Belamcanda chinensis caused by Dickeya fangzhongdai in China. **2023**, 125, 101974	0
273	Phylogenomics and biogeography of arid-adapted Chlamydogobius goby fishes. **2023**, 182, 107757	0
272	Emergence of ehrlichiosis by a new tick-borne Ehrlichia species in China. **2023**, 131, 32-39	0
271	Complete mitochondrial genomes of two click-beetles, Sinelater perroti and Sternocampsus coriaceus (Coleoptera: Elateroidea: Elateridae), and their phylogenetic implications. **2023**, 26, 102059	0
270	A comprehensive phylogeny and revised taxonomy illuminate the origin and diversification of the global radiation of Papilio (Lepidoptera: Papilionidae). **2023**, 183, 107758	0
269	Genomic phylogeography illuminates deep cyto-nuclear discordances in midwife toads (Alytes). **2023**, 183, 107783	0
268	Phylogeny and expression of ADAM10 and ADAM17 homologs in lamprey.	0
267	Unsuspected findings about phylogeny and ultrastructure of the enigmatic cyanobacterium Microcrocis geminata resulted in its epitypification and novel placement in Geminocystaceae. **2023**, 23, 110-121	0
266	The Populus koreana genome provides insights into the biosynthesis of plant aroma. **2023**, 197, 116453	0
265	Genetic diversity of Kappaphycus malesianus (Solieriaceae, Rhodophyta) from the Philippines. **2023**, 187, 103649	0
264	Peripheral and central employment of acid-sensing ion channels during early bilaterian evolution. 12,	0
263	Biodiversity and spatial distribution of ascidian using environmental DNA metabarcoding. **2023**, 185, 105893	0
262	Surveillance of 16 UK native bat species through conservationist networks uncovers coronaviruses with zoonotic potential.	0
261	New genetic lineage of whipworm present in Bactrian camel (Camelus bactrianus). **2023**, 315, 109886	0
260	Microbial Communities on Samples of Commercially Available Fresh-Consumed Leafy Vegetables and Small Berries. **2023**, 9, 150	0
259	Functional differentiation of two general odorant-binding proteins to sex pheromones in Spodoptera frugiperda. **2023**, 191, 105348	0

258	Plasmodium sporozoites require the protein B9 to invade hepatocytes. **2023**, 26, 106056	0
257	Functional HIV-1/HCV cross-reactive antibodies isolated from a chronically co-infected donor. **2023**, 42, 112044	0
256	Lateral gene transfer leaves lasting traces in Rhizaria.	0
255	Cloning and Molecular Characterization of the phlD Gene Involved in the Biosynthesis of Phloroglucinol a Compound with Antibiotic Properties from Plant Growth Promoting Bacteria Pseudomonas spp.. **2023**, 12, 260	2
254	A novel RHH family transcription factor aCcr1 and its viral homologs dictate cell cycle progression in archaea. **2023**, 51, 1707-1723	0
253	High abundance of hydrocarbon-degrading Alcanivorax in plumes of hydrothermally active volcanoes in the South Pacific Ocean. **2023**, 17, 600-610	0
252	A paralog of Pcc1 is the fifth core subunit of the KEOPS tRNA-modifying complex in Archaea. **2023**, 14,	0
251	Unstable EBV latency drives inflammation in multiple sclerosis patient derived spontaneous B cells.	0
250	Morpho-molecular analysis of podolampadacean dinoflagellates (Dinophyceae), with the description of two new genera. **2023**, 62, 117-135	0
249	Chromosome-level genomes of multicellular algal sisters to land plants illuminate signaling network evolution.	0
248	Genetic diversity, phylogenetic position, and co-phylogenetic relationships of Karyolysus, a common blood parasite of lizards in the western Mediterranean. **2023**, 53, 185-196	0
247	Ets-1 transcription factor regulates glial cell regeneration and function in planarians.	0
246	A Revision of the Rhinolophus hipposideros group (Chiroptera: Rhinolophidae) with Definition of an Additional Species from the Middle East. **2023**, 24,	0
245	Pangenomic analysis of Wolbachia provides insight into the evolution of host adaptation and cytoplasmic incompatibility factor genes. 14,	0
244	Genomics discovery of giant fungal viruses from subsurface oceanic crustal fluids. **2023**, 3,	0
243	Genomic Insights and Functional Analysis Reveal Plant Growth Promotion Traits of Paenibacillus mucilaginosus G78. **2023**, 14, 392	0
242	piRNA pathway evolution beyond gonad context: Perspectives from apicomplexa and trypanosomatids. 14,	0
241	Identification of coronaviruses in bats and rodents in northern and central Argentina. **2023**, 168,	0

240	Aim18p and Aim46p are chalcone isomerase domain‐containing mitochondrial hemoproteins in Saccharomyces cerevisiae. **2023**, 299, 102981	0
239	Using Entamoeba muris To Model Fecal-Oral Transmission of Entamoeba in Mice. **2023**, 14,	0
238	Not the Last Piece of the Puzzle: Niphargus Phylogeny in Hungary. **2023**, 15, 223	0
237	Characterization of the Complete Mitochondrial Genome of a Flea Beetle Luperomorpha xanthodera (Coleoptera: Chrysomelidae: Galerucinae) and Phylogenetic Analysis. **2023**, 14, 414	1
236	Taxonomic Advances from Fungal Flora Associated with Ferns and Fern-like Hosts in Northern Thailand. **2023**, 12, 683	0
235	Epidemiological and genomic analysis of dengue cases in Guangzhou, China, from 2010 to 2019. **2023**, 13,	0
234	The identity of Argyria lacteella (Fabricius, 1794) (Lepidoptera, Pyraloidea, Crambinae), synonyms, and related species revealed by morphology and DNA capture in type specimens. 1146, 1-42	0
233	Ants of French Guiana: 16S rRNA sequence dataset. 11,	0
232	A high-quality reference genome for the fission yeast Schizosaccharomyces osmophilus. **2023**, 13,	0
231	Plastid Phylogenomic Insights into the Inter-Tribal Relationships of Plantaginaceae. **2023**, 12, 263	0
230	Metabarcoding to monitor the crustacean zooplankton of a lake improves when using a reference DNA library from local samples. 82,	0
229	Distinct Molecular Patterns of Two-Component Signal Transduction Systems in Thermophilic Cyanobacteria as Revealed by Genomic Identification. **2023**, 12, 271	1
228	Dunaliella viridis TAV01: A Halotolerant, Protein-Rich Microalga from the Algarve Coast. **2023**, 13, 2146	0
227	Transcription factors of lignin biosynthesis respond to cold and drought in Eucalyptus urograndis. **2023**, 35, 17-30	0
226	Using Multiplex Amplicon PCR Technology to Efficiently and Timely Generate Rift Valley Fever Virus Sequence Data for Genomic Surveillance. **2023**, 15, 477	0
225	The origins and diversification of Holarctic brown bear populations inferred from genomes of past and present populations.	0
224	The genome of Magnolia hypoleuca provides a new insight into cold tolerance and the evolutionary position of magnoliids. 14,	0
223	Molecular characterization of a novel victorivirus (order Ghabrivirales, family Totiviridae) infecting Metarhizium anisopliae. **2023**, 168,	0

222	Uncovering bacterial hosts of class 1 integrons in an urban coastal aquatic environment with a single-cell fusion-polymerase chain reaction technology.	0
221	On the mysterious Seychellois endemic spider genus Cenemus (Araneae, Pholcidae). 81, 179-200	0
220	Building a local reference library for metabarcoding survey of lake macrobenthos: oligochaetes and chironomids from Lake Maggiore. **2022**, 13,	0
219	Heterotrimeric G proteins regulate planarian regeneration and behavior. **2023**, 223,	0
218	Diverse DNA virus genomes identified in fecal samples of Mexican free-tailed bats (Tadarida brasiliensis) captured in Chiricahua Mountains of southeast Arizona (USA). **2023**, 580, 98-111	0
217	Long-term epidemiology and evolution of swine influenza viruses in Vietnam.	0
216	The identity of the carrageenophyte red alga Sarcothalia radula (Gigartinaceae, Rhodophyta).	0
215	Selection on many loci drove the origin and spread of a key innovation.	0
214	Identification of potentially zoonotic parasites in captive orangutans and semi-captive mandrills: Phylogeny and morphological comparison. **2023**, 85,	0
213	Molecular phylogeny, systematics and biogeography of the subfamily Nemognathinae (Coleoptera, Meloidae). **2023**, 37, 101-116	0
212	Multiple mutations in the Nav1.4 sodium channel of New Guinean toxic birds provide autoresistance to deadly batrachotoxin.	0
211	Expansion of Kuravirus-like Phage Sequences within the Past Decade, including Escherichia Phage YF01 from Japan, Prompt the Creation of Three New Genera. **2023**, 15, 506	0
210	Natural products from the Picea foliar endophytes Niesslia endophytica sp. nov. and Strasseria geniculata. **2023**, 22,	0
209	Public health interventions successfully mitigated multiple incursions of SARS-CoV-2 Delta variant in the Australian Capital Territory. **2023**, 151,	0
208	GUN Mutants: New Weapons To Unravel Ascospore Germination Regulation in the Model Fungus Podospora anserina. **2023**, 11,	0
207	Sequence Characterization of ITS Regions of Immortelle Helichrysum italicum (Roth) G. Don from the East Adriatic Coast. **2023**, 14, 480	0
206	Biochemical and structural basis of polyamine, lysine and ornithine acetylation catalyzed by spermine/spermidine N -acetyl transferase in moss and maize.	0
205	Physcomitrium patens PpRIC, an ancestral CRIB-domain ROP effector, inhibits auxin-induced differentiation of apical initial cells. **2023**, 42, 112130	0

204	RAREFAN: A webservice to identify REPINs and RAYTs in bacterial genomes. 3,	0
203	Genetic analysis of the tomato russet mite provides evidence of oligophagy and a widespread pestiferous haplotype. **2023**, 89, 171-199	0
202	FHbp variants among meningococci of serogroup B in Italy: Evolution and selective pressure, 2014–2017. **2023**, 18, e0277976	0
201	Diversity, distribution, and expression of opsin genes in freshwater lakes.	0
200	Insights into cryptochrome modulation of ABA signaling to mediate dormancy regulation in Marchantia polymorpha. **2023**, 238, 1479-1497	0
199	Loss of ndrg2 Function Is Involved in Notch Activation in Neuromast Hair Cell Regeneration in Zebrafish.	0
198	Genes encoding cytochrome P450 monooxygenases and glutathione S-transferases associated with herbicide resistance evolved before the origin of land plants. **2023**, 18, e0273594	0
197	Resolving the Sticta fuliginosa Morphodeme (Lichenized Ascomycota: Peltigeraceae) in Northwestern North America. **2023**, 126,	0
196	Humpback spiders from Ecuador: relationships, prosoma “inflation” and genital asymmetry (Araneae: Pholcidae: Mecolaesthus). **2023**, 37, 117-151	0
195	Human pathogens in ticks removed from humans in Hebei, China. **2023**, 9, e13859	0
194	Dynamics of Early Establishment of SARS-CoV-2 VOC Omicron Lineages in Minas Gerais, Brazil. **2023**, 15, 585	0
193	The Potential Fungal Pathogens of Euonymus japonicus in Beijing, China. **2023**, 9, 271	0
192	Discovery of a novel merbecovirus DNA clone contaminating agricultural rice sequencing datasets from Wuhan, China.	0
191	Introductions of Human-Origin Seasonal H3N2, H1N2 and Pre-2009 H1N1 Influenza Viruses to Swine in Brazil. **2023**, 15, 576	0
190	Genome-wide analysis of NBS-LRR genes revealed contribution of disease resistance from Saccharum spontaneum to modern sugarcane cultivar. 14,	0
189	Genomic Epidemiological Analysis of Antimicrobial-Resistant Bacteria with Nanopore Sequencing. **2023**, 227-246	0
188	The “True Colours” of Golden Loaches (Teleostei: Cobitidae). **2023**, 8, 119	0
187	Bacterial community structure in the alcyoniid Lobophytum pauciflorum.	0

186	Thaxterogaster carneus (Cortinariaceae), a new species of Thaxterogaster sect. Vibratiles , from coniferous forests of Kashmir Himalaya, India.	0
185	A new Asian leaf litter toad of the genus Leptobrachella (Amphibia, Anura, Megophryidae) from central south China. 1149, 103-134	0
184	Diversity of the Antimicrobial Peptide Genes in Collembola. **2023**, 14, 215	0
183	Prolonged experimental CD4+ T-cell depletion does not cause disease progression in SIV-infected African green monkeys. **2023**, 14,	0
182	Discovery and Genome Characterization of a Closterovirus from Wheat Plants with Yellowing Leaf Symptoms in Japan. **2023**, 12, 358	0
181	Improved Genomic Prediction of Staphylococcus epidermidis Isolation Sources with a Novel Polygenic Score. **2023**, 61,	0
180	Chromatic polymorphism in Trichomycterus albinotatus (Siluriformes, Trichomycteridae), a mountain catfish from south-eastern Brazil and the role of colouration characters in trichomycterine taxonomy. **2023**, 99, 161-171	0
179	Phylogenomics of darkling beetles (Coleoptera: Tenebrionidae) from the Atacama Desert. 11, e14848	0
178	DNA Barcoding of Moon Jellyfish (Cnidaria, Scyphozoa, Ulmaridae, Aurelia): Two Cryptic Species from the Azores (NE Atlantic, Macaronesia), and Evaluation of the Non-Indigenous Species (NIS). **2023**, 15, 323	0
177	Taxonomic Revision of the Genus Croaker Johnius (Perciformes: Sciaenidae) in Taiwanese Waters. **2023**, 11, 471	1
176	Update on laboratory data of animal rabies at the Centre Pasteur of Cameroon from 2014 to 2021. **2023**, 157, 6-12	0
175	A Global Survey of Hypervirulent Aeromonas hydrophila (vAh) Identified vAh Strains in the Lower Mekong River Basin and Diverse Opportunistic Pathogens from Farmed Fish and Other Environmental Sources. **2023**, 11,	0
174	The Low Variability of Tc24 in Trypanosoma cruzi TcI as an Advantage for Chagas Disease Prophylaxis and Diagnosis in Mexico. **2023**, 12, 368	0
173	Comparative Analysis of Complete Mitochondrial Genome of Ariosoma meeki (Jordan and Snider, 1900), Revealing Gene Rearrangement and the Phylogenetic Relationships of Anguilliformes. **2023**, 12, 348	0
172	Fungal diversity notes 1512–1610: taxonomic and phylogenetic contributions on genera and species of fungal taxa. **2022**, 117, 1-272	2
171	Amblyopinae Mitogenomes Provide Novel Insights into the Paraphyletic Origin of Their Adaptation to Mudflat Habitats. **2023**, 24, 4362	0
170	Rickettsia association with two Macrolophus (Heteroptera: Miridae) species: A comparative study of phylogenies and within-host localization patterns. 13,	0
169	MAP9/MAPH-9 supports axonemal microtubule doublets and modulates motor movement.	0

168	Comparative analysis of adenylate isopentenyl transferase genes in plant growth-promoting bacteria and plant pathogenic bacteria. **2023**, 9, e13955	0
167	Whether including exotic species alters conservation prioritization: a case study in the Min River in southeastern China.	0
166	Metagenome diversity illuminates origins of pathogen effectors.	0
165	Potential Activity of Arthrospira platensis as Antioxidant, Cytotoxic and Antifungal against Some Skin Diseases: Topical Cream Application. **2023**, 21, 160	0
164	IS481EU Shows a New Connection between Eukaryotic and Prokaryotic DNA Transposons. **2023**, 12, 365	0
163	Phylogenetic diversity of cacao (Theobroma cacao L.) genotypes in Colombia. **2022**, 20, 203-214	0
162	Robustness of Felsenstein□ versus Transfer Bootstrap Supports with respect to Taxon Sampling.	0
161	Cautionary note on ribonuclease activity of recombinant PR-10 proteins.	0
160	An X-Domain Phosphoinositide Phospholipase C (PI-PLC-like) of Trypanosoma brucei Has a Surface Localization and Is Essential for Proliferation. **2023**, 12, 386	0
159	Tracking the intensity of the mechanism to produce antigenic diversity by subtelomeric ectopic recombination across the phylogeny ofPlasmodiumparasites.	0
158	Challenges of Whole Genome Sequencing based Molecular Identification of Zoonotic Tuberculosis caused byMycobacterium orygis.	0
157	Genome Sequences of Two Grapevine Rupestris Stem Pitting-Associated Virus Variants from Vitis vinifera cv. Riesling in Idaho, USA. **2023**, 12,	0
156	Association of ISVsa3 with Multidrug Resistance in Salmonella enterica Isolates from Cattle (Bos taurus). **2023**, 11, 631	0
155	The mitochondrial genome of Heterosentis pseudobagri (Wang & Zhang, 1987) Pichelin & Cribb, 1999 reveals novel aspects of tRNA genes evolution in Acanthocephala. **2023**, 24,	0
154	A virus-borne DNA damage signaling pathway controls the lysogeny-induction switch in a group of temperate pleolipoviruses.	0
153	Fingerprints, barcode sequences and quasi-phylogenies□Tools for analysing polyphonic music. **2023**, 18, e0280478	0
152	An earliest Paleocene squirrelfish (Teleostei: Beryciformes: Holocentroidea) and its bearing on the timescale of holocentroid evolution. **2023**, 21,	0
151	Rapid molecular detection of CMY-2, and CTX-M group 1 and 9 variants via recombinase polymerase amplification. **2023**, 5,	0

150	Phylogeny of the flea beetles (Galerucinae: Alticini) and the position of Aulacothorax elucidated through anchored phylogenomics (Coleoptera: Chrysomelidae: Alticini).	1
149	Formation of the Holarctic Fauna: Dated molecular phylogenetic and biogeographic insights from the Quedius-lineage of Ground-Dwelling Rove Beetles (Coleoptera, Staphylinidae). **2023**, 182, 107749	0
148	A New Parasitic Archamoeba Causing Systemic Granulomatous Disease in Goldfish Extends the Diversity of Pathogenic Endolimax spp.. **2023**, 13, 935	0
147	Mutational signatures in wild typeEscherichia colistrains reveal dominance of DNA polymerase errors.	0
146	Comparative metagenomics reveals host-specific functional adaptation of intestinal microbiota across hominids.	0
145	Isolation of ACE2-dependent and -independent sarbecoviruses from Chinese horseshoe bats.	0
144	Transposon-derived transcription factors across metazoans. 11,	0
143	MeC3HDZ1/MeCNA is a strong candidate for cassava storage root productivity improvement.	0
142	Phylogenetic History and Phylogeographic Patterns of the European Wildcat (Felis´silvestris) Populations. **2023**, 13, 953	0
141	Evolution of mitogenomic gene order in Orthoptera.	0
140	Species Delimitation Under Allopatry: Genomic Divergences Within and Across Continents in Lepidoptera.	0
139	Knockout of DDM1 in Physcomitrium patens disrupts DNA methylation with a minute effect on transposon regulation and development. **2023**, 18, e0279688	0
138	Discovery of paralogous GnRH and corazonin signaling systems in an invertebrate chordate.	0
137	The Phaseolus vulgaris Receptor-Like Kinase PvFER1 and the Small Peptides PvRALF1 and PvRALF6 Regulate Nodule Number as a Function of Nitrate Availability. **2023**, 24, 5230	0
136	Phylogenetic Analysis of Spliceosome SF3a2 in Different Plant Species. **2023**, 24, 5232	0
135	Convergent trends and spatiotemporal patterns of arboviruses in Mexico and Central America.	0
134	Genetic variability highlights the invasion route of the Lutzomyia longipalpis complex, the main vector of Visceral Leishmaniasis in Uruguay.	0
133	Discovery of an unrecognized nidovirus associated with granulomatous hepatitis in rainbow trout. **2023**, 26, 106370	0

132	A high soluble-fibre allele in wheat encodes a defective cell wall peroxidase responsible for dimerization of ferulate moieties on arabinoxylan.	0
131	Raveneliopsis, a new genus of ravenelioid rust fungi on Cenostigma (Caesalpinioideae) from the Brazilian Cerrado and Caatinga. **2023**, 115, 263-276	0
130	The allopolyploid origin(s) and diversification of New Caledonian Grevillea (Proteaceae). 1-14	0
129	Two major chromosome evolution events with unrivaled conserved gene content in pomegranate. 14,	0
128	African army ants at the forefront of virome surveillance in a remote tropical forest. 3,	0
127	Comparative genomics analysis of endangered wild Egyptian Moringa peregrina (Forssk.) Fiori plastome, with implications for the evolution of Brassicales order. 14,	0
126	The chalara-like anamorphs of Leotiomycetes. **2023**, 119, 213-490	0
125	Uncovering Bacterial Hosts of Class 1 Integrons in an Urban Coastal Aquatic Environment with a Single-Cell Fusion-Polymerase Chain Reaction Technology. **2023**, 57, 4870-4879	0
124	Molecular phylogeny and morphology reveal four new species of Thelephora (Thelephorales, Basidiomycota) from subtropical China, closely related to T. ganbajun. 14,	0
123	Characterization of Virulent T4-Like Acinetobacter baumannii Bacteriophages DLP1 and DLP2. **2023**, 15, 739	0
122	Carex quixotiana (Cyperaceae), a new Iberian endemic from Don Quixote's land (La Mancha, S Spain). 221, 161-186	0
121	Genetic Diversity and Insights about Distribution of Brown Howler Monkeys (Alouatta guariba Group) (Atelidae, Alouattinae).	0
120	Genetic Diversity, Population Structure and Selection Signatures in Enset (Ensete ventricosum, (Welw.) Cheesman),´an Underutilized and Key Food Security Crop in Ethiopia.	0
119	Historical Landscape Evolution Shaped the Phylogeography and Population History of the Cyprinid Fishes of Acrossocheilus (Cypriniformes: Cyprinidae) According to Mitochondrial DNA in Zhejiang Province, China. **2023**, 15, 425	0
118	Asynchronous phylogeographic and demographic dynamics of rodent community in the low latitude Asia.	0
117	Phylogeny and Evolutionary Timescale of Muscidae (Diptera: Calyptratae) Inferred from Mitochondrial Genomes. **2023**, 14, 286	0
116	Phylogenomic analysis of the genus Rosenbergiella and description of Rosenbergiella gaditana sp. nov., Rosenbergiella metrosideri sp. nov., Rosenbergiella epipactidis subsp. epipactidis subsp. nov., Rosenbergiella epipactidis subsp. californiensis subsp. nov., Rosenbergiella epipactidis subsp. japonicus subsp. nov., Rosenbergiella nectarea subsp. nectarea subsp. nov. and Rosenbergiella [illegible] **2023**, 73,	0
115	Scleromatobacter humisilvae gen. nov., sp. nov., a novel bacterium isolated from oak forest soil. **2023**, 73,	0

114	Natural selection and convergent evolution of the HOX gene family in Carnivora. 11,	0
113	Characterization of Molecular Diversity and Organization of Phycobilisomes in Thermophilic Cyanobacteria. **2023**, 24, 5632	0
112	Deep Structural Analysis of Myriads of Omicron Sub-Variants Revealed Hotspot for Vaccine Escape Immunity. **2023**, 11, 668	0
111	A new species of the red alga Erythrotrichia (Erythropeltales, Rhodophyta) from Korea: Erythrotrichia johnawestii sp. nov. and observations in culture. **2023**,	0
110	’Candidatus Megaira’ are diverse symbionts of algae and ciliates with the potential for defensive symbiosis. **2023**, 9,	0
109	Cervicovaginal Human Papillomavirus Genomes, Microbiota Composition and Cytokine Concentrations in South African Adolescents. **2023**, 15, 758	0
108	Genomic features and heat resistance profiles ofEscherichia coliisolated from Brazilian beef. **2023**, 134,	0
107	Whole-genome sequencing reveals putative underlying mechanisms of biocontrol capability of IBFCBF-5. **2023**, 45,	0
106	Antiviral immune response reveals host-specific virus infections in natural ant populations. 14,	0
105	From the Mountain to the Valley: Drivers of Groundwater Prokaryotic Communities along an Alpine River Corridor. **2023**, 11, 779	0
104	Diverse and Abundant Viruses Exploit Conjugative Plasmids.	0
103	Comprehensive characterization of the complex BAHD acyltransferase family from 218 land plants species: phylogenomic analysis and identification of specificity determinant positions.	0
102	Genome-wide identification, characterization, and validation of the bHLH transcription factors in grass pea. 14,	0
101	One Health Surveillance Highlights Circulation of Viruses with Zoonotic Potential in Bats, Pigs, and Humans in Viet Nam. **2023**, 15, 790	0
100	Epidemiological Survey and Risk Factor Analysis of 14 Potential Pathogens in Golden Snub-Nosed Monkeys at Shennongjia National Nature Reserve, China. **2023**, 12, 483	0
99	Emergence of an ancient and pathogenic mammarenavirus. **2023**, 12,	0
98	From everywhere all at once: Several colonization routes available to Svalbard in the early Holocene. **2023**, 13,	0
97	Morphology, phylogeny and fatty acid profiles of Meyerella similis from freshwater ponds and Meyerella krienitzii sp. nov. from soil (Trebouxiophyceae, Chlorophyta).	0

96	Phylogenomic inference of the higher classification of velvet ants (Hymenoptera: Mutillidae).	0
95	Phylogeographic analysis revealed allopatric distribution pattern and biogeographic processes of the widespread pale chub Opsariichthys acutipinnis-evolans complex (Teleostei: Cyprinidae) in southeastern China. 11,	0
94	From primordial clocks to circadian oscillators. **2023**, 616, 183-189	0
93	The evolution of white-tailed jackrabbit camouflage in response to past and future seasonal climates. **2023**, 379, 1238-1242	0
92	Evolutionary Aspects of the Fructan Syndrome. **2023**, 75-90	0
91	A new hexactinellid-sponge-associated zoantharian (Porifera, Hexasterophora) from the northwestern Pacific Ocean. 1156, 71-85	0
90	Duckweed evolution: from land back to water.	0
89	Egr-2 coordinates intestinal remodeling by promoting midline patterning and pharynx regeneration in planarians.	0
88	Diversity of Gracilariaceae (Rhodophyta) in China: An integrative morphological and molecular assessment including a description of Gracilaria tsengii sp. nov.. **2023**, 71, 103074	0
87	DELLA functions evolved by rewiring of associated transcriptional networks. **2023**, 9, 535-543	0
86	Expanding strain coverage of a Group A Streptococcus pilus-expressing Lactococcus lactis mucosal vaccine.	0
85	Field survey and molecular characterization of apicomplexan parasites in small mammals from military camps in Afghanistan. **2023**, 122, 1199-1211	0
84	Whole-mitochondrial genomes of Nannizziopsis provide insights in evolution and detection. **2023**, 13,	0
83	Repertoire of P-glycoprotein drug transporters in the zoonotic nematode Toxocara canis. **2023**, 13,	0
82	A Novel Dependoparvovirus Identified in Cloacal Swabs of Monk Parakeet (Myiopsitta monachus) from Urban Areas of Spain. **2023**, 15, 850	0
81	Three new species of the Synapturanus rabus complex (Microhylidae: Otophryninae) in Colombia with a review of the genus Synapturanus. **2023**, 5258, 151-196	0
80	Phylobone: A comprehensive database of bone extracellular matrix proteins in human and model organisms.	0
79	Human seven-strand (METTL) methyltransferases - conquering the universe of protein lysine methylation. **2023**, 104661	0

78	High level of novelty under the hood of convergent evolution. **2023**, 379, 1043-1049	0
77	Molecular and morphological analyses disclose the existence of three species of Dolichopoda (Orthoptera: Rhaphidophoridae) in the Calabria region (Italy). **2023**, 57, 372-394	0
76	MORC2 restriction factor silences HIV proviral expression.	0
75	Identification and characterization of odorant-binding protein genes in the brown-winged green bug, Plautia stali.	0
74	Comparative Analysis of the Alkaline Proteolytic Enzymes of Yarrowia Clade Species and Their Putative Applications. **2023**, 24, 6514	0
73	Complete genome analysis of African swine fever virus genotypes II, IX and XV from domestic pigs in Tanzania. **2023**, 13,	0
72	ANO7 African-ancestral genomic diversity and advanced prostate cancer.	0
71	Genome-wide single nucleotide polymorphisms reveal recurrent waves of speciation in niche-pockets, in Europe’s most venomous snake.	0
70	Five new Graphium species from hardwood trees in Poland. 1-18	0
69	Genomics of the tumorigenes clade of the family Rhizobiaceae and description of Rhizobium rhododendri sp. nov.. **2023**, 12,	0
68	In-depth analysis of erythrose reductase homologs in Yarrowia lipolytica.	0
67	Expression analysis of the Tao kinase family of Ste20p-like map kinase kinase kinases during early embryonic development in Xenopus laevis. **2023**, 119318	0
66	CRISPR-Cas9 enrichment, a new strategy in microbial metagenomics to investigate complex genomic regions: The case of an environmental integron.	0
65	Characteristics, Comparative Analysis, and Phylogenetic Relationships of Chloroplast Genomes of Cultivars and Wild Relatives of Eggplant (Solanum melongena). **2023**, 45, 2832-2846	0
64	Insight into the genomes of dominant yeast symbionts of European spruce bark beetle, Ips typographus. 14,	0
63	Geographical subdivision of Alviniconcha snail populations in the Indian Ocean hydrothermal vent regions. 10,	0
62	Description of Neochlorella semenenkoi gen. et. sp. nov. (Chlorophyta, Trebouxiophyceae), a Novel Chlorella-like Alga with High Biotechnological Potential. **2023**, 15, 513	0
61	Fortuitously compatible protein surfaces primed allosteric control in cyanobacterial photoprotection.	0

60	New Insights into the Variation and Admixture of the Cave-Dwelling Spider Trogloneta yunnanensis in South China Karst. **2023**, 13, 1244	0
59	Description of Two Fungal Endophytes Isolated from Fragaria chiloensis subsp. chiloensis f. patagonica: Coniochaeta fragariicola sp. nov. and a New Record of Coniochaeta hansenii. **2023**, 3, 183-203	0
58	Confirming the identity of the Hypogeococcus species (Hemiptera: Pseudococcidae) associated with Harrisia martinii (Labour.) Britton (Cactaceae) in Australia: Implications for biological control.	0
57	First report of Spirometra (Eucestoda; Diphyllobothriidae) naturally occurring in a fish host. 70,	0
56	Expansion and collapse of VEGF diversity in major clades of the animal kingdom.	0
55	Marine conditions in Andaman Sea shape the unique genetic structure of Sargassum plagiophyllum C.Agardh.	0
54	Penicillin Binding Protein Substitutions Cooccur with Fluoroquinolone Resistance in Epidemic Lineages of Multidrug-Resistant Clostridioides difficile.	0
53	RNA Viruses Are Prevalent and Active Tenants of the Predatory Mite Phytoseiulus persimilis (Acari: Phytoseiidae).	0
52	Super-pangenome analyses highlight genomic diversity and structural variation across wild and cultivated tomato species.	0
51	Cnidarian pharyngeal nervous system illustrates prebilaterian neurosecretory regulation of feeding.	0
50	The terpene synthase genes of Melaleuca alternifolia (tea tree) and comparative gene family analysis among Myrtaceae essential oil crops. **2023**, 309,	0
49	Coinfection and circulation of chikungunya virus and dengue virus in pediatric patients in Myanmar, 2019. **2023**, 105129	0
48	Single-specimen systematics resolves the phylogeny and diversity conundrum of enigmatic crustacean y-larvae. **2023**, 107780	0
47	Phyloecology ofnrfA-ammonifiers and their relative importance with denitrifiers in global terrestrial biomes.	0
46	Combining target enrichment and Sanger sequencing data to clarify the systematics of the diverse Neotropical butterfly subtribe Euptychiina (Nymphalidae, Satyrinae).	0
45	Characterization of Pseudofusicoccum Species from Diseased Plantation-Grown Acacia mangium, Eucalyptus spp., and Pinus´massoniana in Southern China. **2023**, 12, 574	0
44	Symbiosis preservation: Putative regulation of fatty acyl-CoA reductase by miR-31a within the symbiont harboring bacteriome through tsetse evolution. 14,	0
43	Vibrio paucivorans sp. nov. and Vibrio qingdaonensis sp. nov., two marine bacteria. **2023**, 73,	0

42	Comparative Clustering (CompaCt) of eukaryote complexomes identifies novel interactions and sheds light on protein complex evolution.	0
41	Complete nucleotide sequence of hackberry virus A, a tentative member of the genus Waikavirus. **2023**, 168,	0
40	Morphology and molecular phylogeny of a widely distributed but little-known sand-dwelling phototrophic dinoflagellate, Coutea sabulosa gen. & sp. nov. (Dinophyceae, Alveolata). 1-15	0
39	A global survey of tapeworms (Cestoda: Proteocephalidae) of 'true' frogs (Amphibia: Ranidae), including a tabulated list of all proteocephalids parasitising amphibians. 70,	0
38	A conserved hymenopteran-specific family of cytochrome P450s protects bee pollinators from toxic nectar alkaloids. **2023**, 9,	0
37	Previously uncharacterized rectangular bacterial structures in the dolphin mouth. **2023**, 14,	0
36	Design and validation of Dolosigranulum pigrum specific PCR primers using the bacterial core genome. **2023**, 13,	0
35	Stable endocytic structures navigate the complex pellicle of apicomplexan parasites. **2023**, 14,	0
34	Chromosomal-Scale Genome Assemblies of Two Coastal Plant Species, Scaevola taccada and S. hainanensis□Insight into Adaptation Outside of the Common Range. **2023**, 24, 7355	0
33	Actinophytocola gossypii sp. nov. and Streptomyces gossypii sp. nov., two novel actinomycetes isolated from rhizosphere soil of cotton. **2023**, 73,	0
32	Phylogenetic analysis of Blaberoidea reveals non-monophyly of taxa and supports the creation of multiple new subfamilies.	0
31	Identification of multiple transcription factor genes potentially involved in the development of electrosensory versus mechanosensory lateral line organs.	0
30	Longitudinal Survey of Astrovirus infection in different bat species in Zimbabwe: Evidence of high genetic Astrovirus diversity.	0
29	The epidemiology and evolutionary dynamics of massive dengue outbreak in China, 2019. 14,	0
28	Trypanosoma cruziVDU deubiquitinase mediates surface protein trafficking and infectivity.	0
27	A rare non-canonical splice site in Trema orientalis SYMRK does not affect its dual symbiotic functioning in endomycorrhiza and rhizobium nodulation.	0
26	The invasive Asian benthic foraminifera Trochammina hadai Uchio, 1962: identification of a new local in Normandy (France) and a discussion on its putative introduction pathways. **2023**, 18, 23-38	0
25	Tilapia lake virus: A structured phylogenetic approach. 14,	0

24	Identification of IPT9 in Brachiaria brizantha (syn. Urochloa brizantha) and expression analyses during ovule development in sexual and apomictic plants.	0
23	Genetic characterization of the zoonotic parasite Ancylostoma caninum in the central and eastern United States. **2023**, 97,	0
22	Genomic features, antimicrobial susceptibility, and epidemiological insights into Burkholderia cenocepacia clonal complex 31 isolates from bloodstream infections in India. 13,	0
21	Tribal assignment of the genus Eumera Staudinger, 1892, using multi-gene analysis, with description of a new species from Iran (Lepidoptera: Geometridae: Ennominae). **2023**, 5270, 92-104	0
20	Kinetic characterization and phylogenetic analysis of human ADP-dependent glucokinase reveal new insights into its regulatory properties. **2023**, 109602	0
19	Mirusviruses link herpesviruses to giant viruses.	0
18	A taxonomic revision of Boiga multomaculata (Boie, 1827) and B. ochracea (Theobald, 1868), with the description of a new subspecies (Squamata, Serpentes, Colubridae). **2023**, 5270, 151-193	0
17	RAPIDprep: A Simple, Fast Protocol for RNA Metagenomic Sequencing of Clinical Samples. **2023**, 15, 1006	0
16	Epidemiological and genomic investigation of chikungunya virus in Rio de Janeiro state, Brazil, between 2015 and 2018.	0
15	Shewanella septentrionalis sp. nov. and Shewanella holmiensis sp. nov., isolated from Baltic Sea water and sediments. **2023**, 73,	0
14	First Isolation and Genome Sequence Analysis of West Nile Virus in Mosquitoes in Brazil. **2023**, 8, 237	0
13	Conservation and variation in the region of the Theileria parva p104 antigen coding gene used for PCR surveillance of the parasite.	0
12	Morphology and molecular analyses reveal three new species of Botryosphaeriales isolated from diseased plant branches in China. 97, 1-19	0
11	First detection and genome analysis of simple nosed bat polyomaviruses in Central Europe. **2023**, 112, 105439	0
10	A farnesyl-dependent structural role for CENP-E in expansion of the fibrous corona.	0
9	Paenibacillus melissococcoides sp. nov., isolated from a honey bee colony affected by European foulbrood disease. **2023**, 73,	0
8	Evolution of stridulatory mechanisms: vibroacoustic communication may be common in leaf-footed bugs and allies (Heteroptera: Coreoidea). **2023**, 10,	0
7	A fungal lytic polysaccharide monooxygenase is required for cell wall integrity, thermotolerance, and virulence of the fungal human pathogen Cryptococcus neoformans. **2023**, 19, e1010946	0

6	The first report of the non-indigenous Chydorus brevilabris Frey, 1980 (Crustacea: Cladocera) in Asian freshwaters.	0
5	The origin, evolution and functional divergence of HOOKLESS1 in plants. **2023**, 6,	0
4	A Long-Standing Hybrid Population Between Pacific and Atlantic Herring in a Subarctic Fjord of Norway. **2023**, 15,	0
3	A first annotated genome sequence for Haliotis midae with genomic insights into abalone evolution and traits of economic importance. **2023**, 70, 101044	0
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