ggtree: an r package for visualization and annotation of phylogenetic trees with their covariates and other associated data

DOI: 10.1111/2041-210x.12628
Methods in Ecology and Evolution, 2017, 8, 28-36.

#	Paper	IF	Citations
2251	.		
2250	Function and Phylogeny of Bacterial Butyryl Coenzyme A:Acetate Transferases and Their Diversity in the Proximal Colon of Swine. **2016**, 82, 6788-6798		17
2249	Phylogenetic analysis of the human antibody repertoire reveals quantitative signatures of immune senescence and aging. **2017**, 114, 1105-1110		69
2248	Application of high-throughput sequencing to whole rabies viral genome characterisation and its use for phylogenetic re-evaluation of a raccoon strain incursion into the province of Ontario. **2017**, 232, 123-133		17
2247	The complete mitochondrial genome of the White-Nose Syndrome pathogen,. **2017**, 2, 48-49		1
2246	Gut metagenomes of type 2 diabetic patients have characteristic single-nucleotide polymorphism distribution in Bacteroides coprocola. **2017**, 5, 15		18
2245	Abundance and Diversity of Psychrotolerant Cultivable Mycobiota in Winter of a Former Aluminous Shale Mine. **2017**, 34, 823-833		12
2244	Cheminformatics Modeling of Amine Solutions for Assessing their CO Absorption Properties. **2017**, 36, 1600143		9
2243	Squamate Conserved Loci (SqCL): A unified set of conserved loci for phylogenomics and population genetics of squamate reptiles. **2017**, 17, e12-e24		20
2242	A maternal-effect selfish genetic element in. **2017**, 356, 1051-1055		48
2241	Comparative Analysis of Extended-Spectrum-Lactamase CTX-M-65-Producing Salmonella enterica Serovar Infantis Isolates from Humans, Food Animals, and Retail Chickens in the United States. **2017**, 61,		70
2240	Characterizing the Chemical Space of ERK2 Kinase Inhibitors Using Descriptors Computed from Molecular Dynamics Trajectories. **2017**, 57, 1286-1299		48
2239	Weaver's historic accessible collection of synthetic dyes: a cheminformatics analysis. **2017**, 8, 4334-4339		23
2238	An integrated approach to identify cytochrome P450 superfamilies in plant species within the malvids. **2017**,		
2237	Integrated analysis of genetic, behavioral, and biochemical data implicates neural stem cell-induced changes in immunity, neurotransmission and mitochondrial function in Dementia with Lewy Body mice. **2017**, 5, 21		5
2236	Floristic response to urbanization: Filtering of the bioregional flora in Indianapolis, Indiana, USA. **2017**, 104, 1179-1187		9
2235	Population admixture in Chinese and European Sus scrofa. **2017**, 7, 13178		4

2234	Identification of Genetically Intact HIV-1 Proviruses in Specific CD4 T Cells from Effectively Treated Participants. **2017**, 21, 813-822	187
2233	Recurrent Reverse Evolution Maintains Polymorphism after Strong Bottlenecks in Commensal Gut Bacteria. **2017**, 34, 2879-2892	21
2232	Large-Scale Phylogenomics of the Group Highlights Taxonomic Inconsistencies and Reveals Novel Clade-Associated Features. **2017**, 2,	56
2231	Forensic Human Identification Using Skin Microbiomes. **2017**, 83,	46
2230	Chromosomal inversion differences correlate with range overlap in passerine birds. **2017**, 1, 1526-1534	55
2229	Genotyping-by-Sequencing-Based Genetic Analysis of African Rice Cultivars and Association Mapping of Blast Resistance Genes Against Magnaporthe oryzae Populations in Africa. **2017**, 107, 1039-1046	10
2228	Mechanisms of Surface Antigenic Variation in the Human Pathogenic Fungus. **2017**, 8,	19
2227	Pandemic H1N1 influenza A viruses suppress immunogenic RIPK3-driven dendritic cell death. **2017**, 8, 1931	27
2226	Elevation in tropical sky islands as the common driver in structuring genes and communities of freshwater organisms. **2017**, 7, 16089	8
2225	The Diversity, Structure, and Function of Heritable Adaptive Immunity Sequences in the Aedes aegypti Genome. **2017**, 27, 3511-3519.e7	104
2224	Integrated view of in the Americas. **2017**, 358, 789-793	79
2223	Genome-Wide Sequence and Expression Analysis of the NAC Transcription Factor Family in Polyploid Wheat. **2017**, 7, 3019-3029	34
2222	Adding loci improves phylogeographic resolution in red mangroves despite increased missing data: comparing microsatellites and RAD-Seq and investigating loci filtering. **2017**, 7, 17598	53
2221	Large-scale determination and characterization of cell type-specific regulatory elements in the human genome. **2017**, 9, 463-476	4
2220	Insight into the population structure of hardhead silverside, (Teleostei: Atherinidae), in Belize and the Florida Keys using. **2017**, 7, 9503-9517	3
2219	Pan-genome Analyses of the Species , and Identification of Genomic Markers Predictive for Species, Subspecies, and Serovar. **2017**, 8, 1345	38
2218	Local Chromatin Features Including PU.1 and IKAROS Binding and H3K4 Methylation Shape the Repertoire of Immunoglobulin Kappa Genes Chosen for V(D)J Recombination. **2017**, 8, 1550	14
2217	Enterotoxin C and Enterotoxin-Like L Associated with Post-partum Mastitis. **2017**, 8, 173	7

2216	Comparative Genomics Analysis of a New Strain from Salar de Huasco Reveals a Repertoire of Stress-Related Genes and Arsenic Resistance. **2017**, 8, 456	24
2215	Horses in Denmark Are a Reservoir of Diverse Clones of Methicillin-Resistant and -Susceptible. **2017** , 8, 543	38
2214	Survey of Antibiotic-producing Bacteria Associated with the Epidermal Mucus Layers of Rays and Skates. **2017**, 8, 1050	15
2213	A phylogenetic transform enhances analysis of compositional microbiota data. **2017**, 6,	144
2212	Clarinet (CLA-1), a novel active zone protein required for synaptic vesicle clustering and release. **2017**, 6,	22
2211	Genome-wide evolutionary dynamics of influenza B viruses on a global scale. **2017**, 13, e1006749	55
2210	The molecular evolutionary dynamics of oxidative phosphorylation (OXPHOS) genes in Hymenoptera. **2017**, 17, 269	23
2209	Genomic innovations, transcriptional plasticity and gene loss underlying the evolution and divergence of two highly polyphagous and invasive Helicoverpa pest species. **2017**, 15, 63	150
2208	Members of the Candidate Phyla Radiation are functionally differentiated by carbon- and nitrogen-cycling capabilities. **2017**, 5, 112	66
2207	Dietary energy drives the dynamic response of bovine rumen viral communities. **2017**, 5, 155	38
2206	Selection on non-antigenic gene segments of seasonal influenza A virus and its impact on adaptive evolution. **2017**, 3, vex034	8
2205	CrusTF: a comprehensive resource of transcriptomes for evolutionary and functional studies of crustacean transcription factors. **2017**, 18, 908	2
2204	Adaptation in a Fibronectin Binding Autolysin of. **2017**, 2,	6
2203	Variability in Disinfection Resistance between Currently Circulating Enterovirus B Serotypes and Strains. **2018**, 52, 3696-3705	33
2202	Sustained transmission of high-level azithromycin-resistant Neisseria gonorrhoeae in England: an observational study. **2018**, 18, 573-581	80
2201	Method to interactively visualize and navigate related information. **2018**, 111, 61-75	2
2200	Cheminformatics Analysis of Dynamic WNK-Inhibitor Interactions. **2018**, 37, e1700138	7
2199	DSYB catalyses the key step of dimethylsulfoniopropionate biosynthesis in many phytoplankton. **2018**, 3, 430-439	61

2198	High genetic diversity of extended-spectrum βlactamases producing Escherichia coli in feces of horses. **2018**, 219, 117-122	12
2197	Filtering nucleotide sites by phylogenetic signal to noise ratio increases confidence in the Neoaves phylogeny generated from ultraconserved elements. **2018**, 126, 116-128	12
2196	RecQ Helicases Function in Development, DNA Repair, and Gene Targeting in. **2018**, 30, 717-736	24
2195	Insight into the Significance of Aspergillus fumigatus cyp51A Polymorphisms. **2018**, 62,	27
2194	Carrot Juice Fermentations as Man-Made Microbial Ecosystems Dominated by Lactic Acid Bacteria. **2018**, 84,	37
2193	Amphibian chytridiomycosis outbreak dynamics are linked with host skin bacterial community structure. **2018**, 9, 693	75
2192	Who Is the Rock Miner and Who Is the Hunter? The Use of Heavy-Oxygen Labeled Phosphate (PO) to Differentiate between C and P Fluxes in a Benzene-Degrading Consortium. **2018**, 52, 1773-1786	2
2191	Variation in Genetic Diversity of Phytophthora infestans Populations in Mexico from the Center of Origin Outwards. **2018**, 102, 1534-1540	9
2190	Fish DNA barcoding around large marine infrastructure for improved biodiversity assessment and monitoring. **2018**, 29, 1174-1179	5
2189	Novel Method Reveals a Narrow Phylogenetic Distribution of Bacterial Dispersers in Environmental Communities Exposed to Low-Hydration Conditions. **2018**, 84,	2
2188	Molecular epidemiology reveals the role of war in the spread of HIV in Ukraine. **2018**, 115, 1051-1056	32
2187	Altered chemomechanical coupling causes impaired motility of the kinesin-4 motors KIF27 and KIF7. **2018**, 217, 1319-1334	16
2186	Convergent Evolution Driven by Rifampin Exacerbates the Global Burden of Drug-Resistant. **2018**, 3,	28
2185	Toward the Rational Design of Sustainable Hair Dyes Using Cheminformatics Approaches: Step 1. Database Development and Analysis. **2018**, 6, 2344-2352	11
2184	Morphology and molecular phylogeny of Holostichides terrae nov. spec. (Ciliophora: Spirotrichea) with discussion on the possible non-monophyly of Holostichides. **2018**, 62, 69-78	11
2183	C photosynthesis evolved in warm climates but promoted migration to cooler ones. **2018**, 21, 376-383	16
2182	An Iranian genomic sequence of Beet mosaic virus provides insights into diversity and evolution of the world population. **2018**, 54, 272-279	6
2181	Multiplexed gene synthesis in emulsions for exploring protein functional landscapes. **2018**, 359, 343-347	69

2180	Pairwise comparisons across species are problematic when analyzing functional genomic data. **2018** , 115, E409-E417	42
2179	Metabarcoding analysis of strongylid nematode diversity in two sympatric primate species. **2018**, 8, 5933	24
2178	The global distribution and spread of the mobilized colistin resistance gene mcr-1. **2018**, 9, 1179	268
2177	The ecology of Roman trade. Reconstructing provincial connectivity with similarity measures. **2018**, 92, 37-47	9
2176	Relentless spread and adaptation of non-typeable vanA vancomycin-resistant Enterococcus faecium: a genome-wide investigation. **2018**, 73, 1487-1491	15
2175	Species delimitation and biogeography of the gnatcatchers and gnatwrens (Aves: Polioptilidae). **2018**, 126, 45-57	10
2174	In silico Predicted Glucose-1-phosphate Uridylyltransferase (GalU) Inhibitors Block a Key Pathway Required for Listeria Virulence. **2018**, 37, e1800004	9
2173	Diversity of Entamoeba spp. in African great apes and humans: an insight from Illumina MiSeq high-throughput sequencing. **2018**, 48, 519-530	17
2172	Microbial metagenome of urinary tract infection. **2018**, 8, 4333	46
2171	Populations of Phytophthora rubi Show Little Differentiation and High Rates of Migration Among States in the Western United States. **2018**, 31, 614-622	11
2170	Resolving a phylogenetic hypothesis for parrots: implications from systematics to conservation. **2018**, 118, 7-21	25
2169	Targeted sequencing of clade-specific markers from skin microbiomes for forensic human identification. **2018**, 32, 50-61	44
2168	A molecular systematic analysis of the Neotropical banner winged damselflies (Polythoridae: Odonata). **2018**, 43, 56-67	2
2167	Integrating patient and whole-genome sequencing data to provide insights into the epidemiology of seasonal influenza A(H3N2) viruses. **2018**, 4,	8
2166	Genomic epidemiology of the commercially important pathogen Renibacterium salmoninarum within the Chilean salmon industry. **2018**, 4,	6
2165	Evaluation of a Novel MALDI Biotyper Algorithm to Distinguish From. **2018**, 9, 3140	14
2164	Unravelling species boundaries in the complex (section): opportunistic human and animal pathogens capable of interspecific hybridization. **2018**, 41, 142-174	38
2163	Genome wide characterization of enterotoxigenic Escherichia coli serogroup O6 isolates from multiple outbreaks and sporadic infections from 1975-2016. **2018**, 13, e0208735	5

2162	Genetic Characterization of Maximilian Sunflower for the Development of a Locally Adapted Perennial Grain Oilseed. **2018**, 58, 2241-2260	1
2161	The gold-standard genome of NRRL 3 enables a detailed view of the diversity of sugar catabolism in fungi. **2018**, 91, 61-78	33
2160	The global origins of resistance-associated variants in the non-structural proteins 5A and 5B of the hepatitis C virus. **2018**, 4, vex041	5
2159	Modeling site-specific amino-acid preferences deepens phylogenetic estimates of viral sequence divergence. **2018**, 4, vey033	10
2158	Demographic histories and genetic diversity across pinnipeds are shaped by human exploitation, ecology and life-history. **2018**, 9, 4836	29
2157	Characterising routes of H5N1 and H7N9 spread in China using Bayesian phylogeographical analysis. **2018**, 7, 184	9
2156	Dynamic linear models guide design and analysis of microbiota studies within artificial human guts. **2018**, 6, 202	30
2155	Genetics and Genomics of an Unusual Selfish Sex Ratio Distortion in an Insect. **2018**, 28, 3864-3870.e4	8
2154	Radiotherapy induces responses of lung cancer to CTLA-4 blockade. **2018**, 24, 1845-1851	379
2153	Habitat or temporal isolation: Unraveling herbivore-parasitoid speciation patterns using double digest RADseq. **2018**, 8, 9803-9816	4
2152	The molecular basis of antigenic variation among A(H9N2) avian influenza viruses. **2018**, 7, 176	15
2151	Numerical taxonomy contributes to delimitation of Iranian and Turkish Hesperis L. (Brassicaceae) species. **2018**, 367, 101	3
2150	Species Designations Belie Phenotypic and Genotypic Heterogeneity in Oral Streptococci. **2018**, 3,	19
2149	Pure early zygotic genes in the Asian malaria mosquito Anopheles stephensi. **2018**, 11, 652	3
2148	Evolution of the Population Structure of in France. **2018**, 9, 3055	16
2147	Uncovering secondary metabolite evolution and biosynthesis using gene cluster networks and genetic dereplication. **2018**, 8, 17957	22
2146	Enrichment of Verrucomicrobia, Actinobacteria and Burkholderiales drives selection of bacterial community from soil by maize roots in a traditional milpa agroecosystem. **2018**, 13, e0208852	28
2145	A New Phylogenetic Framework for the Animal-Adapted Complex. **2018**, 9, 2820	77

2144	Quantifying the risk of hemiplasy in phylogenetic inference. **2018**, 115, 12787-12792	29
2143	Reconstructing the evolutionary history of pandemic foot-and-mouth disease viruses: the impact of recombination within the emerging O/ME-SA/Ind-2001 lineage. **2018**, 8, 14693	36
2142	Inter- and intra-host sequence diversity reveal the emergence of viral variants during an overwintering epidemic caused by dengue virus serotype 2 in southern Taiwan. **2018**, 12, e0006827	10
2141	Microhabitat change drives diversification in pholcid spiders. **2018**, 18, 141	16
2140	The diversity of the proline-rich domain of pneumococcal surface protein A (PspA): Potential relevance to a broad-spectrum vaccine. **2018**, 36, 6834-6843	11
2139	Microbiome composition within a sympatric species complex of intertidal isopods (Jaera albifrons). **2018**, 13, e0202212	5
2138	Comparative genomics reveals the distinct evolutionary trajectories of the robust and complex coral lineages. **2018**, 19, 175	32
2137	The evolution of language families is shaped by the environment beyond neutral drift. **2018**, 2, 816-821	17
2136	Genetic diversity of Microsporidia in the circulatory system of endemic amphipods from different locations and depths of ancient Lake Baikal. **2018**, 6, e5329	9
2135	Two Methods for Mapping and Visualizing Associated Data on Phylogeny Using Ggtree. **2018**, 35, 3041-3043	223
2134	The USDA cucumber (L.) collection: genetic diversity, population structure, genome-wide association studies, and core collection development. **2018**, 5, 64	43
2133	Precision identification of diverse bloodstream pathogens in the gut microbiome. **2018**, 24, 1809-1814	77
2132	Terrestrial species adapted to sea dispersal: Differences in propagule dispersal of two Caribbean mangroves. **2018**, 27, 4612-4626	11
2131	Species-level bacterial community profiling of the healthy sinonasal microbiome using Pacific Biosciences sequencing of full-length 16S rRNA genes. **2018**, 6, 190	64
2130	Identification of Genes Encoding Enzymes Catalyzing the Early Steps of Carrot Polyacetylene Biosynthesis. **2018**, 178, 1507-1521	17
2129	Evolutionary pathway for the 2017 emergence of a novel highly pathogenic avian influenza A(H7N9) virus among domestic poultry in Tennessee, United States. **2018**, 525, 32-39	4
2128	Phylogenomic Classification and the Evolution of Clonal Complex 5 Methicillin-Resistant in the Western Hemisphere. **2018**, 9, 1901	34
2127	Shotgun Proteomics Analysis of Saliva and Salivary Gland Tissue from the Common Octopus Octopus vulgaris. **2018**, 17, 3866-3876	10

2126	Single-cell genomics of co-sorted Nanoarchaeota suggests novel putative host associations and diversification of proteins involved in symbiosis. **2018**, 6, 161	24
2125	Diverse Bacteria Utilize Alginate Within the Microbiome of the Giant Kelp. **2018**, 9, 1914	19
2124	Phylogenetic approach to recover integration dates of latent HIV sequences within-host. **2018**, 115, E8958-E8967	23
2123	Novel insights into the genetic diversity of Parafavella based on mitochondrial CO1 sequences. **2018**, 47, 743-755	9
2122	Genomic Epidemiology Reconstructs the Introduction and Spread of Zika Virus in Central America and Mexico. **2018**, 23, 855-864.e7	60
2121	Autosomal and Mitochondrial Adaptation Following Admixture: A Case Study on the Honeybees of Reunion Island. **2018**, 10, 220-238	8
2120	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity. **2018**, 35, 719-733	68
2119	Dynamic Copy Number Evolution of X- and Y-Linked Ampliconic Genes in Human Populations. **2018**, 209, 907-920	19
2118	Genetic characterization of the HIV-1 reservoir after Vacc-4x and romidepsin therapy in HIV-1-infected individuals. **2018**, 32, 1793-1802	7
2117	One thousand DNA barcodes of piranhas and pacus reveal geographic structure and unrecognised diversity in the Amazon. **2018**, 8, 8387	38
2116	The role of adaptive strategies in plant naturalization. **2018**, 21, 1380-1389	32
2115	Geography but not alternative host species explain the spread of raccoon rabies virus in Vermont. **2018**, 146, 1977-1986	8
2114	Community assembly and diversification in a species-rich radiation of island weevils (Coleoptera: Cratopini). **2018**, 45, 2016-2026	8
2113	Laboratory and molecular surveillance of paediatric typhoidal Salmonella in Nepal: Antimicrobial resistance and implications for vaccine policy. **2018**, 12, e0006408	47
2112	Distinct bacterial metacommunities inhabit the upper and lower respiratory tracts of healthy feedlot cattle and those diagnosed with bronchopneumonia. **2018**, 221, 105-113	43
2111	Defining endemic cholera at three levels of spatiotemporal resolution within Bangladesh. **2018**, 50, 951-955	22
2110	Improved phylogenetic resolution within Siphonophora (Cnidaria) with implications for trait evolution. **2018**, 127, 823-833	11
2109	Resolving the rapid plant radiation of early diverging lineages in the tropical Zingiberales: Pushing the limits of genomic data. **2018**, 128, 55-68	25

2108	Genetic Evidence Supports Sporadic and Independent Introductions of Subtype H5 Low-Pathogenic Avian Influenza A Viruses from Wild Birds to Domestic Poultry in North America. **2018**, 92,	16
2107	Microbial biogeography of 925 geothermal springs in New Zealand. **2018**, 9, 2876	70
2106	Whole Genome Analyses Suggests that sensu lato Contains Two Additional Novel Genera (gen. nov., and gen. nov.): Implications for the Evolution of Diazotrophy and Nodulation in the. **2018**, 9,	115
2105	Characterization of (Cyanobacteria) Genotypes Based on the Internal Transcribed Spacer Region of rRNA by Next-Generation Sequencing. **2018**, 9, 971	11
2104	Epidemiological significance of dengue virus genetic variation in mosquito infection dynamics. **2018** , 14, e1007187	26
2103	Sperm head morphology is associated with sperm swimming speed: A comparative study of songbirds using electron microscopy. **2018**, 72, 1918-1932	20
2102	Anchored hybrid enrichment generated nuclear, plastid and mitochondrial markers resolve the Lepanthes horrida (Orchidaceae: Pleurothallidinae) species complex. **2018**, 129, 27-47	25
2101	Computational analysis of the receptor binding specificity of novel influenza A/H7N9 viruses. **2018**, 19, 88	7
2100	Genome-centric metatranscriptomes and ecological roles of the active microbial populations during cellulosic biomass anaerobic digestion. **2018**, 11, 117	17
2099	Recent Asian origin of chytrid fungi causing global amphibian declines. **2018**, 360, 621-627	229
2098	Epidemiology of Campylobacter, Salmonella and antimicrobial resistant Escherichia coli in free-living Canada geese (Branta canadensis) from three sources in southern Ontario. **2018**, 65, 873-886	10
2097	No association between resistance mutations, empiric antibiotic, and mortality in ceftriaxone-resistant Escherichia coli and Klebsiella pneumoniae bacteremia. **2018**, 8, 12785	7
2096	Columbid circoviruses detected in free ranging pigeons from Southern Brazil: insights on PiCV evolution. **2018**, 163, 3083-3090	6
2095	Bayesian Phylogeography and Pathogenic Characterization of Smallpox Based on HA, ATI, and CrmB Genes. **2018**, 35, 2607-2617	5
2094	Genomic exploration of sequential clinical isolates reveals a distinctive molecular signature of persistent Staphylococcus aureus bacteraemia. **2018**, 10, 65	19
2093	Genome-Wide Comparative Analysis of Aspergillus fumigatus Strains: The Reference Genome as a Matter of Concern. **2018**, 9,	28
2092	The genetic diversity of Borrelia afzelii is not maintained by the diversity of the rodent hosts. **2018**, 11, 454	14
2091	Phylogeny-corrected identification of microbial gene families relevant to human gut colonization. **2018**, 14, e1006242	16

2090	Functional and Genome Sequence-Driven Characterization of Effector Gene Repertoires Reveals Novel Variants With Altered Specificities in Closely Related Malian pv. Strains. **2018**, 9, 1657	17
2089	A High Quality Genome for , a Close Relative of House Mice with Unique Social and Ecological Adaptations. **2018**, 8, 2145-2152	3
2088	Diversity of Bacteria Exhibiting Bile Acid-inducible 7�dehydroxylation Genes in the Human Gut. **2019**, 17, 1016-1019	41
2087	Sex-Specific Linkages Between Taxonomic and Functional Profiles of Tick Gut Microbiomes. **2019**, 9, 298	20
2086	Bayesian phylodynamics of avian influenza A virus H9N2 in Asia with time-dependent predictors of migration. **2019**, 15, e1007189	11
2085	Rapid phenotypic evolution in multidrug-resistant Klebsiella pneumoniae hospital outbreak strains. **2019**, 5,	13
2084	Bacteria are important dimethylsulfoniopropionate producers in coastal sediments. **2019**, 4, 1815-1825	28
2083	Contrasting selective patterns across the segmented genome of bluetongue virus in a global reassortment hotspot. **2019**, 5, vez027	9
2082	A highly resolved food web for insect seed predators in a species-rich tropical forest. **2019**, 22, 1638-1649	23
2081	Population gene introgression and high genome plasticity for the zoonotic pathogen Streptococcus agalactiae. **2019**,	19
2080	Assignment of virus and antimicrobial resistance genes to microbial hosts in a complex microbial community by combined long-read assembly and proximity ligation. **2019**, 20, 153	38
2079	Phylogeny, host use, and diversification in the moth family Momphidae (Lepidoptera: Gelechioidea). **2019**, 14, e0207833	4
2078	A likelihood ratio-based approach for improved source attribution in microbiological forensic investigations. **2019**, 302, 109869	2
2077	Indication of ongoing amphipod speciation in Lake Baikal by genetic structures within endemic species. **2019**, 19, 138	4
2076	Genetic diversity, virulence factors and farm-to-table spread pattern of Vibrio parahaemolyticus food-associated isolates. **2019**, 84, 103270	18
2075	Circulation, Evolution and Transmission of H5N8 virus, 2016-2018. **2019**, 79, 363-372	2
2074	Interspecific variation across angiosperms in global DNA methylation: phylogeny, ecology and plant features in tropical and Mediterranean communities. **2019**, 224, 949-960	6
2073	Real-time whole genome sequencing to control a Streptococcus pyogenes outbreak at a national orthopaedic hospital. **2019**, 103, 21-26	4

2072	Nontuberculous Mycobacteria in Two Drinking Water Distribution Systems and the Role of Residual Disinfection. **2019**, 53, 8563-8573	24
2071	Innate Immune Genes Associated With Newcastle Disease Virus Load in Chick Embryos From Inbred and Outbred Lines. **2019**, 10, 1432	4
2070	Genomic epidemiology of syphilis reveals independent emergence of macrolide resistance across multiple circulating lineages. **2019**, 10, 3255	31
2069	The evolution of vocal duets and migration in New World warblers (Parulidae). **2019**, 136,	3
2068	Depth distributions of nitrite reductase (nirK) gene variants reveal spatial dynamics of thaumarchaeal ecotype populations in coastal Monterey Bay. **2019**, 21, 4032-4045	7
2067	The relative importance of ecological drivers of arbuscular mycorrhizal fungal distribution varies with taxon phylogenetic resolution. **2019**, 224, 936-948	8
2066	Scalable methods for analyzing and visualizing phylogenetic placement of metagenomic samples. **2019**, 14, e0217050	41
2065	One hypervirulent clone, sequence type 283, accounts for a large proportion of invasive Streptococcus agalactiae isolated from humans and diseased tilapia in Southeast Asia. **2019**, 13, e0007421	23
2064	Cheminformatics approach to exploring and modeling trait-associated metabolite profiles. **2019**, 11, 43	3
2063	Implications of kappa-casein evolutionary diversity for the self-assembly and aggregation of casein micelles. **2019**, 6, 190939	5
2062	Memory CD4 + T-Cells Expressing HLA-DR Contribute to HIV Persistence During Prolonged Antiretroviral Therapy. **2019**, 10, 2214	21
2061	Ecological and geographical speciation in : The evolution of amphibian obligate parasitism. **2019**, 10, 218-230	5
2060	Evaluating Chromatin Accessibility Differences Across Multiple Primate Species Using a Joint Modeling Approach. **2019**, 11, 3035-3053	3
2059	Switching the Post-translational Modification of Translation Elongation Factor EF-P. **2019**, 10, 1148	10
2058	MaizeSNPDB: A comprehensive database for efficient retrieve and analysis of SNPs among 1210 maize lines. **2019**, 17, 1377-1383	3
2057	Duplication and diversification of trehalase confers evolutionary advantages on lepidopteran insects. **2019**, 28, 5282-5298	13
2056	Transcriptional Structure of Petunia Clock in Leaves and Petals. **2019**, 10,	4
2055	Altered chromosomal topology drives oncogenic programs in SDH-deficient GISTs. **2019**, 575, 229-233	81

2054	Molecular mechanism of azithromycin resistance among typhoidal Salmonella strains in Bangladesh identified through passive pediatric surveillance. **2019**, 13, e0007868	52
2053	A global overview of cassava genetic diversity. **2019**, 14, e0224763	14
2052	A Simple and Robust Statistical Method to Define Genetic Relatedness of Samples Related to Outbreaks at the Genomic Scale - Application to Retrospective Foodborne Outbreak Investigations. **2019**, 10, 2413	7
2051	Phylogenetic Analyses of Xanthomonads Causing Bacterial Leaf Spot of Tomato and Pepper: Revealed Homologous Populations Despite Distant Geographical Distribution. **2019**, 7,	4
2050	Molecular epidemiological study of enterovirus D68 in hospitalised children in Hong Kong in 2014-2015 and their complete coding sequences. **2019**, 6, e000437	1
2049	Off-target capture data, endosymbiont genes and morphology reveal a relict lineage that is sister to all other singing cicadas. **2019**, 128, 865-886	7
2048	Limited gene exchange between two sister species of leaf beetles within a hybrid zone in the Alps. **2019**, 32, 1406-1417	2
2047	Environmental variables associated with population structure and Swiss needle cast severity in Western Oregon and Washington. **2019**, 9, 11379-11394	2
2046	Genomic Epidemiology of Major Extraintestinal Pathogenic Lineages Causing Urinary Tract Infections in Young Women Across Canada. **2019**, 6, ofz431	11
2045	The Snapdragon LATE ELONGATED HYPOCOTYL Plays A Dual Role in Activating Floral Growth and Scent Emission. **2019**, 8,	8
2044	High Heat Tolerance Is Negatively Correlated with Heat Tolerance Plasticity in Nudibranch Mollusks. **2019**, 92, 430-444	15
2043	Plasticity in the Human Gut Microbiome Defies Evolutionary Constraints. **2019**, 4,	26
2042	Consistent Biomarkers and Related Pathogenesis Underlying Asthma Revealed by Systems Biology Approach. **2019**, 20,	9
2041	Assessing the viral content of uncultured picoeukaryotes in the global-ocean by single cell genomics. **2019**, 28, 4272-4289	14
2040	A Genome-Based Species Taxonomy of the Genus Complex. **2019**, 4,	27
2039	The role of long-distance dispersal and mycorrhizas on plant colonisation within mainland Germany. **2019**, 258, 151443	1
2038	Capability for arsenic mobilization in groundwater is distributed across broad phylogenetic lineages. **2019**, 14, e0221694	6
2037	The Genomics of Carriage Isolates from UK Children and Their Household Contacts, Pre-PCV7 to Post-PCV13. **2019**, 10,	6

2036	The complete mitochondrial genome of record-breaking migrant Arctic tern. **2019**, 4, 2738-2739	1
2035	Informal genomic surveillance of regional distribution of Salmonella Typhi genotypes and antimicrobial resistance via returning travellers. **2019**, 13, e0007620	29
2034	The higher prevalence of extended spectrum beta-lactamases among Escherichia coli ST131 in Southeast Asia is driven by expansion of a single, locally prevalent subclone. **2019**, 9, 13245	9
2033	Genomic Analysis of Hexachlorocyclohexane-Degrading WS5A3p Strain in the Context of the Pangenome of. **2019**, 10,	9
2032	Inferring host roles in bayesian phylodynamics of global avian influenza A virus H9N2. **2019**, 538, 86-96	8
2031	Selection and gene flow shape niche-associated variation in pheromone response. **2019**, 3, 1455-1463	17
2030	Geography Shapes the Population Genomics of Salmonella enterica Dublin. **2019**, 11, 2220-2231	9
2029	Identification of the Bloom Forming Ulva and Macroalgal Assemblage in Jamaica Bay, New York, USA. **2019**, 120, 269	
2028	Diversity of opisthokont septin proteins reveals structural constraints and conserved motifs. **2019**, 19, 4	6
2027	Back to the Salt Mines: Genome and Transcriptome Comparisons of the Halophilic Fungus and Its Halotolerant Relative. **2019**, 10,	3
2026	Arsenite Oxidation by a Newly Isolated Betaproteobacterium Possessing Genes and Diversity of the Gene Cluster in Bacterial Genomes. **2019**, 10, 1210	6
2025	DNA barcoding of the rodent genus (Cricetidae: Sigmodontinae): mitogenomic-anchored database and identification of nuclear mitochondrial translocations (Numts). **2019**, 30, 702-712	3
2024	Description of strongly heat-inducible heat shock protein 70 transcripts from Baikal endemic amphipods. **2019**, 9, 8907	7
2023	Microevolution of antimicrobial resistance and biofilm formation of Salmonella Typhimurium during persistence on pig farms. **2019**, 9, 8832	18
2022	Should I stay or should I go? Pollinator shifts rather than cospeciation dominate the evolutionary history of South African Rediviva bees and their Diascia host plants. **2019**, 28, 4118-4133	6
2021	Incongruence between gene trees and species trees and phylogenetic signal variation in plastid genes. **2019**, 138, 219-232	74
2020	A Systematic Approach to Identify and Characterize the Effectiveness and Safety of Novel Probiotic Strains to Control Foodborne Pathogens. **2019**, 10, 1108	19
2019	Phylodynamic and transmission pattern of rabies virus in China and its neighboring countries. **2019**, 164, 2119-2129	2

2018	Hybrid enrichment of poorly preserved museum specimens refines homology hypotheses in a group of minute litter bugs (Hemiptera: Dipsocoromorpha: Schizopteridae). **2019**, 44, 985-995	3
2017	Understanding microbial community dynamics to improve optimal microbiome selection. **2019**, 7, 85	61
2016	Discovery and inhibition of an interspecies gut bacterial pathway for Levodopa metabolism. **2019**, 364,	217
2015	The Complete Chloroplast Genomes of and a Comparison with Other Species in Lythraceae. **2019**, 20,	25
2014	Investigation of round goby viral haemorrhagic septicaemia outbreak in New York. **2019**, 42, 1023-1033	4
2013	Clustering of Isolates Using MLST and Whole-Genome Phylogenetics and Protein Motif Fingerprinting. **2019**, 7, 66	3
2012	HIV Diversity and Genetic Compartmentalization in Blood and Testes during Suppressive Antiretroviral Therapy. **2019**, 93,	17
2011	A systematic study towards evolutionary and epidemiological dynamics of currently predominant H5 highly pathogenic avian influenza viruses in Vietnam. **2019**, 9, 7723	11
2010	Lineage specific histories of Mycobacterium tuberculosis dispersal in Africa and Eurasia. **2019**, 28, 3241-3256	45
2009	Expanding the biodiversity of Oenococcus oeni through comparative genomics of apple cider and kombucha strains. **2019**, 20, 330	6
2008	The origin of aerobic methanotrophy within the Proteobacteria. **2019**, 366,	8
2007	Sequential horizontal gene transfers from different hosts in a widespread Eurasian parasitic plant, Cynomorium coccineum. **2019**, 106, 679-689	13
2006	Conserved, breed-dependent, and subline-dependent innate immune responses of Fayoumi and Leghorn chicken embryos to Newcastle disease virus infection. **2019**, 9, 7209	4
2005	Characterization of a large cluster of HIV-1 A1 infections detected in Portugal and connected to several Western European countries. **2019**, 9, 7223	7
2004	Dated language phylogenies shed light on the ancestry of Sino-Tibetan. **2019**, 116, 10317-10322	48
2003	The Petunia CHANEL Gene is a ZEITLUPE Ortholog Coordinating Growth and Scent Profiles. **2019**, 8,	16
2002	Genetics and evidence for balancing selection of a sex-linked colour polymorphism in a songbird. **2019**, 10, 1852	28
2001	De Novo Transcriptome Assembly and Functional Annotation in Five Species of Bats. **2019**, 9, 6222	13

2000	Susceptibility (re)-testing of a large collection of Listeria monocytogenes from foods in China from 2012 to 2015 and WGS characterization of resistant isolates. **2019**, 74, 1786-1794	9
1999	Emergence of human infection with Jingmen tick virus in China: A retrospective study. **2019**, 43, 317-324	41
1998	Duplication of a domestication locus neutralized a cryptic variant that caused a breeding barrier in tomato. **2019**, 5, 471-479	35
1997	Characterizing a Murine Model for Astrovirus Using Viral Isolates from Persistently Infected Immunocompromised Mice. **2019**, 93,	12
1996	Direct quantitative real-time PCR assay for detection of the emerging pathogen Neonectria neomacrospora. **2019**, 49, e12509	2
1995	Co-circulation of genetically distinct highly pathogenic avian influenza A clade 2.3.4.4 (H5N6) viruses in wild waterfowl and poultry in Europe and East Asia, 2017-18. **2019**, 5, vez004	37
1994	Genome of 'Charleston Gray', the principal American watermelon cultivar, and genetic characterization of 1,365 accessions in the U.S. National Plant Germplasm System watermelon collection. **2019**, 17, 2246-2258	41
1993	The Patchy Distribution of Restriction?Modification System Genes and the Conservation of Orphan Methyltransferases in Halobacteria. **2019**, 10,	18
1992	COI-based species delimitation in Indochinese Tetraserica chafers reveal hybridisation despite strong divergence in male copulation organs. **2019**, 19, 277-286	4
1991	Differential gene expression associated with fungal trophic shifts along the senescence gradient of the moss Dicranum scoparium. **2019**, 21, 2273-2289	7
1990	Recruit symbiosis establishment and Symbiodiniaceae composition influenced by adult corals and reef sediment. **2019**, 38, 405-415	12
1989	Evolutionary history and palaeoecology of brown bear in North-East Siberia re-examined using ancient DNA and stable isotopes from skeletal remains. **2019**, 9, 4462	17
1988	Morphological and Molecular Analysis of Australian Earwigs (Dermaptera) Points to Unique Species and Regional Endemism in the Anisolabididae Family. **2019**, 10,	2
1987	Shotgun Metagenomics of a Water Kefir Fermentation Ecosystem Reveals a Novel Species. **2019**, 10, 479	41
1986	Tumor Microenvironment Characterization in Gastric Cancer Identifies Prognostic and Immunotherapeutically Relevant Gene Signatures. **2019**, 7, 737-750	301
1985	Towards resolving and redefining Amphipyrinae (Lepidoptera, Noctuoidea, Noctuidae): a massively polyphyletic taxon. **2019**, 44, 451-464	6
1984	Culture of Clinical Specimens Reveals Extensive Diversity of Legionella pneumophila Strains in Arizona. **2019**, 4,	4
1983	Taxonomic novelties in grammitid ferns (Polypodiaceae) from the Neotropics and Madagascar supported by molecular data. **2019**, 394, 176	0

1982	Transmission Trees on a Known Pathogen Phylogeny: Enumeration and Sampling. **2019**, 36, 1333-1343	8
1981	Cluster-Transition Determining Sites Underlying the Antigenic Evolution of Seasonal Influenza Viruses. **2019**, 36, 1172-1186	4
1980	Resolving Phylogenetic Relationships for Streptococcus mitis and Streptococcus oralis through Core- and Pan-Genome Analyses. **2019**, 11, 1077-1087	14
1979	Aneuploidy and Ethanol Tolerance in. **2019**, 10, 82	32
1978	Mechanism of a Standalone □Lactone Synthetase: New Continuous Assay for a Widespread ANL Superfamily Enzyme. **2019**, 20, 1701-1711	5
1977	Phylogenetic Clustering by Linear Integer Programming (PhyCLIP). **2019**, 36, 1580-1595	21
1976	Potential for Microbially Mediated Natural Attenuation of Diluted Bitumen on the Coast of British Columbia (Canada). **2019**, 85,	12
1975	A congruent topology for deep gastropod relationships. **2019**, 286, 20182776	39
1974	Climate is a strong predictor of near-infrared reflectance but a poor predictor of colour in butterflies. **2019**, 286, 20190234	13
1973	Molecular phylogeny of Oreochromis (Cichlidae: Oreochromini) reveals mito-nuclear discordance and multiple colonisation of adverse aquatic environments. **2019**, 136, 215-226	17
1972	Genomic signatures of G-protein-coupled receptor expansions reveal functional transitions in the evolution of cephalopod signal transduction. **2019**, 286, 20182929	4
1971	TORMES: an automated pipeline for whole bacterial genome analysis. **2019**, 35, 4207-4212	33
1970	hicap: Serotyping of the Haemophilus influenzae Capsule Locus. **2019**, 57,	16
1969	Extreme genetic structure and dynamic range evolution in a montane passerine bird: implications for tropical diversification. **2019**, 126, 487-506	15
1968	Can Multi-Element Fingerprinting of Soils Inform Assessments of Chemical Connectivity Between Depressional Wetlands?. **2019**, 39, 1015-1027	4
1967	The Charosphere Promotes Mineralization of 13C-Phenanthrene by Psychrotrophic Microorganisms in Greenland Soils. **2019**, 48, 559-567	6
1966	overexpresses a wound-inducible enzyme, , that affects jasmonate catabolism, sex determination, and plant architecture in maize. **2019**, 2, 114	22
1965	Human pantothenate kinase 4 is a pseudo-pantothenate kinase. **2019**, 28, 1031-1047	13

1964	Envelope-Specific Recognition Patterns of HIV Vaccine-Induced IgG Antibodies Are Linked to Immunogen Structure and Sequence. **2019**, 10, 717	5
1963	Microbial Community Diversity Within Sediments from Two Geographically Separated Hadal Trenches. **2019**, 10, 347	34
1962	Within-farm prevalence and environmental distribution of livestock-associated methicillin-resistant Staphylococcus aureus in farmed mink (Neovison vison). **2019**, 231, 80-86	5
1961	Human and Extracellular DNA Depletion for Metagenomic Analysis of Complex Clinical Infection Samples Yields Optimized Viable Microbiome Profiles. **2019**, 26, 2227-2240.e5	54
1960	Deep Learning Architecture Search by Neuro-Cell-Based Evolution with Function-Preserving Mutations. **2019**, 243-258	6
1959	Speciation Rate Is Independent of the Rate of Evolution of Morphological Size, Shape, and Absolute Morphological Specialization in a Large Clade of Birds. **2019**, 193, E78-E91	18
1958	Population genomic analysis of mango (Mangifera indica) suggests a complex history of domestication. **2019**, 222, 2023-2037	21
1957	Land-plant Phylogenomic and Pomegranate Transcriptomic Analyses Reveal an Evolutionary Scenario of CYP75 Genes Subsequent to Whole Genome Duplications. **2019**, 62, 48-60	9
1956	Genomic insights into neonicotinoid sensitivity in the solitary bee Osmia bicornis. **2019**, 15, e1007903	40
1955	Characterization of Emetic and Diarrheal Strains From a 2016 Foodborne Outbreak Using Whole-Genome Sequencing: Addressing the Microbiological, Epidemiological, and Bioinformatic Challenges. **2019**, 10, 144	50
1954	Putting keyhole limpets on the map: phylogeny and biogeography of the globally distributed marine family Fissurellidae (Vetigastropoda, Mollusca). **2019**, 135, 249-269	4
1953	Combining MALDI-TOF and genomics in the study of methicillin resistant and multidrug resistant Staphylococcus pseudintermedius in New Zealand. **2019**, 9, 1271	16
1952	Circulation of Plasmids Harboring Resistance Genes to Quinolones and/or Extended-Spectrum Cephalosporins in Multiple Serotypes from Swine in the United States. **2019**, 63,	10
1951	Phylofactorization: a graph partitioning algorithm to identify phylogenetic scales of ecological data. **2019**, 89, e01353	33
1950	New species reveal unexpected interspecific microhabitat diversity in the genus Uthina Simon, 1893 (Araneae : Pholcidae). **2019**,	2
1949	Conserved Patterns of Symmetric Inversion in the Genome Evolution of Respiratory Pathogens. **2019**, 4,	10
1948	Evolution of Serotype 3 in England and Wales: A Major Vaccine Evader. **2019**, 10,	15
1947	Genus level analysis of PKS-NRPS and NRPS-PKS hybrids reveals their origin in Aspergilli. **2019**, 20, 847	9

1946	A Phylogenomic Analysis of the Floral Transcriptomes of Sexually Deceptive and Rewarding European Orchids, and. **2019**, 10, 1553	16
1945	An Escherichia coli ST131 pangenome atlas reveals population structure and evolution across 4,071 isolates. **2019**, 9, 17394	39
1944	A family of Type VI secretion system effector proteins that form ion-selective pores. **2019**, 10, 5484	27
1943	Phylogenetic comparative methods improve the selection of characters for generic delimitations in a hyperdiverse Neotropical orchid clade. **2019**, 9, 15098	7
1942	Interspecific hybridization facilitates niche adaptation in beer yeast. **2019**, 3, 1562-1575	41
1941	Evolution and phylogeography of densovirus. **2019**, 5, vez053	3
1940	Sensory coding mechanisms revealed by optical tagging of physiologically defined neuronal types. **2019**, 366, 1384-1389	12
1939	Re-assessing the diversity of negative strand RNA viruses in insects. **2019**, 15, e1008224	43
1938	Evolution and Global Transmission of a Multidrug-Resistant, Community-Associated Methicillin-Resistant Staphylococcus aureus Lineage from the Indian Subcontinent. **2019**, 10,	22
1937	New Insights on Phylogeny Based on a Comparative Phylogenomic Study Using Complete Plastome Sequences. **2019**, 8,	6
1936	Phylogenetic Relationship Among Wild and Cultivated Grapevine in Sicily: A Hotspot in the Middle of the Mediterranean Basin. **2019**, 10, 1506	12
1935	Basal Rot of : Understanding Pathogenicity in f. sp.. **2019**, 10, 2905	6
1934	The Genetic Structure of Populations of the Douglas-Fir Swiss Needle Cast Fungus Nothophaeocryptopus gaeumannii in New Zealand. **2019**, 109, 446-455	1
1933	Isolation and identification of a novel salmon gill poxvirus variant from Atlantic salmon in Eastern Canada. **2019**, 42, 315-318	6
1932	Spatial patterns along an elevation gradient in high altitude grasslands, Brazil. **2019**, 37,	6
1931	Niche Differentiation among Three Closely Related Clades at a Full-Scale Activated Sludge Wastewater Treatment Plant and Putative Linkages to Process Performance. **2019**, 85,	4
1930	Developing a High-Throughput SNP-Based Marker System to Facilitate the Introgression of Traits From Species Into Bread Wheat (). **2018**, 9, 1993	14
1929	Bacteriome-associated Wolbachia of the parthenogenetic termite Cavitermes tuberosus. **2019**, 95,	13

1928	Monographic treatment of Paraholosticha muscicola (Ciliophora, Keronopsidae), including morphological and molecular biological characterization of a brackish water population from Korea. **2019**, 68, 48-67	24
1927	Contrasting patterns of coding and flanking region evolution in mammalian keratin associated protein-1 genes. **2019**, 133, 352-361	4
1926	High-Resolution Evolutionary Analysis of Within-Host Hepatitis C Virus Infection. **2019**, 219, 1722-1729	8
1925	Meningococcal Disease Among College-Aged Young Adults: 2014-2016. **2019**, 143,	25
1924	Soybean Sudden Death Syndrome Causal Agent Present in Michigan. **2019**, 103, 1234-1243	11
1923	Patterns of cross-resistance and collateral sensitivity between clinical antibiotics and natural antimicrobials. **2019**, 12, 878-887	5
1922	Commensal Enterobacteriaceae Protect against Salmonella Colonization through Oxygen Competition. **2019**, 25, 128-139.e5	70
1921	Remote tropical island colonization does not preclude symbiotic specialists: new evidence of mycorrhizal specificity across the geographic distribution of the Hawaiian endemic orchid Anoectochilus sandvicensis. **2019**, 123, 657-666	3
1920	Real time monitoring of Aeromonas salmonicida evolution in response to successive antibiotic therapies in a commercial fish farm. **2019**, 21, 1113-1123	12
1919	Genetic Diversity of Verticillium dahliae Populations From Olive and Potato in Lebanon. **2019**, 103, 656-667	2
1918	Vestured pits and scalariform perforation plate morphology modify the relationships between angiosperm vessel diameter, climate and maximum plant height. **2019**, 221, 1802-1813	10
1917	From shallow to deep divergences: mixed messages from Amazon Basin cichlids. **2019**, 832, 317-329	3
1916	High risk Epstein-Barr virus variants characterized by distinct polymorphisms in the EBER locus are strongly associated with nasopharyngeal carcinoma. **2019**, 144, 3031-3042	29
1915	Detecting Amino Acid Coevolution with Bayesian Graphical Models. **2019**, 1851, 105-122	3
1914	Of puzzles and pavements: a quantitative exploration of leaf epidermal cell shape. **2019**, 221, 540-552	40
1913	A repeated cross-sectional study of the epidemiology of Campylobacter and antimicrobial resistant Enterobacteriaceae in free-living Canada geese in Guelph, Ontario, Canada. **2019**, 66, 60-72	4
1912	Forensic human identification with targeted microbiome markers using nearest neighbor classification. **2019**, 38, 130-139	28
1911	Understand the genomic diversity and evolution of fungal pathogen Candida glabrata by genome-wide analysis of genetic variations. **2020**, 176, 82-90	7

1910	Gnrh receptor gnrhr2bb is expressed exclusively in lhb-expressing cells in Atlantic salmon male parr. **2020**, 285, 113293	11
1909	Comparative Genomic Analysis of the Pheromone Receptor Class 1 Family (V1R) Reveals Extreme Complexity in Mouse Lemurs (Genus, Microcebus) and a Chromosomal Hotspot across Mammals. **2020**, 12, 3562-3579	10
1908	Microbial genomes retrieved from High Arctic lake sediments encode for adaptation to cold and oligotrophic environments. **2020**, 65, S233	7
1907	StrainHub: a phylogenetic tool to construct pathogen transmission networks. **2020**, 36, 945-947	14
1906	Bacterial colonization of minerals in grassland soils is selective and highly dynamic. **2020**, 22, 917-933	12
1905	Identification of genetic families based on mitochondrial D-loop sequence in population of the Tatra chamois (Rupicapra rupicapra tatrica). **2020**, 75, 121-128	2
1904	Plant phylogenetic history explains in-stream decomposition at a global scale. **2020**, 108, 17-35	20
1903	The first transcriptomic resource for the flatworm Triaenophorus nodulosus (Cestoda: Bothriocephalidea), a common parasite of holarctic freshwater fish. **2020**, 51, 100702	0
1902	BactMAP: An R package for integrating, analyzing and visualizing bacterial microscopy data. **2020**, 113, 297-308	13
1901	Molecular insights into evolution, mutations and receptor-binding specificity of influenza A and B viruses from outpatients and hospitalized patients in Singapore. **2020**, 90, 84-96	2
1900	The Green Revolution shaped the population structure of the rice pathogen Xanthomonas oryzae pv. oryzae. **2020**, 14, 492-505	16
1899	Genetic basis for the cooperative bioactivation of plant lignans by Eggerthella lenta and other human gut bacteria. **2020**, 5, 56-66	29
1898	Natural variation in HsfA2 pre-mRNA splicing is associated with changes in thermotolerance during tomato domestication. **2020**, 225, 1297-1310	24
1897	Treeio: An R Package for Phylogenetic Tree Input and Output with Richly Annotated and Associated Data. **2020**, 37, 599-603	118
1896	The metagenome-assembled genome of Candidatus Oenococcus aquikefiri from water kefir represents the species Oenococcus sicerae. **2020**, 88, 103402	12
1895	Structural Insights Into PfARO and Characterization of its Interaction With PfAIP. **2020**, 432, 878-896	7
1894	Gonadotropin-inhibitory hormone in teleosts: New insights from a basal representative, the eel. **2020**, 287, 113350	7
1893	All these Fantastic Cultures? Research History and Regionalization in the Late Palaeolithic Tanged Point Cultures of Eastern Europe. **2020**, 23, 162-185	10

1892	High-density SNP-based genetic diversity and heterotic patterns of tropical maize breeding lines. **2020**, 60, 779-787	2
1891	Neotropical migratory and resident birds occurring in sympatry during winter have distinct haemosporidian parasite assemblages. **2020**, 47, 748-759	11
1890	A Bioinformatic Analysis of Integrative Mobile Genetic Elements Highlights Their Role in Bacterial Adaptation. **2020**, 27, 140-153.e9	47
1889	Primary dermal fibroblasts and pectoralis muscle show similar patterns of oxidative stress in tropical and temperate birds despite differing life-histories. **2020**, 51,	2
1888	Unexpected mitochondrial genome diversity revealed by targeted single-cell genomics of heterotrophic flagellated protists. **2020**, 5, 154-165	23
1887	Comparative skeletal anatomy of neonatal ursids and the extreme altriciality of the giant panda. **2020**, 236, 724-736	3
1886	The Genome of the Blind Soil-Dwelling and Ancestrally Wingless Dipluran Campodea augens: A Key Reference Hexapod for Studying the Emergence of Insect Innovations. **2020**, 12, 3534-3549	2
1885	Function-driven single-cell genomics uncovers cellulose-degrading bacteria from the rare biosphere. **2020**, 14, 659-675	29
1884	Origin and transmission of bovine viral diarrhea virus type 1 in China revealed by phylodynamic analysis. **2020**, 128, 162-169	6
1883	Towards a unified classification for human respiratory syncytial virus genotypes. **2020**, 6, veaa052	8
1882	Large-scale survey reveals pervasiveness and potential function of endogenous geminiviral sequences in plants. **2020**, 6, veaa071	8
1881	Geographical isolation, habitat shifts and hybridisation in the diversification of the Macaronesian endemic genus Argyranthemum (Asteraceae). **2020**, 228, 1953-1971	6
1880	Prolonged Outbreak of Multidrug-Resistant Shigella sonnei Harboring in Victoria, Australia. **2020**, 64,	7
1879	New Insights Into the Evolutionary History of Melatonin Receptors in Vertebrates, With Particular Focus on Teleosts. **2020**, 11, 538196	5
1878	Warming Climate Is Reducing the Diversity of Dominant Microbes in the Largest High Arctic Lake. **2020**, 11, 561194	3
1877	Unraveling the Spiraling Radiation: A Phylogenomic Analysis of Neotropical L. **2020**, 11, 1195	1
1876	Unlocking plant resources to support food security and promote sustainable agriculture. **2020**, 2, 421-445	54
1875	UCE data reveal multiple origins of rose gallers in North America: Global phylogeny of Diplolepis Geoffroy (Hymenoptera: Cynipidae). **2020**, 153, 106949	1

1874	DoubleRecViz: a web-based tool for visualizing transcript-gene-species tree reconciliation. **2021**, 37, 1920-1922	0
1873	Differential activities of maize plant elicitor peptides as mediators of immune signaling and herbivore resistance. **2020**, 104, 1582-1602	10
1872	Genomic and transcriptional analysis of genes containing fibrinogen and IgSF domains in the schistosome vector Biomphalaria glabrata, with emphasis on the differential responses of snails susceptible or resistant to Schistosoma mansoni. **2020**, 14, e0008780	5
1871	No Assembly Required: Using BTyper3 to Assess the Congruency of a Proposed Taxonomic Framework for the Group With Historical Typing Methods. **2020**, 11, 580691	10
1870	Genome Sequence and Characterization of Five Bacteriophages Infecting and : Alderaan, Coruscant, Dagobah, Endor1 and Endor2. **2020**, 12,	1
1869	A Collinearity-Incorporating Homology Inference Strategy for Connecting Emerging Assemblies in the Triticeae Tribe as a Pilot Practice in the Plant Pangenomic Era. **2020**, 13, 1694-1708	30
1868	Visualization of evolutionary relationships through geologic time in Timescale Creator. **2020**, 8, 100037	
1867	Ecology and evolution of cycad-feeding Lepidoptera. **2020**, 23, 1862-1877	10
1866	Imaginal disc growth factor maintains cuticle structure and controls melanization in the spot pattern formation of Bombyx mori. **2020**, 16, e1008980	6
1865	Genomic characterization of a diazotrophic microbiota associated with maize aerial root mucilage. **2020**, 15, e0239677	5
1864	The New ST152 Variants with Hypermucoviscous Phenotype Isolated from Renal Transplant Recipients with Asymptomatic Bacteriuria-Genetic Characteristics by WGS. **2020**, 11,	6
1863	Analysis of Whole Genome Resequencing Datasets from a Worldwide Sample of Sheep Breeds to Identify Potential Causal Mutations Influencing Milk Composition Traits. **2020**, 10,	2
1862	Adaptation of Arginine Synthesis among Uropathogenic Branches of the Escherichia coli Phylogeny Reveals Adjustment to the Urinary Tract Habitat. **2020**, 11,	4
1861	First detection and molecular characterisation of pseudocowpox virus in a cattle herd in Zambia. **2020**, 17, 152	2
1860	Large-scale genome sequencing of mycorrhizal fungi provides insights into the early evolution of symbiotic traits. **2020**, 11, 5125	86
1859	A global test of Allen's rule in rodents. **2020**, 29, 2248-2260	7
1858	Patterns of speciation are similar across mountainous and lowland regions for a Neotropical plant radiation (Costaceae: Costus). **2020**, 74, 2644-2661	7
1857	Unlocking the relationships among population structure, plant architecture, growing season, and environmental adaptation in Henan wheat cultivars. **2020**, 20, 469	0

1856	Vesicle Transport in Plants: A Revised Phylogeny of SNARE Proteins. **2020**, 16, 1176934320956575	7
1855	CerealsDB-new tools for the analysis of the wheat genome: update 2020. **2020**, 2020,	11
1854	Chagas vectors Panstrongylus chinai (Del Ponte, 1929) and Panstrongylus howardi (Neiva, 1911): chromatic forms or true species?. **2020**, 13, 226	5
1853	Asterid Phylogenomics/Phylotranscriptomics Uncover Morphological Evolutionary Histories and Support Phylogenetic Placement for Numerous Whole-Genome Duplications. **2020**, 37, 3188-3210	21
1852	Rapid implementation of SARS-CoV-2 sequencing to investigate cases of health-care associated COVID-19: a prospective genomic surveillance study. **2020**, 20, 1263-1272	200
1851	CeMbio - The Microbiome Resource. **2020**, 10, 3025-3039	29
1850	The Identification and Evolutionary Trends of the Solute Carrier Superfamily in Arthropods. **2020**, 12, 1429-1439	5
1849	Genome-wide patterns of differentiation over space and time in the Queensland fruit fly. **2020**, 10, 10788	8
1848	Identification of copy number variation and population analysis of the sacred lotus (). **2020**, 84, 2037-2044	0
1847	Characterizing the impact of an exotic soybean line on elite cultivar development. **2020**, 15, e0235434	1
1846	A molecular and epidemiological study of Vibrio cholerae isolates from cholera outbreaks in southern Ghana. **2020**, 15, e0236016	3
1845	Pathogenic Differences of Type 1 Restriction-Modification Allele Variants in Experimental Meningitis. **2020**, 10, 590657	1
1844	Evolution of Oxidative Phosphorylation (OXPHOS) Genes Reflecting the Evolutionary and Life Histories of Fig Wasps (Hymenoptera, Chalcidoidea). **2020**, 11,	0
1843	Equine-Like H3 Avian Influenza Viruses in Wild Birds, Chile. **2020**, 26, 2887-2898	1
1842	No evidence for increased transmissibility from recurrent mutations in SARS-CoV-2. **2020**, 11, 5986	165
1841	Ghosts of a Structured Past: Impacts of Ancestral Patterns of Isolation-by-Distance on Divergence-Time Estimation. **2020**, 111, 573-582	2
1840	DHFR and DHPS Mutations Are Associated With HIV-1 Co-Infection and a Novel DHPS Mutation I504T Is Identified in Western Kenya. **2020**, 10, 600112	2
1839	Mercury Methylation Genes Identified across Diverse Anaerobic Microbial Guilds in a Eutrophic Sulfate-Enriched Lake. **2020**, 54, 15840-15851	12

1838	Estimation of Full-Length TprK Diversity in Treponema pallidum subsp.. **2020**, 11,	3
1837	Virulence characterization and comparative genomics of Listeria monocytogenes sequence type 155 strains. **2020**, 21, 847	7
1836	Immune challenge reduces gut microbial diversity and triggers fertility-dependent gene expression changes in a social insect. **2020**, 21, 816	1
1835	Epidemiology and biology of a herpesvirus in rabies endemic vampire bat populations. **2020**, 11, 5951	5
1834	A comprehensive analysis of cotton VQ gene superfamily reveals their potential and extensive roles in regulating cotton abiotic stress. **2020**, 21, 795	6
1833	Multi-locus sequence analyses reveal a clonal L. borgpetersenii genotype in a heterogeneous invasive Rattus spp. community across the City of Johannesburg, South Africa. **2020**, 13, 570	0
1832	Population genetic structure of turbot (Scophthalmus maximus L., 1758) in the Black Sea. **2020**, 97, 1154-1164	8
1831	Partitiviruses Infecting Drosophila melanogaster and Aedes aegypti Exhibit Efficient Biparental Vertical Transmission. **2020**, 94,	17
1830	Population Structure of Non-ST6 Isolated in the Red Meat and Poultry Value Chain in South Africa. **2020**, 8,	6
1829	Comparison of Molecular Subtyping and Antimicrobial Resistance Detection Methods Used in a Large Multistate Outbreak of Extensively Drug-Resistant Campylobacter jejuni Infections Linked to Pet Store Puppies. **2020**, 58,	4
1828	A Race against Time: Reduced Azithromycin Susceptibility in Serovar Typhi in Pakistan. **2020**, 5,	14
1827	Molecular characterization of Pseudomonas from Agaricus bisporus caps reveal novel blotch pathogens in Western Europe. **2020**, 21, 505	4
1826	Diverse variola virus (smallpox) strains were widespread in northern Europe in the Viking Age. **2020** , 369,	42
1825	Fungi, bacteria and oomycota opportunistically isolated from the seagrass, Zostera marina. **2020**, 15, e0236135	15
1824	Genetic Population Structure of the Hard Clam Meretrix meretrix Along the Chinese Coastlines Revealed by Microsatellite DNA Markers. **2020**, 7,	1
1823	Evaluation of an ensemble-based distance statistic for clustering MLST datasets using epidemiologically defined clusters of cyclosporiasis. **2020**, 148, e172	7
1822	A seventeenth-century Mycobacterium tuberculosis genome supports a Neolithic emergence of the Mycobacterium tuberculosis complex. **2020**, 21, 201	17
1821	Ancient Bacterial Genomes Reveal a High Diversity of Treponema pallidum Strains in Early Modern Europe. **2020**, 30, 3788-3803.e10	21

1820	Coronaviruses in the Sea. **2020**, 11, 1795	18
1819	Ecological factors associated with persistent circulation of multiple highly pathogenic avian influenza viruses among poultry farms in Taiwan during 2015-17. **2020**, 15, e0236581	6
1818	BnaSNPDB: An interactive web portal for the efficient retrieval and analysis of SNPs among 1,007 rapeseed accessions. **2020**, 18, 2766-2773	4
1817	The diversity of maternal-age effects upon pre-adult survival across animal species. **2020**, 287, 20200972	14
1816	High Prevalence of Human-Associated in Wetlands Located in Eastern France. **2020**, 11, 552566	5
1815	Butterfly dichromatism primarily evolved via Darwin's, not Wallace's, model. **2020**, 4, 545-555	5
1814	MIR2111-5 locus and shoot-accumulated mature miR2111 systemically enhance nodulation depending on HAR1 in Lotus japonicus. **2020**, 11, 5192	10
1813	Structural-based connectivity and omic phenotype evaluations (SCOPE): a cheminformatics toolbox for investigating lipidomic changes in complex systems. **2020**, 145, 7197-7209	3
1812	Antimicrobial Susceptibility and Phylogenetic Relations in a German Cohort Infected with Mycobacterium abscessus. **2020**, 58,	3
1811	Tissue Tropisms of Avian Influenza A Viruses Affect Their Spillovers from Wild Birds to Pigs. **2020**, 94,	3
1810	African Arowana Genome Provides Insights on Ancient Teleost Evolution. **2020**, 23, 101662	1
1809	Contribution of Podoviridae and Myoviridae bacteriophages to the effectiveness of anti-staphylococcal therapeutic cocktails. **2020**, 10, 18612	10
1808	Systematic revision and morphological phylogenetic analysis of ́Anchylorhynchus Schoenherr, 1836 (Coleoptera, Curculionidae: Derelomini). **2020**, 4839, zootaxa.4839.1.1	2
1807	Bradymonabacteria, a novel bacterial predator group with versatile survival strategies in saline environments. **2020**, 8, 126	11
1806	A comparison of humans and baboons suggests germline mutation rates do not track cell divisions. **2020**, 18, e3000838	23
1805	Genome-wide analysis of the polyamine oxidase gene family in wheat (Triticum aestivum L.) reveals involvement in temperature stress response. **2020**, 15, e0236226	1
1804	Characterization of integrated prophages within diverse species of clinical nontuberculous mycobacteria. **2020**, 17, 124	8
1803	Diversity in the intrinsic apoptosis pathway of nematodes. **2020**, 3, 478	0

1802	Assessing the legacy of land use trajectories on stream fish communities of southern Brazil. **2020**, 1	1
1801	The Best-Practice Organism for Single-Species Studies of Antimicrobial Efficacy against Biofilms Is. **2020**, 10,	2
1800	Sex-biased patterns shaped the genetic history of Roma. **2020**, 10, 14464	3
1799	Genetic Basis of Antigenic Variation of SAT3 Foot-And-Mouth Disease Viruses in Southern Africa. **2020**, 7, 568	1
1798	The evolutionary history of Neanderthal and Denisovan Y chromosomes. **2020**, 369, 1653-1656	35
1797	Long-term Sculpting of the B-cell Repertoire following Cancer Immunotherapy in Patients Treated with Sipuleucel-T. **2020**, 8, 1496-1507	2
1796	Twentieth-century emergence of antimicrobial resistant human- and bovine-associated Salmonella enterica serotype Typhimurium lineages in New York State. **2020**, 10, 14428	2
1795	Extensive Homoplasy but No Evidence of Convergent Evolution of Repeat Numbers at MIRU Loci in Modern Lineages. **2020**, 8, 455	
1794	Epidemiological and Genomic Analysis of SARS-CoV-2 in 10 Patients From a Mid-Sized City Outside of Hubei, China in the Early Phase of the COVID-19 Outbreak. **2020**, 8, 567621	1
1793	Extensive haplotypes are associated with population differentiation and environmental adaptability in Upland cotton (Gossypium hirsutum). **2020**, 133, 3273-3285	4
1792	New Genomes From the China-Myanmar Border. **2020**, 11, 1930	2
1791	Rapid Detection of Azole-Resistant Aspergillus fumigatus in Clinical and Environmental Isolates by Use of a Lab-on-a-Chip Diagnostic System. **2020**, 58,	7
1790	Diazotrophic bacteria from maize exhibit multifaceted plant growth promotion traits in multiple hosts. **2020**, 15, e0239081	4
1789	Amalgamated cross-species transcriptomes reveal organ-specific propensity in gene expression evolution. **2020**, 11, 4459	11
1788	The Nubeam reference-free approach to analyze metagenomic sequencing reads. **2020**, 30, 1364-1375	2
1787	A CYC/TB1-type TCP transcription factor controls spikelet meristem identity in barley. **2020**, 71, 7118-7131	9
1786	Evolutionary and structural analyses of SARS-CoV-2 D614G spike protein mutation now documented worldwide. **2020**, 10, 14031	120
1785	A horizontally acquired expansin gene increases virulence of the emerging plant pathogen Erwinia tracheiphila. **2020**, 10, 21743	2

1784	Discovery of Genomic Characteristics and Selection Signatures in Southern Chinese Local Cattle. **2020**, 11, 533052	4
1783	Identification of BELL Transcription Factors Involved in Nodule Initiation and Development in the Legumes and. **2020**, 9,	6
1782	The Role of Symbiotic Microorganisms, Nutrient Uptake and Rhizosphere Bacterial Community in Response of Pea (L.) Genotypes to Elevated Al Concentrations in Soil. **2020**, 9,	3
1781	Whole-Genome Sequence Analysis of an Extensively Drug-Resistant Salmonella enterica Serovar Agona Isolate from an Australian Silver Gull () Reveals the Acquisition of Multidrug Resistance Plasmids. **2020**, 5,	8
1780	Foliar fungal endophyte community structure is independent of phylogenetic relatedness in an Asteraceae common garden. **2020**, 10, 13895-13912	4
1779	Thiosulfate Reduction Coupled with Anaerobic Ammonium Oxidation by Ralstonia sp. GX3-BWBA. **2020**, 4, 2426-2434	6
1778	Using metacommunity ecology to understand environmental metabolomes. **2020**, 11, 6369	13
1777	Plant TDP1 (Tyrosyl-DNA Phosphodiesterase 1): A Phylogenetic Perspective and Gene Expression Data Mining. **2020**, 11,	2
1776	Full genome viral sequences inform patterns of SARS-CoV-2 spread into and within Israel. **2020**, 11, 5518	66
1775	Indo-European phylogenetics with R. **2020**, 8, 110-180	1
1774	Metagenomic Approach with the NetoVIR Enrichment Protocol Reveals Virus Diversity within Ethiopian Honey Bees (). **2020**, 12,	9
1773	Genome-scale phylogeny and contrasting modes of genome evolution in the fungal phylum Ascomycota. **2020**, 6,	24
1772	The distribution of mutations and hotspots in transcription regulators of resistance-nodulation-cell division efflux pumps in tigecycline non-susceptible Acinetobacter baumannii in China. **2020**, 310, 151464	4
1771	Genetic Diversity, Compartmentalization, and Age of HIV Proviruses Persisting in CD4 T Cell Subsets during Long-Term Combination Antiretroviral Therapy. **2020**, 94,	9
1770	Dissemination of Quinolone-Resistant Escherichia coli in the Norwegian Broiler and Pig Production Chains and Possible Persistence in the Broiler Production Environment. **2020**, 86,	7
1769	Emergence of genomic diversity and recurrent mutations in SARS-CoV-2. **2020**, 83, 104351	500
1768	Extended-Spectrum-□Lactamase- and Plasmid AmpC-Producing Escherichia coli Causing Community-Onset Bloodstream Infection: Association of Bacterial Clones and Virulence Genes with Septic Shock, Source of Infection, and Recurrence. **2020**, 64,	3
1767	Oxidosqualene cyclases involved in the biosynthesis of triterpenoids in Quercus suber cork. **2020**, 10, 8011	10

1766	Under-the-Radar Dengue Virus Infections in Natural Populations of Aedes aegypti Mosquitoes. **2020**, 5,		9
1765	Genomic Epidemiology of Invasive Methicillin-Resistant Staphylococcus aureus Infections Among Hospitalized Individuals in Ontario, Canada. **2020**, 222, 2071-2081		5
1764	Development of an inactivated vaccine candidate for SARS-CoV-2. **2020**, 369, 77-81		823
1763	Ecological and genomic analyses of candidate phylum WPS-2 bacteria in an unvegetated soil. **2020**, 22, 3143-3157		16
1762	Insights into the evolutionary history and epidemiological characteristics of the emerging lineage 1 porcine reproductive and respiratory syndrome viruses in China. **2020**, 67, 2630-2641		9
1761	Multi-task learning sparse group lasso: a method for quantifying antigenicity of influenza A(H1N1) virus using mutations and variations in glycosylation of Hemagglutinin. **2020**, 21, 182		1
1760	Lineage-specific evolution and gene flow in Listeria monocytogenes are independent of bacteriophages. **2020**, 22, 5058-5072		7
1759	Ecological succession in the vaginal microbiota during pregnancy and birth. **2020**, 14, 2325-2335		18
1758	Significant host- and environment-dependent differentiation among highly sporadic fungal endophyte communities in cereal crops-related wild grasses. **2020**, 22, 3357-3374		13
1757	The genome of a Bacteroidetes inhabitant of the human gut encodes a structurally distinct enoyl-acyl carrier protein reductase (FabI). **2020**, 295, 7635-7652		3
1756	A DNA Repair Inhibitor Isolated from an Ecuadorian Fungal Endophyte Exhibits Synthetic Lethality in PTEN-Deficient Glioblastoma. **2020**, 83, 1899-1908		2
1755	Toxigenic evolution and establishment of reservoirs in aquatic ecosystems. **2020**, 117, 7897-7904		12
1754	Mutant EZH2 Induces a Pre-malignant Lymphoma Niche by Reprogramming the Immune Response. **2020**, 37, 655-673.e11		47
1753	Tracking echovirus eleven outbreaks in Guangdong, China: a metatranscriptomic, phylogenetic, and epidemiological study. **2020**, 6, veaa029		5
1752	Climate, and not fire, drives the phylogenetic clustering of species with hard-coated seeds in Mediterranean Basin communities. **2020**, 45, 125545		7
1751	nosoi: A stochastic agent-based transmission chain simulation framework in r. *Methods in Ecology and Evolution*, **2020**, 11, 1002-1007	7.7	6
1750	Supermatrix phylogeny resolves goby lineages and reveals unstable root of Gobiaria. **2020**, 151, 106862		11
1749	Convergent evolution and possible constraint in the posterodorsal retraction of the external nares in pelagic crocodylomorphs. **2020**, 189, 494-520		4

1748	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus Pycnoporus. **2020**, 27,	13
1747	Low Symbiodiniaceae diversity in a turbid marginal reef environment. **2020**, 39, 545-553	10
1746	Insights into high mobility group A (HMGA) proteins from Poaceae family: An in silico approach for studying homologs. **2020**, 87, 107306	
1745	Regional Transmission and Reassortment of 2.3.4.4b Highly Pathogenic Avian Influenza (HPAI) Viruses in Bulgarian Poultry 2017/18. **2020**, 12,	6
1744	Development of an Inactivated Vaccine Candidate, BBIBP-CorV, with Potent Protection against SARS-CoV-2. **2020**, 182, 713-721.e9	381
1743	Characterizing coral reef biodiversity: genetic species delimitation in brachyuran crabs of Palmyra Atoll, Central Pacific. **2020**, 31, 178-189	2
1742	Genetic and functional diversification of chemosensory pathway receptors in mosquito-borne filarial nematodes. **2020**, 18, e3000723	12
1741	Comparative Genome Analyses of Wild Type- and Quinolone Resistant Indicate Dissemination of QREC in the Norwegian Broiler Breeding Pyramid. **2020**, 11, 938	2
1740	Coexistence of genetically different Rhizophagus irregularis isolates induces genes involved in a putative fungal mating response. **2020**, 14, 2381-2394	4
1739	Whole Genome Sequencing and Spatial Analysis Identifies Recent Tuberculosis Transmission Hotspots in Ghana. **2020**, 7, 161	3
1738	A Large-Scale Outbreak of Echovirus 30 in Gansu Province of China in 2015 and Its Phylodynamic Characterization. **2020**, 11, 1137	6
1737	Molecular Mechanism of Regulation of the Purine Salvage Enzyme XPRT by the Alarmones pppGpp, ppGpp, and pGpp. **2020**, 432, 4108-4126	18
1736	Decoding a highly mixed Kazakh genome. **2020**, 139, 557-568	3
1735	Using ggtree to Visualize Data on Tree-Like Structures. **2020**, 69, e96	233
1734	Comparative analysis of phenotypic and genotypic antibiotic susceptibility patterns in Mycobacterium avium complex. **2020**, 93, 320-328	9
1733	A comparative genomics approach identifies contact-dependent growth inhibition as a virulence determinant. **2020**, 117, 6811-6821	16
1732	Low mutational load and high mutation rate variation in gut commensal bacteria. **2020**, 18, e3000617	26
1731	Disentangling the assembly mechanisms of ant cuticular bacterial communities of two Amazonian ant species sharing a common arboreal nest. **2020**, 29, 1372-1385	4

1730	Rapid speciation and ecological divergence into North American alpine habitats: the Nipponpremebria (Coleoptera: Carabidae) species complex. **2020**, 130, 18-33	4
1729	Impact of UV irradiation at full scale on bacterial communities in drinking water. **2020**, 3,	10
1728	Effects of underfeeding and oral vancomycin on gut microbiome and nutrient absorption in humans. **2020**, 26, 589-598	34
1727	Detection of H3N8 influenza A virus with multiple mammalian-adaptive mutations in a rescued Grey seal () pup. **2020**, 6, veaa016	8
1726	Novel approach in whole genome mining and transcriptome analysis reveal conserved RiPPs in Trichoderma spp. **2020**, 21, 258	10
1725	Genome-wide discovery, and computational and transcriptional characterization of an AIG gene family in the freshwater snail Biomphalaria glabrata, a vector for Schistosoma mansoni. **2020**, 21, 190	10
1724	Genomic Stability of Composite SCC ACME and COMER-Like Genetic Elements in Correlates With Rate of Excision. **2020**, 11, 166	5
1723	Strain Dynamics in a Raccoon () Population in Southern Ontario, Canada: High Prevalence and Rapid Subtype Turnover. **2020**, 7, 27	5
1722	Influenza A Virus Field Surveillance at a Swine-Human Interface. **2020**, 5,	14
1721	Insight into unique somitogenesis of yak (Bos grunniens) with one additional thoracic vertebra. **2020**, 21, 201	2
1720	Morphologically similar but not closely related: the long-spored species of Subulicystidium (Trechisporales, Basidiomycota). **2020**, 19, 691-703	2
1719	The evolving landscape of cell surface pattern recognition across plant immune networks. **2020**, 56, 135-146	12
1718	Phylogenetic analysis of SARS-CoV-2 genomes in Turkey. **2020**, 44, 146-156	12
1717	Thermal bottlenecks in the life cycle define climate vulnerability of fish. **2020**, 369, 65-70	142
1716	Massive haplotypes underlie ecotypic differentiation in sunflowers. **2020**, 584, 602-607	81
1715	Revealing COVID-19 transmission in Australia by SARS-CoV-2 genome sequencing and agent-based modeling. **2020**, 26, 1398-1404	174
1714	Historical biogeography of Vochysiaceae reveals an unexpected perspective of plant evolution in the Neotropics. **2020**, 107, 1004-1020	7
1713	An exploration of the complex biogeographical history of the Neotropical banner-wing damselflies (Odonata: Polythoridae). **2020**, 20, 74	4

1712	Whole Genome Sequencing and Comparative Genomics of Two Nematicidal Strains Reveals a Wide Range of Possible Virulence Factors. **2020**, 10, 881-890		6
1711	Distribution of Bacterial □1,3-Galactosyltransferase Genes in the Human Gut Microbiome. **2019**, 10, 3000		22
1710	A transcriptomic and proteomic atlas of expression in the Nezara viridula (Heteroptera: Pentatomidae) midgut suggests the compartmentalization of xenobiotic metabolism and nutrient digestion. **2020**, 21, 129		5
1709	Identification of Hidden Population Structure in Time-Scaled Phylogenies. **2020**, 69, 884-896		5
1708	Expansion of known ssRNA phage genomes: From tens to over a thousand. **2020**, 6, eaay5981		49
1707	Macroevolutionary bursts and constraints generate a rainbow in a clade of tropical birds. **2020**, 20, 32		8
1706	Substantial Antigenic Drift in the Hemagglutinin Protein of Swine Influenza A Viruses. **2020**, 12,		13
1705	Assessment of a multiplex PCR and Nanopore-based method for dengue virus sequencing in Indonesia. **2020**, 17, 24		11
1704	Genomic epidemiology of Vibrio cholerae reveals the regional and global spread of two epidemic non-toxigenic lineages. **2020**, 14, e0008046		6
1703	Metaphylogenetic analysis of global sewage reveals that bacterial strains associated with human disease show less degree of geographic clustering. **2020**, 10, 3033		1
1702	Four high-quality draft genome assemblies of the marine heterotrophic nanoflagellate Cafeteria roenbergensis. **2020**, 7, 29		11
1701	Population structure and antimicrobial resistance patterns of Salmonella Typhi isolates in urban Dhaka, Bangladesh from 2004 to 2016. **2020**, 14, e0008036		16
1700	Genesis and Gappa: processing, analyzing and visualizing phylogenetic (placement) data. **2020**, 36, 3263-3265		69
1699	moveVis: Animating movement trajectories in synchronicity with static or temporally dynamic environmental data in r. *Methods in Ecology and Evolution*, **2020**, 11, 664-669	7.7	9
1698	Genomics Evolutionary History and Diagnostics of the Species Group Including Apple and Asian Pear Pathotypes. **2019**, 10, 3124		21
1697	Variation of chemical compounds in wild Heliconiini reveals ecological factors involved in the evolution of chemical defenses in mimetic butterflies. **2020**, 10, 2677-2694		10
1696	Genomic Acquisitions in Emerging Populations of pv. Infecting Corn in the United States and Argentina. **2020**, 110, 1161-1173		9
1695	Association of leaf silicon content with chronic wind exposure across and within herbaceous plant species. **2020**, 29, 711-721		2

1694	Phylogenetic informativeness analyses to clarify past diversification processes in Cucurbitaceae. **2020**, 10, 488	9
1693	Genomic Analysis of Wolbachia from Laodelphax striatellus (Delphacidae, Hemiptera) Reveals Insights into Its "Jekyll and Hyde" Mode of Infection Pattern. **2020**, 12, 3818-3831	27
1692	Molecular epidemiology of clinically high-risk Pseudomonas aeruginosa strains: Practical overview. **2020**, 64, 331-344	4
1691	Parallel evolutionary paths to produce more than one biofilm phenotype. **2020**, 6, 2	16
1690	The diversity of microsporidian parasites infecting the Holarctic amphipod Gammarus lacustris from the Baikal region is dominated by the genus Dictyocoela. **2020**, 170, 107330	5
1689	Genomic insight into the origins and dispersal of the Brazilian coastal natives. **2020**, 117, 2372-2377	11
1688	Genomic dynamics of species and mobile genetic elements in a prolonged blaIMP-4-associated carbapenemase outbreak in an Australian hospital. **2020**, 75, 873-882	14
1687	Structural evolution drives diversification of the large LRR-RLK gene family. **2020**, 226, 1492-1505	15
1686	Protein Profile Changes in Circulating Placental Extracellular Vesicles in Term and Preterm Births: A Longitudinal Study. **2020**, 161,	19
1685	Expanded complement of Niemann-Pick type C2-like protein genes in Clonorchis sinensis suggests functions beyond sterol binding and transport. **2020**, 13, 38	1
1684	Stem Cell Transcriptional Networks. **2020**,	1
1683	Global cellulose biomass, horizontal gene transfers and domain fusions drive microbial expansin evolution. **2020**, 226, 921-938	9
1682	Full genomic characterization of a porcine rotavirus strain detected in an asymptomatic piglet in Accra, Ghana. **2020**, 16, 11	1
1681	Comparative genomics of Lactobacillus fermentum suggests a free-living lifestyle of this lactic acid bacterial species. **2020**, 89, 103448	11
1680	A landscape of genomic alterations at the root of a near-untreatable tuberculosis epidemic. **2020**, 18, 24	10
1679	"Frozen evolution" of an RNA virus suggests accidental release as a potential cause of arbovirus re-emergence. **2020**, 18, e3000673	7
1678	Amycolatopsis BX17: An actinobacterial strain isolated from soil of a traditional milpa agroecosystem with potential biocontrol against Fusarium graminearum. **2020**, 147, 104285	2
1677	Mitochondrial Genome Polymorphisms in the Human Pathogenic Fungus. **2020**, 11, 706	13

1676	Emergence of Fluoroquinolone-Resistant and among Australian Chickens in the Absence of Fluoroquinolone Use. **2020**, 86,	23
1675	Outbreak Severity of Highly Pathogenic Avian Influenza A(H5N8) Viruses Is Inversely Correlated to Polymerase Complex Activity and Interferon Induction. **2020**, 94,	6
1674	Proposal of a Taxonomic Nomenclature for the Bacillus cereus Group Which Reconciles Genomic Definitions of Bacterial Species with Clinical and Industrial Phenotypes. **2020**, 11,	53
1673	Design and evaluation of degassed anaerobic membrane biofilm reactors for improved methane recovery. **2020**, 10, 100407	8
1672	A deeper meaning for shallow-level phylogenomic studies: nested anchored hybrid enrichment offers great promise for resolving the tiger moth tree of life (Lepidoptera: Erebidae: Arctiinae). **2020**, 45, 874-893	8
1671	Cheminformatics Analysis and Modeling with MacrolactoneDB. **2020**, 10, 6284	9
1670	Bighorn sheep gut microbiomes associate with genetic and spatial structure across a metapopulation. **2020**, 10, 6582	13
1669	Baby Genomics: Tracing the Evolutionary Changes That Gave Rise to Placentation. **2020**, 12, 35-47	7
1668	Emergence of a Novel Salmonella enterica Serotype Reading Clonal Group Is Linked to Its Expansion in Commercial Turkey Production, Resulting in Unanticipated Human Illness in North America. **2020**, 5,	12
1667	Distribution and diversity of olefins and olefin-biosynthesis genes in Gram-positive bacteria. **2020**, 13, 70	2
1666	Persistence of Brucella abortus lineages revealed by genomic characterization and phylodynamic analysis. **2020**, 14, e0008235	6
1665	Comparative genomics and full-length Tprk profiling of Treponema pallidum subsp. pallidum reinfection. **2020**, 14, e0007921	6
1664	Epidemiology of Respiratory Syncytial Virus Across Five Influenza Seasons Among Adults and Children One Year of Age and Older-Washington State, 2011/2012-2015/2016. **2021**, 223, 147-156	2
1663	Cutting the Gordian knot: a historical and taxonomic revision of the Jurassic crocodylomorph Metriorhynchus. **2021**, 192, 510-553	1
1662	The rise and fall of globins in the amphibia. **2021**, 37, 100759	0
1661	Genetic population structure of the striped venus clam Chamelea gallina across its range. **2021**, 234, 105758	0
1660	Phylogenetic relationships and revised classification of the true bug infraorder Dipsocoromorpha (Insecta: Hemiptera: Heteroptera). **2021**, 37, 248-275	0
1659	Food or just a free ride? A meta-analysis reveals the global diversity of the Plastisphere. **2021**, 15, 789-806	37

1658	Genomic analyses reveal the genetic basis of early maturity and identification of loci and candidate genes in upland cotton (Gossypium hirsutum L.). **2021**, 19, 109-123	12
1657	Exploring the : differences in uropygial gland volume and haemosporidian infection in palearctic and neotropical birds. **2021**, 67, 147-156	2
1656	Wildland fire as an atmospheric source of viable microbial aerosols and biological ice nucleating particles. **2021**, 15, 461-472	9
1655	A Novel Species-Level Group of Exhibits Variation in Phytopathogenicity Despite Conservation of Virulence Loci. **2021**, 34, 39-48	2
1654	Molecular Phylogenomics and Population Structure of. **2021**, 111, 108-115	7
1653	A targeted phylogenetic approach helps explain New World functional diversity patterns of two eudicot lineages. **2021**, 48, 202-215	1
1652	The impacts of climate change on fish growth: A summary of conducted studies and current knowledge. **2021**, 121, 106976	14
1651	Genomic Characterization of Emerging Bacterial Uropathogen Neisseria meningitidis, Which Was Misidentified as Neisseria gonorrhoeae by Nucleic Acid Amplification Testing. **2021**, 59,	5
1650	The Aegilops ventricosa 2NS segment in bread wheat: cytology, genomics and breeding. **2021**, 134, 529-542	13
1649	Identification of the Aedes aegypti nAChR gene family and molecular target of spinosad. **2021**, 77, 1633-1641	5
1648	Diversity, community composition, and bioactivity of cultivable fungal endophytes in saline and dry soils in deserts. **2021**, 49, 101019	4
1647	Genome-wide prediction and comparative transcriptomic analysis reveals the G protein-coupled receptors involved in gonadal development of Apostichopus japonicus. **2021**, 113, 967-978	1
1646	Special Care Is Needed in Applying Phylogenetic Comparative Methods to Gene Trees with Speciation and Duplication Nodes. **2021**, 38, 1614-1626	1
1645	Demographic analyses of marine and terrestrial snakes (Elapidae) using whole genome sequences. **2021**, 30, 545-554	4
1644	Phylogenetic patterns and ontogenetic origins of limb length variation in ecologically diverse lacertine lizards. **2021**, 132, 283-296	1
1643	Phylogenetic analysis of SARS-CoV-2 in Boston highlights the impact of superspreading events. **2021**, 371,	111
1642	Eusociality Shapes Convergent Patterns of Molecular Evolution across Mitochondrial Genomes of Snapping Shrimps. **2021**, 38, 1372-1383	6
1641	Horizontal chromosome transfer and independent evolution drive diversification in Fusarium oxysporum f. sp. fragariae. **2021**, 230, 327-340	3

1640	Phylogenetic and geographical analysis of a retrovirus during the early stages of endogenous adaptation and exogenous spread in a new host. **2021**, 30, 2626-2640	6
1639	Different functional characteristics can explain different dimensions of plant invasion success. **2021** , 109, 1524-1536	1
1638	The role of functional strategies in global plant distribution. **2021**, 44, 493-503	4
1637	Quantifying range structure to inform management in invaded landscapes. **2021**, 58, 338-349	1
1636	Elevation filters seed traits and germination strategies in the eastern Tibetan Plateau. **2021**, 44, 242-254	1
1635	Desert truffle genomes reveal their reproductive modes and new insights into plant-fungal interaction and ectendomycorrhizal lifestyle. **2021**, 229, 2917-2932	6
1634	The HLA diversity of the Anthony Nolan register. **2021**, 97, 15-29	4
1633	Evolution of pollination syndromes and corolla symmetry in Balsaminaceae reconstructed using phylogenetic comparative analyses. **2021**, 127, 267-280	1
1632	Genome-wide functional analysis of hot pepper immune receptors reveals an autonomous NLR clade in seed plants. **2021**, 229, 532-547	10
1631	Effectors, chaperones, and harpins of the Type III secretion system in the fire blight pathogen Erwinia amylovora: a review. **2021**, 103, 25-39	7
1630	Comparative transcriptomics of ice-crawlers demonstrates cold specialization constrains niche evolution in a relict lineage. **2021**, 14, 360-382	1
1629	Discovery and surveillance of viruses from salmon in British Columbia using viral immune-response biomarkers, metatranscriptomics, and high-throughput RT-PCR. **2021**, 7, veaa069	8
1628	Spatiotemporal reconstruction and transmission dynamics during the 2016-17 H5N8 highly pathogenic avian influenza epidemic in Italy. **2021**, 68, 37-50	4
1627	Full Issue PDF. **2021**, 34, 1-139	
1626	Human B cell lineages engaged by germinal centers following influenza vaccination are measurably evolving.	1
1625	Unveiling the Importance and Evolution of Design Components Through the ▯ree of Blockchain▯ **2021**, 3,	5
1624	Resolving generic limits in Cyperaceae tribe Abildgaardieae using targeted sequencing. **2021**, 196, 163-187	5
1623	GEViTRec: Data Reconnaissance Through Recommendation Using a Domain-Specific Visualization Prevalence Design Space. **2021**, PP,	0

1622	Genomic epidemiology of a densely sampled COVID-19 outbreak in China. **2021**, 7, veaa102	8
1621	Enrichment and description of novel bacteria performing syntrophic propionate oxidation at high ammonia level. **2021**, 23, 1620-1637	6
1620	Ion channel profiling of the Lymnaea stagnalis ganglia via transcriptome analysis. **2021**, 22, 18	1
1619	Genetic diversity and heterotic grouping of sorghum lines using SNP markers. **2021**, 78,	5
1618	Plant-derived benzoxazinoids act as antibiotics and shape bacterial communities.	1
1617	Genetic architecture of wild soybean (Glycine soja Sieb. and Zucc.) populations originating from different East Asian regions. **2021**, 68, 1577-1588	
1616	Interaction study of Pasteurella multocida with culturable aerobic bacteria isolated from porcine respiratory tracts using coculture in conditioned media. **2021**, 21, 19	0
1615	Sexual size dimorphism and its allometry in Chinese lizards. **2021**, 35, 323-335	1
1614	Plasticity versus Evolutionary Divergence: What Causes Habitat Partitioning in Urban-Adapted Birds?. **2021**, 197, 60-74	3
1613	Diversification of mammalian deltaviruses by host shifting. **2021**, 118,	14
1612	Development of interactive biological web applications with R/Shiny. **2021**,	3
1611	Genomic epidemiology of persistently circulating MDR Shigella sonnei strains associated with men who have sex with men (MSM) in Belgium (2013-19). **2021**,	4
1610	Taxonomic updates in (Bignoniaceae): A new Mexican species and the re-establishment of the giant-leaved. **2021**, 171, 75-90	0
1609	Anomalous influenza seasonality in the United States and the emergence of novel influenza B viruses. **2021**, 118,	2
1608	Morphological evolution in relationship to sidewinding, arboreality and precipitation in snakes of the family Viperidae. **2021**, 132, 328-345	0
1607	Protist communities along freshwater□marine transition zones in Hudson Bay (Canada). **2021**, 9,	4
1606	Detection of Trypanosoma cruzi in the saliva of diverse neotropical bats. **2021**, 68, 271-276	6
1605	The mA methylome of SARS-CoV-2 in host cells. **2021**, 31, 404-414	28

1604	AusTraits □a curated plant trait database for the Australian flora.	1
1603	A computational method for immune repertoire mining that identifies novel binders from different clonotypes, demonstrated by identifying anti-pertussis toxoid antibodies. **2021**, 13, 1869406	11
1602	Identification and Downstream Analyses of Domains Amplified in Plant Genomes: The Case of StAR-Related Lipid Transfer (START) Domains in Rice. **2021**, 2238, 325-338	
1601	Viromics of extant insect orders unveil the evolution of the flavi-like superfamily. **2021**, 7, veab030	6
1600	Germline IGHV3-53-encoded RBD-targeting neutralizing antibodies are commonly present in the antibody repertoires of COVID-19 patients. **2021**, 10, 1097-1111	6
1599	Receptor-Like Kinase (RLK) as a candidate gene conferring resistance to Hemileia vastatrix in coffee. **2021**, 78,	7
1598	Phylogenetic Methods for Genome-Wide Association Studies in Bacteria. **2021**, 2242, 205-220	1
1597	Ancient balancing selection maintains incompatible versions of the galactose pathway in yeast. **2021**, 371, 415-419	6
1596	Indigenous rhizobial strains SEMIA 4108 and SEMIA 4107 for common bean inoculation: A biotechnological tool for cleaner and more sustainable agriculture. **2021**, 57, 57-67	
1595	Pathogenomic analyses of an ESX-1-deleted member of the complex causing disease in various hosts. **2021**, 7,	8
1594	First phylogenetic analysis of Dryophthorinae (Coleoptera, Curculionidae) based on structural alignment of ribosomal DNA reveals Cenozoic diversification. **2021**, 11, 1984-1998	1
1593	High-throughput functional analysis of natural variants in yeast.	0
1592	Genotypic and Phenotypic Characterization of Isolates from the Respiratory Tract in Mechanically-Ventilated Patients. **2021**, 13,	3
1591	A statewide analysis of SARS-CoV-2 transmission in New York.	1
1590	Phylogenetic Characterization of Crimean-Congo Hemorrhagic Fever Virus Detected in African Blue Ticks Feeding on Cattle in a Ugandan Abattoir. **2021**, 9,	2
1589	Frequent intergenotypic recombination between the non-structural and structural genes is a major driver of epidemiological fitness in caliciviruses.	2
1588	Phylogenomics of reveals a new lineage and a complex evolutionary history. **2021**, 7,	29
1587	Evolutionary analyses of the major variant surface antigen-encoding genes reveal population structure of Plasmodium falciparum within and between continents. **2021**, 17, e1009269	5

1586	Genome assembly and population genomic analysis provide insights into the evolution of modern sweet corn. **2021**, 12, 1227	9
1585	Diploid chromosome-scale assembly of the Muscadinia rotundifolia genome supports chromosome fusion and disease resistance gene expansion during Vitis and Muscadinia divergence. **2021**, 11,	8
1584	An Expanded Gene Catalog of Mouse Gut Metagenomes. **2021**, 6,	4
1583	Alterations in the gut microbiome and metabolic profile in rats acclimated to high environmental temperature. **2021**,	6
1582	Altitude and the distributional typology of language structure: Ejectives and beyond. **2021**, 16, e0245522	4
1581	Size Variation of the Nonrecombining Region on the Mating-Type Chromosomes in the Fungal Podospora anserina Species Complex. **2021**, 38, 2475-2492	0
1580	Cry75Aa (Mpp75Aa) Insecticidal Proteins for Controlling the Western Corn Rootworm, , (Coleoptera: Chrysomelidae), Isolated from the Insect Pathogenic Bacteria. **2020**,	5
1579	Genomic architecture of 5S rDNA cluster and its variations within and between species.	2
1578	Phylogenetic diversity of the picocyanobacterial community from a novel winter bloom in Lake Biwa. **2021**, 22, 161-167	1
1577	Target enrichment and extensive population sampling help untangle the recent, rapid radiation of Oenothera sect. Calylophus.	0
1576	Q Fever: Seroprevalence, Risk Factors in Slaughter Livestock and Genotypes of in South Africa. **2021**, 10,	1
1575	Rapid molecular evolution of symbionts of. **2021**, 7,	8
1574	The Distribution of Several Genomic Virulence Determinants Does Not Corroborate the Established Serotyping Classification of. **2021**, 22,	1
1573	Gut Microbiota in Decapod Shrimps: Evidence of Phylosymbiosis. **2021**, 82, 994-1007	0
1572	A comprehensive and high-quality collection of genomes and their genes. **2021**, 7,	12
1571	Characterizing and Evaluating the Zoonotic Potential of Novel Viruses Discovered in Vampire Bats. **2021**, 13,	9
1570	Continental-Scale Gene Flow Prevents Allopatric Divergence of Pelagic Freshwater Bacteria. **2021**, 13,	4
1569	Waves Out of the Korean Peninsula and Inter- and Intra-Species Replacements in Freshwater Fishes in Japan. **2021**, 12,	4

1568	Wide range of metabolic adaptations to the acquisition of the Calvin cycle revealed by comparison of microbial genomes. **2021**, 17, e1008742	2
1567	PhyKIT: a broadly applicable UNIX shell toolkit for processing and analyzing phylogenomic data. **2021**,	8
1566	Streptomyces sp. M54: an actinobacteria associated with a neotropical social wasp with high potential for antibiotic production. **2021**, 114, 379-398	2
1565	Different evolutionary trends form the twilight zone of the bacterial pan-genome.	
1564	Comparative analysis of host-associated variation in Phytophthora cactorum.	
1563	Resolving Recalcitrant Clades in the Pantropical Ochnaceae: Insights From Comparative Phylogenomics of Plastome and Nuclear Genomic Data Derived From Targeted Sequencing. **2021**, 12, 638650	2
1562	Genetic diversity and population structure of popcorn germplasm resources using genome-wide SNPs through genotyping-by-sequencing. **2021**, 68, 2379-2389	2
1561	Overexpression of vesicle-associated membrane protein PttVAP27-17 as a tool to improve biomass production and the overall saccharification yields in Populus trees. **2021**, 14, 43	4
1560	Global Geographic and Temporal Analysis of SARS-CoV-2 Haplotypes Normalized by COVID-19 Cases During the Pandemic. **2021**, 12, 612432	8
1559	Intra-host variation and evolutionary dynamics of SARS-CoV-2 populations in COVID-19 patients. **2021**, 13, 30	36
1558	One hundred and sixty years of taxonomic confusion resolved: Belonocnema (Hymenoptera: Cynipidae: Cynipini) gall wasps associated with live oaks in the USA.	2
1557	Diversification, disparification and hybridization in the desert shrubs Encelia. **2021**, 230, 1228-1241	1
1556	Population Genomic Analysis of From Food Reveals Substrate-Specific Genome Variation. **2021**, 12, 620033	1
1555	Genetic and epigenetic variation in transposable element expression responses to abiotic stress in maize. **2021**, 186, 420-433	3
1554	Sex Ratios in a Warming World: Thermal Effects on Sex-Biased Survival, Sex Determination, and Sex Reversal. **2021**, 112, 155-164	5
1553	Population structure and uropathogenic potential of extended-spectrum cephalosporin-resistant Escherichia coli from retail chicken meat. **2021**, 21, 94	1
1552	Triclosan Tolerance Is Driven by a Conserved Mechanism in Diverse Species. **2021**, 87,	3
1551	Comparative viral metagenomics from chicken feces and farm dust in the Netherlands.	0

1550	The endophytic microbiota of Citrus limon is transmitted from seed to shoot highlighting differences of bacterial and fungal community structures. **2021**, 11, 7078	7
1549	Reconstructing Squamate Biogeography in Afro-Arabia Reveals the Influence of a Complex and Dynamic Geologic Past. **2021**,	2
1548	Adding leaves to the Lepidoptera tree: capturing hundreds of nuclear genes from old museum specimens. **2021**, 46, 649-671	8
1547	Analysis of Fungal Genomes Reveals Commonalities of Intron Gain or Loss and Functions in Intron-Poor Species. **2021**, 38, 4166-4186	5
1546	MSA-Regularized Protein Sequence Transformer toward Predicting Genome-Wide Chemical-Protein Interactions: Application to GPCRome Deorphanization. **2021**, 61, 1570-1582	2
1545	Large-Scale Genome Scanning within Exonic Regions Revealed the Contributions of Selective Sweep Prone Genes to Host Divergence and Adaptation in Species Complex. **2021**, 9,	0
1544	Isolation, Characterization, and Genomic Investigation of a Phytopathogenic Strain of. **2021**, PHYTO11200501R	4
1543	Genomic epidemiology of COVID-19 in care homes in the east of England. **2021**, 10,	8
1542	Lynnia grapsolytica n. gen, n. sp. (Ciliophora: Apostomatida: Colliniidae), a Deadly Blood Parasite of Crabs with a Novel Pseudocytopharynx. **2021**, 68, e12847	0
1541	Breast tumours maintain a reservoir of subclonal diversity during expansion. **2021**, 592, 302-308	33
1540	Physiological Functions of Bacterial "Multidrug" Efflux Pumps. **2021**, 121, 5417-5478	22
1539	Rubisco Adaptation Is More Limited by Phylogenetic Constraint Than by Catalytic Trade-off. **2021**, 38, 2880-2896	8
1538	Detection of a SARS-CoV-2 variant of concern in South Africa. **2021**, 592, 438-443	685
1537	LuxR Solos from Environmental Fluorescent Pseudomonads. **2021**, 6,	2
1536	Ignoring errors causes inaccurate timing of single-cell phylogenies.	0
1535	Targeted sequencing supports morphology and embryo features in resolving the classification of Cyperaceae tribe Fuireneae s.l.. **2021**, 59, 809-832	5
1534	A tale of three SARS-CoV-2 variants with independently acquired P681H mutations in New York State.	11
1533	Prevalence and Diversity of Avian Haemosporidians May Vary with Anthropogenic Disturbance in Tropical Habitats in Myanmar. **2021**, 13, 111	6

1532	Extensive structural variation in the Bowman-Birk inhibitor family in common wheat (Triticum aestivum L.). **2021**, 22, 218	2
1531	Long insert clone experimental evidence for assembly improvement and chimeric chromosomes detection in an allopentaploid beer yeast. **2021**,	
1530	Exploration of the 2016 Yellowstone River fish kill and proliferative kidney disease in wild fish populations. **2021**, 12, e03436	6
1529	Seed Banks as Incidental Fungi Banks: Fungal Endophyte Diversity in Stored Seeds of Banana Wild Relatives. **2021**, 12, 643731	3
1528	Parallel molecular mechanisms for enzyme temperature adaptation. **2021**, 371,	11
1527	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. **2020**, 9, 1246	1
1526	Stage-specific transcriptomic analysis of the model cestode Hymenolepis microstoma. **2021**, 113, 620-632	1
1525	Genome Analysis of and spp., Closest Phylogenetic Relatives of , Highlights the Role of Amastins in Shaping Pathogenicity. **2021**, 12,	2
1524	Estimating maximal microbial growth rates from cultures, metagenomes, and single cells via codon usage patterns. **2021**, 118,	18
1523	Genomic diversity of SARS-CoV-2 during early introduction into the Baltimore-Washington metropolitan area. **2021**, 6,	17
1522	Comparative Genomics of and pv. Strains Isolated from a Single Walnut Host Tree. **2021**, 9,	3
1521	Ecophysiological differentiation between life stages in filmy ferns (Hymenophyllaceae).	
1520	Genomic network analysis of environmental and livestock F-type plasmid populations. **2021**, 15, 2322-2335	4
1519	A Comprehensive Phylogenetic Analysis of the Serpin Superfamily. **2021**, 38, 2915-2929	8
1518	The LOTUS Initiative for Open Natural Products Research: Knowledge Management through Wikidata.	15
1517	Ecological opportunity and the rise and fall of crocodylomorph evolutionary innovation. **2021**, 288, 20210069	15
1516	Bacterial diversity and flavor profile of Zha-Chili, a traditional fermented food in China. **2021**, 141, 110112	19
1515	Island songbirds as windows into evolution in small populations. **2021**, 31, 1303-1310.e4	15

1514	A co-opted steroid synthesis gene, maintained in sorghum but not maize, is associated with a divergence in leaf wax chemistry. **2021**, 118,	4
1513	Water and nitrogen shape winter annual plant diversity and community composition in near-urban Sonoran Desert preserves.. **2021**, 91, 1-19	2
1512	Aggression heuristics underlie animal dominance hierarchies and provide evidence of group-level social information. **2021**, 118,	20
1511	Searching for regulators that interact with BELL1 transcription factor and control the legume-rhizobial symbiosis development. **2021**, 19, 37-45	
1510	The Destructive Tree Pathogen Originates from the Laurosilva Forests of East Asia. **2021**, 7,	11
1509	Isolation and Characterization of Phages for Phage Therapy. **2021**, 2, 26-42	9
1508	Forest are robust to seasonal biotic and abiotic changes. **2021**, 11, 6604-6619	0
1507	Genomic insights into the origin, domestication and genetic basis of agronomic traits of castor bean. **2021**, 22, 113	10
1506	Population Genomics of from U.S. Cystic Fibrosis Care Centers. **2021**, 18, 1960-1969	11
1505	Bifidobacterium Lactis Probio-M8 regulates gut microbiota to alleviate Alzheimer's disease in the APP/PS1 mouse model. **2021**, 60, 3757-3769	9
1504	Molecular Epidemiology of Salmonellosis in Florida, USA, 2017-2018. **2021**, 8, 656827	0
1503	Exploring the genomic diversity and antimicrobial susceptibility of Bifidobacterium pseudocatenulatum in the Vietnamese population to aid probiotic design.	
1502	Unexpected distribution of the 4-formylaminooxyvinylglycine (FVG) biosynthetic pathway in Pseudomonas and beyond. **2021**, 16, e0247348	2
1501	Use of an Alignment-Free Method for the Geographical Discrimination of GTPVs Based on the GPCR Sequences. **2021**, 9,	
1500	An endangered flightless grasshopper with strong genetic structure maintains population genetic variation despite extensive habitat loss. **2021**, 11, 5364-5380	5
1499	Pervasive transmission of E484K and emergence of VUI-NP13L with evidence of SARS-CoV-2 co-infection events by two different lineages in Rio Grande do Sul, Brazil. **2021**, 296, 198345	61
1498	Phylogeography of infectious disease: genetic diversity and connectivity of the Ostreid herpesvirus 1 population in France.	
1497	Comparative genomics of the coconut crab and other decapod crustaceans: exploring the molecular basis of terrestrial adaptation. **2021**, 22, 313	0

1496	Diversity and host assemblage of avian haemosporidians in different terrestrial ecoregions of Peru.. **2022**, 68, 27-40	3
1495	Molecular surveillance of coxsackievirus A16 in southern China, 2008-2019. **2021**, 166, 1653-1659	0
1494	Evolution of specialization in a plant-microbial mutualism is explained by the oscillation theory of speciation. **2021**, 75, 1070-1086	5
1493	SARS-CoV-2 ORF6 Disrupts Bidirectional Nucleocytoplasmic Transport through Interactions with Rae1 and Nup98. **2021**, 12,	26
1492	Patient and Microbial Genomic Factors Associated with Carbapenem-Resistant Klebsiella pneumoniae Extraintestinal Colonization and Infection. **2021**, 6,	3
1491	Quantitative analysis of spore shapes improves identification of fungi.	
1490	Identification of Candidate Susceptibility Genes to f. sp. in Wheat. **2021**, 12, 657796	1
1489	The impact of porcine reproductive and respiratory syndrome virus (PRRSV) genotypes, established on the basis of ORF-5 nucleotide sequences, on three production parameters in Ontario sow farms. **2021**, 189, 105312	2
1488	Recircumscription of the Canary Island endemics Argyranthemum broussonetii and A. callichrysum (Asteraceae: Anthemideae) based on evolutionary relationships and morphology. **2021**, 51,	1
1487	Rephine.r: a pipeline for correcting gene calls and clusters to improve phage pangenomes and phylogenies.	
1486	Population Genomics of the Maize Pathogen Ustilago maydis: Demographic History and Role of Virulence Clusters in Adaptation. **2021**, 13,	1
1485	Fungus-bacterium associations are widespread in fungal cultures isolated from a semi-arid natural grassland in Germany. **2021**, 97,	1
1484	Evolution of the codling moth pheromone via an ancient gene duplication. **2021**, 19, 83	4
1483	Functional leaf traits indicate phylogenetic signals in forests across an elevational gradient in the central Himalaya. **2021**, 134, 753-764	1
1482	Mix and match: Patchwork domain evolution of the land plant-specific Ca2+-permeable mechanosensitive channel MCA. **2021**, 16, e0249735	5
1481	A Mother's Story, Mitogenome Relationships in the Genus. **2021**, 11,	4
1480	Insights about the epidemiology of Salmonella Typhimurium isolates from different sources in Brazil using comparative genomics. **2021**, 13, 27	1
1479	Primate phageomes are structured by superhost phylogeny and environment. **2021**, 118,	6

1478	Balancing selection maintains hyper-divergent haplotypes in Caenorhabditis elegans. **2021**, 5, 794-807	12
1477	Tissue-specific transcriptome analysis of drought stress and rehydration in at seedling. **2021**, 9, e10933	1
1476	Discriminating arboviral species. **2021**, 102,	1
1475	High Differentiation among Populations of Green Foxtail, Setaria viridis, in Taiwan and Adjacent Islands Revealed by Microsatellite Markers. **2021**, 13, 159	0
1474	LCM and RNA-seq analyses revealed roles of cell cycle and translational regulation and homoeolog expression bias in cotton fiber cell initiation. **2021**, 22, 309	3
1473	Amazon tree dominance across forest strata. **2021**, 5, 757-767	5
1472	SARS-CoV-2 shifting transmission dynamics and hidden reservoirs potentially limit efficacy of public health interventions in Italy. **2021**, 4, 489	13
1471	Niche and local geography shape the pangenome of wastewater- and livestock-associated Enterobacteriaceae. **2021**, 7,	12
1470	Great chemistry between us: The link between plant chemical defenses and butterfly evolution. **2021**, 11, 8595-8613	2
1469	Co-activation pattern alterations in autism spectrum disorder-A volume-wise hierarchical clustering fMRI study. **2021**, 11, e02174	1
1468	Aquaculture mediates global transmission of a viral pathogen to wild salmon. **2021**, 7,	10
1467	Quantifying the Persistence of Vaccine-Related T Cell Epitopes in Circulating Swine Influenza A Strains from 2013-2017. **2021**, 9,	0
1466	RevGadgets: an R Package for visualizing Bayesian phylogenetic analyses from RevBayes.	2
1465	SARS-CoV-2 B.1.617.2 Delta variant replication, sensitivity to neutralising antibodies and vaccine breakthrough.	62
1464	The evolution and changing ecology of the African hominid oral microbiome. **2021**, 118,	20
1463	Strain engraftment competition and functional augmentation in a multi-donor fecal microbiota transplantation trial for obesity. **2021**, 9, 107	12
1462	Homopeptide and homocodon levels across fungi are coupled to GC/AT-bias and intrinsic disorder, with unique behaviours for some amino acids. **2021**, 11, 10025	1
1461	Taxonomic, phylogenetic and functional diversity of understorey plants respond differently to environmental conditions in European forest edges. **2021**, 109, 2629-2648	3

1460	Using aggregated field collection data and the novel r package fungarium to investigate fungal fire association. **2021**, 113, 842-855	0
1459	Exploring the phylogeography and population dynamics of the giant deer () using Late Quaternary mitogenomes. **2021**, 288, 20201864	3
1458	Pathogenic potential assessment of the Shiga toxin-producing by a source attribution-considered machine learning model. **2021**, 118,	1
1457	treeclimbR pinpoints the data-dependent resolution of hierarchical hypotheses. **2021**, 22, 157	2
1456	Density-based binning of gene clusters to infer function or evolutionary history using GeneGrouper.	1
1455	Zymomonas diversity and potential for biofuel production. **2021**, 14, 112	5
1454	Population structure and transmission of in Ethiopia. **2021**, 7,	4
1453	Inferring Mycobacterium bovis transmission between cattle and badgers using isolates from the Randomised Badger Culling Trial.	
1452	Complex introgression among three diverged largemouth bass lineages.	
1451	miRNAs of Aedes aegypti (Linnaeus 1762) conserved in six orders of the class Insecta. **2021**, 11, 10706	
1450	Phylogenetic and phylodynamic analysis of a classical swine fever virus outbreak in Japan (2018-2020). **2021**,	5
1449	Genetic Origins and Sex-Biased Admixture of the Huis. **2021**, 38, 3804-3819	4
1448	Microevolution in the pansecondary metabolome of and its potential macroevolutionary implications for filamentous fungi. **2021**, 118,	8
1447	Natural variation in fecundity is correlated with species-wide levels of divergence in Caenorhabditis elegans. **2021**, 11,	0
1446	Genomic epidemiology of SARS-CoV-2 in Esteio, Rio Grande do Sul, Brazil. **2021**, 22, 371	8
1445	Role of Phylogenetic Structure in the Dynamics of Coastal Viral Assemblages. **2021**, 87,	2
1444	The Austronesian Game Taxonomy: A cross-cultural dataset of historical games. **2021**, 8,	1
1443	Intra-host evolutionary dynamics of the hepatitis C virus among people who inject drugs. **2021**, 11, 9986	1

1442	Identification and characterization of proteins of unknown function (PUFs) in Clostridium thermocellum DSM 1313 strains as potential genetic engineering targets. **2021**, 14, 116	1
1441	The diversity of opsins in Lake Baikal amphipods (Amphipoda: Gammaridae). **2021**, 21, 81	2
1440	Molecular Analysis of East African Lumpy Skin Disease Viruses Reveals a Mixed Isolate with Features of Both Vaccine and Field Isolates. **2021**, 9,	1
1439	Genomic and temporal analyses of in southern Brazil. **2021**, 7,	2
1438	Microbially Guided Discovery and Biosynthesis of Biologically Active Natural Products. **2021**, 10, 1505-1519	3
1437	Capturing noroviruses circulating in the population: sewage surveillance in Guangdong, China (2013-2018). **2021**, 196, 116990	4
1436	Toward a Stable Global Noctuidae (Lepidoptera) Taxonomy. **2021**, 5,	3
1435	Ancient horse genomes reveal the timing and extent of dispersals across the Bering Land Bridge. **2021**, 30, 6144-6161	7
1434	Neutralization diversity of HIV-1 Indian subtype C envelopes obtained from cross sectional and followed up individuals against broadly neutralizing monoclonal antibodies having distinct gp120 specificities. **2021**, 18, 12	
1433	Hidden viral sequences in public sequencing data and warning for future emerging diseases.	
1432	Integrative species delimitation based on COI, ITS, and morphological evidence illustrates a unique evolutionary history of the genus (Odonata: Coenagrionidae). **2021**, 9, e11459	2
1431	Regional Spread of blaNDM-1-Containing Klebsiella pneumoniae ST147 in Post-Acute Care Facilities. **2021**, 73, 1431-1439	1
1430	Rapid protein sequence evolution via compensatory frameshift is widespread in RNA virus genomes. **2021**, 22, 251	0
1429	Genomic and phenotypic divergence informs translocation strategies for an endangered freshwater fish. **2021**, 30, 3394-3407	1
1428	The interaction of resource use and gene flow on the phenotypic divergence of benthic and pelagic morphs of Icelandic Arctic charr (). **2021**, 11, 7315-7334	2
1427	100-My history of bornavirus infections hidden in vertebrate genomes. **2021**, 118,	8
1426	Retrospective Characterization of the 2006-2007 Swine Vesicular Disease Epidemic in Northern Italy by Whole Genome Sequence Analysis. **2021**, 13,	
1425	SARS-CoV-2 variants of concern dominate in Lahore, Pakistan in April 2021.	

1424	St. Louis Encephalitis Virus in the Southwestern United States: A Phylogeographic Case for a Multi-Variant Introduction Event. **2021**, 12, 667895	0
1423	Phenotypic and Genotypic Properties of Fluoroquinolone-Resistant, -Carrying Isolated from the German Food Chain in 2017. **2021**, 9,	3
1422	Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. **2021**, 7,	15
1421	Measuring Metal Uptake and Loss in Individual Organisms: A Novel Double Stable Isotope Method and its Application in Explaining Body Size Effects on Cadmium Concentration in Mussels. **2021**, 55, 9979-9988	2
1420	Global dispersal and diversification of the genus Schoenus (Cyperaceae) from the Western Australian biodiversity hotspot. **2021**, 59, 791-808	2
1419	The influence of habitat association on swimming performance in marine teleost fish larvae. **2021**, 22, 1187	3
1418	Microbiota and Metabolite Modifications after Dietary Exclusion of Dairy Products and Reduced Consumption of Fermented Food in Young and Older Men. **2021**, 13,	1
1417	Sequence of the supernumerary B chromosome of maize provides insight into its drive mechanism and evolution. **2021**, 118,	8
1416	A Molecular Analysis of Microalgae from Around the Globe to Revise Raphidonema (Trebouxiophyceae, Chlorophyta). **2021**, 57, 1419-1432	2
1415	Cultivating the Bacterial Microbiota of Roots. **2021**, 6, e0130620	5
1414	The novel Rab5 effector FERRY links early endosomes with the translation machinery.	0
1413	An Antigenic Thrift-Based Approach to Influenza Vaccine Design. **2021**, 9,	0
1412	A new classification of Cyperaceae (Poales) supported by phylogenomic data. **2021**, 59, 852-895	8
1411	Arabinogalactan-proteins from non-coniferous gymnosperms have unusual structural features. **2021**, 261, 117831	5
1410	Analysis of 56K genomes identifies the relationship between antibiotic and metal resistance co-Occurrence and the spread of multidrug-resistant non-typhoidal Salmonella.	
1409	Fitness barriers to spread of colistin-resistant Klebsiella pneumoniae overcome by establishing niche in patient population with elevated colistin use.	1
1408	Testing cophylogeny between coral reef invertebrates and their bacterial and archaeal symbionts. **2021**, 30, 3768-3782	1
1407	Effects of Different Organic Fertilizers on Improving Soil from Newly Reclaimed Land to Crop Soil. **2021**, 11, 560	7

1406	Large-scale genome sampling reveals unique immunity and metabolic adaptations in bats. **2021**, 30, 6449-6467	5
1405	Cultivable Yeast Microbiota from the Marine Fish Species and. **2021**, 7,	2
1404	Potential G-quadruplexes and i-Motifs in the SARS-CoV-2. **2021**, 16, e0250654	10
1403	Genomic epidemiology of the first epidemic wave of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in Palestine. **2021**, 7,	2
1402	Single-cell immunophenotyping of the skin lesion erythema migrans identifies IgM memory B cells. **2021**, 6,	0
1401	Genome-Inferred Correspondence between Phylogeny and Metabolic Traits in the Wild Drosophila Gut Microbiome. **2021**, 13,	0
1400	Antigenic evolution of contemporary clade 2.3.4.4 HPAI H5 influenza A viruses and impact on vaccine use for mitigation and control. **2021**, 39, 3794-3798	0
1399	rMAP: the Rapid Microbial Analysis Pipeline for ESKAPE bacterial group whole-genome sequence data. **2021**, 7,	0
1398	Unexpected Discovery of Hypermutator Phenotype Sounds the Alarm for Quality Control Strains. **2021**, 13,	0
1397	ggtreeExtra: Compact Visualization of Richly Annotated Phylogenetic Data. **2021**, 38, 4039-4042	15
1396	Bioinformatics tools used for whole-genome sequencing analysis of Neisseria gonorrhoeae: a literature review. **2021**,	1
1395	Five years of citizen science and standardised field surveys in an informal urban green space reveal a threatened Eden for wild bees in Brussels, Belgium. **2021**, 14, 868	1
1394	Emergence of immune escape at dominant SARS-CoV-2 killer T-cell epitope.	4
1393	The effect of recombination on the evolution of a population of. **2021**,	0
1392	Asexual reproduction and vegetative growth of in response to temperature and photoperiod. **2021** , 11, 10515-10525	0
1391	Genomic insights into the adaptation and evolution of the nautilus, an ancient but evolving "living fossil". **2021**,	0
1390	Evolutionary origins of viviparity consistent with palaeoclimate and lineage diversification. **2021**, 34, 1167-1176	4
1389	A New Pathway for Forming Acetate and Synthesizing ATP during Fermentation in Bacteria. **2021**, 87, e0295920	5

1388	Evaluation of Virulence Determinants Using Whole-Genome Sequencing and Phenotypic Biofilm Analysis of Outbreak-Linked Isolates. **2021**, 12, 687625	2
1387	Phytogeographic History of the Tea Family Inferred Through High-Resolution Phylogeny and Fossils. **2021**, 70, 1256-1271	2
1386	Evolutionary and Ecological Drivers Shape the Emergence and Extinction of Foot-and-Mouth Disease Virus Lineages. **2021**, 38, 4346-4361	3
1385	Characterization of the gut microbiota in Chinese children with overweight and obesity using 16S rRNA gene sequencing. **2021**, 9, e11439	4
1384	Temporal phylogeny and molecular characterization of echovirus 30 associated with aseptic meningitis outbreaks in China. **2021**, 18, 118	0
1383	Duck wastes as a potential reservoir of novel antibiotic resistance genes. **2021**, 771, 144828	2
1382	Spatial patterns in the size of Chinese lizards are driven by multiple factors. **2021**, 11, 9621-9630	0
1381	Ecophysiological differentiation between life stages in filmy ferns (Hymenophyllaceae). **2021**, 134, 971-988	4
1380	Structure of Chimpanzee Gut Microbiomes across Tropical Africa. **2021**, 6, e0126920	1
1379	Exploring the Potential of Culture Supernatant With Resuscitation-Promoting Factor for Enhancing the Culturability of Soil Bacteria. **2021**, 12, 685263	1
1378	Limited evidence for a positive relationship between hybridization and diversification across seed plant families. **2021**, 75, 1966-1982	1
1377	Cryogenian Origin and Subsequent Diversification of the Plant Cell-Wall Enzyme XTH Family. **2021**,	4
1376	A comprehensive phylogenomic study of the monocot order Commelinales, with a new classification of Commelinaceae. **2021**, 108, 1066-1086	5
1375	Temporal Comparison of Microbial Community Structure in an Australian Winery. **2021**, 7, 134	0
1374	Settling a family feud: a high-level phylogenomic framework for the Gentianales based on 353 nuclear genes and partial plastomes. **2021**, 108, 1143-1165	8
1373	Heterothermy, body size, and locomotion as ecological predictors of migration in mammals.	3
1372	A nuclear phylogenomic study of the angiosperm order Myrtales, exploring the potential and limitations of the universal Angiosperms353 probe set. **2021**, 108, 1087-1111	20
1371	Comparative Analysis of Host-Associated Variation in. **2021**, 12, 679936	1

1370	Genotype-Specific Expression and NLR Repertoire Contribute to Phenotypic Resistance Diversity in. **2021**, 12, 675760	0
1369	Species-wide phylogenomics of the Staphylococcus aureus agr operon reveals convergent evolution of frameshift mutations.	
1368	Generalizing Bayesian phylogenetics to infer shared evolutionary events.	
1367	Revison of Coquillett (Diptera: Tachinidae) with description of five new species from Area de Conservaci□ Guanacaste in northwestern Costa Rica. **2021**, 9, e68598	
1366	SARS-CoV-2 variant evolution in the United States: High accumulation of viral mutations over time likely through serial Founder Events and mutational bursts. **2021**, 16, e0255169	12
1365	Validation of a novel associative transcriptomics pipeline in Brassica oleracea: identifying candidates for vernalisation response. **2021**, 22, 539	1
1364	Comparative and functional genomics of the ABC transporter superfamily across arthropods. **2021**, 22, 553	4
1363	regentrans: a framework and R package for using genomics to study regional pathogen transmission.	1
1362	Characterization and identification of SFDC-1, a novel AmpC-type □lactamase in Serratia fonticola. **2021**,	
1361	The Wild Sugarcane and Sorghum Kinomes: Insights Into Expansion, Diversification, and Expression Patterns. **2021**, 12, 668623	3
1360	Interstrain Variability of Human Vaginal for Metabolism of Biogenic Amines and Antimicrobial Activity against Urogenital Pathogens. **2021**, 26,	4
1359	Genomic insights into molecular adaptation to intertidal environments in the mangrove Aegiceras corniculatum. **2021**, 231, 2346-2358	4
1358	Oral administration of maternal vaginal microbes at birth to restore gut microbiome development in infants born by caesarean section: A pilot randomised placebo-controlled trial. **2021**, 69, 103443	12
1357	Genomic Elucidation of a COVID-19 Resurgence and Local Transmission of SARS-CoV-2 in Guangzhou, China. **2021**, 59, e0007921	2
1356	Tree-aggregated predictive modeling of microbiome data. **2021**, 11, 14505	2
1355	tinselR-an R Shiny Application for Annotating Phylogenetic Trees. **2021**, 10, e0022721	
1354	A higher-level nuclear phylogenomic study of the carrot family (Apiaceae). **2021**, 108, 1252-1269	6
1353	Whole-genome analysis of giraffe supports four distinct species. **2021**, 31, 2929-2938.e5	8

1352	Novel microbial syntrophies identified by longitudinal metagenomics.	
1351	Stable Carbon Isotope Depletions in Lipid Biomarkers Suggest Subsurface Carbon Fixation in Lava Caves. **2021**, 126, e2021JG006430	1
1350	Diversity and Pathogenicity of Pectobacterium Species Responsible for Causing Soft Rot and Blackleg of Potato in the Columbia Basin. **2021**, 98, 267	
1349	MOSGA 2: Comparative genomics and validation tools.	
1348	Understanding the Genetic Diversity of Picobirnavirus: A Classification Update Based on Phylogenetic and Pairwise Sequence Comparison Approaches. **2021**, 13,	3
1347	Complexity and Local Specificity of the Virome Associated with Tospovirus-Transmitting Thrips Species. **2021**, 95, e0059721	6
1346	Genomic Surveillance of SARS-CoV-2 in Erie County, New York.	1
1345	Evolution in the understorey: The Sulawesi babbler Pellorneum celebense (Passeriformes: Pellorneidae) has diverged rapidly on land-bridge islands in the Wallacean biodiversity hotspot. **2021**, 293, 314-325	1
1344	Sex-biased gene expression and recent sex chromosome turnover. **2021**, 376, 20200107	5
1343	Novel Integrative Modeling of Molecules and Morphology across Evolutionary Timescales. **2021**,	2
1342	microViz: an R package for microbiome data visualization and statistics. **2021**, 6, 3201	13
1341	A molecularphylogeny offorktail damselflies(genus Ischnura)revealsa dynamic macroevolutionary history of female colour polymorphisms. **2021**, 160, 107134	5
1340	Genomic characterization of sporadic isolates of the dominant clone of Mycobacterium abscessus subspecies massiliense. **2021**, 11, 15336	5
1339	Comparative genomic insights into the epidemiology and virulence of plant pathogenic pseudomonads from Turkey. **2021**, 7,	0
1338	Analysis of 56,348 Genomes Identifies the Relationship between Antibiotic and Metal Resistance and the Spread of Multidrug-Resistant Non-Typhoidal Salmonella. **2021**, 9,	0
1337	Spatiotemporal dissemination pattern of SARS-CoV-2 B1.1.28-derived lineages introduced into Uruguay across its southeastern border with Brazil.	1
1336	Kveik brewing yeasts demonstrate wide flexibility in beer fermentation temperature and flavour metabolite production and exhibit enhanced trehalose accumulation.	
1335	Spatial Genetic Structure of the Insect-Vectored Conifer Pathogen Leptographium wageneri Suggests Long Distance Gene Flow Among Douglas-fir Plantations in Western Oregon. **2021**, 4,	

1334	Reconstructing Dipsacales phylogeny using Angiosperms353: issues and insights. **2021**, 108, 1122-1142	4
1333	Emergence and spread of a B.1.1.28-derived lineage with Q675H and Q677H Spike mutations in Uruguay.	
1332	Revealing enzyme functional architecture via high-throughput microfluidic enzyme kinetics. **2021**, 373,	19
1331	Geometric morphometric analysis of spore shapes improves identification of fungi. **2021**, 16, e0250477	
1330	Fungal microbiomes are determined by host phylogeny and exhibit widespread associations with the bacterial microbiome. **2021**, 288, 20210552	2
1329	Whole-genome sequencing of Schistosoma mansoni reveals extensive diversity with limited selection despite mass drug administration. **2021**, 12, 4776	12
1328	Horizontal Transfer of Microbial Toxin Genes to Gall Midge Genomes. **2021**, 13,	1
1327	Genomic divergence during feralization reveals both conserved and distinct mechanisms of parallel weediness evolution. **2021**, 4, 952	0
1326	Wild Goffin's cockatoos flexibly manufacture and use tool sets. **2021**, 31, 4512-4520.e6	5
1325	Integrated Whole-Genome Sequencing Infrastructure for Outbreak Detection and Source Tracing of Serotype Enteritidis. **2021**, 18, 582-589	2
1324	Multiresistance to Nonazole Fungicides in Aspergillus fumigatus TR/L98H Azole-Resistant Isolates. **2021**, 65, e0064221	3
1323	High-Throughput Single-Cell Technology Reveals the Contribution of Horizontal Gene Transfer to Typical Antibiotic Resistance Gene Dissemination in Wastewater Treatment Plants. **2021**, 55, 11824-11834	3
1322	A new nomenclature for the livestock-associated Mycobacterium tuberculosis complex based on phylogenomics. 1, 100	0
1321	Diversity of maize (Zea mays L.) rhizobacteria with potential to promote plant growth. **2021**, 52, 1807-1823	0
1320	Ancestral Physical Stress and Later Immune Gene Family Expansions Shaped Bivalve Mollusc Evolution. **2021**, 13,	2
1319	Monitoring the Antimicrobial Resistance Dynamics of Salmonella enterica in Healthy Dairy Cattle Populations at the Individual Farm Level Using Whole-Genome Sequencing.	
1318	SemiBin: Incorporating information from reference genomes with semi-supervised deep learning leads to better metagenomic assembled genomes (MAGs).	1
1317	Hidden Viral Sequences in Public Sequencing Data and Warning for Future Emerging Diseases. **2021** , 12, e0163821	2

1316	Predominance of the SARS-CoV-2 Lineage P.1 and Its Sublineage P.1.2 in Patients from the Metropolitan Region of Porto Alegre, Southern Brazil in March 2021. **2021**, 10,	5
1315	Distinct patterns of within-host virus populations between two subgroups of human respiratory syncytial virus. **2021**, 12, 5125	3
1314	Rephine.r: a pipeline for correcting gene calls and clusters to improve phage pangenomes and phylogenies. **2021**, 9, e11950	2
1313	Distribution and phasing of sequence motifs that facilitate CRISPR adaptation. **2021**, 31, 3515-3524.e6	2
1312	Evolution of gene expression across species and specialized zooids in Siphonophora.	0
1311	Lycophyte transcriptomes reveal two whole-genome duplications in Lycopodiaceae: Insights into the polyploidization of Phlegmariurus. **2021**,	0
1310	Novel K23-Specific Bacteriophages From Different Families: Similarity of Depolymerases and Their Therapeutic Potential. **2021**, 12, 669618	4
1309	Data-driven, participatory characterization of traditional farmer varieties discloses teff (Eragrostis tef) adaptive and breeding potential under current and future climates.	0
1308	Vibrio cholerae multifaceted adaptive strategies in response to bacteriophage predation in an endemic region of the Democratic Republic of the Congo.	0
1307	Diversity of Deep-Sea Scale-Worms (Annelida, Polynoidae) in the Clarion-Clipperton Fracture Zone. **2021**, 8,	0
1306	Genetic Background and Antibiotic Resistance Profiles of NDM-1 Strains Isolated from UTI, ABU, and the GI Tract, from One Hospital in Poland, in Relation to Strains Nationally and Worldwide. **2021**, 12,	1
1305	Blockage of bacterial FimH prevents mucosal inflammation associated with Crohn’s disease. **2021**, 9, 176	5
1304	Evolutionary dynamics of multidrug resistant Salmonella enterica serovar 4,[5],12:i:- in Australia. **2021**, 12, 4786	4
1303	Temporal lineage dynamics of the ORF5 gene of porcine reproductive and respiratory syndrome virus in Korea in 2014-2019. **2021**, 166, 2803-2815	7
1302	Egg Incubation Mechanics of Giant Birds. **2021**, 10,	1
1301	Recovery of high quality metagenomessembled genomes from fullcale activated sludge microbial communities in a tropical climate using longitudinal metagenome sampling.	
1300	Long-term maize-Desmodium intercropping shifts structure and composition of soil microbiome with stronger impact on fungal communities. **2021**, 467, 437	1
1299	First molecular characterization of poxviruses in cattle, sheep, and goats in Botswana. **2021**, 18, 167	0

1298	Genomic Diversity and Antimicrobial Resistance of Haemophilus Colonizing the Airways of Young Children with Cystic Fibrosis. **2021**, e0017821	1
1297	Transcriptome-wide SNPs for Botrychium lunaria ferns enable fine-grained analysis of ploidy and population structure. **2021**,	0
1296	Legionella pneumophila CRISPR-Cas Suggests Recurrent Encounters with One or More Phages in the Family. **2021**, 87, e0046721	0
1295	Cross-Scale Analyses of Animal and Human Gut Microbiome Assemblies from Metacommunity to Global Landscape. **2021**, 6, e0063321	4
1294	Mutations that adapt SARS-CoV-2 to mustelid hosts do not increase fitness in the human airway.	2
1293	Effects of continuous cropping of Pinellia ternata (Thunb.) Breit. on soil physicochemical properties, enzyme activities, microbial communities and functional genes. **2021**, 8,	2
1292	Reactivation of transposable elements following hybridization in fission yeast.	
1291	Genome-wide identification and evolutionary analysis of MLO gene family in Rosaceae plants. **2021**, 8, 110-110	1
1290	Whole Genome Sequencing of Methicillin-Resistant Clinical Isolates Reveals Variable Composite SCC ACME among Different STs in a Tertiary Care Hospital in Oman. **2021**, 9,	1
1289	Suitability of a dual COI marker for marine zooplankton DNA metabarcoding. **2021**, 170, 105444	0
1288	Clonal dynamics in early human embryogenesis inferred from somatic mutation. **2021**, 597, 393-397	17
1287	Response of Methanogen Communities to the Elevation of Cathode Potentials in Bioelectrochemical Reactors Amended with Magnetite. **2021**, 87, e0148821	
1286	Whole genome sequencing reveals the genomic diversity, taxonomic classification, and evolutionary relationships of the genus Nocardia. **2021**, 15, e0009665	4
1285	Surface touch network structure determines bacterial contamination spread on surfaces and occupant exposure. **2021**, 416, 126137	4
1284	Megabase-scale presence-absence variation with Tripsacum origin was under selection during maize domestication and adaptation. **2021**, 22, 237	6
1283	Genome-Wide Comparative Analysis of Genetic Diversity of Regular and Specialty Maize Inbred Lines Through Genotyping by Target Sequencing (GBTS). 1	
1282	Genome-Wide SNP Discovery and Population Genetic Analysis of in China Seas. **2021**, 12, 717764	2
1281	Survey of Ticks and Tick-Borne Rickettsial and Protozoan Pathogens in Eswatini. **2021**, 10,	3

1280	Phylogeny, body morphology, and trophic level shape intestinal traits in coral reef fishes. **2021**, 11, 13218-13231	0
1279	Different evolutionary trends form the twilight zone of the bacterial pan-genome. **2021**, 7,	3
1278	Engineered Promoter-Switched Viruses Reveal the Role of Poxvirus Maturation Protein A26 as a Negative Regulator of Viral Spread. **2021**, 95, e0101221	0
1277	Single-cell exome sequencing reveals multiple subclones in metastatic colorectal carcinoma. **2021**, 13, 148	1
1276	Microbiome degrading linear alkylbenzene sulfonate in activated sludge. **2021**, 418, 126365	5
1275	Density-dependent microbial calcium carbonate precipitation by drinking water bacteria via amino acid metabolism and biosorption. **2021**, 202, 117444	1
1274	DEVOLUTION-A method for phylogenetic reconstruction of aneuploid cancers based on multiregional genotyping data. **2021**, 4, 1103	1
1273	Spatiotemporal analyses illuminate the competitive advantage of a SARS-CoV-2 variant of concern over a variant of interest.	0
1272	The link between avian brachial index, flight capability and the neornithine evolutionary radiation. **2021**, 282, 1698-1707	2
1271	Evolution of protective symbiosis in palaemonid shrimps (Decapoda: Caridea) with emphases on host spectrum and morphological adaptations. **2021**, 162, 107201	6
1270	MOSGA 2: Comparative genomics and validation tools. **2021**, 19, 5504-5509	0
1269	Pathogenicity effector candidates and accessory genome revealed by pan-genomic analysis of Parastagonospora nodorum.	
1268	Comparative Genomic Analysis of Novel subsp. Strains Reveals Functional Divergence in the Human Gut Microbiota. **2021**, 9,	0
1267	Local patterns of spread of influenza A(H3N2) virus in coastal Kenya over a one-year period revealed through virus sequence data.	
1266	The Physiological Landscape and Specificity of Antibody Repertoires.	1
1265	The nasal mutualist AMBR11 supports homeostasis via multiple mechanisms. **2021**, 24, 102978	2
1264	Full genome Nobecovirus sequences from Malagasy fruit bats define a unique evolutionary history for this coronavirus clade.	
1263	Study on the diversity of epiphytic bacteria on corn and alfalfa using Illumina MiSeq/NovaSeq high-throughput sequencing system. **2021**, 71,	

1262	Longitudinal Genomic Characterization of Carbapenemase-producing Enterobacteriaceae (CPE) Reveals Changing Pattern of CPE Isolated in Hong Kong Hospitals. **2021**, 58, 106430	0
1261	Testing the potential contribution of Wolbachia to speciation when cytoplasmic incompatibility becomes associated with host-related reproductive isolation. **2021**,	2
1260	Complex photobiont diversity in the marine lichen Lichina pygmaea. 1-8	1
1259	Genomic Update of Phenotypic Prediction Rule for Methicillin-Resistant Staphylococcus aureus (MRSA) USA300 Discloses Jail Transmission Networks with Increased Resistance. **2021**, 9, e0037621	1
1258	Flanker: a tool for comparative genomics of gene flanking regions. **2021**, 7,	1
1257	Diversification of the Type VI Secretion System in Agrobacteria. **2021**, 12, e0192721	3
1256	Mycobiome Transplant Increases Resistance to Austropuccinia psidii in an Endangered Hawaiian Plant.	6
1255	Kaistella beijingensis sp. nov., Isolated from a Municipal Wastewater Treatment Plant, Is Involved in Sludge Foaming. **2021**, 87, e0153421	1
1254	Whole genome sequence analysis of Salmonella Typhi in Papua New Guinea reveals an established population of genotype 2.1.7 sensitive to antimicrobials.	0
1253	Data-driven approaches for genetic characterization of SARS-CoV-2 lineages.	1
1252	Genetic characterization of melon accessions in the U.S. National Plant Germplasm System and construction of a melon core collection. **2021**, 1,	2
1251	Exploring in Healthy Poultry Reveals High Genetic Diversity, Good Biofilm-Forming Abilities and Higher Prevalence in Turkeys Than Broilers. **2021**, 12, 725414	3
1250	Comparative genomics of in vitro and in vivo evolution of probiotics reveals energy restriction not the main evolution driving force in short term. **2021**, 113, 3373-3380	1
1249	from a soldier from the 1652 siege of Barcelona (Spain) supports historical transatlantic epidemic contacts. **2021**, 24, 103021	1
1248	A single dose of the Biontech/Pfizer BNT162b2 vaccine protected elderly residents from severe COVID-19 during a SARS-coronavirus-2 outbreak in a senior citizen home in Germany. **2021**, 9, 1809-1814	1
1247	Long-term balancing selection in highly dynamic mating loci generates trans-species polymorphisms in fungi.	
1246	Frequent intergenotypic recombination between the non-structural and structural genes is a major driver of epidemiological fitness in caliciviruses. **2021**, 7, veab080	3
1245	Molecular epidemiology of dengue in a setting of low reported endemicity: Kupang, East Nusa Tenggara province, Indonesia. **2021**, 115, 1304-1316	

1244	Exploring the Genomic Diversity and Antimicrobial Susceptibility of Bifidobacterium pseudocatenulatum in a Vietnamese Population. **2021**, 9, e0052621	0
1243	Genomic Epidemiology and Antimicrobial Resistance Mechanisms of Imported Typhoid in Australia. **2021**, 65, e0120021	1
1242	Ecological and behavioural drivers of offspring size in marine teleost fishes. **2021**, 30, 2407	1
1241	Investigating Sources of Conflict in Deep Phylogenomics of Vetigastropod Snails. **2021**,	0
1240	Repeated dietary shifts in elapid snakes (Squamata: Elapidae) revealed by ancestral state reconstruction.	1
1239	SARS-CoV-2 B.1.617.2 Delta variant replication and immune evasion. **2021**, 599, 114-119	334
1238	How mitonuclear discordance and geographic variation have confounded species boundaries in a widely studied snake. **2021**, 162, 107194	5
1237	Faster Rates of Molecular Sequence Evolution in Reproduction-Related Genes and in Species with Hypodermic Sperm Morphologies. **2021**, 38, 5685-5703	0
1236	Whole-genome analysis uncovers loss of blaZ associated with carriage isolates belonging to methicillin-resistant Staphylococcus aureus (MRSA) clone ST5-VI in Cape Verde. **2021**, 26, 77-83	1
1235	Emergence and Spread of a B.1.1.28-Derived P.6 Lineage with Q675H and Q677H Spike Mutations in Uruguay. **2021**, 13,	0
1234	Genome-wide analysis provides a deeper understanding of the population structure of the serotype Paratyphi B complex in Bangladesh. **2021**, 7,	1
1233	Increased fidelity of protein synthesis extends lifespan. **2021**, 33, 2288-2300.e12	16
1232	Dissemination of Mycobacterium abscessus via global transmission networks. **2021**, 6, 1279-1288	4
1231	High Prevalence of Coinfecting Enteropathogens in Suspected Rotavirus Vaccine Breakthrough Cases. **2021**, 59, e0123621	0
1230	Genetic and Ecogeographic Controls on Species Cohesion in Australia's Most Diverse Lizard Radiation.. **2022**, 199, E57-E75	1
1229	Revision of the montane New Guinean skink genus Lobulia (Squamata: Scincidae), with the description of four new genera and nine new species.	
1228	Sex- and stage-dependent expression patterns of odorant-binding and chemosensory protein genes in. **2021**, 9, e12132	1
1227	Identity of Fish Fry from the ▯Tet▯Fishery in Eastern Cuba. **2021**, 51,	1

1226	Structure of Geobacter pili reveals secretory rather than nanowire behaviour. **2021**, 597, 430-434	19
1225	Immune responses in COVID-19 respiratory tract and blood reveal mechanisms of disease severity.	
1224	Description and functional analysis of the transcriptome from malting barley. **2021**, 113, 3310-3324	1
1223	Revision of the group (Diptera: Mycetophilidae). **2021**, 9, e67134	0
1222	AusTraits, a curated plant trait database for the Australian flora. **2021**, 8, 254	6
1221	Multiple introductions of multidrug-resistant typhoid associated with acute infection and asymptomatic carriage, Kenya. **2021**, 10,	4
1220	Mutation hotspots and spatiotemporal distribution of SARS-CoV-2 lineages in Brazil, February 2020-2021. **2021**, 304, 198532	6
1219	Whole-genome sequencing analysis of uncommon Shiga toxin-producing Escherichia coli from cattle: Virulence gene profiles, antimicrobial resistance predictions, and identification of novel O-serogroups. **2021**, 99, 103821	2
1218	Plants used traditionally as antimalarials in Latin America: Mining the tree of life for potential new medicines. **2021**, 279, 114221	2
1217	Phenoloxidases in Plants-How Structural Diversity Enables Functional Specificity. **2021**, 12, 754601	3
1216	Global trade in parrots □Influential factors of trade and implications for conservation. **2021**, 30, e01784	4
1215	Reduced sialidase activity of influenza A(H3N2) neuraminidase associated with positively charged amino acid substitutions. **2021**, 102,	2
1214	Ecology of avian influenza viruses in migratory birds wintering within the Yangtze River wetlands. **2021**, 66, 2014-2024	2
1213	The evolutionary history of vines in a neotropical biodiversity hotspot: Phylogenomics and biogeography of a large passion flower clade (Passiflora section Decaloba). **2021**, 164, 107260	2
1212	Protocol for post-processing of bacterial pangenome data using Pagoo pipeline. **2021**, 2, 100802	0
1211	Elevated diversity in loci linked to facial morphology is consistent with the hypothesis that individual facial recognition is important across hominoids. **2021**, 174, 785-791	
1210	Differential disease severity and whole-genome sequence analysis for human influenza A/H1N1pdm virus in 2015-2016 influenza season. **2021**, 7, veab044	1
1209	Mitochondrial genome of (Gastropoda: Lymnaeoidea): Implications for snail systematics and schistosome epidemiology.. **2021**, 1, 100017	1

1208	Links between gut microbiome composition and fatty liver disease in a large population sample. **2021**, 13, 1-22	12
1207	The history of foot-and-mouth disease virus serotype C: the first known extinct serotype?. **2021**, 7,	10
1206	Testing which axes of species differentiation underlie covariance of phylogeographic similarity among montane sedge species. **2021**, 75, 349-364	4
1205	Mode and dynamics of vanA-type vancomycin resistance dissemination in Dutch hospitals. **2021**, 13, 9	6
1204	Reproductive phasiRNA loci and DICER-LIKE5, but not microRNA loci, diversified in monocotyledonous plants. **2021**, 185, 1764-1782	5
1203	Exposure of Salmonella biofilms to antibiotic concentrations rapidly selects resistance with collateral tradeoffs. **2021**, 7, 3	15
1202	Dinoflagellates alter their carbon and nutrient metabolic strategies across environmental gradients in the central Pacific Ocean. **2021**, 6, 173-186	9
1201	A comprehensive analysis of genetic diversity of EBV reveals potential high-risk subtypes associated with nasopharyngeal carcinoma in China. **2021**, 7, veab010	4
1200	Lower Recovery of Nontuberculous Mycobacteria from Outdoor Hawai'i Environmental Water Biofilms Compared to Indoor Samples. **2021**, 9,	4
1199	Molecular characterization of lumpy skin disease virus (LSDV) emerged in Bangladesh reveals unique genetic features compared to contemporary field strains. **2021**, 17, 61	12
1198	OUP accepted manuscript.	3
1197	Pervasive duplication of tumor suppressors in Afrotherians during the evolution of large bodies and reduced cancer risk. **2021**, 10,	10
1196	High dispersal capacity and biogeographic breaks shape the genetic diversity of a globally distributed reef-dwelling calcifier. **2020**, 10, 5976-5989	11
1195	Phylogenomics of the tropical plant family Ochnaceae using targeted enrichment of nuclear genes and 250+ taxa. **2021**, 70, 48-71	3
1194	Genotyping for Species Identification and Diversity Assessment Using Double-Digest Restriction Site-Associated DNA Sequencing (ddRAD-Seq). **2020**, 2107, 159-187	2
1193	Gene Ontology Semantic Similarity Analysis Using GOSemSim. **2020**, 2117, 207-215	30
1192	Diverse coral reef invertebrates exhibit patterns of phylosymbiosis. **2020**, 14, 2211-2222	12
1191	Early high rates and disparity in the evolution of ichthyosaurs. **2020**, 3, 68	12

1190	Reconciling material cultures in archaeology with genetic data requires robust cultural evolutionary taxonomies. **2019**, 5,	14
1189	Nanopore Amplicon Sequencing Reveals Molecular Convergence and Local Adaptation of Rhodopsin in Great Lakes Salmonids. **2021**, 13,	2
1188	The Balance Hypothesis for the Avian Lumbosacral Organ and an Exploration of Its Morphological Variation. **2020**, 2, obaa024	2
1187	Genomic epidemiology of coxsackievirus A16 in mainland of China, 2000-18. **2020**, 6, veaa084	8
1186	Simulating within host human immunodeficiency virus 1 genome evolution in the persistent reservoir. **2020**, 6, veaa089	2
1185	Easy phylotyping of the EzClermont web app and command-line tool. **2020**, 2, acmi000143	14
1184	Polyphasic data support the splitting of Aspergillus candidus into two species; proposal of Aspergillus dobrogensis sp. nov. **2018**, 68, 995-1011	15
1183	A taxonomic note on the genus : Description of 23 novel genera, emended description of the genus Beijerinck 1901, and union of and. **2020**, 70, 2782-2858	824
1182	sp. nov., isolated from skin ulcers of sea-farmed fish, and description of sp. nov. with subdivision into genomovars and. **2020**, 70, 6079-6090	7
1181	Analysis of partial sequences of the RNA-dependent RNA polymerase gene as a tool for genus and subgenus classification of coronaviruses. **2020**, 101, 1261-1269	6
1180	Matrix-assisted laser desorption/ionization time-of-flight MS for the accurate identification of complex and in the clinical microbiology laboratory. **2020**, 69, 1105-1113	4
1179	Australian porcine clonal complex 10 (CC10) Escherichia coli belong to multiple sublineages of a highly diverse global CC10 phylogeny. **2019**, 5,	16
1178	Whole genome sequence analysis of Australian avian pathogenic Escherichia coli that carry the class 1 integrase gene. **2019**, 5,	31
1177	Comparative genome analysis of , an understudied member of the group. **2019**, 5,	3
1176	Clonal ST131-22 strains from a healthy pig and a human urinary tract infection carry highly similar resistance and virulence plasmids. **2019**, 5,	18
1175	Coinfinder: detecting significant associations and dissociations in pangenomes. **2020**, 6,	12
1174	Comparing serotyping with whole-genome sequencing for subtyping of non-typhoidal : a large-scale analysis of 37 serotypes with a public health impact in the USA. **2020**, 6,	6
1173	Exploration into the origins and mobilization of di-hydrofolate reductase genes and the emergence of clinical resistance to trimethoprim. **2020**, 6,	6

1172	Whole-genome epidemiology links phage-mediated acquisition of a virulence gene to the clonal expansion of a pandemic serovar Typhimurium clone. **2020**, 6,	7
1171	Genomic analysis of trimethoprim-resistant extraintestinal pathogenic and recurrent urinary tract infections. **2020**, 6,	10
1170	Pairwise comparisons across species are problematic when analyzing functional genomic data.	3
1169	Microbial metagenome of urinary tract infection.	1
1168	PHYLOSCANNER: Inferring Transmission from Within- and Between-Host Pathogen Genetic Diversity.	2
1167	Evolutionary stasis of an RNA virus indicates arbovirus re-emergence triggered by accidental release.	2
1166	Resolving brain organoid heterogeneity by mapping single cell genomic data to a spatial reference.	2
1165	Three genomes of Osteoglossidae shed light on ancient teleost evolution.	3
1164	Global gut content data synthesis and phylogeny delineate reef fish trophic guilds.	2
1163	Deconstructing the association between abiotic factors and species assemblages in the global ocean microbiome.	1
1162	Mercury methylation trait dispersed across diverse anaerobic microbial guilds in a eutrophic sulfate-enriched lake.	3
1161	A 21-year survey of Escherichia coli from bloodstream infections (BSIs) in a tertiary hospital reveals how community-hospital dynamics, influence local BSI rates, the trends of the B2 phylogroup and the STc131 pandemic clone.	2
1160	Tissue tropisms of avian influenza A viruses affect their spillovers from wild birds to pigs.	1
1159	Revealing COVID-19 Transmission by SARS-CoV-2 Genome Sequencing and Agent Based Modelling.	26
1158	Genomic characterization of a diazotrophic microbiota associated with maize aerial root mucilage.	2
1157	Infection Groups Differential (IGD) Score Reveals Infection Ability Difference between SARS-CoV-2 and Other Coronaviruses.	2
1156	Intra-host Variation and Evolutionary Dynamics of SARS-CoV-2 Population in COVID-19 Patients.	9
1155	No evidence for increased transmissibility from recurrent mutations in SARS-CoV-2.	38

1154	Phylogenetic analysis of migration, differentiation, and class switching in B cells.	8
1153	treeclimbR pinpoints the data-dependent resolution of hierarchical hypotheses.	6
1152	Ancient bacterial genomes reveal a formerly unknown diversity of Treponema pallidum strains in early modern Europe.	2
1151	Phylogenomics of Mycobacterium africanum reveals a new lineage and a complex evolutionary history.	4
1150	No Assembly Required: Using BTyper3 to Assess the Congruency of a Proposed Taxonomic Framework for the Bacillus cereus group with Historical Typing Methods.	1
1149	Isolation and characterisation of Klebsiella phages for phage therapy.	1
1148	Machine learning models to identify patient and microbial genetic factors associated with carbapenem-resistant Klebsiella pneumoniae infection.	1
1147	Links between gut microbiome composition and fatty liver disease in a large population sample.	2
1146	CellPhy: accurate and fast probabilistic inference of single-cell phylogenies from scDNA-seq data.	4
1145	Genome-wide Prediction of Small Molecule Binding to Remote Orphan Proteins Using Distilled Sequence Alignment Embedding.	0
1144	ANALYSIS OF SARS-COV-2 GENOME SEQUENCES FROM THE PHILIPPINES: GENETIC SURVEILLANCE AND TRANSMISSION DYNAMICS.	1
1143	Genomic assessment of within-host population variation in Neisseria gonorrhoeae: Implications for gonorrhoea transmission.	0
1142	Genomic epidemiology of COVID-19 in care homes in the East of England.	2
1141	Tree-Aggregated Predictive Modeling of Microbiome Data.	2
1140	The dirty north: Evidence for multiple colonisations and Wolbachia infections shaping the genetic structure of the widespread butterfly Polyommatus icarus in the British Isles.	1
1139	Pervasive duplication of tumor suppressors in Afrotherians during the evolution of large bodies and reduced cancer risk.	0
1138	An expanded gene catalog of the mouse gut metagenome.	1
1137	A deep learning framework for elucidating whole-genome chemical interaction space.	2

1136	Phylostems: a new graphical tool to investigate temporal signal of heterochronous sequences at various evolutionary scales.	0
1135	Clonal dynamics in early human embryogenesis inferred from somatic mutation.	0
1134	Reconstructing Squamate Biogeography in Afro-Arabia Reveals the Influence of a Complex and Dynamic Geologic Past.	1
1133	Phylofactorization: a graph-partitioning algorithm to identify phylogenetic scales of ecological data.	3
1132	Novel Integrative Modeling of Molecules and Morphology across Evolutionary Timescales.	9
1131	Dynamic linear models guide design and analysis of microbiota studies within artificial human guts.	2
1130	Easily phylotyping E. coli via the EzClermont web app and command-line tool.	3
1129	Scalable methods for analyzing and visualizing phylogenetic placement of metagenomic samples.	2
1128	Informal genomic surveillance of regional distribution of Salmonella Typhi genotypes and antimicrobial resistance via returning travellers.	1
1127	Bayesian Tip-dated Phylogenetics: Topological Effects, Stratigraphic Fit and the Early Evolution of Mammals.	5
1126	Genomics, evolutionary history and diagnostics of theAlternaria alternataspecies group including apple and Asian pear pathotypes.	1
1125	A genome-based species taxonomy of the Lactobacillus Genus Complex.	1
1124	Low Mutational Load Allows for High Mutation Rate Variation in Gut Commensal Bacteria.	1
1123	Mitigating Pandemic Risk with Influenza A Virus Field Surveillance at a Swine-Human Interface.	6
1122	The genome of the blind soil-dwelling and ancestrally wingless dipluran Campodea augens, a key reference hexapod for studying the emergence of insect innovations.	1
1121	Genomic acquisitions in emerging populations ofXanthomonas vasicolapv.vasculoruminfecting corn in the U.S. and Argentina.	1
1120	Antibiotics select for novel pathways of resistance in biofilms.	7
1119	From morphogenesis to pathogenesis: A cellulose loosening protein is one of the most widely distributed tools in nature.	2

1118	Molecular and transcriptional structure of the petal and leaf circadian clock in Petunia hybrida.	1
1117	Genesis and Gappa: Processing, Analyzing and Visualizing Phylogenetic (Placement) Data.	5
1116	StrainHub: A phylogenetic tool to construct pathogen transmission networks.	2
1115	Population Genomics of Nontuberculous Mycobacteria Recovered from United States Cystic Fibrosis Patients.	7
1114	Population structure and antimicrobial resistance patterns of Salmonella Typhi isolates in Bangladesh from 2004 to 2016.	2
1113	A horizontally acquired expansin gene increases virulence of the emerging plant pathogen Erwinia tracheiphila.	2
1112	Identification of hidden population structure in time-scaled phylogenies.	0
1111	Climate change negatively impacts dominant microbes in the sediments of a High Arctic lake.	4
1110	An Escherichia coli ST131 pangenome atlas reveals population structure and evolution across 4,071 isolates.	0
1109	Microbial genomes retrieved from High Arctic lake sediments encode for adaptation to cold and oligotrophic environments.	2
1108	Proposal of a taxonomic nomenclature for theBacillus cereusgroup which reconciles genomic definitions of bacterial species with clinical and industrial phenotypes.	2
1107	Emergence of a novelSalmonella entericaserotype Reading clone is linked to its expansion in commercial turkey production, resulting in unanticipated human illness in North America.	1
1106	Phylogeography and host range of Armillaria gallica in riparian forests of the northern Great Plains, USA. **2021**, 51,	2
1105	Single-cell repertoire tracing identifies rituximab-resistant B cells during myasthenia gravis relapses. **2020**, 5,	16
1104	Expanding the Orthologous Matrix (OMA) programmatic interfaces: REST API and the packages for R and Python. **2019**, 8, 42	6
1103	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. **2020**, 9, 1246	1
1102	RhierBAPS: An R implementation of the population clustering algorithm hierBAPS. **2018**, 3, 93	81
1101	Design of synthetic bacterial communities for predictable plant phenotypes. **2018**, 16, e2003962	106

1100	Delineating reef fish trophic guilds with global gut content data synthesis and phylogeny. **2020**, 18, e3000702	6
1099	Daptomycin treatment impacts resistance in off-target populations of vancomycin-resistant Enterococcus faecium. **2020**, 18, e3000987	3
1098	Increased virulence of Puccinia coronata f. sp.avenae populations through allele frequency changes at multiple putative Avr loci. **2020**, 16, e1009291	6
1097	An investig-ation into the epidemiology of chikungunya virus across neglected regions of Indonesia. **2020**, 14, e0008934	3
1096	Screening of a long-term sample set reveals two Ranavirus lineages in British herpetofauna. **2017**, 12, e0184768	12
1095	Molecular diversity and genetic structure of Saccharum complex accessions. **2020**, 15, e0233211	7
1094	A spatio-temporal assessment of simian/human immunodeficiency virus (SHIV) evolution reveals a highly dynamic process within the host. **2017**, 13, e1006358	15
1093	Characterising the epidemic spread of influenza A/H3N2 within a city through phylogenetics. **2020**, 16, e1008984	5
1092	Phylogenomics of 8,839 Clostridioides difficile genomes reveals recombination-driven evolution and diversification of toxin A and B. **2020**, 16, e1009181	7
1091	The Ancestral Cuticle Suppresses. **2020**, 10, 2385-2395	3
1090	The Occurrence of Physaloptera Hispida and a Mastophorus Sp. in Pulmonary Vessels of Hispid Cotton Rats (Sigmodon hispidus) from Georgia, U.S.A.. **2019**, 105, 718	2
1089	LAS: an integrated language analysis tool for multiple languages. **2016**, 1, 35	4
1088	Emergence of diversity in carbapenemase-producing ST131, England, January 2014 to June 2016. **2019**, 24,	8
1087	Investigating the natural resistance of blackfoot p-a%%KERN_ERR%%ua Haliotis iris to abalone viral ganglioneuritis using whole transcriptome analysis. **2019**, 135, 107-119	3
1086	Molecular-Assisted Distinctness and Uniformity Testing Using SLAF-Sequencing Approach in Soybean. **2020**, 11,	9
1085	Genomic Analysis of Antimicrobial Resistance Genotype-to-Phenotype Agreement in. **2020**, 9,	5
1084	The great greenbriers gall mystery resolved? New species of Aprostocetus Westwood (Hymenoptera, Eulophidae) gall inducer and two new parasitoids (Hymenoptera, Eurytomidae) associated with Smilax L. in southern Florida, USA. 80, 71-98	0
1083	The fruticose genera in the Ramalinaceae (Ascomycota, Lecanoromycetes): their diversity and evolutionary history. **2020**, 73, 1-68	7

1082	Pooled Deep Sequencing of Drug Resistance Loci from Parasites across Ethiopia. **2019**, 101, 1139-1143	3
1081	Do mycorrhizal fungi create below-ground links between native plants and <i>Acacia longifolia</i>? A case study in a coastal maritime pine forest in Portugal. **2018**, 18, 105-114	2
1080	Parallel evolution of influenza across multiple spatiotemporal scales. **2017**, 6,	89
1079	Expansion of the fatty acyl reductase gene family shaped pheromone communication in Hymenoptera. **2019**, 8,	11
1078	Improved characterisation of MRSA transmission using within-host bacterial sequence diversity. **2019**, 8,	11
1077	Deep sampling of Hawaiian reveals high genetic diversity and admixture with global populations. **2019**, 8,	28
1076	HA stabilization promotes replication and transmission of swine H1N1 gamma influenza viruses in ferrets. **2020**, 9,	12
1075	Asynchrony between virus diversity and antibody selection limits influenza virus evolution. **2020**, 9,	12
1074	Evidence of cryptic lineages within a small South American crocodilian: the Schneider's dwarf caiman (Alligatoridae: Caimaninae). **2019**, 7, e6580	19
1073	Alteration of the gut microbiota associated with childhood obesity by 16S rRNA gene sequencing. **2020**, 8, e8317	33
1072	, a new species of combtooth blenny from the Central Pacific, illuminates the origins of the Hawaiian fish fauna. **2020**, 8, e8852	3
1071	Ancient genetic divergence in bumblebee catfish of the genus (Pseudopimelodidae: Siluriformes) from northwestern South America. **2020**, 8, e9028	6
1070	A vanA vancomycin-resistant Enterococcus faecium ST80 outbreak resulting from a single importation event. **2021**,	0
1069	Multilocus phylogeny, natural history traits and classification of natricine snakes (Serpentes: Natricinae).	2
1068	Characterizing the Countrywide Epidemic Spread of Influenza A(H1N1)pdm09 Virus in Kenya between 2009 and 2018. **2021**, 13,	0
1067	Dynamics of gut mucosal colonisation with extended spectrum beta-lactamase producing Enterobacterales in Malawi.	0
1066	Differential pathogenesis of closely related 2018 Nigerian outbreak clade III Lassa virus isolates. **2021**, 17, e1009966	2
1065	Arbuscular mycorrhizal fungal communities of a mangrove forest along a salinity gradient on Iriomote Island. 1	0

1064	Complex introgression among three diverged largemouth bass lineages.. **2021**, 14, 2815-2830	0
1063	Genomic Characterization of Endemic and Ecdemic Non-typhoidal Lineages Circulating Among Animals and Animal Products in South Africa. **2021**, 12, 748611	2
1062	Pulse grazing by reindeer () can increase the phylogenetic diversity of vascular plant communities in the Fennoscandian tundra. **2021**, 11, 14598-14614	0
1061	Sugar-seeking insects as a source of diverse bread-making yeasts with enhanced attributes. **2021**,	0
1060	RecPD: A Recombination-Aware Measure of Phylogenetic Diversity.	
1059	Genomic analysis of extended-spectrum beta-lactamase (ESBL) producing Escherichia coli colonising adults in Blantyre, Malawi reveals previously undescribed diversity.	0
1058	Genomic and antigenic diversity of carried Klebsiella pneumoniae isolates mirrors that of invasive isolates in Blantyre, Malawi.	
1057	Local adaptation and spatiotemporal patterns of genetic diversity revealed by repeated sampling of Caenorhabditis elegans across the Hawaiian Islands.	0
1056	Drought Sensitivity of Sugarcane Cultivars Shapes Rhizosphere Bacterial Community Patterns in Response to Water Stress. **2021**, 12, 732989	0
1055	Habitat and phylogeny, but not morphology, are linked to fruit consumption in the most ecologically diverse bird family, the Furnariidae. 1-8	
1054	Estimating the maximal growth rates of eukaryotic microbes from cultures and metagenomes via codon usage patterns.	0
1053	Virophages and retrotransposons colonize the genomes of a heterotrophic flagellate. **2021**, 10,	2
1052	Prediction of antimicrobial resistance in clinical isolates using a rules-based analysis of whole genome sequences. **2021**, AAC0119621	0
1051	Efficient breeding of industrial brewing yeast strains using CRISPR/Cas9-aided mating-type switching. **2021**, 105, 8359-8376	4
1050	Large-scale discovery of candidate type VI secretion effectors with antibacterial activity.	
1049	Genetic diversity of Salmonella Paratyphi A isolated from enteric fever patients in Bangladesh from 2008 to 2018. **2021**, 15, e0009748	2
1048	A Previously Undescribed Highly Prevalent Phage Identified in a Danish Enteric Virome Catalog. **2021**, 6, e0038221	0
1047	Assessing species coverage and assembly quality of rapidly accumulating sequenced genomes.	0

1046	Multiple evolutionary origins and losses of tooth complexity in squamates. **2021**, 12, 6001	4
1045	Phylogenetic Analysis Indicates That Evasin-Like Proteins of Ixodid Ticks Fall Into Three Distinct Classes. **2021**, 11, 769542	0
1044	Adaptation of the polony technique to quantify Gokushovirinae, a diverse group of single-stranded DNA phage. **2021**, 23, 6622-6636	1
1043	A new Hendra virus genotype found in Australian flying foxes. **2021**, 18, 197	5
1042	Pathogenesis-related protein 1 (PR-1) genes in soybean: Genome-wide identification, structural analysis and expression profiling under multiple biotic and abiotic stresses. **2022**, 809, 146013	3
1041	Use of filamentous fungi as biocatalysts in the oxidation of 5-(hydroxymethyl)furfural (HMF). **2022**, 344, 126169	4
1040	Biogeographical distributions of nitrogen-cycling functional genes in a subtropical estuary.	2
1039	Population connectivity across a highly fragmented distribution: Phylogeography of the Chalcophaps doves. **2022**, 166, 107333	
1038	Transmission of Klebsiella strains and plasmids within and between Grey-headed flying fox colonies.	0
1037	Diagnosis delays in the UK according to pre or postmigration acquisition of HIV.. **2022**, 36, 415-422	0
1036	Molecular Adaptation to Folivory and the Conservation Implications for Madagascar’s Lemurs. **2021** , 9,	0
1035	Nuclear genome of a pedinophyte pinpoints genomic innovation and streamlining in the green algae.	
1034	The gastrointestinal nematodes of plains and Grevy’s zebras: Phylogenetic relationships and host specificity. **2021**, 16, 228-235	3
1033	Evolutionary thrift: mycobacteria repurpose plasmid diversity during adaptation of type VII secretion systems.	
1032	A phylogenetic transform enhances analysis of compositional microbiota data.	3
1031	Integrating patient and whole genome sequencing data to provide insights into the epidemiology of seasonal influenza A(H3N2) viruses.	0
1030	Adaptation in a fibronectin binding autolysin ofStaphylococcus saprophyticus.	
1029	Genome-wide sequence and expression analysis of the NAC transcription factor family in polyploid wheat.	

1028	Mechanisms of surface antigenic variation in the human pathogenic fungusPneumocystis jirovecii.	
1027	Switching the Post-Translational Modification of Elongation Factor P.	
1026	Genetic Variation in a Cellular Adhesin Suggests Self-Discrimination Driven by Ecological Competition in Yeast.	
1025	Comparative genomics ofPseudomonas syringaereveals convergent gene gain and loss associated with specialisation onto cherry (Prunus avium).	0
1024	Genomic Exploration of Within-Host Microevolution Reveals a Distinctive Molecular Signature of PersistentStaphylococcus aureusBacteraemia.	0
1023	Species delimitation and biogeography of the gnatcatchers and gnatwrens (Aves: Polioptilidae).	
1022	The molecular basis of antigenic variation among A(H9N2) avian influenza viruses.	1
1021	Cost-efficient high throughput capture of museum arthropod specimen DNA using PCR-generated baits.	0
1020	Expansion of the fatty acyl reductase gene family shaped pheromone communication in Hymenoptera.	
1019	A New Phylogenetic Framework for the Animal-adaptedMycobacterium tuberculosisComplex.	0
1018	Diversification in the microlepidopteran genus Mompha (Lepidoptera: Gelechioidea: Momphidae) is explained more by tissue specificity than host plant family.	0
1017	treesiftr: An R package and server for viewing phylogenetic trees and data. **2019**, 2, 35	
1016	Expanding the Orthologous Matrix (OMA) programmatic interfaces: REST API and the OmaDB packages for R and Python. **2019**, 8, 42	5
1015	The Patchy Distribution of Restriction-Modification System Genes and the Conservation of Orphan Methyltransferases in Halobacteria.	2
1014	Comparative genome analysis ofLactobacillus mudanjiangensis, an understudied member of theLactobacillus plantarumgroup.	
1013	Dynamics in coastal RNA viruses and bacteriophages are driven by shifts in the community phylogenetic structure.	
1012	Geography Shapes the Population Genomics ofSalmonella entericaDublin.	
1011	Elaborate expansion of syntenic V1R hotspots correlates with high species diversity in nocturnal mouse and dwarf lemurs.	

1010	A molecular logic of sensory coding revealed by optical tagging of physiologically-defined neuronal types.	2
1009	Hybridization and diversification are positively correlated across vascular plant families.	1
1008	A phylogenomic framework for Vetigastropoda (Mollusca).	
1007	Measuring Perceptual Distance of Organismal Color Pattern using the Features of Deep Neural Networks.	1
1006	exploration of the pv. genome using transposon insertion sequencing and comparative genomics to discriminate between core and contextual essential genes. **2019**, 7,	3
1005	Genomic Epidemiology of Methicillin-Resistant Staphylococcus aureus in Two Cohorts of High-Risk Military Trainees.	0
1004	Coinfinder: Detecting Significant Associations and Dissociations in Pangenomes.	
1003	Out of the Qinghai-Tibetan Plateau and get flourishing - the evolution of Neodon voles (Rodentia: Cricetidae) revealed by systematic sampling and low coverage whole genome sequencing.	
1002	The ancestralC. eleganscuticle suppressesrol-1.	
1001	Molecular Ecology of Coral Reef Microorganisms in the Western Indian Ocean coast of Kenya.	
1000	Asynchrony between virus diversity and antibody selection limits influenza virus evolution.	1
999	Forest Saccharomyces paradoxus are robust to seasonal biotic and abiotic changes.	
998	The effect of recombination on the evolution of a population ofNeisseria meningitidis.	
997	Genus-wide characterization of bumblebee genomes reveals variation associated with key ecological and behavioral traits of pollinators.	
996	Diazotrophic bacteria from maize exhibit multifaceted plant growth promotion traits in multiple hosts.	
995	Phylogenetic Analysis of SARS-CoV-2 Genomes in Turkey.	2
994	Negative frequency-dependent selection and asymmetrical transformation stabilise multi-strain bacterial population structures.	
993	Partitiviruses infecting Drosophila melanogaster and Aedes aegypti exhibit efficient biparental vertical transmission.	

992	A computational method for immune repertoire mining that identifies novel binders from different clonotypes, demonstrated by identifying anti-Pertussis toxoid antibodies.		1
991	sp. nov., isolated from birds and water in New Zealand. **2020**, 70, 3775-3784		4
990	Phylogenetic Analysis of St. Louis Encephalitis Virus within Two Southwestern United State Counties: a case for a bulk introduction event into the southwest United States.		
989	Genetic and epigenetic contributions to variation in transposable element expression responses to abiotic stress in maize.		2
988	Capturing noroviruses circulating in the population: sewage surveillance in Guangdong, China (2013-2018).		
987	Pseudomonas alliivorans sp. nov., a plant-pathogenic bacterium isolated from onion foliage in Georgia, USA. **2021**, 45, 126278		1
986	RevGadgets: An R package for visualizing Bayesian phylogenetic analyses from RevBayes. *Methods in Ecology and Evolution*,	7.7	2
985	Genomic Analysis of a Hospital-Associated Outbreak of : Implications on Transmission. **2021**, JCM0154721		2
984	Universal features shaping organelle gene retention.		1
983	Drivers of methicillin-resistant Staphylococcus aureus (MRSA) lineage replacement in China. **2021**, 13, 171		4
982	Phylogeny of the damselfishes (Pomacentridae) and patterns of asymmetrical diversification in body size and feeding ecology. **2021**, 16, e0258889		2
981	Pan-phylum genome-wide identification of sodium calcium exchangers reveal heterogeneous expansions and possible roles in nematode parasitism. **2021**, 146052		0
980	Highly Variable and Non-complex Diazotroph Communities in Corals From Ambient and High CO2 Environments. **2021**, 8,		1
979	Variation in Leishmania chemokine suppression driven by diversification of the GP63 virulence factor. **2021**, 15, e0009224		1
978	Genetic Diversity and Transmission of Multidrug-Resistant Mycobacterium tuberculosis strains in Lusaka, Zambia. **2021**, 114, 142-150		1
977	Genetic Analysis of SARS-CoV-2 Variants in Mexico during the First Year of the COVID-19 Pandemic. **2021**, 13,		4
976	An Effective Preprocessing Method for High-Quality Pan-Genome Analysis of Bacillus subtilis and Escherichia coli. **2022**, 2377, 371-390		0
975	DNA metabarcoding of the phytoplankton of Great Salt Lake□ Gilbert Bay: Spatiotemporal assemblage changes and comparisons to microscopy. **2021**, 48, 110-110		3

974	Intragenomic variation in mutation biases causes underestimation of selection on synonymous codon usage.	
973	Surveillance for spp. in Game Birds and Cage-Free, Floor-Raised Poultry in Pennsylvania. **2020**, 64, 210-215	1
972	Phylogenetic Analyses of Chemokine Receptors from Sequence Retrieval to Phylogenetic Trees. **2020**, 2108, 313-343	
971	Causes of Outcome Learning: A causal inference-inspired machine learning approach to disentangling common combinations of potential causes of a health outcome.	2
970	Rasgos gen�icos poblacionales aclaran el estatus taxon�ico del narciso de Villafuerte y respaldan su conservaci�. **2021**, 15-18	
969	A workflow with R: Phylogenetic analyses and visualizations using mitochondrial cytochrome b gene sequences. **2020**, 15, e0243927	1
968	Species Identification of Shed Snake Skins by Scanning Electron Microscopy, with Verification of Intraspecific Variations and Phylogenetic Comparative Analyses of Microdermatoglyphics. **2020**, 34,	0
967	Evolution of the Codling Moth Pheromone Through the Member of an Ancient Desaturase Expansion.	
966	Homologous Recombination in Mediates Diversification of Cell Surface Features and Transport Systems. **2020**, 5,	3
965	Trypanosoma (Herpetosoma) diversity in rodents and lagomorphs of New Mexico with a focus on epizootological aspects of infection in Southern Plains woodrats (Neotoma micropus). **2020**, 15, e0244803	
964	From Prevention to Disease Perturbations: A Multi-Omic Assessment of Exercise and Myocardial Infarctions. **2020**, 11,	0
963	The nucleotide messenger (p)ppGpp is a co-repressor of the purine synthesis transcription regulator PurR in Firmicutes.	1
962	Genomic rearrangements uncovered by genome-wide co-evolution analysis of a major nosocomial pathogen,. **2020**, 6,	2
961	One hundred million years history of bornavirus infections hidden in vertebrate genomes.	0
960	Partial RdRp sequences offer a robust method for Coronavirus subgenus classification.	
959	The evolutionary history of Neandertal and Denisovan Y chromosomes.	0
958	Ghosts of a structured past: Impacts of ancestral patterns of isolation-by-distance on divergence-time estimation.	
957	All small things considered: the diversity of fungi, bacteria and oomycota isolated from the seagrass, Zostera marina.	

956	Island songbirds as windows into evolution in small populations.	1
955	The balance hypothesis for the avian lumbosacral organ and an exploration of its morphological variation.	
954	Multiple evolutionary origins and losses of tooth complexity in squamates.	
953	Primate phageomes are structured by superhost phylogeny and environment.	
952	Regional transmission and reassortment of 2.3.4.4b highly pathogenic avian influenza (HPAI) viruses in Bulgarian poultry 2017/18.	1
951	Daptomycin Resistance Occurs Predominantly in -Type Vancomycin-Resistant in Australasia and Is Associated With Heterogeneous and Novel Mutations. **2021**, 12, 749935	1
950	Accumulating candidate genes for broad-spectrum resistance to rice blast in a drought-tolerant rice cultivar. **2021**, 11, 21502	0
949	ANI, Mash and Dashing equally differentiate between Klebsiella species.	
948	Use of Slaughterhouses as Sentinel Points for Genomic Surveillance of Foot-and-Mouth Disease Virus in Southern Vietnam. **2021**, 13,	1
947	Density-based binning of gene clusters to infer function or evolutionary history using GeneGrouper. **2021**,	1
946	New insights into the phylogeny and evolution of Podocarpaceae inferred from transcriptomic data. **2022**, 166, 107341	1
945	Emergence of Ceftazidime- and Avibactam-Resistant Klebsiella pneumoniae Carbapenemase-Producing Pseudomonas aeruginosa in China. **2021**, e0078721	8
944	Germinal centre-driven maturation of B cell response to SARS-CoV-2 vaccination. **2021**,	14
943	Phylogenomics of 8,839 Clostridioides difficile genomes reveals recombination-driven evolution and diversification of toxin A and B.	0
942	Global Geographic and Temporal Analysis of SARS-CoV-2 Haplotypes Normalized by COVID-19 Cases during the Pandemic.	4
941	Diversification, disparification, and hybridization in the desert shrubsEncelia.	
940	Genomic network analysis of an environmental and livestock IncF plasmid population.	
939	Genome-wide analysis of the polyamine oxidase gene family in wheat (Triticum aestivum L.) reveals involvement in temperature stress response.	1

938	Fine-scale Population Structure and Demographic History of Han Chinese Inferred from Haplotype Network of 111,000 Genomes.	
937	Recurrent mobilization of ancestral and novel variants of the chromosomal di-hydrofolate reductase gene drives the emergence of clinical resistance to trimethoprim.	
936	Waves out of the Korean Peninsula and inter- and intra-species replacements in freshwater fishes in Japan.	
935	Genome-wide identification and transcriptional analyses of the R2R3-MYB gene family in wheat.	0
934	Genome sequence and characterization of five bacteriophages infecting Streptomyces coelicolor and Streptomyces venezuelae: Alderaan, Coruscant, Dagobah, Endor1 and Endor2.	
933	A new species of (Paullinieae, Sapindaceae) from the Amazon and its phylogenetic placement. **2020** , 165, 115-126	1
932	A comprehensive phylogenetic analysis of the serpin superfamily.	
931	Rubisco adaptation is more limited by phylogenetic constraint than by catalytic trade-off.	
930	The sugarcane and sorghum kinomes: insights into evolutionary expansion and diversification.	
929	Divergence in environmental adaptation between terrestrial clades of the Bacillus cereus group. **2020**, 97,	2
928	Magnaporthe oryzae populations in Sub-Saharan Africa are diverse and show signs of local adaptation.	0
927	Population structure and transmission ofMycobacterium bovisin Ethiopia.	
926	Response of methanogen community to elevation of cathode potentials in the presence of magnetite.	
925	(Hydrostachyaceae), a new species from Madagascar. **2020**, 167, 45-56	
924	Ecoregion Rather Than Sympatric Legumes Influences Symbiotic Bradyrhizobium Associations in Invasive Scotch Broom (Cytisus scoparius) in the Pacific Northwest. **2020**, 94,	
923	Full Issue PDF. **2021**, 5, 249-366	
922	Non-starter bacterial communities in aged Cheddar cheese: Patterns on two timescales. **2021**, AEM0193921	1
921	Genomic landscape of SARS-CoV-2 pandemic in Brazil suggests an external P.1 variant origin.	1

920	Human B cell lineages associated with germinal centers following influenza vaccination are measurably evolving. **2021**, 10,	5
919	Mapping the hidden diversity of the species group (Cichlidae: Geophagini) from the Amazon basin.. **2021**, 9, e12443	1
918	Inferring Mycobacterium bovis transmission between cattle and badgers using isolates from the Randomised Badger Culling Trial. **2021**, 17, e1010075	3
917	Diversity of archaea and niche preferences among putative ammonia-oxidizing Nitrososphaeria dominating across European arable soils. **2021**,	1
916	Anammox bacteria drive fixed nitrogen loss in hadal trench sediments. **2021**, 118,	4
915	Derivedness Index for Estimating Degree of Phenotypic Evolution of Embryos: A Study of Comparative Transcriptomic Analyses of Chordates and Echinoderms.. **2021**, 9, 749963	0
914	Danish Whole-Genome-Sequenced and Samples Fit into Globally Prevalent Clades. **2021**, 7,	0
913	Independent infections of porcine deltacoronavirus among Haitian children. **2021**, 600, 133-137	29
912	Phylogenetic Analysis of the Membrane Attack Complex/Perforin Domain-Containing Proteins in and the Role of in Cotton Under Cold Stress. **2021**, 12, 684227	0
911	Single-nucleotide mosaicism in citrus: Estimations of somatic mutation rates and total number of variants. **2021**, e20162	0
910	Global phylogeny of Treponema pallidum lineages reveals recent expansion and spread of contemporary syphilis. **2021**, 6, 1549-1560	2
909	Analysis of pir gene expression across the Plasmodium life cycle. **2021**, 20, 445	0
908	Complex adaptive architecture underlies adaptation to quantitative host resistance in a fungal plant pathogen. **2021**,	
907	Phylogenetic Distribution of WhiB- and Lsr2-Type Regulators in Actinobacteriophage Genomes. **2021**, e0072721	0
906	Genetic Characterisation of Chestnut Cultivars in Crete. **2021**, 12, 1659	0
905	Diversification of plasmids in a genus of pathogenic and nitrogen-fixing bacteria. **2022**, 377, 20200466	4
904	Regulation of dhurrin pathway gene expression during Sorghum bicolor development. **2021**, 254, 119	2
903	SARS-CoV-2 variants of concern dominate in Lahore, Pakistan in April 2021. **2021**, 7,	3

902	Population analysis of retrotransposons in giraffe genomes supports RTE decline and widespread LINE1 activity in Giraffidae. **2021**, 12, 27	0
901	Eubacterium coprostanoligenes and Methanoculleus identified as potential producers of metabolites that contribute to swine manure foaming. **2021**,	0
900	Slow and fast evolutionary rates in the history of lepidosaurs.	2
899	Key roles for the freezing line and disturbance in driving the low plant species richness of temperate regions. **2022**, 31, 280	1
898	Antimicrobial Resistance in Spp. Isolated from a Beef Processing Plant and Retail Ground Beef. **2021**, e0198021	1
897	SNP and Phylogenetic Characterization of Low Viral Load SARS-CoV-2 Specimens by Target Enrichment. 1,	1
896	Emergence and global spread of main clinical clonal complex. **2021**, 7, eabj9805	4
895	Genomic Analysis of Global Strains Reveals Distinct Lineages With Differing Virulence and Antibiotic Resistance Gene Content.. **2021**, 12, 795173	2
894	Porcine circovirus-2 in Africa: Identification of continent-specific clusters and evidence of independent viral introductions from Europe, North America and Asia. **2021**,	1
893	A new nomenclature for the livestock-associated Mycobacterium tuberculosis complex based on phylogenomics. 1, 100	1
892	Genome-Wide Identification and Gene Expression Analysis of Acyl-Activating Enzymes Superfamily in Tomato () Under Aluminum Stress.. **2021**, 12, 754147	4
891	The genome sequence of the Australian filarial nematode, Cercopithifilaria johnstoni. 6, 259	0
890	Metabarcoding in two isolated populations of wild roe deer (Capreolus capreolus) reveals variation in gastrointestinal nematode community composition between regions and among age classes. **2021**, 14, 594	3
889	Enriching for Orthologs Increases Support for Xenacoelomorpha and Ambulacraria Sister Relationship.	
888	Robust expansion of phylogeny for fast-growing genome sequence data.	
887	Memory persistence and differentiation into antibody-secreting cells accompanied by positive selection in longitudinal BCR repertoires.	
886	Genome sequences of the five Sitopsis species of Aegilops and the origin of polyploid wheat B-subgenome.. **2021**,	3
885	Comparative phylotranscriptomics reveals putative sex differentiating genes across eight diverse bivalve species.. **2021**, 41, 100952	

884	Dissemination of multidrug resistant bacteria to the polar environment - Role of the longest migratory bird Arctic tern (Sterna paradisaea).. **2021**, 815, 152727	1
883	Biome-specific distribution of Ni-containing carbon monoxide dehydrogenases.. **2022**, 26, 9	0
882	Large-scale characterization of the macrolide resistome reveals high diversity and several new pathogen-associated genes.. **2022**, 8,	1
881	Proteomics, phylogenetics, and co-expression analyses indicate novel interactions in the plastid CLP chaperone-protease system.. **2022**, 101609	0
880	Secreted Toxins From Strains Isolated From Keratinocyte Skin Cancers Mediate Pro-tumorigenic Inflammatory Responses in the Skin.. **2021**, 12, 789042	1
879	Distinct developmental phenotypes result from mutation of Set8/KMT5A and histone H4 lysine 20 in Drosophila melanogaster.	
878	A spatiotemporal atlas of the lepidopteran pest Helicoverpa armigera midgut provides insights into nutrient processing and pH regulation.. **2022**, 23, 75	0
877	Viral infection and transmission in a large, well-traced outbreak caused by the SARS-CoV-2 Delta variant.. **2022**, 13, 460	88
876	GAL08, an Uncultivated Group of , Is a Dominant Bacterial Clade in a Neutral Hot Spring.. **2021**, 12, 787651	0
875	CellPhy: accurate and fast probabilistic inference of single-cell phylogenies from scDNA-seq data.. **2022**, 23, 37	1
874	Conservation Genomics of Two Threatened Subspecies of Northern Giraffe: The West African and the Kordofan Giraffe.. **2022**, 13,	0
873	Distribution and Evolutionary History of Sialic Acid Catabolism in the Phylum .. **2022**, e0238021	0
872	Morphological characters in light of new molecular phylogenies: the caudal-fin skeleton of Ovalentaria.. **2022**, 9, 211605	1
871	Down, then up: non-parallel genome size changes and a descending chromosome series in a recent radiation of Australian allotetraploid plant species, Nicotiana section Suaveolentes (Solanaceae).. **2022**,	6
870	Tenacibaculosis in Norwegian Atlantic salmon (Salmo salar) cage-farmed in cold sea water is primarily associated with Tenacibaculum finnmarkense genomovar finnmarkense.. **2022**,	2
869	A Highly Contiguous Genome Assembly of Arthrinium puccinoides.. **2022**,	0
868	OUP accepted manuscript.	
867	Comparative Transcriptomics Uncover the Uniqueness of Oocyte Development in the Donkey.. **2022**, 13, 839207	1

866	ggComp enables dissection of germplasm resources and construction of a multiscale germplasm network in wheat.. **2022**,	0
865	Large-scale WGS of carbapenem-resistant Acinetobacter baumannii isolates reveals patterns of dissemination of ST clades associated with antibiotic resistance.. **2022**,	1
864	Redefining the coenzyme A transferase superfamily with a large set of manually-annotated proteins.. **2022**,	2
863	Lineage replacement and evolution captured by the United Kingdom Covid Infection Survey.	1
862	The phylogenomic landscape of the genus Serratia.	0
861	Prevalence of SARS-CoV-2 Variants of Concern and Variants of Interest in COVID-19 Breakthrough Infections in a Hospital in Monterrey, Mexico.. **2022**, 14,	2
860	A network analysis of global cephalopod trade.. **2022**, 12, 322	1
859	VDJ Gene Usage in IgM Repertoires of Rhesus and Cynomolgus Macaques.. **2021**, 12, 815680	1
858	OUP accepted manuscript.	0
857	Fine-Scale Reconstruction of the Evolution of FII-33 Multidrug Resistance Plasmids Enables High-Resolution Genomic Surveillance.. **2022**, e0083121	3
856	Plastid phylogenomics of tribe Perseeae (Lauraceae) yields insights into the evolution of East Asian subtropical evergreen broad-leaved forests.. **2022**, 22, 32	0
855	Antigenic evolution of SARS-CoV-2 in immunocompromised hosts.	2
854	Emergence of rare carbapenemases (FRI, GES-5, IMI, SFC and SFH-1) in Enterobacterales isolated from surface waters in Japan.. **2022**,	1
853	The diversity of Isolates Collected from Tomato Plants in US high tunnels.. **2022**,	1
852	Species-Wide Phylogenomics of the Staphylococcus aureus Operon Revealed Convergent Evolution of Frameshift Mutations.. **2022**, e0133421	0
851	Describing biodiversity in the genomics era: A new species of Nearctic Cynipidae gall wasp and its genome. **2022**, 47, 94-112	0
850	The reference genome of camellia chekiangoleosa provides insights into camellia evolution and tea oil biosynthesis.. **2022**,	1
849	Optimising genomic approaches for identifying vancomycin-resistant Enterococcus faecium transmission in healthcare settings.. **2022**, 13, 509	2

848	regentrans: a framework and R package for using genomics to study regional pathogen transmission.. **2022**, 8,	
847	Evolution of gene expression across species and specialized zooids in Siphonophora.. **2022**,	1
846	Mutations that adapt SARS-CoV-2 to mink or ferret do not increase fitness in the human airway.. **2022**, 110344	10
845	A chromosome-level, fully phased genome assembly of the oat crown rust fungus Puccinia coronata f. sp. avenae: a resource to enable comparative genomics in the cereal rusts.	1
844	A catalogue of resistance gene homologs and a chromosome-scale reference sequence support resistance gene mapping in winter wheat.	
843	The rise of grasslands is linked to atmospheric CO decline in the late Palaeogene.. **2022**, 13, 293	3
842	Growth, Antigenicity, and Immunogenicity of SARS-CoV-2 Spike Variants Revealed by a Live rVSV-SARS-CoV-2 Virus.. **2021**, 8, 793437	1
841	Evaluation of Bacterial Diversity and Evolutionary Dynamics of Gut Bifidobacterium longum Isolates Obtained from Older Individuals in Hubei Province, China.. **2022**, e0144221	
840	An analysis of LysM domain function in LytE when fulfilling the D,L-endopeptidase requirement for viability in Bacillus subtilis.	
839	Nuclear genome of a pedinophyte pinpoints genomic innovation and streamlining in the green algae.. **2021**,	0
838	F Plasmid Lineages in Escherichia coli ST95: Implications for Host Range, Antibiotic Resistance, and Zoonoses.. **2022**, e0121221	4
837	sp. nov., isolated from leaves of a strawberry plant ().. **2022**, 72,	0
836	Insights into agar and secondary metabolite pathways from the genome of the red alga Gracilaria domingensis (Rhodophyta: Gracilariales).. **2022**,	0
835	Evolution of host-microbe cell adherence by receptor domain shuffling.. **2022**, 11,	0
834	Changes in the skin microbiome associated with squamous cell carcinoma in transplant recipients. **2022**, 2,	0
833	A Bayesian Multi-Outcome Analysis of Fine Particulate Matter and Cardiorespiratory Hospitalizations.. **2022**, 33, 176-184	
832	Similar geographic patterns but distinct assembly processes of abundant and rare bacterioplankton communities in river networks of the Taihu Basin.. **2022**, 211, 118057	3
831	Comparative genomic analysis of the first Ehrlichia canis detections in Australia.. **2022**, 13, 101909	2

830	Population Structure and Genetic Diversity of the Pepper Weevil (Coleoptera: Curculionidae) Using the COI Barcoding Region.. **2022**, 22,	
829	On the covariance of phylogenetic quantitative trait evolution models and their matrix condition. 1-20	0
828	Identification of enhancer-like elements defines regulatory networks active in planarian adult stem cells.	
827	Full Genome Sequences From Malagasy Fruit Bats Define a Unique Evolutionary History for This Coronavirus Clade.. **2022**, 10, 786060	1
826	Adaptive evolution of major histocompatibility complex class I immune genes and disease associations in coastal juvenile sea turtles.. **2022**, 9, 211190	0
825	Resequencing and genome-wide association studies of autotetraploid potato. **2022**, 2,	1
824	Evolution of chromosome number in grasshoppers (Orthoptera: Caelifera: Acrididae). 1	1
823	Escape from recognition of SARS-CoV-2 variant spike epitopes but overall preservation of T cell immunity. **2022**, 14,	14
822	Why does pollen morphology vary? Evolutionary dynamics and morphospace occupation in the largest angiosperm order (Asterales).. **2022**,	0
821	A highly virulent variant of HIV-1 circulating in the Netherlands.. **2022**, 375, 540-545	5
820	Characterization of Genetic Elements Carrying Gene in Escherichia coli from the Community and Hospital Settings in Vietnam.. **2022**, e0135621	0
819	Narrow transmission bottlenecks and limited within-host viral diversity during a SARS-CoV-2 outbreak on a fishing boat.. **2022**,	1
818	The evolutionary history of serotype 6 in Asia.. **2021**, 7,	0
817	Genomic Analysis of 18th-Century Kazakh Individuals and Their Oral Microbiome.. **2021**, 10,	1
816	Bayesian inference of clonal expansions in a dated phylogeny. **2021**,	0
815	Treponema pallidum genome sequencing from six continents reveals variability in vaccine candidate genes and dominance of Nichols clade strains in Madagascar.. **2021**, 15, e0010063	2
814	Global phylogeny and taxonomic reassessment of the lichen genus Dendriscosticta (Ascomycota: Peltigerales). **2022**, 71, 256-287	2
813	Paxilloboletus gen. nov., a new lamellate bolete genus from tropical Africa. **2022**, 21, 243-256	0

812	The early SARS-CoV-2 epidemic in Senegal was driven by the local emergence of B.1.416 and the introduction of B.1.1.420 from Europe.. **2022**, 8, veac025	0
811	Archival Mitogenomes Uncover the Synergistic Roles of Environment and Infection in an Amphibian Extinction.	
810	Phycova - a tool for exploring covariates of pathogen spread.. **2022**, 8, veac015	0
809	Polymorphism of <i>HvDRO1</i> and <i>HvqSOR1</i> associated with root growth angle in barley accessions. **2022**, 16, 1-10	
808	Succession of founding microbiota in an anaerobic baffled bioreactor treating low-temperature raw domestic wastewater. **2022**, 8, 792-806	0
807	OUP accepted manuscript.	
806	OUP accepted manuscript.	
805	Assessing species coverage and assembly quality of rapidly accumulating sequenced genomes.. **2022**, 11,	3
804	RecPD: A Recombination-aware measure of phylogenetic diversity.. **2022**, 18, e1009899	0
803	Utility of Triti-Map for bulk-segregated mapping of causal genes and regulatory elements in Triticeae. **2022**, 100304	1
802	Germinal centre-driven maturation of B cell response to mRNA vaccination.. **2022**,	15
801	Biotyping reveals loss of motility in two distinct Yersinia ruckeri lineages exclusive to Norwegian aquaculture.. **2022**, 45, 641-653	0
800	Integrating phylogenetic and functional data in microbiome studies.	
799	Local adaptation and spatiotemporal patterns of genetic diversity revealed by repeated sampling of Caenorhabditis elegans across the Hawaiian Islands.. **2022**,	0
798	Nigericin and Geldanamycin Are Phytotoxic Specialized Metabolites Produced by the Plant Pathogen sp. 11-1-2.. **2022**, e0231421	1
797	Population genomics of from an anthrax hyperendemic area reveals transmission processes across spatial scales and unexpected within-host diversity.. **2022**, 8,	0
796	Microbiome-host phylogeny relationships in animal gastrointestinal tract microbiomes.. **2022**,	0
795	Clade-wide variation in bite-force performance is determined primarily by size, not ecology.. **2022**, 289, 20212493	1

794	Evaluating Impacts of Syntenic Block Detection Strategies on Rearrangement Phylogeny Using M. tuberculosis Isolates.	1
793	Cross-kingdom metagenomic profiling of Lake Hillier reveals pigment-rich polyextremophiles and wide-ranging metabolic adaptations.	0
792	Global plant diversity as a reservoir of micronutrients for humanity.. **2022**,	1
791	Ecology drives patterns of spectral transmission in the ocular lenses of frogs and salamanders. **2022**, 36, 850-864	1
790	in Municipal Shower Systems in Stavanger, Norway; A Longitudinal Surveillance Study Using Whole Genome Sequencing in Risk Management.. **2022**, 10,	0
789	Complex patterns of ploidy in a holocentric plant clade (Schoenus, Cyperaceae) in the Cape biodiversity hotspot.. **2022**,	0
788	Highly Resolved Papilionoid Legume Phylogeny Based on Plastid Phylogenomics.. **2022**, 13, 823190	2
787	Population Genomics Approaches for Genetic Characterization of SARS-CoV-2 Lineages.. **2022**, 9, 826746	1
786	Nuclear genome of Bulinus truncatus, an intermediate host of the carcinogenic human blood fluke Schistosoma haematobium.. **2022**, 13, 977	0
785	Phytochytrium and Sparrowiella, two new polycentric genera in Cladochytriales. **2022**, 21, 1	
784	Discovery of Flaviviridae-derived endogenous viral elements in shrew genomes provide novel insights into Pestivirus ancient history.	0
783	Highly divergent white-tailed deer SARS-CoV-2 with potential deer-to-human transmission.	10
782	Global Distribution of Gene Variants in 214K Metagenomic Samples.. **2022**, e0010522	0
781	Dual Adhesive Unipolar Polysaccharides Synthesized by Overlapping Biosynthetic Pathways in Agrobacterium tumefaciens.. **2022**,	0
780	Disentangle genus microdiversity within a complex microbial community by using a multi-distance long-read binning method: example of Candidatus Accumulibacter.. **2022**,	0
779	Patterns of Traditional and Modern Uses of Wild Edible Native Plants of Chile: Challenges and Future Perspectives.. **2022**, 11,	1
778	Genomic and antigenic diversity of colonizing isolates mirrors that of invasive isolates in Blantyre, Malawi.. **2022**, 8,	0
777	Mycorrhizal symbiosis pathway and edaphic fertility frame root economics space among tree species.. **2022**,	1

776	DNA Metabarcoding Enables High-Throughput Detection of Spotted Wing Drosophila (Drosophila suzukii) Within Unsorted Trap Catches. **2022**, 10,	0
775	Genomic Epidemiology of SARS-CoV-2 in Tocantins State and the Diffusion of P.1.7 and AY.99.2 Lineages in Brazil.. **2022**, 14,	1
774	SARS-CoV-2 transmission risk upon return to work in RNA-positive healthcare workers.. **2022**,	2
773	The contributions of Nettie Stevens to the field of sex chromosome biology.. **2022**, 377, 20210215	1
772	Mineral protection and resource limitations combine to explain profile-scale soil carbon persistence.	1
771	SIEVE: joint inference of single-nucleotide variants and cell phylogeny from single-cell DNA sequencing data.	0
770	The virota and its transkingdom interactions in the healthy infant gut.. **2022**, 119, e2114619119	2
769	Correlated evolution of parental care with dichromatism, colours, and patterns in anurans.. **2022**,	0
768	Dactylogyridae 2022: a meta-analysis of phylogenetic studies and generic diagnoses of parasitic flatworms using published genetic and morphological data.. **2022**,	0
767	Starvation causes changes in the intestinal transcriptome and microbiome that are reversed upon refeeding.. **2022**, 23, 225	0
766	Resolving clonal substructure from single cell genomic data using CopyKit.	0
765	An isolated population of the secretive, endemic Aztec Rail (Rallus tenuirostris) in Chihuahua, Mexico. **2022**, 133,	
764	Large-scale fungal strain sequencing unravels the molecular diversity in mating loci maintained by long-term balancing selection.. **2022**, 18, e1010097	0
763	Addressing IGHV Gene Structural Diversity Enhances Immunoglobulin Repertoire Analysis: Lessons From Rhesus Macaque.. **2022**, 13, 818440	0
762	Meta-analysis of the species complex (RSSC) based on comparative evolutionary genomics and reverse ecology.. **2022**, 8,	3
761	Kveik Brewing Yeasts Demonstrate Wide Flexibility in Beer Fermentation Temperature Tolerance and Exhibit Enhanced Trehalose Accumulation.. **2022**, 13, 747546	0
760	Global population structure of the complex and identification of hospital-adapted lineages in the complex.. **2022**, 8,	1
759	Broad- and fine-scale structure across the distribution of the relict dace (Relictus solitarius) in the Great Basin desert, USA.	

758	Horizontal transmission enables flexible associations with locally adapted symbiont strains in deep-sea hydrothermal vent symbioses.. **2022**, 119, e2115608119	2
757	Complete chloroplast genome of Roem. var. (Franch.) Hand.-Mazz (Meliaceae), 'Chinese mahogany'.. **2022**, 7, 495-497	0
756	Integrated metagenomics identifies a crucial role for trimethylamine-producing Lachnoclostridium in promoting atherosclerosis.. **2022**, 8, 11	1
755	Implementation of a COVID-19 Genomic Surveillance Regional Network for Latin America and Caribbean region.. **2022**, 17, e0252526	0
754	Synergies between Heat Disturbance and Inoculum Size Promote the Invasion Potential of a Bacterial Pathogen in Soil.. **2022**, 10,	
753	Metagenome-Assembled Genomes Reveal Mechanisms of Carbohydrate and Nitrogen Metabolism of Schistosomiasis-Transmitting Vector .. **2022**, e0184321	1
752	Genomic Epidemiology of SARS-CoV-2 in Seychelles, 2020-2021.	0
751	Image_7.PDF. **2018**,	
750	Image_8.PDF. **2018**,	
749	Image_9.PDF. **2018**,	
748	Table_1.XLSX. **2018**,	
747	Image_1.tif. **2020**,	
746	Image_2.tif. **2020**,	
745	Image_3.tif. **2020**,	
744	Table_1.docx. **2020**,	
743	Table_1.DOCX. **2019**,	
742	Data_Sheet_1.PDF. **2019**,	
741	Table_1.DOCX. **2019**,	

740 Table_2.DOCX. **2019**,

739 Table_3.xlsx. **2019**,

738 Table_4.DOCX. **2019**,

737 Table_5.DOCX. **2019**,

736 Data_Sheet_1.xlsx. **2019**,

735 Data_Sheet_2.pdf. **2019**,

734 Data_Sheet_3.fasta. **2019**,

733 Data_Sheet_4.pdf. **2019**,

732 Data_Sheet_1.xlsx. **2019**,

731 Image_1.pdf. **2019**,

730 Image_2.tif. **2019**,

729 Image_1.TIF. **2019**,

728 Image_2.TIF. **2019**,

727 Table_1.DOCX. **2019**,

726 Data_Sheet_1.PDF. **2019**,

725 Table_2.DOCX. **2019**,

724 Table_3.DOCX. **2019**,

723 Table_1.XLSX. **2019**,

722 Table_2.XLSX. **2019**,

721 Table_3.XLSX. **2019**,

720 Table_4.XLSX. **2019**,

719 Image_1.JPEG. **2020**,

718 Image_10.JPEG. **2020**,

717 Image_11.JPEG. **2020**,

716 Image_12.JPEG. **2020**,

715 Image_2.JPEG. **2020**,

714 Image_3.JPEG. **2020**,

713 Image_4.JPEG. **2020**,

712 Image_5.JPEG. **2020**,

711 Image_6.JPEG. **2020**,

710 Image_7.JPEG. **2020**,

709 Image_8.JPEG. **2020**,

708 Image_9.JPEG. **2020**,

707 Table_1.DOCX. **2020**,

706 Table_2.csv. **2020**,

705 Image_1.TIFF. **2018**,

704 Table_1.DOCX. **2018**,

703 Table_2.DOCX. **2018**,

702 Table_3.DOCX. **2018**,

701 Table_1.XLSX. **2020**,

700 Image_1.JPEG. **2020**,

699 Image_10.JPEG. **2020**,

698 Image_2.JPEG. **2020**,

697 Image_3.JPEG. **2020**,

696 Image_4.JPEG. **2020**,

695 Image_5.JPEG. **2020**,

694 Image_6.JPEG. **2020**,

693 Image_7.JPEG. **2020**,

692 Image_8.JPEG. **2020**,

691 Image_9.jpg. **2020**,

690 Table_1.XLSX. **2020**,

689 Table_2.XLSX. **2020**,

688 Image_1.TIF. **2019**,

687 Image_2.TIF. **2019**,

686 Image_3.TIF. **2019**,

685 Image_4.TIF. **2019**,

684 Table_1.XLSX. **2019**,

683 Table_2.XLSX. **2019**,

682 Table_3.XLSX. **2019**,

681 Data_Sheet_1.docx. **2018**,

680 Image_1.TIF. **2018**,

679 Table_1.xlsx. **2018**,

678 Data_Sheet_1.docx. **2018**,

677 Data_Sheet_2.CSV. **2018**,

676 Data_Sheet_3.CSV. **2018**,

675 Data_Sheet_4.CSV. **2018**,

674 Data_Sheet_5.CSV. **2018**,

673 Data_Sheet_6.CSV. **2018**,

672 Data_Sheet_7.CSV. **2018**,

671 Data_Sheet_8.CSV. **2018**,

670 Table_1.XLSX. **2018**,

669 Table_2.XLSX. **2018**,

668 Table_3.XLSX. **2018**,

667 Data_Sheet_1.PDF. **2019**,

666 Data_Sheet_1.docx. **2019**,

665 Data_Sheet_2.xls. **2019**,

664 Image_1.tif. **2018**,

663 Table_1.xlsx. **2018**,

662 Table_2.xlsx. **2018**,

661 Data_Sheet_1.PDF. **2020**,

660 Data_Sheet_2.PDF. **2020**,

659 Data_Sheet_3.PDF. **2020**,

658 Table_1.XLSX. **2020**,

657 Table_2.XLSX. **2020**,

656 Table_3.XLSX. **2020**,

655 Table_4.XLSX. **2020**,

654 Table_5.XLSX. **2020**,

653 Table_6.XLSX. **2020**,

652 Table_7.XLSX. **2020**,

651 Data_Sheet_1.docx. **2019**,

650 Table_1.XLSX. **2020**,

649 Table_2.XLSX. **2020**,

648 Table_3.XLSX. **2020**,

647 Table_4.XLSX. **2020**,

646 Table_1.xls. **2019**,

645 Data_Sheet_1.XLSX. **2020**,

644 Data_Sheet_2.docx. **2020**,

643 Data_Sheet_1.XLSX. **2020**,

642 Data_Sheet_2.PDF. **2020**,

641 Data_Sheet_1.PDF. **2019**,

640 Data_Sheet_2.PDF. **2019**,

639 Data_Sheet_3.PDF. **2019**,

638 Data_Sheet_4.PDF. **2019**,

637 Data_Sheet_5.PDF. **2019**,

636 Table_1.XLSX. **2019**,

635 Table_2.XLSX. **2019**,

634 Table_3.XLSX. **2019**,

633 Table_4.PDF. **2019**,

632 Data_Sheet_1.PDF. **2018**,

631 Data_Sheet_1.xlsx. **2018**,

630 Data_Sheet_1.PDF. **2020**,

629 Data_Sheet_1.docx. **2020**,

628 Table_1.xlsx. **2020**,

627 Data_Sheet_1.PDF. **2020**,

626 Data_Sheet_1.xlsx. **2019**,

625 Data_Sheet_2.xlsx. **2019**,

624 Data_Sheet_3.xlsx. **2019**,

623 Data_Sheet_4.xlsx. **2019**,

622 DataSheet_1.pdf. **2020**,

621 Data_Sheet_1.docx. **2019**,

620 Table_1.XLSX. **2020**,

619 DataSheet_1.xlsx. **2019**,

618 DataSheet_2.xlsx. **2019**,

617 Image_1.jpg. **2019**,

616 Image_2.jpg. **2019**,

615 Table_1.pdf. **2019**,

614	Table_2.pdf. **2019**,	
613	Table_3.pdf. **2019**,	
612	Table_4.pdf. **2019**,	
611	DataSheet_1.pdf. **2019**,	
610	Image_1.pdf. **2020**,	
609	Image_1.PDF. **2020**,	
608	Image_2.PDF. **2020**,	
607	Table_1.PDF. **2020**,	
606	Table_2.PDF. **2020**,	
605	Data_Sheet_1.PDF. **2020**,	
604	endosymbionts in two species indicates independent acquisitions and lack of prophage elements.. **2022**, 8,	0
603	SubPhaser: A robust allopolyploid subgenome phasing method based on subgenome-specific k-mers.. **2022**,	0
602	Phylogenetic analysis of migration, differentiation, and class switching in B cells.. **2022**, 18, e1009885	2
601	Sorghum hybrids grown in hydroponics contrast for phosphorus use efficiency.. **2022**, 84, e253083	
600	OUP accepted manuscript.	2
599	OUP accepted manuscript.	3
598	Functional Insights of Salinity Stress-Related Pathways in Metagenome-Resolved Genomes.. **2022**, e0244921	0
597	Ecological and Anthropogenic Spatial Gradients Shape Patterns of Dispersal of Foot-and-Mouth Disease Virus in Uganda. **2022**, 11, 524	

596	Improving Association Studies and Genomic Predictions for Climbing Beans With Data From Bush Bean Populations.. **2022**, 13, 830896	0
595	Functional characterization of putative ecdysone transporters in lepidopteran pests.	
594	A deep siamese neural network improves metagenome-assembled genomes in microbiome datasets across different environments.. **2022**, 13, 2326	4
593	First Report of Lumpy Skin Disease in Myanmar and Molecular Analysis of the Field Virus Isolates. **2022**, 10, 897	2
592	ORIGINS AND DIVERSITY OF PERIPHERAL POPULATIONS OF RIO GRANDE SUCKER (PANTOSTEUS PLEBEIUS) IN THE SOUTHWESTERN UNITED STATES. **2022**, 66,	
591	Somewhere I belong: phylogeny and morphological evolution in a species-rich lineage of ectoparasitic flatworms infecting cichlid fishes.. **2022**,	2
590	Antigenic characterization and pandemic risk assessment of North American H1 influenza A viruses circulating in swine.	0
589	Genetic Diversity and Connectivity of the Ostreid Herpesvirus 1 Populations in France: A First Attempt to Phylogeographic Inference for a Marine Mollusc Disease.	1
588	Evolution of coastal forests based on a full set of mangrove genomes.. **2022**,	5
587	A metagenomic study of the bacteria in snow algae microbiomes.. **2022**,	
586	Strain Variation in Clostridioides difficile Cytotoxicity Associated with Genomic Variation at Both Pathogenic and Nonpathogenic Loci.	
585	An NGS-Based Phylogeny of Orthotricheae (Orthotrichaceae, Bryophyta) With the Proposal of the New Genus Rehubryum From Zealandia. **2022**, 13,	0
584	Plasmodium falciparum genetic diversity in coincident human and mosquito hosts.	0
583	Signatures of selection in core and accessory genomes indicate different ecological drivers of diversification among Bacillus cereus clades.. **2022**,	0
582	Characterisation of Enteritidis ST11 and ST1925 Associated with Human Intestinal and Extra-Intestinal Infections in Singapore.. **2022**, 19,	0
581	Host and pathogen response to bacteriophage engineered against Mycobacterium abscessus lung infection.. **2022**,	7
580	Rapid diversification of the Variable Seedeater superspecies complex despite widespread gene flow.. **2022**, 107510	0
579	Unsuspected clonal spread of Methicillin-resistant Staphylococcus aureus causing bloodstream infections in hospitalized adults detected using whole genome sequencing.. **2022**,	

578	Plasmid overlap and evolution between Enterobacterales isolates from bloodstream infections and non-human compartments.	
577	Evaluation of genomic selection for high salinity tolerance trait in Pacific white shrimp Litopeneaus vannamei. **2022**, 738320	0
576	Biogeography of Micro-Eukaryotic Communities in Sediment of Thermokarst Lakes Are Jointly Controlled by Spatial, Climatic, and Physicochemical Factors Across the Qinghai-Tibet Plateau. **2022** , 10,	0
575	Phylogenomic comparison of Neisseria gonorrhoeae causing disseminated gonococcal infections and uncomplicated gonorrhea in Georgia, United States.	0
574	Discovery of lignin-transforming bacteria and enzymes in thermophilic environments using stable isotope probing.. **2022**,	2
573	Whole-genome sequencing of Mycobacterium tuberculosis from Cambodia.. **2022**, 12, 7693	0
572	Development of recombinant monoclonal antibodies targeting conserved VlsE epitopes in Lyme disease pathogens.	
571	Antibody Evasion of SARS-CoV-2 Omicron BA.1, BA.1.1, BA.2 and BA.3 Sub-lineages. **2022**,	10
570	Composition, Structure and Diversity of Soil Bacterial Communities before, during and after Transit through the Gut of the Earthworm Aporrectodea caliginosa. **2022**, 10, 1025	0
569	DMSP Production by Coral-Associated Bacteria. **2022**, 9,	1
568	A comprehensive analysis of Usutu virus (USUV) genomes revealed lineage-specific codon usage patterns and host adaptation.	
567	Specific utilization of biopolymers of plant and fungal origin reveals the existence of substrate-specific guilds for bacteria in temperate forest soils. **2022**, 108696	2
566	PhyloCloud: an online platform for making sense of phylogenomic data.. **2022**,	0
565	Species limits and introgression in Pimelodus from the Magdalena-Cauca River basin.. **2022**, 107517	0
564	Viruses of Rhodophyta: lack of cultures and genomic resources pose a threat to the growing red algal aquaculture industry. 1-15	1
563	A catalogue of resistance gene homologs and a chromosome-scale reference sequence support resistance gene mapping in winter wheat.. **2022**,	1
562	Photoreceptor distributions, visual pigments and the opsin repertoire of Atlantic halibut (Hippoglossus hippoglossus).. **2022**, 12, 8062	0
561	Identifying Candidate Genes for Short Gestation Length Trait in Chinese Qingping Pigs by Whole-Genome Resequencing and RNA Sequencing. **2022**, 13,	

560	SARS-CoV-2 infection results in immune responses in the respiratory tract and peripheral blood that suggest mechanisms of disease severity.. **2022**, 13, 2774	0
559	Co-infection with SARS-CoV-2 Omicron and Delta variants revealed by genomic surveillance.. **2022**, 13, 2745	2
558	Investigating plant disease outbreaks with long-read metagenomics: sensitive detection and highly resolved phylogenetic reconstruction applied to .. **2022**, 8,	0
557	Transmission of Klebsiella strains and plasmids within and between Grey-headed flying fox colonies.. **2022**,	
556	Multiple-Locus Variable-Number Tandem-Repeat Analysis (MLVA) Genotypes of Listeria monocytogenes isolated from Farms, Abattoirs, and Retail in Gauteng Province, South Africa.. **2022**,	0
555	Metatranscriptomic comparison of viromes in endemic and introduced passerines in New Zealand.	1
554	Assessing risk for butterflies in the context of climate change, demographic uncertainty, and heterogenous data sources.	1
553	Metagenomics Combined with Activity-Based Proteomics Point to Gut Bacterial Enzymes that Reactivate Mycophenolate.	
552	Insights into the genomics of clownfish adaptive radiation: the genomic substrate of the diversification.	0
551	Characterization and application of bacteriophages for the biocontrol of Shiga-toxin producing Escherichia coli in Romaine lettuce. **2022**, 140, 109109	0
550	Exploring the diversity and genetic structure of the U.S. National Cultivated Strawberry Collection.	2
549	Sweepstakes reproductive success via pervasive and recurrent selective sweeps.	1
548	SARS-CoV-2 genomic surveillance in Rwanda: Introductions and local transmission of the B.1.617.2 (Delta) variant of concern.	
547	Ongoing evolution of Beet necrotic yellow vein virus towards Rz1 resistance- breaking in Europe.	0
546	Transmission of SARS-CoV-2 from humans to animals and potential host adaptation. **2022**, 13,	5
545	SCONCE2: jointly inferring single cell copy number profiles and tumor evolutionary distances.	
544	A deeply conserved protease, acylamino acid-releasing enzyme (AARE), acts in plant aging.	
543	Metagenomic Analysis Using Phylogenetic PlacementA Review of the First Decade. **2022**, 2,	2

542	Myriapod genomes reveal ancestral horizontal gene transfer and hormonal gene loss in millipedes. **2022**, 13,		1
541	Termite dispersal is influenced by their diet. **2022**, 289,		0
540	The LOTUS initiative for open knowledge management in natural products research. 11,		7
539	Lineage BA.2 dominated the Omicron SARS-CoV-2 epidemic wave in the Philippines.		0
538	Dominance of Three Sublineages of the SARS-CoV-2 Delta Variant in Mexico. **2022**, 14, 1165		0
537	Genomic dissection of Klebsiella pneumoniae infections in hospital patients reveals insights into an opportunistic pathogen. **2022**, 13,		3
536	Antibiotic-resistant organisms establish reservoirs in new hospital built environments and are related to patient blood infection isolates. **2022**, 2,		0
535	Detection of Genus and Three Important Species of Cronobacter Using Novel Genus- and Species-Specific Genes Identified by Large-Scale Comparative Genomic Analysis. **2022**, 13,		
534	Identification and characterization of 3-ketosphinganine reductase activity encoded at the BT_0972 locus in Bacteroides thetaiotaomicron. **2022**, 100236		1
533	Dynamics of Salmonella enterica and antimicrobial resistance in the Brazilian poultry industry and global impacts on public health. **2022**, 18, e1010174		1
532	Comparative phyloproteomics identifies conserved plasmodesmal proteins.		0
531	Genome sequencing and evolutionary analysis of a new endophytic Trichoderma species isolated from orchid roots with reduced repertoire of protein-coding genes. **2022**, 21,		
530	Diversity and community structure of eukaryotic microalgae in surface sediments in the central Bohai Sea, China, based on a metabarcoding approach.		
529	Phase & Power in Genomic Harmonic Analysis. **2022**,		
528	Antimicrobial resistance genes predict plasmid generalism and network structure in wastewater.		
527	The phylodynamics of SARS-CoV-2 during 2020 in Finland. **2022**, 2,		0
526	Genomic Epidemiology of SARS-CoV-2 in Seychelles, 2020�2021. **2022**, 14, 1318		1
525	Principled, practical, flexible, fast: a new approach to phylogenetic factor analysis. *Methods in Ecology and Evolution*,	7.7	1

524	Discordance between HIV-1 Population in Plasma at Rebound after Structured Treatment Interruption and Archived Provirus Population in Peripheral Blood Mononuclear Cells.	
523	The Perfect Storm of 2019: An immunological and phylodynamic analysis of Cambodia's unprecedented dengue outbreak.	
522	Rifampicin Resistance Associated with rpoB Mutations in Neisseria gonorrhoeae Clinical Strains Isolated in Austria, 2016 to 2020.	0
521	Variation in Grain Zinc and Iron Concentrations, Grain Yield and Associated Traits of Biofortified Bread Wheat Genotypes in Nepal. 13,	0
520	Accounting for errors in data improves divergence time estimates in single-cell cancer evolution.	0
519	A Reference Genome Assembly of the Bobcat, Lynx rufus.	0
518	Cryptic diversity and spatial genetic variation in the coral Acropora tenuis and its endosymbionts across the Great Barrier Reef.	1
517	Functional and phylogenetic analyses of camel rumen microbiota associated with different lignocellulosic substrates. **2022**, 8,	0
516	The Viral Susceptibility of the Haloferax Species. **2022**, 14, 1344	0
515	SARS-CoV-2: Two Years in the Pandemic: What Have We Observed from Genome Sequencing Results in Lithuania?. **2022**, 10, 1229	
514	Intragenomic variation in non-adaptive nucleotide biases causes underestimation of selection on synonymous codon usage. **2022**, 18, e1010256	
513	Joint profiling of gene expression and chromatin accessibility during amphioxus development at single-cell resolution. **2022**, 39, 110979	2
512	Cultivated hawthorn (Crataegus pinnatifida var. major) genome sheds light on the evolution of Maleae (apple tribe).	1
511	Discovery and Genomic Characterization of a Novel Henipavirus, Angavokely virus, from fruit bats in Madagascar.	0
510	Dynamic plastid and mitochondrial genomes in Chaetopeltidales (Chlorophyceae) and characterization of a new chlorophyte taxon. **2022**, 109, 939-951	0
509	Resolving Deep Evolutionary Relationships within the RNA Virus Phylum Lenarviricota.	1
508	Comparative genomic analysis reveals contraction of gene families with putative roles in pathogenesis in the fungal boxwood pathogens Calonectria henricotiae and C. pseudonaviculata. **2022**, 22,	0
507	Rapid adaptation of a complex trait during experimental evolution of Mycobacterium tuberculosis. 11,	0

506	Metatranscriptomic Comparison of Viromes in Endemic and Introduced Passerines in New Zealand. **2022**, 14, 1364	0
505	Potential Inter-variant and Intra-variant Recombination of Delta and Omicron Variants.	1
504	A polar bear paleogenome reveals extensive ancient gene flow from polar bears into brown bears.	1
503	Robust phylodynamic analysis of genetic sequencing data from structured populations.	0
502	Leptospira enrichment culture followed by ONT Nanopore sequencing allows better detection of Leptospira presence and diversity in water and soil samples.	
501	The impact of species-wide gene expression variation on Caenorhabditis elegans complex traits. **2022**, 13,	0
500	Recovery of High Quality Metagenome-Assembled Genomes From Full-Scale Activated Sludge Microbial Communities in a Tropical Climate Using Longitudinal Metagenome Sampling. 13,	0
499	Deep haplotype analyses of target-site resistance locus ACCase in blackgrass enabled by pool-based amplicon sequencing.	
498	Phylogenomic Analysis of Protein-Coding Genes Resolves Complex Gall Wasp Relationships.	0
497	Narrow Transmission Bottlenecks and Limited Within-Host Viral Diversity During a SARS-CoV-2 Outbreak on a Fishing Boat.	0
496	Biosynthetic potential of the global ocean microbiome.	6
495	Transcriptional response of Meloidogyne incognita to non-fumigant nematicides. **2022**, 12,	
494	Strain tracking of Candidatus Liberibacter asiaticus citrus greening disease pathogen, enabled by high-resolution microbiome analysis of the Asian citrus psyllid.	0
493	Plant secondary metabolites and primate food choices: A meta-analysis and future directions.	0
492	Comparative transcriptomic analysis reveals that TPX2 and AURXA are involved in porcine PCV2 infection. **2022**, 834, 146649	0
491	Grasshoppers exhibit asynchrony and spatial non-stationarity in response to the El Niño/Southern and Pacific Decadal Oscillations. **2022**, 471, 110043	0
490	Applying Synteny Networks (SynNet) to Study Genomic Arrangements of Protein-Coding Genes in Plants. **2022**, 199-215	
489	Soil-derived bacteria endow Camellia weevil with more ability to resist plant chemical defense. **2022**, 10,	3

488	Origins and Evolution of Seasonal Human Coronaviruses.		1
487	Phylogenetic evidence of the re-evolution of planktotrophy in Australian periwinkles. **2022**, 136, 574-585		
486	A chromosome-level genome assembly of the orange wheat blossom midge, Sitodiplosis mosellana G�hin (Diptera: Cecidomyiidae) provides insights into the evolution of a detoxification system.		
485	Craniodental Morphology and Phylogeny of Marsupials. **2022**, 457,		6
484	Fine-grain population structure and transmission patterns of Mycobacterium tuberculosis in southern Mozambique, a high TB/HIV burden area. **2022**, 8,		
483	Contrasting coloured ventral wings are a visual collision avoidance signal in birds. **2022**, 289,		0
482	The RadOrgMiner pipeline: Automated genotyping of organellar loci from RADseq data. *Methods in Ecology and Evolution*,	7.7	
481	A Physcomitrella PIN protein acts in spermatogenesis and sporophyte abortion.		
480	Multispecies comparative analysis reveals transcriptional specificity during Mongolian horse testicular development.		
479	Influence of insertion sequences on population structure of phytopathogenic bacteria in the Ralstonia solanacearum species complex.		0
478	Generalizing Bayesian phylogenetics to infer shared evolutionary events. **2022**, 119,		1
477	No news from old drawings? Stomach anatomy in muroid rodents in relation to body size and ecology.		
476	Watershed-scale liming reveals the short- and long-term effects of pH on the forest soil microbiome and carbon cycling.		0
475	Determining the International Spread of B.1.1.523 SARS-CoV-2 Lineage with a Set of Mutations Highly Associated with Reduced Immune Neutralization. **2022**, 10, 1356		0
474	Vibrio cholerae O139 genomes provide a clue to why it may have failed to usher in the eighth cholera pandemic. **2022**, 13,		2
473	Recent transposable element bursts triggered by insertions near genes in a fungal pathogen.		0
472	Comparative Genomics and Pan-Genome Driven Prediction of a Reduced Genome of Akkermansia muciniphila. **2022**, 10, 1350		1
471	A new species of Astronotus (Teleostei, Cichlidae) from the Orinoco River and Gulf of Paria basins, northern South America. 1113, 111-152		

470	A natural uORF variant confers phosphorus acquisition diversity in soybean. **2022**, 13,	0
469	Co-Circulation of Different Hepatitis E Virus Genotype 3 Subtypes in Pigs and Wild Boar in North-East Germany, 2019. **2022**, 11, 773	1
468	Epidemiological and microbiological investigation of a large increase in vibriosis, northern Europe, 2018. **2022**, 27,	2
467	Novel Viral and Microbial Species in a Translocated Toutouwai (Petroica longipes) Population from Aotearoa/New Zealand.	
466	Origins and Evolution of Seasonal Human Coronaviruses. **2022**, 14, 1551	0
465	Untangling an AGS Outbreak Caused by the Recombinant GII.12[P16] Norovirus With Nanopore Sequencing. 12,	0
464	Genomic Sequencing of Dengue Virus Strains Associated with Papua New Guinean Outbreaks in 2016 Reveals Endemic Circulation of DENV-1 and DENV-2. **2022**,	1
463	Characterisation of the RNA Virome of Nine Ochlerotatus Species in Finland. **2022**, 14, 1489	1
462	Diversity and Evolution of Computationally Predicted T Cell Epitopes against Human Respiratory Syncytial Virus.	
461	Gamma variant vertically transmitted from a mild symptomatic pregnant woman associated with fatal neonatal COVID. **2022**, 102385	
460	Emergence of immune escape at dominant SARS-CoV-2 killer T-cell epitope. **2022**,	5
459	Genomic surveillance reveals antibiotic resistance gene transmission via phage recombinases within sheep mastitis-associated Streptococcus uberis. **2022**, 18,	0
458	Cellular stress affects the fate of microbial resistance to folate inhibitors in treatment wetlands. **2022**, 845, 157318	0
457	Genetic redundancy of 4-hydroxybenzoate 3-hydroxylase genes ensures the catabolic safety of Pigmentiphaga sp. H8 in 3-bromo-4-hydroxybenzoate-contaminated habitats.	
456	Butterfly–parasitoid–hostplant interactions in Western Palaearctic Hesperiidae: a DNA barcoding reference library.	3
455	Genome Wide Association Mapping in Sunflower (Helianthus annuus L.) reveals Common Loci and Putative Candidate Genes for resistance to Diaporthe gulyae and D. helianthi causing Phomopsis Stem Canker.	0
454	Differential survival of potentially pathogenic, septicemia- and meningitis-causing E. coli across the wastewater treatment train. **2022**, 5,	
453	Ancient herpes simplex 1 genomes reveal recent viral structure in Eurasia. **2022**, 8,	0

452	Climate Ecology as a Driver of Global Breeding Periods in Anurans.	
451	Acquisition and evolution of enhanced mutualism�n underappreciated mechanism for invasive success?.	0
450	A joint learning approach for genomic prediction in polyploid grasses. **2022**, 12,	0
449	Parallel duplication and loss of aquaporin-coding genes during the �out of the sea�transition paved the way for animal terrestrialization.	
448	Highly pathogenic avian influenza H5N1 virus infections in wild red foxes (Vulpes vulpes) show neurotropism and adaptive virus mutations.	1
447	Novel internalin P homologs in Listeria. **2022**, 8,	
446	covSampler: A subsampling method with balanced genetic diversity for large-scale SARS-CoV-2 genome data sets. **2022**, 8,	0
445	Stemness Analysis Uncovers That The Peroxisome Proliferator-Activated Receptor Signaling Pathway Can Mediate Fatty Acid Homeostasis In Sorafenib-Resistant Hepatocellular Carcinoma Cells. 12,	0
444	Robust Phylodynamic Analysis of Genetic Sequencing Data from Structured Populations. **2022**, 14, 1648	
443	Biogas slurry application alters soil properties, reshapes the soil microbial community, and alleviates root rot of Panax notoginseng. 10, e13770	
442	The Structures of the Steroid Binding CYP142 Cytochrome P450 Enzymes from Mycobacterium ulcerans and Mycobacterium marinum. **2022**, 8, 1606-1617	0
441	RNA viromes from terrestrial sites across China expand environmental viral diversity. **2022**, 7, 1312-1323	1
440	Body mass and cell size shape the tolerance of fishes to low oxygen in a temperature-dependent manner.	3
439	Characterization of resistance to newer antimicrobials among carbapenem-resistant Klebsiella pneumoniae in the post�acute-care setting. 1-4	
438	In search of the Aplysia immunome: an in silico study. **2022**, 23,	0
437	Seed Development and Protein Accumulation Patterns in Faba Bean (Vicia faba, L.). **2022**, 70, 9295-9304	0
436	Triazole resistance in Aspergillus fumigatus isolates in Africa: a systematic review. **2022**, 60,	0
435	Constraints on the evolution of toxin-resistant Na,K-ATPases have limited dependence on sequence divergence. **2022**, 18, e1010323	1

434	Freshwater macrophytes harbor viruses representing all five major phyla of the RNA viral kingdom Orthornavirae. 10, e13875	0
433	Revving an Engine of Human Metabolism: Activity Enhancement of Triosephosphate Isomerase via Hemi-Phosphorylation.	0
432	Genome-wide identification and expression analysis of the SlNAC gene family in tomato based on a high-quality genome.	
431	Exploring strain diversity of dominant human skin bacterial species using single-cell genome sequencing. 13,	0
430	State-dependent evolutionary models reveal modes of solid tumor growth.	
429	Improved detection and classification of plasmids from circularized and fragmented assemblies.	1
428	Genome-resolved community structure and function of freshwater bacteria at a continental scale.	0
427	Genomic epidemiology of the first two waves of SARS-CoV-2 in Canada. 11,	1
426	Identification of early quassinoid biosynthesis in the invasive tree of heaven (Ailanthus altissima) confirms evolutionary origin from protolimonoids. 13,	1
425	Molecular characterization of circulating Salmonella Typhi strains in an urban informal settlement in Kenya. **2022**, 16, e0010704	0
424	Managing genetic diversity in breeding programs of small populations: the case of French local chicken breeds. **2022**, 54,	0
423	Phylogenomic analysis of the parrots of the world distinguishes artifactual from biological sources of gene tree discordance.	0
422	Evolutionary analysis of swimming speed in early vertebrates challenges the New Head Hypothesis**2022**, 5,	0
421	Phylodynamics of SARS-CoV-2 transmissions in France, Europe and the world during 2020.	
420	Dolichospermum blooms in Lake Superior: DNA-based approach provides insight to the past, present and future of blooms. **2022**,	0
419	Dysfunction of Ras-GAP protein AfgapA contributes to hypoxia fitness in Aspergillus fumigatus.	
418	Epidemiology and genomic analysis of Klebsiella oxytoca from a single hospital network in Australia. **2022**, 22,	2
417	SCONCE2: jointly inferring single cell copy number profiles and tumor evolutionary distances. **2022**, 23,	

416	Genome-wide characterization of the common bean kinome: catalog and insights into expression patterns and genetic organization.	0
415	Leek Yellow Stripe Virus Can Adjust for Host Adaptation by Trimming the N-Terminal Domain to Allow the P1 Protein to Function as an RNA Silencing Suppressor. **2022**, 38, 383-394	
414	First detection and origin of multi-drug resistant Klebsiella pneumoniae ST15 harboring and OXA-48 in South America. **2022**,	
413	Genomic evidence of contemporary hybridization between Schistosoma species. **2022**, 18, e1010706	0
412	Genomes from Uncultivated Pelagiphages Reveal Multiple Phylogenetic Clades Exhibiting Extensive Auxiliary Metabolic Genes and Cross-Family Multigene Transfers.	1
411	Dynamics of transposable element accumulation in the non-recombining regions of mating-type chromosomes in anther-smut fungi.	
410	Identification of clinical and ecological determinants of strain engraftment after fecal microbiota transplantation using metagenomics. **2022**, 3, 100711	0
409	Pericentriolar matrix (PCM) integrity relies on cenexin and polo-like kinase (PLK)1. **2022**, 33,	
408	Multilayered Networks of SalmoNet2 Enable Strain Comparisons of the Salmonella Genus on a Molecular Level.	0
407	Phylogenetic lineages of tuberculosis isolates and their association with patient demographics in Tanzania. **2022**, 23,	
406	Metagenomics combined with activity-based proteomics point to gut bacterial enzymes that reactivate mycophenolate. **2022**, 14,	0
405	Lineage BA.2 Dominated the Omicron SARS-CoV-2 Epidemic Wave in the Philippines.	0
404	Transcriptome and Population Structure of Glassy-winged Sharpshooters (Homalodisca vitripennis) with Varying Insecticide Resistance in Southern California.	
403	Comparative genomics of Streptococcus oralis identifies large scale homologous recombination and a genetic variant associated with infection.	
402	The landscape in the gut microbiome of long-lived families reveals new insights on longevity and aging relevant neural and immune function. **2022**, 14,	1
401	Vibrio cholerae circulating throughout a mass vaccination campaign in the Forcibly Displaced Myanmar National population in Coxs Bazar, Bangladesh.	
400	Phylotranscriptomics reveals the reticulate evolutionary history of a widespread diatom species complex.	0
399	Molecular Epidemiology of Mycobacterium abscessus Isolates Recovered from German Cystic Fibrosis Patients.	0

398	Leaf side determines the relative importance of dispersal versus host filtering in the phyllosphere microbiome.	
397	Contrasting long-term dynamics of antimicrobial resistance and virulence plasmids in Salmonella Typhimurium from animals. **2022**, 8,	
396	Fundamental metabolic strategies of heterotrophic bacteria.	
395	Understanding early pandemic SARS-CoV-2 transmission in a medical center by incorporating public sequencing databases to mitigate bias.	0
394	Metagenomic data from cerebrospinal fluid permits tracing the origin and spread of Neisseria meningitidis CC4821 in China. **2022**, 5,	
393	Disentangling the Role of Poultry Farms and Wild Birds in the Spread of Highly Pathogenic Avian Influenza Virus in Europe.	
392	A multi-omics framework reveals strawberry flavor genes and their regulatory elements.	0
391	Integrating Genome-Resolved Metagenomics with Trait-Based Process Modeling to Determine Biokinetics of Distinct Nitrifying Communities within Activated Sludge. **2022**, 56, 11670-11682	0
390	Cobamide Sharing Is Predicted in the Human Skin Microbiome.	0
389	Skimming for barcodes: rapid production of mitochondrial genome and nuclear ribosomal repeat reference markers through shallow shotgun sequencing. 10, e13790	1
388	High-throughput nanopore sequencing of Treponema pallidum tandem repeat genes arp and tp0470 reveals clade-specific patterns and recapitulates global whole genome phylogeny.	
387	Massive expansion of P-selectin genes in two Venerida species, Sinonovacula constricta and Mercenaria mercenaria: evidence from comparative genomics of Bivalvia. **2022**, 23,	0
386	Andrographolide exerted anti-inflammatory effects thereby reducing sex hormone synthesis in LPS-induced female rats, but had no effect on hormone production in healthy ones. 13,	0
385	Genomic Surveillance of Carbapenem-Resistant Klebsiella pneumoniae from a Major Public Health Hospital in Singapore.	0
384	Genome-centric metagenomics insights into functional divergence and horizontal gene transfer of denitrifying bacteria in anammox consortia. **2022**, 224, 119062	0
383	Identification of genes involved in oleoresin biosynthesis in Pinus massoniana through the combination of SMRT and Illumina sequencing. **2022**, 188, 115553	0
382	Identification and characterization of a recombinant cysteine peptidase (AsCathL) from leaf-cutting ant Atta sexdens Linnaeus, 1758 (Hymenoptera, Formicidae). **2023**, 201, 106174	0
381	Carbon Substrate Selects for Different Lineages of N2O Reducing Communities in Soils Under Anoxic Conditions.	0

380	Metagenomic approaches for understanding microbial communities in contaminated environments: Bioinformatic tools, case studies and future outlook. **2023**, 103-156	0
379	Development and Characterization of Microsatellite Markers Based on the Chloroplast Genome of Tree Peony. **2022**, 13, 1543	0
378	Rhodnius (St□ 1859) (Hemiptera, Triatominae) genus in Bolivian Amazonia: a risk for human populations?. **2022**, 15,	0
377	Differential Oral Microbial Input Determines Two Microbiota Pneumo-Types Associated with Health Status. 2203115	0
376	Genomic Characterization of Salmonella Typhimurium Isolated from Guinea Pigs with Salmonellosis in Lima, Peru. **2022**, 10, 1726	0
375	Dynamic changes in the transcriptome landscape of Arabidopsis thaliana in response to cold stress. 13,	0
374	Genomic characterization of Staphylococcus aureus isolates causing osteoarticular infections in otherwise healthy children. **2022**, 17, e0272425	0
373	Myotis fimbriatus Virome, a Window to Virus Diversity and Evolution in the Genus Myotis. **2022**, 14, 1899	0
372	The Importance of Contact Zones for Distinguishing Interspecific from Intraspecific Geographic Variation.	0
371	Data-driven, participatory characterization of farmer varieties discloses teff breeding potential under current and future climates. 11,	0
370	Functional characterization of putative ecdysone transporters in lepidopteran pests. **2022**, 103830	1
369	The genus Serratia revisited by genomics. **2022**, 13,	1
368	Evolution of the vls Antigenic Variability Locus of the Lyme Disease Pathogen and Development of Recombinant Monoclonal Antibodies Targeting Conserved VlsE Epitopes.	1
367	Immune Imprinting Drives Human Norovirus Potential for Global Spread.	1
366	The evolution of conspicuousness in frogs: When to signal toxicity?.	0
365	SPREAD 4: online visualization of pathogen phylogeographic reconstructions.	0
364	Genomic Sequencing and Phylogenomics of Cowpox Virus. **2022**, 14, 2134	2
363	Establishing farm dust as a useful viral metagenomic surveillance matrix. **2022**, 12,	1

362	Discovery and Genomic Characterization of a Novel Henipavirus, Angavokely Virus, from Fruit Bats in Madagascar. **2022**, 96,	0
361	Persistence of Rare Salmonella Typhi Genotypes Susceptible to First-Line Antibiotics in the Remote Islands of Samoa.	1
360	A Preliminary Molecular Phylogeny for Stiria (Noctuidae, Stiriinae) and Description of a New Species from Texas. **2022**, 76,	0
359	Geological drivers of diversification in Papuan microhylid frogs.	0
358	High-throughput nanopore sequencing of Treponema pallidum tandem repeat genes arp and tp0470 reveals clade-specific patterns and recapitulates global whole genome phylogeny. 13,	0
357	Extended genomic analyses of the broad-host-range phages vB_KmiM-2Di and vB_KmiM-4Dii reveal slopekviruses have highly conserved genomes. **2022**, 168,	0
356	Transcriptomic heterochrony and completely cleistogamous flower development in the mycoheterotrophic orchid Gastrodia.	0
355	Potential of conserved antigenic sites in development of universal SARS-like coronavirus vaccines. 13,	0
354	Identification of Signatures of Selection for Litter Size and Pubertal Initiation in Two Sheep Populations. **2022**, 12, 2520	0
353	Endogenous viral elements in shrew genomes provide insights into Pestivirus ancient history.	0
352	Natural recombination among Type I restriction-modification systems creates diverse genomic methylation patterns among Xylella fastidiosa strains.	0
351	Distinct origins and transmission pathways of blaKPC Enterobacterales across three U.S. states.	0
350	Associations between brood size, gut microbiome diversity and survival in great tit (Parus major) nestlings.	0
349	A variable gene family encoding nodule-specific cysteine-rich peptides in pea (Pisum sativum L.). 13,	0
348	Orthologous microsatellites, transposable elements, and DNA deletions correlate with generation time and body mass in neoavian birds. **2022**, 8,	0
347	Genome of elegance coral Catalaphyllia jardinei (Euphylliidae). 9,	0
346	Colonization dynamics of extended-spectrum beta-lactamase-producing Enterobacterales in the gut of Malawian adults. **2022**, 7, 1593-1604	0
345	The likely extinction of hundreds of palm species threatens their contributions to people and ecosystems.	1

344	Characterizing Antimicrobial Resistance in Clinically Relevant Bacteria Isolated at the Human/Animal/Environment Interface Using Whole-Genome Sequencing in Austria. **2022**, 23, 11276	0
343	Genetic Diversity of Actinobacillus pleuropneumoniae Serovars in Hungary. **2022**, 9, 511	0
342	A global phylogenomic and metabolic reconstruction of the large intestine bacterial community of domesticated cattle. **2022**, 10,	0
341	The genetic mechanisms underlying the convergent evolution of pollination syndromes in the Neotropical radiation of Costus L.. 13,	0
340	Meta-transcriptomics reveals potential virus transfer between Aedes communis mosquitoes and their parasitic water mites.	0
339	Carbohydrate utilization by the gut microbiome determines host health responsiveness to whole grain type and processing methods. **2022**, 14,	0
338	Dynamics of SARS-CoV-2 Variants of Concern in Vaccination Model City in the State of Sao Paulo, Brazil. **2022**, 14, 2148	1
337	Bacterial composition in Swedish raw drinking water reveals three major interacting ubiquitous metacommunities. **2022**, 11,	0
336	The rapid radiation of Bomarea (Alstroemeriaceae: Liliales), driven by the rise of the Andes.	0
335	Guidelines for standardizing the application of discriminant analysis of principal components to genotype data.	0
334	Population structure and evolution of Salmonella enterica serotype Typhi in Zimbabwe before a typhoid conjugate vaccine immunization campaign.	0
333	Evolutionary inference across eukaryotes identifies universal features shaping organelle gene retention. **2022**,	1
332	Memory persistence and differentiation into antibody-secreting cells accompanied by positive selection in longitudinal BCR repertoires. 11,	0
331	Emergence and Persistent Dominance of Omicron BA.2.3.7 Variant in Community Outbreaks in Taiwan.	0
330	Ggtree : A serialized data object for visualization of a phylogenetic tree and annotation data.	1
329	Investigating CRISPR spacer targets and their impact on genomic diversification of Streptococcus mutans. 13,	1
328	Plasmodium falciparum Genetic Diversity in Coincident Human and Mosquito Hosts.	0
327	Comparative genomics of Rothia species reveals diversity in novel biosynthetic gene clusters and ecological adaptation to different eukaryotic hosts and host niches. **2022**, 8,	0

326	Functional and phylogenetic responses of motile cryptofauna to habitat degradation.	1
325	tidy tree: a new layout for phylogenetic trees.	0
324	Population genomic analysis of the Speckled Dace species complex (Rhinichthys osculus) identifies three distinct lineages in California.	1
323	Epidemiology and infection control of Methicillin-resistant Staphylococcus aureus in a German tertiary neonatal intensive and intermediate care unit: A retrospective study (2013–2020). **2022**, 17, e0275087	0
322	Identification of a novel aminoglycoside O-nucleotidyltransferase AadA33 in Providencia vermicola. 13,	0
321	Microscopic marine invertebrates are reservoirs for cryptic and diverse protists and fungi. **2022**, 10,	0
320	Integrating Phylogenetic and Functional Data in Microbiome Studies.	0
319	Polyphyly in widespread Salmonella enterica serovars and using genomic proximity to choose the best reference genome for bioinformatics analyses. 10,	1
318	Discovering candidate SNPs for resilience breeding of red clover. 13,	0
317	Back-to-Africa introductions of Mycobacterium tuberculosis as the main cause of tuberculosis in Dar es Salaam, Tanzania.	0
316	Generalist nematodes dominate the nemabiome of roe deer in sympatry with sheep at a regional level. **2022**,	0
315	A comprehensive database of amphibian heat tolerance. **2022**, 9,	0
314	Novel trends of genome´evolution in highly complex tropical sponge microbiomes. **2022**, 10,	0
313	Mating strategy predicts gene presence/absence patterns in a genus of simultaneously hermaphroditic flatworms.	0
312	A high-quality Buxus austro-yunnanensis (Buxales) genome provides new insights into karyotype evolution in early eudicots. **2022**, 20,	0
311	Activation of TnSmu1, an integrative and conjugative element, by an ImmR-like transcriptional regulator in Streptococcus mutans. **2022**, 168,	0
310	Cortinarius subgenus Leprocybe (Agaricales) in New Zealand. 1-22	0
309	Host Phylogeny Shapes Viral Transmission Networks in an Island Ecosystem.	0

308	Characterization and Identification of Probiotic Features in Lacticaseibacillus Paracasei Using a Comparative Genomic Analysis Approach.	0
307	Haplotype assignment of longitudinal viral deep-sequencing data using co-variation of variant frequencies.	0
306	Marine surf to freshwater: a molecular phylogeny of Donacidae (Bivalvia: Heterodonta). **2022**, 36, 984	0
305	The Perennial Horse Gram (Macrotyloma axillare) Genome, Phylogeny, and Selection Across the Fabaceae. **2022**, 255-279	0
304	Phylogeny, taxonomy, and character evolution in Entoloma subgenus Nolanea. **2022**,	0
303	Horizontal transfer and phylogenetic distribution of the immune evasion factor tarP. 13,	0
302	Leptospira enrichment culture followed by ONT metagenomic sequencing allows better detection of Leptospira presence and diversity in water and soil samples. **2022**, 16, e0010589	0
301	Comparative transcriptomic analysis of normal and abnormal in vitro flowers in Cymbidium nanulum Y. S. Wu et S. C. Chen identifies differentially expressed genes and candidate genes involved in flower formation. 13,	0
300	Detection of maternal transmission of resistant Gram-negative bacteria in a Cambodian hospital setting.	0
299	A divide-and-conquer approach for genomic prediction in rubber tree using machine learning. **2022**, 12,	0
298	Crop management shapes the diversity and activity of DNA and RNA viruses in the rhizosphere. **2022**, 10,	0
297	Barley FASCIATED EAR genes determine inflorescence meristem size and yield traits. **2022**,	0
296	Multiple waves of viral invasions in Symbiodiniaceae algal genomes.	0
295	Genome-wide association study reveals novel QTLs and candidate genes for seed vigor in rice. 13,	0
294	Population genomics of Puccinia graminis f.sp. tritici highlights the role of admixture in the origin of virulent wheat rust races. **2022**, 13,	0
293	Novel viral and microbial species in a translocated Toutouwai (Petroica longipes) population from Aotearoa/New Zealand. **2022**, 4,	0
292	Transcriptome and population structure of glassy-winged sharpshooters (Homalodisca vitripennis) with varying insecticide resistance in southern California. **2022**, 23,	0
291	Genomic and phylogenomic insights into the family Streptomycetaceae lead to the proposal of six novel genera. **2022**, 72,	1

290	Can the extinction risk of Irish vascular plants be predicted using leaf traits?.	0
289	Culture collections as a source of historic strains for genomic studies in plant pathology.	0
288	Regional epidemic dynamics and Delta variant diversity resulted in varying rates of spread of Omicron-BA.1 in Mexico.	0
287	Genomic epidemiology of SARS-CoV-2 within households in coastal Kenya: a case ascertained cohort study.	0
286	Small islands and large biogeographic barriers have driven contrasting speciation patterns in Indo-Pacific sunbirds (Aves: Nectariniidae).	0
285	Genomic Epidemiology Reveals the Circulation of the Chikungunya Virus East/Central/South African Lineage in Tocantins State, North Brazil. **2022**, 14, 2311	0
284	New insights into the novel sequences of the chicken pangenome by liquid chip.	0
283	Cell size is a key ecological trait associated with biogeographic patterns of microbial eukaryotes in coastal waters. 9,	0
282	Metabolic genes on conjugative plasmids are highly prevalent in Escherichia coli and can protect against antibiotic treatment.	0
281	Thermal proteome profiling reveals Haemonchus orphan protein HCO_011565 as a target of the nematocidal small molecule UMW-868. 13,	0
280	Strain and serovar variants ofSalmonella entericaexhibit diverse tolerance to food chain-related stress.	0
279	Tumour microbiomes and Fusobacterium genomics in Vietnamese colorectal cancer patients. **2022**, 8,	0
278	Tree2GD: a phylogenomic method to detect large-scale gene duplication events.	0
277	Continued evolution of the Eurasian avian-like H1N1 swine influenza viruses in China.	0
276	Draft Genome Resource for the Forest Pathogen Coniferiporia weirii a Pathogen of Thuja plicata and Callitropsis nootkatensis.	0
275	Increased cases of influenza C virus in children and adults in Austria, 2022.	0
274	Biogeographical events, not cospeciation, might be the main drivers in the historical association between Noctiliostrebla species (Streblidae) and their bulldog bat hosts.	0
273	Incipiently social carpenter bees (Xylocopa) host distinctive gut bacterial communities and display geographical structure as revealed by full-length PacBio 16S rRNA sequencing.	1

272	Comparative Genomics of Streptococcus oralis Identifies Large Scale Homologous Recombination and a Genetic Variant Associated with Infection.	0
271	ggmotif: An R Package for the extraction and visualization of motifs from MEME software. **2022**, 17, e0276979	0
270	Application of ecosystem-specific reference databases for increased taxonomic resolution in soil microbial profiling. 13,	0
269	Antigenic Characterization and Pandemic Risk Assessment of North American H1 Influenza A Viruses Circulating in Swine.	0
268	Genetic structure of Plasmopara halstedii populations across Europe and South Russia.	1
267	Genomic evolution of SARS-CoV-2 in Reunion Island. **2022**, 106, 105381	0
266	Phylogeography, hybridization, and species discovery in the Etheostoma nigrum complex (Percidae: Etheostoma: Boleosoma). **2023**, 178, 107645	0
265	Active microbial communities during biodegradation of biodegradable plastics by mesophilic and thermophilic anaerobic digestion. **2023**, 443, 130208	1
264	De novo transcriptome assembly and identification of G-Protein-Coupled-Receptors (GPCRs) in two species of monogenean parasites of fish. **2022**, 29, 51	1
263	Opposing directions of stage-specific body shape change in a close relative of C. elegans. **2022**, 7,	0
262	Immune landscape of isocitrate dehydrogenase stratified human gliomas.	0
261	The media drives public interest in invasive plants in the US.	0
260	Filtering artifactual signal increases support for Xenacoelomorpha and Ambulacraria sister relationship in the animal tree of life. **2022**,	0
259	Divergent SARS-CoV-2 variant emerges in white-tailed deer with deer-to-human transmission.	6
258	Efficient Tracing of the SARS-CoV-2 Omicron Variants in Santa Barbara County Using a Rapid Quantitative Reverse Transcription PCR Assay. **2022**, 12, 2805	0
257	Phylogenetic analyses of Salmonella detected along the broiler production chain in Trinidad and Tobago. **2022**, 102322	0
256	Whole-Genome Sequencing-Based Species Classification, Multilocus Sequence Typing, and Antimicrobial Resistance Mechanism Analysis of the Enterobacter cloacae Complex in Southern China.	0
255	Combining phylogenomic and morphological data reveals new patterns of diversity in the national tree of Brasil, Paubrasilia echinata.	0

254	Is there hybridisation between diploid and tetraploid Euphrasia in a secondary contact zone?.	0
253	Genetic Dissection of Phosphorus Use Efficiency and Genotype-by-Environment Interaction in Maize. **2022**, 23, 13943	0
252	Targeted metagenomics using probe capture detects a larger diversity of nitrogen and methane cycling genes in complex microbial communities than traditional metagenomics.	0
251	Functional validation of transposable element derivedcis-regulatory elements in Atlantic salmon.	0
250	Increased phage resistance through lysogenic conversion accompanying emergence of monophasic Salmonella Typhimurium ST34 pandemic strain. **2022**, 8,	0
249	Diversity of rhizobia, symbiotic effectiveness, and potential of inoculation in Acacia mearnsii seedling production.	0
248	Detection and phylogenetic assessment of PRV-1 via sampling of biological materials released from salmon farms in British Columbia.	0
247	Virus classification based on in-depth sequence analyses and development of demarcation criteria using the Betaflexiviridae as a case study. **2022**, 103,	0
246	Epidemiological and genetic characteristics of respiratory syncytial virus infection in children from Hangzhou after the peak of COVID-19. **2023**, 158, 105354	0
245	Genome sequence, phylogenetic analysis, and structure-based annotation reveal metabolic potential of Chlorella sp. SLA-04. **2023**, 69, 102943	0
244	Genetic potential for exopolysaccharide synthesis in activated sludge bacteria uncovered by genome-resolved metagenomics. **2023**, 229, 119485	0
243	Carbon substrate selects for different lineages of N2O reducing communities in soils under anoxic conditions. **2023**, 177, 108909	0
242	Independent recruitment of FRUITFULL-like transcription factors in the convergent origins of vernalization-responsive grass flowering. **2023**, 179, 107678	0
241	Structural evolution of an amphibian-specific globin: A computational evolutionary biochemistry approach. **2023**, 45, 101055	0
240	Genome-wide characterization of the common bean kinome: Catalog and insights into expression patterns and genetic organization. **2023**, 855, 147127	0
239	Divergence times of the Rhoadsia clade (Characiformes: Characidae). **2022**, 20,	0
238	Effects of Klebsiella pneumoniae Bacteriophages on IRAK3 Knockdown/Knockout THP-1 Monocyte Cell Lines. **2022**, 14, 2582	0
237	Aquatic insects differentially affect lake sturgeon larval phenotypes and egg surface microbial communities. **2022**, 17, e0277336	0

236	Rouxiella badensis, a new bacterial pathogen of onion causing bulb rot. 13,	0
235	Molecular detection and characterisation of the first Japanese encephalitis virus belonging to genotype IV acquired in Australia. **2022**, 16, e0010754	2
234	Facultative symbionts are potential agents of symbiont-mediated RNAi in aphids. 13,	1
233	Associating Biological Activity and Predicted Structure of Antimicrobial Peptides from Amphibians and Insects. **2022**, 11, 1710	0
232	Genome Sequence of a Recombinant SARS-CoV-2 Lineage XAM (BA.1.1/BA.2.9) Strain from a Clinical Sample in Santo Domingo, Dominican Republic.	0
231	Gut to lung translocation and antibiotic mediated selection shape the dynamics of Pseudomonas aeruginosa in an ICU patient. **2022**, 13,	1
230	Functional diversification despite structural congruence in the HipBST toxin-antitoxin system ofLegionella pneumophila.	0
229	sitePath: a visual tool to identify polymorphism clades and help find fixed and parallel mutations. **2022**, 23,	0
228	Spatial scale influences taxon conservation in the eukaryotic virome of a mosquito.	0
227	Re-emergence of cholera in Haiti linked to environmentalV. choleraeO1 Ogawa strains.	1
226	Not all pathways are the same unique adaptations to submerged environments emerge from comparative seagrass genomics.	0
225	SIEVE: joint inference of single-nucleotide variants and cell phylogeny from single-cell DNA sequencing data. **2022**, 23,	0
224	Transcriptome mining extends the host range of theFlaviviridaeto non-bilaterians.	0
223	Many-to-one function of cat-like mandibles highlights a continuum of sabre-tooth adaptations. **2022**, 289,	0
222	Investigating the genetic diversity of H5 avian influenza in the UK 2020-2022.	0
221	smot: a python package and CLI tool for contextual phylogenetic subsampling. **2022**, 7, 4193	1
220	Highly contiguous genome assembly and population sequencing reveal three distinct populations and signatures of insecticide resistance ofTuta absolutain Latin America.	0
219	Microbiome and metagenomic analysis of Lake Hillier Australia reveals pigment-rich polyextremophiles and wide-ranging metabolic adaptations. **2022**, 17,	0

218	Genomic landscape of the SARS-CoV-2 pandemic in Brazil suggests an external P.1 variant origin. 13,	0
217	Genomic comparison of two strains of Mycobacterium avium subsp. paratuberculosis with contrasting pathogenic phenotype. **2022**, 102299	0
216	Human microbiota drives hospital-associated antimicrobial resistance dissemination in the urban environment and mirrors patient case rates. **2022**, 10,	0
215	A quantitative global test of the complexity trade-off hypothesis: the case of nominal and verbal grammatical marking. **2022**,	0
214	Genetic Diversity and Population Differentiation of Dongxiang Wild Rice (Oryza rufipogon Griff.) Based on SNP Markers. **2022**, 12, 3056	0
213	High prevalence of ArmA-16S rRNA methyltransferase among aminoglycoside-resistant Klebsiella pneumoniae bloodstream isolates. **2022**, 71,	0
212	Deciphering the role of host species for two Mycobacterium bovis genotypes from the European 3 clonal complex circulation within a cattle-badger-wild boar multihost system. **2023**, 12,	0
211	Targeted single-cell genomics reveals novel host adaptation strategies of the symbiotic bacteria Endozoicomonas in Acropora tenuis coral. **2022**, 10,	0
210	Transcriptome mining extends the host range of the Flaviviridae to non-bilaterians.	0
209	Genome size does not influence extinction risk in the world's amphibians.	0
208	Dynamics of extended-spectrum cephalosporin resistance genes in Escherichia coli from Europe and North America. **2022**, 13,	1
207	Identification of a covert evolutionary pathway between two protein folds.	1
206	Pyruvate: Ferredoxin oxidoreductase is involved in IgA-related microbiota dysbiosis and intestinal inflammation. 13,	0
205	The bacteria of Yangtze finless porpoise (Neophocaena asiaeorientalis asiaeorientalis) are site-specific and distinct from freshwater environment. 13,	0
204	Alternative splicing and genetic variation of mhc-e: implications for rhesus cytomegalovirus-based vaccines. **2022**, 5,	0
203	Ecology, Not Host Phylogeny, Shapes the Oral Microbiome in Closely Related Species. **2022**, 39,	0
202	Adaptive immune responses to SARS-CoV-2 persist in the pharyngeal lymphoid tissue of children.	1
201	Molecular Basis of the Toxigenic Vibrio cholerae O1 Serotype Switch from Ogawa to Inaba in Haiti.	0

200	A Conserved, Serine-Rich Protein Plays Opposite Roles in N-Mediated Immunity against TMV and N-Triggered Cell Death. **2023**, 15, 26	0
199	Effects of chronic exposure to arsenic on the fecal carriage of antibiotic-resistant Escherichia coli among people in rural Bangladesh. **2022**, 18, e1010952	0
198	Genomic epidemiology of SARS-CoV-2 in Cambodia, January 2020 to February 2021.	0
197	A comprehensive list of bacterial pathogens infecting humans. **2022**, 168,	1
196	Changes in endemic patterns of respiratory syncytial virus infection in pediatric patients under the pressure of nonpharmaceutical interventions for COVID-19 in Beijing, China. **2023**, 95,	0
195	Using genetic data to identify transmission risk factors: Statistical assessment and application to tuberculosis transmission. **2022**, 18, e1010696	0
194	Occurrence and Genomic Characterization of mcr-1-Harboring Escherichia coli Isolates from Chicken and Pig Farms in Lima, Peru. **2022**, 11, 1781	0
193	Phylogenomics and the first higher taxonomy of Placozoa, an ancient and enigmatic animal phylum. 10,	0
192	Diversity, duplication, and genomic organization of homeobox genes in Lepidoptera. gr.277118.122	0
191	Mass Mortality Caused by Highly Pathogenic Influenza A(H5N1) Virus in Sandwich Terns, the Netherlands, 2022. **2022**, 28, 2538-2542	2
190	Spatial and Temporal Patterns of Genetic Diversity and Structure in Danish Populations of the Alcon Blue Butterfly Phengaris alcon (Denis & Schifferm□ler). **2022**, 14, 1098	0
189	Deciphering the determinants of recombinant protein yield across the human secretome.	0
188	A large population sample of African HIV genomes from the 1980s reveals a reduction in subtype D over time associated with propensity for CXCR4 tropism. **2022**, 19,	0
187	New perspectives on an old grouping: The genomic and phenotypic variability of Oxalobacter formigenes and the implications for calcium oxalate stone prevention. 13,	1
186	Climate warming triggers the emergence of native viruses in Iberian amphibians. **2022**, 25, 105541	0
185	Cyclospora cayetanensis comprises at least three species that cause human cyclosporiasis. 1-56	0
184	Conifer and broadleaf trees show a strong co-evolution with rhizosphere diazotrophic microbiome.	0
183	Characterization of Pantoea ananatis from rice planthoppers reveals a clade of rice-associated P. ananatis undergoing genome reduction. **2022**, 8,	0

182	Post-vaccine epidemiology of serotype 3 pneumococci identifies transformation inhibition through prophage-driven alteration of a non-coding RNA. **2022**, 14,	0
181	Evaluating the ecological hypothesis: early life salivary microbiome assembly predicts dental caries in a longitudinal case-control study. **2022**, 10,	0
180	Omicron-BA.1 Dispersion Rates in Mexico Varied According to the Regional Epidemic Patterns and the Diversity of Local Delta Subvariants. **2023**, 15, 243	0
179	Reconstructing the phylodynamic history and geographic spread of the CRF01_AE-predominant HIV-1 epidemic in the Philippines from PR/RT sequences sampled from 2008-2018.	0
178	Multivariate chemogenomic screening prioritizes new macrofilaricidal leads. **2023**, 6,	0
177	The complete ITS2 barcoding region for Strongylus vulgaris and Strongylus edentatus.	0
176	Origin Matters: Using a Local Reference Genome Improves Measures in Population Genomics.	0
175	Entry receptors □the gateway to alphavirus infection. **2023**, 133,	0
174	Pharmacological Profiling of a Brugia malayi Muscarinic Acetylcholine Receptor as a Putative Antiparasitic Target.	0
173	Genomic diversity, pathogenicity and antimicrobial resistance of Escherichia coli isolated from poultry in the southern United States. **2023**, 23,	0
172	Expanded catalogue of metagenome-assembled genomes reveals resistome characteristics and athletic performance-associated microbes in horse. **2023**, 11,	0
171	A comprehensive analysis of Usutu virus (USUV) genomes revealed lineage-specific codon usage patterns and host adaptations. 13,	0
170	Invasive Aedes japonicus Mosquitoes Dominate the Aedes Fauna Collected with Gravid Traps in Wooster, Northeastern Ohio, USA. **2023**, 14, 56	0
169	Metavirome of 31 tick species provides a compendium of 1,801 RNA virus genomes. **2023**, 8, 162-173	0
168	Gene gain facilitated endosymbiotic evolution of Chlamydiae. **2023**, 8, 40-54	0
167	Genetic diversity and population structure of barley landraces from Southern Ethiopia□ Gumer district: Utilization for breeding and conservation. **2023**, 18, e0279737	0
166	A deeply conserved protease, acylamino acid-releasing enzyme (AARE), acts in ageing in Physcomitrella and Arabidopsis. **2023**, 6,	0
165	The phenotype and genotype of fermentative microbes.	0

164	Competitiveness and symbiotic efficiency in alfalfa of Rhizobium favelukesii ORY1 strain in which homologous genes of peptidases HrrP and SapA that negatively affect symbiosis were identified. 4,	0
163	Genomic Epidemiology Linking Nonendemic Coccidioidomycosis to Travel. **2023**, 29, 110-117	0
162	Population genomics of Australian indigenous Mesorhizobium reveals diverse nonsymbiotic genospecies capable of nitrogen-fixing symbioses following horizontal gene transfer. **2023**, 9,	0
161	Diversity and evolution of computationally predicted T cell epitopes against human respiratory syncytial virus. **2023**, 19, e1010360	0
160	Silencing of a Pectin Acetylesterase (PAE) Gene Highly Expressed in Tobacco Pistils Negatively Affects Pollen Tube Growth. **2023**, 12, 329	0
159	Genetic diversity of North American popcorn germplasm and the effect of population structure on nicosulfuron response.	0
158	Comparative phyloproteomics identifies conserved plasmodesmal proteins.	0
157	Integrated transcriptome and proteome analyses reveal candidate genes for ginsenoside biosynthesis in Panax japonicus C. A. Meyer. 13,	0
156	A systematic outbreak investigation of SARS-CoV-2 transmission clusters in a tertiary academic care center.	0
155	Soil depth as a driver of microbial and carbon dynamics in a planted forest (Pinus radiata) pumice soil. **2023**, 9, 55-70	0
154	A Phylogeographic Analysis of Porcine Parvovirus 1 in Africa. **2023**, 15, 207	0
153	Discovery and Heterologous Expression of Unspecific Peroxygenases. **2023**, 13, 206	1
152	Genomic Epidemiology Linking Nonendemic Coccidioidomycosis to Travel. **2023**, 29, 110-117	0
151	A bittersweet fate: detection of serotype switching in Pseudomonas aeruginosa. **2023**, 9,	0
150	Natural Recombination among Type I Restriction-Modification Systems Creates Diverse Genomic Methylation Patterns among Xylella fastidiosa Strains.	0
149	Auxin- and pH-induced guttation in Phycomyces sporangiophores: relation between guttation and diminished elongation growth.	0
148	Effect of a karst system (France) on extended spectrum beta-lactamase (ESBL)-producing Escherichia coli. **2023**, 230, 119582	0
147	A combined approach detected novel species diversity and distribution of dinoflagellate cysts in the Yellow Sea, China. **2023**, 187, 114567	0

146	Effects of Phycosphere Bacteria on Their Algal Host Are Host Species-Specific and Not Phylogenetically Conserved. **2023**, 11, 62	0
145	The redlegged earth mite draft genome provides new insights into pesticide resistance evolution and demography in its invasive Australian range.	0
144	High number of SARS-CoV-2 persistent infections uncovered through genetic analysis of samples from a large community-based surveillance study.	0
143	Zoonotic Mutation of Highly Pathogenic Avian Influenza H5N1 Virus Identified in the Brain of Multiple Wild Carnivore Species. **2023**, 12, 168	0
142	Comparison of Chayote (Sechium edule (Jacq.) Sw.) Accessions from Mexico, Japan, and Myanmar Using Reproductive Characters and Microsatellite Markers. **2023**, 12, 476	0
141	Phylogeography as a Proxy for Population Connectivity for Spatial Modeling of Foot-and-Mouth Disease Outbreaks in Vietnam. **2023**, 15, 388	0
140	Association mapping in multiple yam species (Dioscorea spp.) of quantitative trait loci for yield-related traits.	0
139	Highly Pathogenic Avian Influenza H5N1 Virus Infections in Wild Red Foxes (Vulpes vulpes) Show Neurotropism and Adaptive Virus Mutations.	1
138	Parallel duplication and loss of aquaporin-coding genes during the out of the sea transition as potential key drivers of animal terrestrialization.	0
137	Updated Virophage Taxonomy and Distinction from Polinton-like Viruses. **2023**, 13, 204	0
136	Molecular Epidemiology and Diversity of SARS-CoV-2 in Ethiopia, 2020-2022.	0
135	Correlated evolution of social organization and lifespan in mammals. **2023**, 14,	0
134	Molecular and morphological analyses support recognition of Prostanthera volucris (Lamiaceae), a new species from the Central Tablelands of New South Wales. **2023**, 36, 1	0
133	Glacier-Fed Stream Biofilms Harbor Diverse Resistomes and Biosynthetic Gene Clusters.	0
132	APOBEC mutagenesis is a common process in normal human small intestine.	0
131	Strain and serovar variants of Salmonella enterica exhibit diverse tolerance to food chain-related stress. **2023**, 112, 104237	0
130	High Throughput Reproducible Literate Phylogenetic Analysis. **2022**,	0
129	How do fish functional traits respond to dams at the global scale?.	0

128	Molecular epidemiology of continued Plasmodium falciparum disease transmission after an outbreak in Ecuador. 4,	0
127	The Relationship between Cadmium-Related Gene Sequence Variations in Rice and Cadmium Accumulation. **2023**, 13, 800	0
126	The species coalescent indicates possible bat and pangolin origins of the COVID-19 pandemic. **2023** , 13,	0
125	Phylogeography of Francisella tularensis subspecies holarctica and epidemiology of tularemia in Switzerland. 14,	0
124	Rev-Rev Response Element Activity Selection Bias at the HIV Transmission Bottleneck.	0
123	Stratified microbial communities in Australia's only anchialine cave are taxonomically novel and drive chemotrophic energy production via coupled nitrogen-sulphur cycling.	0
122	Legume-wide comparative analysis of pod shatter locus PDH1 reveals phaseoloid specificity, high cowpea expression, and stress responsive genomic context.	0
121	Impact of pathogen genetics on clinical phenotypes in a population ofTalaromyces marneffeifrom Vietnam.	0
120	The global epidemiology and clinical diagnosis of Acanthamoeba keratitis. **2023**, 16, 841-852	0
119	Tracing recent outdoor geolocation by analyzing microbiota from shoe soles and shoeprints even after indoor walking. **2023**, 65, 102869	0
118	Mechanisms of carbon dioxide detection in the earthworm Dendrobaena veneta..	0
117	Activity and diversity of prophages harbored by wheat phyllosphere bacteria.	0
116	A 2D Geometric Morphometric Assessment of Chrono-Cultural Trends in Osseous Barbed Points of the European Final Palaeolithic and Early Mesolithic. **2023**, 9,	0
115	A Physcomitrella PIN protein acts in spermatogenesis and sporophyte retention. **2023**, 237, 2118-2135	0
114	Comparative genomic study of the Penicillium genus elucidates a diverse pangenome and 15 lateral gene transfer events. **2023**, 14,	0
113	Three-quarters of insect species are insufficiently represented by protected areas. **2023**, 6, 139-146	1
112	Modulation of Mechanical Properties of Short Bioinspired Peptide Materials by Single Amino-Acid Mutations. **2023**, 145, 3382-3393	0
111	MicrobiotaProcess: A comprehensive R package for deep mining microbiome. **2023**, 4, 100388	0

110	Targeting influenza A virus by splicing inhibitor herboxidiene reveals the importance of subtype-specific signatures around splice sites. **2023**, 30,	0
109	Genetic Structure and Phylogeography of Commercial Mytilus unguiculatus in China Based on Mitochondrial COI and Cytb Sequences. **2023**, 8, 89	0
108	Insights into the genome of Methylobacterium sp. NMS14P, a novel bacterium for growth promotion of maize, chili, and sugarcane. **2023**, 18, e0281505	0
107	An updated assessment of the soybean-Phytophthora sojae pathosystem.	0
106	The rubber tree kinome: Genome-wide characterization and insights into coexpression patterns associated with abiotic stress responses. 14,	0
105	Macroevolutionary diversity of traits and genomes in the model yeast genus Saccharomyces. **2023**, 14,	0
104	Temporal Dynamics of Genetically Heterogeneous Extended-Spectrum Cephalosporin ResistantEscherichia coliBloodstream Infections.	0
103	Public health interventions successfully mitigated multiple incursions of SARS-CoV-2 Delta variant in the Australian Capital Territory. **2023**, 151,	0
102	Plasmids manipulate bacterial behaviour through translational regulatory crosstalk. **2023**, 21, e3001988	0
101	Recent transposable element bursts are associated with the proximity to genes in a fungal plant pathogen. **2023**, 19, e1011130	0
100	Genome-Wide Identification and Characterization of the PPO Gene Family in Cotton (Gossypium) and Their Expression Variations Responding to Verticillium Wilt Infection. **2023**, 14, 477	0
99	Universal Dynamics of Microbial Communities in Full-Scale Textile Wastewater Treatment Plants and System Prediction by Machine Learning. **2023**, 57, 3345-3356	0
98	Phylotranscriptomics and evolution of key genes for terpene biosynthesis in Pinaceae. 14,	0
97	Deep haplotype analyses of target-site resistance locus ACCase in blackgrass enabled by pool-based amplicon sequencing.	0
96	A phylogenomic analysis of Lonicera and its bearing on the evolution of organ fusion.	0
95	Reconstruction of the tumor spatial microenvironment along the malignant-boundary-nonmalignant axis. **2023**, 14,	0
94	Sweepstakes reproductive success via pervasive and recurrent selective sweeps. 12,	0
93	DAISIEprep: an R package for the extraction and formatting of data for the island biogeography model DAISIE.	0

92	Histone deacetylase OsHDA706 increases salt tolerance via H4K5/K8 deacetylation of OsPP2C49 in rice.	0
91	Morphological disparity and evolutionary rates of cranial and postcranial characters in sloths (Mammalia, Pilosa, Folivora). **2023**, 66,	1
90	Detection of Streptococcus pyogenes M1UK in Australia and characterization of the mutation driving enhanced expression of superantigen SpeA. **2023**, 14,	0
89	Age-associated B cells are heterogeneous and dynamic drivers of autoimmunity in mice. **2023**, 220,	0
88	Optimizing hierarchical tree dissection parameters using historic epidemiologic data as ground truth**2023**, 18, e0282154	0
87	Comparative analysis of adenylate isopentenyl transferase genes in plant growth-promoting bacteria and plant pathogenic bacteria. **2023**, 9, e13955	0
86	SARS-CoV-2 Omicron variant of concern in the Seychelles: Introduction and spread. 8, 105	0
85	Biogeography and Genetic Diversity of Terrestrial Mites in the Ross Sea Region, Antarctica. **2023**, 14, 606	0
84	The Space Environment Activates Capsular Polysaccharide Production in Lacticaseibacillus rhamnosus Probio-M9 by Mutating the wze (ywqD) Gene. **2023**, 11,	0
83	Evaluation of the rbcL marker for metabarcoding of marine diatoms and inference of population structure of selected genera. 14,	0
82	Variety of rumen microbial populations involved in biohydrogenation related to individual milk fat percentage of dairy cows. 10,	0
81	Comparative Genomic and Transcriptomic Analyses Reveal the Impacts of Genetic Admixture in Kazaks, Uyghurs, and Huis. **2023**, 40,	0
80	Adulis and the transshipment of baboons during classical antiquity.	0
79	A molecular framework for grain number determination in barley. **2023**, 9,	0
78	Tapping Culture Collections for Fungal Endophytes: First Genome Assemblies for Three Genera and Five Species in theAscomycota. **2023**, 15,	0
77	Phylogenomics sheds new light on the drivers behind a long-lasting systematic riddle: the figwort family Scrophulariaceae.	0
76	Divergent vertebral formulae shape the evolution of axial complexity in mammals. **2023**, 7, 367-381	0
75	Combined analysis of transposable elements and structural variation in maize genomes reveals genome contraction outpaces expansion.	0

74	Comparative metagenomics reveals host-specific functional adaptation of intestinal microbiota across hominids.	o
73	The antiviral activity of a small molecule drug targeting the NSP1-ribosome complex against Omicron, especially in elderly patients. 13,	o
72	2b or not 2b? 2bRAD is an effective alternative to ddRAD for phylogenomics. **2023**, 13,	o
71	State-dependent evolutionary models reveal modes of solid tumour growth. **2023**, 7, 581-596	o
70	Dispersal versus local recruitment - the central role of seed banks for meta-populaton dynamics in an aquatic plant.	o
69	An Automated Bioinformatics Pipeline Informing Near-Real-Time Public Health Responses to New HIV Diagnoses in a Statewide HIV Epidemic. **2023**, 15, 737	o
68	Widespread Distribution and Evolution of Poxviral Entry-Fusion Complex Proteins in Giant Viruses. **2023**, 11,	o
67	Molecular Epidemiology and Diversity of SARS-CoV-2 in Ethiopia, 2020�2022. **2023**, 14, 705	o
66	Field Resistance to Rose Rosette Disease as Determined by Multi-Year Evaluations in Tennessee and Delaware. **2023**, 12, 439	o
65	Phylostems: a new graphical tool to investigate temporal signal of heterochronous sequences datasets. **2023**, 3,	o
64	Environmental factors and host genotype control foliar epiphytic microbial community of wild soybeans across China. 14,	o
63	Transmission of SARS-CoV-2 Omicron Variant under a Dynamic Clearance Strategy in Shandong, China. **2023**, 11,	o
62	Host shift and natural long-distance dispersal to an oceanic island of a host-specific parasite. **2023**, 19,	o
61	Phylogeny and Evolutionary Timescale of Muscidae (Diptera: Calyptratae) Inferred from Mitochondrial Genomes. **2023**, 14, 286	o
60	Population genomics unravels the Holocene history of bread wheat and its relatives. **2023**, 9, 403-419	o
59	Hyperactive nanobacteria with host-dependent traits pervade Omnitrophota. **2023**, 8, 727-744	o
58	A novel phylogenetic comparative method for evaluating the strength of branch-specific directional selection. **2023**, 77, 63-82	o
57	Systematic analysis of prophage elements in actinobacterial genomes reveals a remarkable phylogenetic diversity. **2023**, 13,	o

56	Chlorine Dioxide Reprograms Rhizosphere Microbial Communities to Enrich Interactions with Tobacco (Nicotiana tabacum). **2023**, 72, 47-60	0
55	Deciphering the mechanism of fungal pathogen-induced disease-suppressive soil.	0
54	CanFlyet: Habitat Zone and Diet Trait Dataset for Diptera Species of Canada and Greenland.	0
53	A Novel Strategy to Identify Endolysins with Lytic Activity against Methicillin-Resistant Staphylococcus aureus. **2023**, 24, 5772	0
52	Relatedness within colonies of three North American species of carpenter ants (Subgenus: Camponotus) and a comparison with relatedness estimates across Formicinae.	0
51	Perennial alternative crops for biogas production increase arthropod abundance and diversity after harvest - results of suction sampling and metabarcoding. 120, 59-69	0
50	A synthesis on the role of mycorrhizal fungal traits for understanding forest tree functions.	0
49	Metagenomic analysis of coastal Kenya female Aedes aegypti mosquito RNA metaviromes reveal presence of diverse insect specific viruses. 8, 136	0
48	Global scenario of the RmtE pan-aminoglycoside-resistance mechanism: emergence of the rmtE4 gene in South America associated with a hospital-related IncL plasmid. **2023**, 9,	0
47	Seed functional ecology in Brazilian rock outcrop vegetation: an integrative synthesis.	0
46	No evidence for associations between brood size, gut microbiome diversity and survival in great tit (Parus major) nestlings. **2023**, 5,	0
45	UropathogenicEscherichia colipopulation structure and antimicrobial susceptibility in Norfolk, UK.	0
44	Whitish truffles found in Finland: soil characteristics, and identification based on morphological and molecular properties. **2023**, 205,	0
43	Trends in Bacterial Pathogens of Bats: Global Distribution and Knowledge Gaps. **2023**, 2023, 1-17	0
42	Genomic dissection of endemic carbapenem resistance: metallo-beta-lactamase gene dissemination through clonal, plasmid and integron transfer pathways.	0
41	MetaInvert: A new soil invertebrate genome resource provides insights into below-ground biodiversity and evolution.	0
40	High-resolution single-molecule long-fragment rRNA gene amplicon sequencing of bacterial and eukaryotic microbial communities. **2023**, 3, 100437	0
39	The Baikal subtype of tick-borne encephalitis virus is evident of recombination between Siberian and Far-Eastern subtypes. **2023**, 17, e0011141	0

38	Karyotype Evolution in Triatominae (Hemiptera, Reduviidae): The Role of Chromosomal Rearrangements in the Diversification of Chagas Disease Vectors. **2023**, 24, 6350	0
37	Dwarfism and gigantism drive human-mediated extinctions on islands. **2023**, 379, 1054-1059	0
36	Genomic Diversity and Phenotypic Variation in Fungal Decomposers Involved in Bioremediation of Persistent Organic Pollutants. **2023**, 9, 418	0
35	Emigration patterns of motile cryptofauna and their implications for trophic functioning in coral reefs. **2023**, 13,	1
34	Streptococcus canis genomic epidemiology reveals the potential for zoonotic transfer. **2023**, 9,	0
33	Characterization of a Novel African Swine Fever Virus p72 Genotype II from Nigeria. **2023**, 15, 915	0
32	Back-to-Africa introductions of Mycobacterium tuberculosis as the main cause of tuberculosis in Dar es Salaam, Tanzania. **2023**, 19, e1010893	0
31	Plant domestication shapes rhizosphere microbiome assembly and metabolic functions. **2023**, 11,	0
30	Fauna-microbe diversity coupling lost in agricultural soils: Implications from the bacteria hidden in earthworm gut. **2023**,	0
29	Phylogenomic analysis uncovers a 9-year variation of Uganda influenza type-A strains from the WHO-recommended vaccines and other Africa strains. **2023**, 13,	0
28	ADAR1 Biology Can Hinder Effective Antiviral RNA Interference.	0
27	Quantifying Shared and Unique Gene Content across 17 Microbial Ecosystems.	0
26	Phyloecology ofnrfA-ammonifiers and their relative importance with denitrifiers in global terrestrial biomes.	0
25	Root phosphatase activity is a competitive trait affiliated with the conservation gradient in root economic space. **2023**, 10, 100111	0
24	Combining target enrichment and Sanger sequencing data to clarify the systematics of the diverse Neotropical butterfly subtribe Euptychiina (Nymphalidae, Satyrinae).	0
23	Sensory specializations drive octopus and squid behaviour. **2023**, 616, 378-383	0
22	A2TEA: Identifying trait-specific evolutionary adaptations. 11, 1137	0
21	Genome-wide gene birth-death dynamics are associated with diet breadth variation in Lepidoptera.	0

20	The SARS-CoV-2 Alpha variant was associated with increased clinical severity of COVID-19 in Scotland: A genomics-based retrospective cohort analysis. **2023**, 18, e0284187	0
19	Novel recombinant SARS-CoV-2 lineage detected through genomic surveillance in Wales, UK. **2023**, 9,	0
18	Detection of maternal transmission of resistant Gram-negative bacteria in a Cambodian hospital setting. 14,	0
17	PlantNLRatlas: a comprehensive dataset of full- and partial-length NLR resistance genes across 100 chromosome-level plant genomes. 14,	0
16	Anguillids in the upper NuSalween River, South-East Asia: species composition, distributions, natal sources and conservation implications. **2023**,	0
15	Unravelling the genetic diversity and population structure of common walnut in the Iranian Plateau. **2023**, 23,	0
14	Genomic features, antimicrobial susceptibility, and epidemiological insights into Burkholderia cenocepacia clonal complex 31 isolates from bloodstream infections in India. 13,	0
13	Genetic analysis of global faba bean diversity, agronomic traits and selection signatures. **2023**, 136,	0
12	The evolution of two transmissible cancers in Tasmanian devils. **2023**, 380, 283-293	0
11	A systematic outbreak investigation of SARS-CoV-2 transmission clusters in a tertiary academic care center. **2023**, 12,	0
10	Metagenomic Detection of Divergent Insect- and Bat-Associated Viruses in Plasma from Two African Individuals Enrolled in Blood-Borne Surveillance. **2023**, 15, 1022	0
9	Microbiome Diversity and Cellulose Decomposition Processes by Microorganisms on the Ancient Wooden Seawall of Qiantang River of Hangzhou, China.	0
8	Comparative genomics and phylogenomics of Campylobacter unveil potential novel species and provide insights into niche segregation. **2023**, 184, 107786	0
7	Phylodynamics of SARS-CoV-2 in France, Europe, and the world in 2020. 12,	0
6	Diverse but desolate landscape of gut microbial azoreductases: A rationale for idiopathic IBD drug response. **2023**, 15,	0
5	Range restricted old and young lineages show the southern Western Ghats to be both a museum and a cradle of diversity for woody plants. **2023**, 290,	0
4	The bacterial community of the European spruce bark beetle in space and time.	0
3	The Elevational Gradient of Bird Beta Diversity in the Meili Snow Mountains, Yunnan Province, China. **2023**, 13, 1567	0

2	Using Genomics To Investigate an Outbreak of Vancomycin-Resistant Enterococcus faecium ST78 at a Large Tertiary Hospital in Queensland.	0
1	The Principles of SARS-CoV-2 Intervariant Competition Are Exemplified in the Pre-Omicron Era of the Colombian Epidemic.	0