OrthoMCL: identification of ortholog groups for eukaryotic genomes

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213	Comparative Genome Analysis Reveals the Genomic Basis of Semi-Aquatic Adaptation in American Mink (Neovison vison). **2022**, 12, 2385	1
212	Transcriptome analysis provides insight into adaptive mechanisms of scallops under environmental stress. 9,	1

211	The complete mitochondrial genome of Isochrysis galbana harbors a unique repeat structure and a specific trans-spliced cox1 gene. 13,	0
210	First Report and Comparative Genomic Analysis of a Mycoplasma mycoides Subspecies capri HN-A in Hainan Island. **2022**, 10, 1908	0
209	The giant diploid faba genome unlocks variation in a global protein crop.	0
208	Cluster-driven evolution and modularity uncover paths of cholera emergence.	0
207	Development and Optimization of a Selective Whole-Genome Amplification To Study Plasmodium ovale Spp..	0
206	Jack of all trades: genome assembly of Wild Jack and comparative genomics of Artocarpus.	0
205	The genetic architecture of phenotypic diversity in the Betta fish (Betta splendens). **2022**, 8,	1
204	Elevation of Clavibacter michiganensis subsp. californiensis to species level as Clavibacter californiensis sp. nov., merging and re-classification of Clavibacter michiganensis subsp. chilensis and Clavibacter michiganensis subsp. phaseoli as Clavibacter phaseoli sp. nov. based on complete genome in silico analyses. **2022**, 72,	0
203	Transcriptome profiling of barley and tomato shoot and root meristems unravels physiological variations underlying photoperiodic sensitivity. **2022**, 17, e0265981	0
202	IPGA: A handy integrated prokaryotes genome and pan-genome analysis web service.	1
201	TOGA integrates gene annotation with orthology inference at scale.	1
200	The coral Acropora loripes genome reveals an alternative pathway for cysteine biosynthesis in animals. **2022**, 8,	0
199	De novo assembly and annotation of the CHOZN GS / genome supports high-throughput genome-scale screening.	0
198	Chromosome-level genome assembly and functional characterization of terpene synthases provide insights into the volatile terpenoid biosynthesis of Wurfbainia villosa.	0
197	The chromosome-level genome of Water-Wisteria establishes an ecological plant model and provides insight into the molecular mechanisms underlying heterophylly in amphibious plants.	0
196	A genome for Cissus illustrates features underlying the evolutionary success in dry savannas.	0
195	Chromosome-level genome assembly and resequencing of camphor tree (Cinnamomum camphora) provides insight into phylogeny and diversification of terpenoid and triglyceride biosynthesis of Cinnamomum.	0
194	Pan-Genome Analysis of Campylobacter: Insights on the Genomic Diversity and Virulence Profile.	0

193	Identification of Candidate Ice Nucleation Activity (INA) Genes in Fusarium avenaceum by Combining Phenotypic Characterization with Comparative Genomics and Transcriptomics. **2022**, 8, 958	0
192	A chromosome-level genome assembly of the potato grouper (Epinephelus tukula). **2022**, 114, 110473	0
191	Evolution of isoform-level gene expression patterns across tissues during lotus species divergence.	0
190	Pan-genome evolution and its association with divergence of metabolic functions in Bifidobacterium genus. **2022**, 38,	0
189	Novel genome sequence of Chinese cavefish (Triplophysa rosa) reveals pervasive relaxation of natural selection in cavefish genomes.	0
188	The draft genome and multi-omics analyses reveal new insights into geo-herbalism properties of Citrus grandis Tomentosa**2022**, 111489	0
187	Comparative genomics of Sarcoptes scabiei provide new insights into adaptation to permanent parasitism and within-host species divergence.	1
186	A chromosome-level genome assembly for Dracaena cochinchinesis reveals molecular basis of its longevity and formation of dragon blood. **2022**, 100456	0
185	Comparative transcriptomics analysis pipeline for the meta-analysis of phylogenetically divergent datasets (CoRMAP). **2022**, 23,	0
184	The complex genome and adaptive evolution of polyploid Chinese pepper (Zanthoxylum armatum and Zanthoxylum bungeanum).	0
183	HSDatabase database of highly similar duplicate genes from plants, animals, and algae. **2022**, 2022,	0
182	Phylogenomics provides insights into the evolution of cactophily and host plant shifts in Drosophila. **2022**, 107653	0
181	Chromosome-Level Assembly of Male Opsariichthys bidens Genome Provides Insights into the Regulation of the GnRH Signaling Pathway and Genome Evolution. **2022**, 11, 1500	0
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179	EchinoDB: an update to the web-based application for genomic and transcriptomic data on echinoderms. **2022**, 23,	0
178	Whole-genome sequencing and comparative genomic analysis of a pathogenic Enterocytozoon hepatopenaei strain isolated from Litopenaeus vannamei.	0
177	The chromosome-level genome of Akebia trifoliata as an important resource to study plant evolution and environmental adaptation in the Cretaceous.	2
176	Identification of shared bacterial strains in the vaginal microbiota of related and unrelated reproductive-age mothers and daughters using genome-resolved metagenomics. **2022**, 17, e0275908	0

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174	OrthoSNAP: A tree splitting and pruning algorithm for retrieving single-copy orthologs from gene family trees. **2022**, 20, e3001827	0
173	Genomic insights into the physiology of Quinella, an iconic uncultured rumen bacterium. **2022**, 13,	0
172	The Chromosome-level genome of Aesculus wilsonii provides new insights into terpenoid biosynthesis and Aesculus evolution. 13,	0
171	Integrated Omic Approaches Reveal Molecular Mechanisms of Tolerance during Soybean and Meloidogyne incognita Interactions. **2022**, 11, 2744	0
170	Haladaptatus halobius sp. nov. and Haladaptatus salinisoli sp. nov., two extremely halophilic archaea isolated from Gobi saline soil. **2022**, 72,	0
169	De novo genome assembly and annotation of Holothuria scabra (Jaeger, 1833) from nanopore sequencing reads.	0
168	De-novo genome assembly and annotation of sobaity seabream Sparidentex hasta. 13,	0
167	An overview of online resources for intra-species detection of gene duplications. 13,	0
166	A Chromosome-Scale Genome Assembly of Mitragyna speciosa (Kratom) and the Assessment of Its Genetic Diversity in Thailand. **2022**, 11, 1492	1
165	Massive genome investigations reveal insights of prevalent introgression for environmental adaptation and triterpene biosynthesis in Ganoderma.	0
164	Thirteen Dipterocarpoideae genomes provide insights into their evolution and borneol biosynthesis. **2022**, 100464	0
163	A chromosome-level genome of Semiothisa cinerearia provides insights into its genome evolution and control. **2022**, 23,	0
162	Comparative transcriptome and proteome analyses of the longissimus dorsi muscle for explaining the difference between donkey meat and other meats. 1-14	0
161	Genome Evolution of a Symbiont Population for Pathogen Defence in Honeybees.	0
160	The GEN-ERA toolbox: unified and reproducible workflows for research in microbial genomics.	0
159	CRISPR-based oligo recombineering prioritizes apicomplexan cysteines for drug discovery. **2022**, 7, 1891-1905	1
158	Comparative genomic analysis of 31 Phytophthora genomes reveal genome plasticity and horizontal gene transfer.	0

157	Worms and gills, plates and spines: the evolutionary origins and incredible disparity of deuterostomes revealed by fossils, genes, and development.	0
156	In-silico approach of identifying novel therapeutic targets against Yersinia pestis using pan and subtractive genomic analysis. **2022**, 107784	0
155	Chromosome-level genome assembly of the bar-headed goose (Anser indicus). **2022**, 9,	0
154	Phylogenomics as an effective approach to untangle cross-species hybridization event: A case study in the family Nymphaeaceae. 13,	0
153	A secreted protease-like protein inZymoseptoria triticiis responsible for avirulence onStb9resistance gene in wheat.	0
152	Olfactory and gustatory receptor genes in fig wasps: Evolutionary insights from comparative studies. **2023**, 850, 146953	0
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150	The Soursop Genome (Annona muricata L., Annonaceae). **2022**, 149-174	0
149	Identification of sex-linked marker and candidate sex determination gene in ornamental fish, African scat (Scatophagus tetracanthus). **2023**, 563, 739023	0
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147	NGSEP 4: Efficient and accurate identification of orthogroups and whole-genome alignment.	0
146	A high-quality chromosome-level genome assembly of Pelteobagrus vachelli provides insights into its environmental adaptation and population history. 13,	0
145	CoreGenes5.0: An Updated User-Friendly Webserver for the Determination of Core Genes from Sets of Viral and Bacterial Genomes. **2022**, 14, 2534	3
144	Chromosome-level genome assembly of Dongxiang wild rice (Oryza rufipogon) provides insights into resistance to disease and freezing. 13,	1
143	Flagellar genes are associated with the colonization persistence phenotype of theDrosophila melanogastermicrobiota.	0
142	Whole-genome resequencing reveals complex effects of geographic-paleoclimatic interactions on diversification of Moustache toads in East Asia.	0
141	De nova assembly, annotation and comparative genomics study on the draft genome of Indian brackish water shrimp Caridina pseudogracilirostris.	0
140	HGTree v2.0: a comprehensive database update for horizontal gene transfer (HGT) events detected by the tree-reconciliation method.	0

139	Deciphering divergent trypanosomatid nuclear complexes by analyzing interactomic datasets with AlphaFold2 and genetic approaches.	0
138	Co-occurrence of essential gene dispensability and bypass suppressor mutations across species.	0
137	Metagenome-assembled genome extraction and analysis from microbiomes using KBase.	0
136	OrthoDB v11: annotation of orthologs in the widest sampling of organismal diversity.	0
135	Dissection of Besnoitia besnoiti intermediate host life cycle stages: From morphology to gene expression. **2022**, 18, e1010955	1
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131	Transcriptomics-based Analysis of the Response of Sugar Content in Litchi Pulp to Foliar Calcium Fertilizer Treatment. **2023**, 148, 9-20	0
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129	New Papiliotrema laurentii UFV-1 strains with improved acetic acid tolerance selected by adaptive laboratory evolution. **2023**, 164, 103765	0
128	Phylogeny Trees as´a´Tool to´Compare Inference Algorithms of´Orthologs. **2022**, 128-139	0
127	First Report and Comparative Genomic Analysis of Mycoplasma capricolum subsp. capricolum HN-B in Hainan Island, China. **2022**, 10, 2298	0
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121	Functional diversification despite structural congruence in the HipBST toxin-antitoxin system ofLegionella pneumophila.	0
120	The first genome sequence of Phomopsis vexans: a fungal pathogen causing Phomopsis blight in eggplant.	1
119	A new order, Entrophosporales, and three new Entrophospora species in Glomeromycota. 13,	0
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116	Diverse, abundant and stable coastal RNA viruses identified by spatiotemporal metatranscriptomics.	0
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114	Genomics of Preaxostyla Flagellates Illuminates Evolutionary Transitions and the Path Towards Mitochondrial Loss.	1
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112	A conserved complex of microneme proteins mediates rhoptry discharge inToxoplasma.	0
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110	Comparative genomics of five Valsa species gives insights on their pathogenicity evolution.	0
109	Comparative Genomics for Evolutionary Cell Biology Using AMOEBAE: Understanding the Golgi and Beyond. **2023**, 431-452	0
108	Linolenic Acid-Derived Oxylipins Inhibit Aflatoxin Biosynthesis in Aspergillus flavus through Activation of Imizoquin Biosynthesis. **2022**, 70, 15928-15944	0
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106	Molecular evolution and signatures of selective pressures on Bos, focusing on the Nelore breed (Bos indicus). **2022**, 17, e0279091	0
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103	Karyotype evolution of the Asterids insights from the first genome sequences of the family Cornaceae.	0
102	A highly quality genome sequence of Penicillium oxalicum species isolated from the root of Ixora chinensis in Vietnam.	0
101	Transcriptome Analysis on the Underlying Physiological Mechanism of Calcium and Magnesium Resolving Sugar Receding in Feizixiao Litchi Pulp. **2022**, 8, 1197	0
100	Jack of all trades: Genome assembly of Wild Jack and comparative genomics of Artocarpus. 13,	0
99	Syringa oblata genome provides new insights into molecular mechanism of flower color differences among individuals and biosynthesis of its flower volatiles. 13,	0
98	The Sugar Metabolic Model of Aspergillus niger Can Only Be Reliably Transferred to Fungi of Its Phylum. **2022**, 8, 1315	0
97	Differences in genetic flux in invasive Streptococcus pneumoniae associated with bacteraemia and meningitis. **2022**, 8, e12229	0
96	Haploid-resolved and chromosome-scale genome assembly in hexa-autoploid sweetpotato (Ipomoea batatas (L.) Lam).	0
95	High-quality genome of Diaphanosoma dubium provides insights into molecular basis of its broad ecological adaptation. **2023**, 106006	0
94	A chromosome-level genome assembly of the Henosepilachna vigintioctomaculata provides insights into the evolution of ladybird beetles.	0
93	Biased mutations and gene losses underlying diploidization of the tetraploid broomcorn millet genome.	0
92	Sipunculus nudus genome provides insights into evolution of spiralian phyla and development. 9,	0
91	Comparative transcriptome analyses of three Gentiana species provides signals for the molecular footprints of selection effects and the phylogenetic relationships.	0
90	Profiling the bloodstream form and procyclic formTrypanosoma bruceicell cycle using single cell transcriptomics.	0
89	Comprehensive analysis of 84 Faecalibacterium prausnitzii strains uncovers their genetic diversity, functional characteristics, and potential risks. 12,	0
88	Single-cell transcriptomics unveils xylem cell development and evolution. **2023**, 24,	0
87	A chromosome-level genome assembly of radish (Raphanus sativus L.) reveals insights into genome adaptation and differential bolting regulation.	0
86	Legionella maioricensis sp. nov., a new species isolated from the hot water distribution systems of a hospital and a shopping center during routine sampling. **2023**, 73,	0

85	High-quality genome sequence reveals a young polyploidization and provides insights into cellulose and lignin biosynthesis in water dropwort (Oenanthe sinensis). **2023**, 193, 116203	0
84	Phylogenomic resolution of order- and family-level monocot relationships using 602 single-copy nuclear genes and 1375 BUSCO genes. 13,	0
83	Phylotranscriptomic analyses of mycoheterotrophic monocots show a continuum of convergent evolutionary changes in expressed nuclear genes from three independent nonphotosynthetic lineages.	0
82	Genomic insight into Myroides oncorhynchi sp. nov., a new member of the Myroides genus, isolated from the internal organ of rainbow trout (Oncorhynchus mykiss).	0
81	Characterization and acceleration of genome shuffling and ploidy reduction in synthetic allopolyploids by genome sequencing and editing. **2023**, 51, 198-217	0
80	The Chromosome-Scale Genomes of Exserohilum rostratum and Bipolaris zeicola Pathogenic Fungi Causing Rice Spikelet Rot Disease. **2023**, 9, 177	0
79	Resolving the haplotypes of arbuscular mycorrhizal fungi highlights the role of two nuclear populations in host interactions.	0
78	PlantTribes2: Tools for comparative gene family analysis in plant genomics. 13,	0
77	Population genetic analysis of the microsporidium Ordospora colligata reveals the role of natural selection and phylogeography on its extremely compact and reduced genome.	0
76	A Robust Methodology for Assessing Homoeolog-Specific Expression. **2023**, 251-258	0
75	Leveraging genomic redundancy to improve inference and alignment of orthologous proteins.	0
74	Characterization and genome-wide sequence analysis of an ectomycorrhizal fungus Pisolithus albus, a potential source for reclamation of degraded lands. **2023**, 13,	0
73	A novel order-level lineage of ammonia-oxidizingThaumarchaeotais widespread in marine and terrestrial environments.	0
72	Spatial-temporal expression analysis of lineage-restricted shell matrix proteins reveals shell field regionalization and distinct cell populations in the slipper snailCrepidula atrasolea.	0
71	Chromosome-level genome assembly provides insights into adaptive evolution of chromosome and important traits in the geckoGekko japonicus.	0
70	Gossypium purpurascens genome provides insight into the origin and domestication of upland cotton. **2023**,	0
69	Analyses of a chromosome-scale genome assembly reveal the origin and evolution of cultivated chrysanthemum. **2023**, 14,	0
68	Whole-genome sequencing and analysis of Apocynum cannabinum.	0

67	The genome sequence and demographic history of Przewalskia tangutica (Solanaceae), an endangered alpine plant on the Qinghai-Tibet Plateau.	0
66	Chromosome-level genome of the bean bug Megacopta cribraria in native range, provides insights into adaptation and pest management. **2023**, 237, 123989	0
65	Phylogenomic analyses of Camellia support reticulate evolution among major clades. **2023**, 182, 107744	0
64	Seeing is believing: Understanding functions of NPR1 and its paralogs in plant immunity through cellular and structural analyses. **2023**, 73, 102352	0
63	Insights into identifying resistance genes for cold and disease stresses through chromosome-level reference genome analyses of Poncirus polyandra. **2023**, 115, 110617	0
62	The Populus koreana genome provides insights into the biosynthesis of plant aroma. **2023**, 197, 116453	0
61	Sugars and sucrose transporters in pollinia of Phalaenopsis aphrodite (Orchidaceae). **2023**, 74, 2556-2571	0
60	Apical Secretory Glycoprotein Complex Contributes to Cell Attachment and Entry by Cryptosporidium parvum. **2023**, 14,	0
59	The chromosome-level genome and key genes associated with mud-dwelling behavior and adaptations of hypoxia and noxious environments in loach (Misgurnus anguillicaudatus). **2023**, 21,	0
58	Inference of Ancient Polyploidy from Genomic Data. **2023**, 3-18	0
57	Genome-based reclassification of Anoxybacillus salavatliensis Cihan et al. 2011 as a later heterotypic synonym of Anoxybacillus gonensis Belduz et al. 2003.	0
56	Chromosome-Level Assembly of Flowering Cherry (Prunus campanulata) Provides Insight into Anthocyanin Accumulation. **2023**, 14, 389	0
55	PANAS: Pipeline and a Case Study to Obtain Synonymous and Nonsynonymous Substitution Rates in Genes of Platyhelminthes. **2023**, 90,	0
54	Interplay between transcriptional regulators and VapBC toxin‐antitoxin loci during thermal stress response in extremely thermoacidophilic archaea.	0
53	Genome and haplotype provide insights into the population differentiation and breeding improvement of Gossypium barbadense. **2023**,	0
52	The genome of Magnolia hypoleuca provides a new insight into cold tolerance and the evolutionary position of magnoliids. 14,	0
51	Genome assembly, resequencing and genome-wide association analyses provide novel insights into the origin, evolution and flower colour variations of flowering cherry.	0
50	An improved reference genome for Trifolium subterraneum L. provides insight into molecular diversity and intra-specific phylogeny. 14,	0

49	Physiological and genomic insights into abiotic stress of halophilic archaeon Natrinema altunense 4.1R isolated from a saline ecosystem of Tunisian desert. **2023**, 151, 133-152	0
48	Genomic diversity in Fructobacillus spp. isolated from fructose-rich niches. **2023**, 18, e0281839	0
47	Identification and Phylogenetic Analysis of the R2R3-MYB Subfamily in Brassica napus. **2023**, 12, 886	0
46	OrthoPhy: A Program to Construct Ortholog Data Sets Using Taxonomic Information. **2023**, 15,	0
45	Genomic characterization of coexisting anatoxin-producing and non-toxigenic Microcoleus subspecies in benthic mats from the Wolastoq, New Brunswick, Canada. **2023**, 124, 102405	0
44	Challenges and opportunities of strain diversity in gut microbiome research. 14,	0
43	Comparative Genomic Analysis and Physiological Properties of Limosilactobacillus fermentum SMFM2017-NK2 with Ability to Inflammatory Bowel Disease. **2023**, 11, 547	0
42	A chromosome-level genome assembly for Erianthus fulvus provides insights into its biofuel potential and facilitates breeding for improvement of sugarcane. **2023**, 100562	0
41	Transcript annotation of Chinese sturgeon (Acipenser sinensis) using Iso-seq and RNA-seq data. **2023**, 10,	0
40	Synteny Identifies Reliable Orthologs for Phylogenomics and Comparative Genomics of the Brassicaceae. **2023**, 15,	0
39	Genomic characterization and molecular dating of the novel bacterium Permianibacter aggregans HW001T, which originated from Permian ground water. **2023**, 5, 12-27	0
38	ProteInfer, deep neural networks for protein functional inference. 12,	1
37	Draft Genome and Biological Characteristics of Fusarium solani and Fusarium oxysporum Causing Black Rot in Gastrodia elata. **2023**, 24, 4545	0
36	Deep origins of eukaryotic multicellularity revealed by the Acrasis kona genome and developmental transcriptomes.	0
35	Chromosome-level reference genome of Tetrastigma hemsleyanum (Vitaceae) provides insights into genomic evolution and the biosynthesis of phenylpropanoids and flavonoids.	0
34	De novo assembly of a chromosome-level reference genome of the ornamental butterfly Sericinus montelus based on nanopore sequencing and Hi-C analysis. 14,	0
33	The giant diploid faba genome unlocks variation in a global protein crop. **2023**, 615, 652-659	0
32	Chromosome-level genome assembly of Phrynocephalus forsythii using third-generation DNA sequencing and Hi-C analysis. **2023**, 30,	0

31	A phylogenomic analysis of Limosilactobacillus reuteri reveals ancient and stable evolutionary relationships with rodents and birds and zoonotic transmission to humans. **2023**, 21,	0
30	The origin and structural evolution ofde novogenes inDrosophila.	0
29	Revealing evolution of tropane alkaloid biosynthesis by analyzing two genomes in the Solanaceae family. **2023**, 14,	0
28	Evolution of chemosensory and detoxification gene families across herbivorous Drosophilidae.	0
27	Genomic Analysis of the Deep-Sea Bacterium Shewanella sp. MTB7 Reveals Backgrounds Related to Its Deep-Sea Environment Adaptation. **2023**, 11, 798	0
26	Toward novel treatment against filariasis: Insight into genome-wide co-evolutionary analysis of filarial nematodes and Wolbachia. 14,	0
25	High-Quality Chromosome-Level De Novo Assembly of the Trifolium repens.	0
24	Rapid adaptations of Legionella pneumophila to the human host. **2023**, 9,	0
23	Comparative Genomics Analysis of Ganoderma Orthologs Involved in Plant-Pathogenesis. **2023**, 14, 653	0
22	Genome-wide comparative analysis between Cranoglanis bouderius and Pangasianodon hypophthalmus : Reveal the genes related to resistance to low-temperature stress.	0
21	Chromosome-aware phylogenomics of Assassin Bugs (Hemiptera: Reduvioidea) elucidates ancient gene conflict.	0
20	Duckweed evolution: from land back to water.	0
19	Artificially cultivated duckweed: a high-efficiency starch producer.	0
18	Characterization and Genome Analysis of Cladobotryum mycophilum, the Causal Agent of Cobweb Disease of Morchella sextelata in China. **2023**, 9, 411	0
17	Evolution of an alternative genetic code in theProvidenciasymbiont of the haematophagous leechHaementeria acuecueyetzin.	0
16	Highly contiguous genomes of human clinical isolates of Giardia duodenalis reveal assemblage- and sub-assemblage-specific presence–absence variation in protein-coding genes. **2023**, 9,	0
15	De novoassembly of the black flounder genome. Why do pleuronectiformes have such a small genome size?.	0
14	LncRNA-encoded peptides: the case of the lncRNA gene located downstream of EIN2. **2023**, 23,	0

13	Two haplotype-resolved genomes of highly heterozygous AAB allotriploid bananas provide insights into subgenome asymmetric evolution and banana wilt control.	0
12	Microspore-expressed SCULP1 is required for p -coumaroylation of sporopollenin, exine integrity, and pollen development in wheat.	0
11	Gene loss during a transition to multicellularity. **2023**, 13,	0
10	Transcriptomic insights into archaeal nitrification in the Amundsen Sea Polynya, Antarctica.	0
9	Monkeypox virus: phylogenomics, host‐pathogen interactome and mutational cascade. **2023**, 9,	0
8	High-quality chromosome-level genome assembly of the plant bug Pachypeltis micranthus provides insights into the availability of Mikania micrantha control.	0
7	Flagellar Genes Are Associated with the Colonization Persistence Phenotype of the Drosophila melanogaster Microbiota.	0
6	Genome Organization of Four Brazilian Xanthomonas albilineans Strains Does Not Correlate with Aggressiveness.	0
5	Systematical Characterization of the AT-Hook Gene Family in Juglans regia L. and the Functional Analysis of the JrAHL2 in Flower Induction and Hypocotyl Elongation. **2023**, 24, 7244	0
4	Novel lytic and lysogenic cyanophages predicted to infectMicrocoleusassociated with anatoxin-producing benthic mats.	0
3	Integrating Metabolic Modeling and High-Throughput Data to Characterize Diatoms Metabolism. **2023**, 165-191	0
2	Origin and diversification of a Himalayan orchid genus Pleione. **2023**, 107797	0
1	First report of whole genome sequence of septicemic Pasteurella multocida serovar B:2 Soron strain isolated from swine.	0