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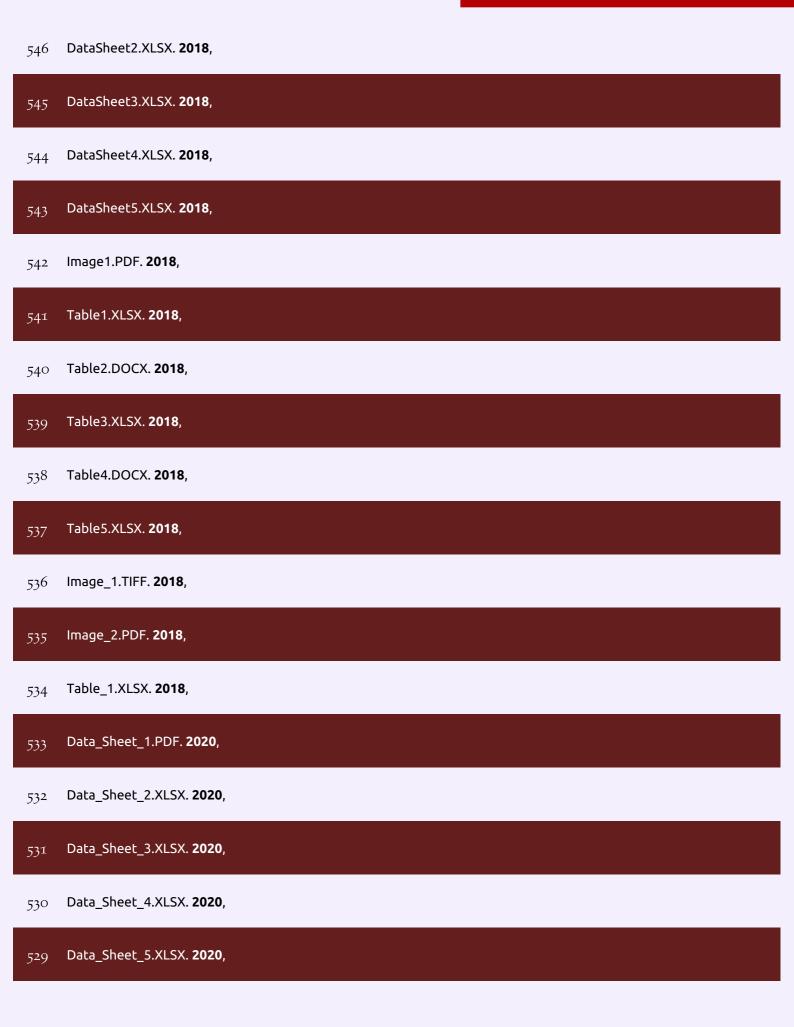
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261	The parthenogenesis mechanism and venom complement of the parasitoid wasp Microctonus hyperodae, a declining biocontrol agent.	О
260	Using machine learning to predict protein-protein interactions between a zombie ant fungus and its carpenter ant host.	0
259	Metagenomics and Metatranscriptomics. 2022 , 147-184	О

258	Prediction of RNA editing sites and genome-wide characterization of PERK gene family in maize (Zea mays L.) in response to drought stress. 2022 , 34, 102293	O
257	Genome-wide identification and characterization of the fatty acid desaturase gene family in Vanilla planifolia. 2022 , 150, 813-820	O
256	The role of gene duplication in the divergence of the sweet cherry. 2022 , 32, 100379	O
255	Synthesizing glycine betaine via choline oxidation pathway as an osmoprotectant strategy in Haloferacales. 2022 , 847, 146886	1
254	The first transcriptome dataset of roselle (Hibiscus sabdariffa L.) calyces during maturation. 2022 , 45, 108613	O
253	Bioinformatics Resources, Tools, and Strategies in Designing Therapeutic Proteins. 2022 , 91-123	O
252	Predicting Drug-Target Interactions Binding Affinity by Using Dual Updating Multi-task Learning. 2022 , 66-76	O
251	Genome architecture and diverged selection shaping pattern of genomic differentiation in wild barley.	O
250	Biological control and plant growth promotion properties of Streptomyces albidoflavus St-220 isolated from Salvia miltiorrhiza rhizosphere. 13,	2
249	The long non-coding RNA GhlncRNA149.1 împroves cotton defense response to aphid damage as a positive regulator.	O
248	Genome-wide identification of wheat ABC1K gene family and functional dissection of TaABC1K3 and TaABC1K6 involved in drought tolerance. 13,	O
247	Genome-wide identification and expression analysis of the WRKY gene family in five legumes.	O
246	A chromosome-scale genome assembly of Quercus gilva: Insights into the evolution of Quercus section Cyclobalanopsis (Fagaceae). 13,	O
245	Full-Length Transcriptomic Sequencing and Temporal Transcriptome Expression Profiling Analyses Offer Insights into Terpenoid Biosynthesis in Artemisia argyi. 2022 , 27, 5948	1
244	Genome mining of Fusarium reveals structural and functional diversity of pectin lyases: a bioinformatics approach. 2022 , 12,	O
243	The Molecular Network behind Volatile Aroma Formation in Pear (Pyrus spp. Panguxiang) Revealed by Transcriptome Profiling via Fatty Acid Metabolic Pathways. 2022 , 12, 1494	1
242	Genomic Profiling of Non-O157 Shiga Toxigenic Escherichia coli-Infecting Bacteriophages from South Africa.	О
241	Genome-guided prediction of acid resistance mechanisms in acidophilic methanotrophs of phylogenetically deep-rooted Verrucomicrobia isolated from geothermal environments. 13,	O

240	A genome-wide search of Toll/Interleukin-1 receptor (TIR) domain-containing adapter molecule (TICAM) and their evolutionary divergence from other TIR domain containing proteins. 2022 , 17,	O
239	Genome-Wide Identification of Histone Modification (HM) Gene Family and Their Expression Patterns Under Abiotic Stress and Different Developmental Stages of Tea (Camellia assamica).	O
238	Screening of immune-related genes against bacterial infection in Ostrinia furnacalis (Lepidoptera: Crambidae). 119, 388-397	0
237	Safety assessment of Mpp75Aa1.1, a new ETX_MTX2 protein from Brevibacillus laterosporus that controls western corn rootworm. 2022 , 17, e0274204	O
236	Identification and characterization of putative effectors from Plasmodiophora brassicae that suppress or induce cell death in Nicotiana benthamiana. 13,	O
235	First Report and Comparative Genomic Analysis of a Mycoplasma mycoides Subspecies capri HN-A in Hainan Island. 2022 , 10, 1908	0
234	PTG-PLM: Predicting Post-Translational Glycosylation and Glycation Sites Using Protein Language Models and Deep Learning. 2022 , 11, 469	0
233	The RNAome landscape of tomato during arbuscular mycorrhizal symbiosis reveals an evolving RNA layer symbiotic regulatory network. 2022 , 100429	Ο
232	CorA gene rearrangement triggered the salinity-driven speciation of Poseidoniales.	0
231	GeneralizedDTA: combining pre-training and multi-task learning to predict drug-target binding affinity for unknown drug discovery. 2022 , 23,	O
230	Genome-Wide Identification and Molecular Evolution of the Magnesium Transporter (MGT) Gene Family in Citrullus lanatus and Cucumis sativus. 2022 , 12, 2253	0
229	Insight into molecular interaction between shrimp and white spot syndrome virus through MjsvCL-VP28 complex: an in-silico approach. 1-11	O
228	In host evolution of Exophiala dermatitidis in cystic fibrosis lung micro-environment.	O
227	mobileOG-db: a Manually Curated Database of Protein Families Mediating the Life Cycle of Bacterial Mobile Genetic Elements. 2022 , 88,	O
226	Complete Genome Sequence of an Uncultivated Freshwater Flavobacterium sp. Strain.	0
225	The Aphelenchoides genomes reveal major events of horizontal gene transfers in clade IV nematodes.	O
224	Genome-wide identification, characterization, and expression analysis of UDP-glycosyltransferase genes associated with secondary metabolism in alfalfa (Medicago sativa L.). 13,	0
223	Decoding the formation of diverse petal colors of Lagerstroemia indica by integrating the data from transcriptome and metabolome. 13,	Ο

222	Genome-wide analysis suggests the potential role of lncRNAs during seed development and seed size/weight determination in chickpea. 2022 , 256,	0
221	Study of Complete Genome Sequence of Uncultivated Hyphomonadaceae sp	O
220	Learning probabilistic protein DNA recognition codes from DNA-binding specificities using structural mappings. 2022 , 32, 1776-1786	O
219	Complete Genome Sequence of an Uncultivated Freshwater Bacteroidota Lineage.	O
218	In silico prediction methods of self-interacting proteins: an empirical and academic survey. 2023 , 17,	O
217	Neural Network for Screening Active Sites on Proteins. 2022 , 225-246	O
216	SUBTLE DIFFERENCES IN FINE POLYSACCHARIDE STRUCTURES GOVERN SELECTION AND SUCCESSION OF HUMAN GUT MICROBIOTA.	O
215	Methylation level of potato gene OMT30376 regulates tuber anthocyanin transformations. 13,	1
214	Complete genome sequencing and in silico genome mining reveal the promising metabolic potential in Streptomyces strain CS-7. 13,	O
213	Floral organ transcriptome in Camellia sasanqua provided insight into stamen petaloid. 2022 , 22,	O
212	Bartonella choladocola sp. nov. and Bartonella apihabitans sp. nov., two novel species isolated from honey bee gut. 2022 , 126372	0
211	Physiological and transcriptomic analysis uncovers salinity stress mechanisms in a facultative crassulacean acid metabolism plant Dendrobium officinale. 13,	O
210	Characterization of AnCUT3, a plastic-degrading paucimannose cutinase from Aspergillus niger expressed in Pichia pastoris. 2022 ,	0
209	Domain Evolution of Vertebrate Blood Coagulation Cascade Proteins.	O
208	HSDatabase database of highly similar duplicate genes from plants, animals, and algae. 2022 , 2022,	O
207	Leaf-transcriptome profiles of phoebe bournei provide insights into temporal drought stress responses. 13,	O
206	Identification and molecular evolution of the La and LARP genes in 16 plant species: A focus on the Gossypium hirsutum. 2022 ,	O
205	Molecular Characterization of bHLH Transcription Factor Family in Rose (Rosa chinensis Jacq.) under Botrytis cinerea Infection. 2022 , 8, 989	O

204	Tn6553, a Tn7-family transposon encoding putative iron uptake functions found in Acinetobacter. 2022 , 204,	O
203	Transcriptome and metabolome analyses provide insights into the relevance of pericarp thickness variations in Camellia drupifera and Camellia oleifera. 13,	1
202	Genome-wide identification and expression analysis of SBP-box gene family reveal their involvement in hormone response and abiotic stresses in Chrysanthemum nankingense. 10, e14241	O
201	Chemosensory-Related Genes in Marine Copepods. 2022 , 20, 681	O
200	Genome-wide identification and characterization of lncRNAs in sunflower endosperm. 2022, 22,	1
199	Characterization and evolutionary diversification of the phospholipase D gene family in mosses. 13,	O
198	Creating De Novo Overlapped Genes. 2023 , 95-120	О
197	Genome Sequence Resource of Trichothecium roseum (ZM-Tr2021), the causal agent of postharvest pink rot.	O
196	PIGN-Related Disease in Two Lithuanian Families: A Report of Two Novel Pathogenic Variants, Molecular and Clinical Characterisation. 2022 , 58, 1526	О
195	A microfluidic platform combined with bacteriophage receptor binding proteins for multiplex detection of Escherichia coli and Pseudomonas aeruginosa in blood. 2022 , 132917	1
194	Low-abundance populations distinguish microbiome performance in plant cell wall deconstruction. 2022 , 10,	О
193	Genome-wide identification of biotin carboxyl carrier subunits of acetyl-CoA carboxylase in Brassica and their role in stress tolerance in oilseed Brassica napus. 2022 , 23,	O
192	Transcriptomic, cytological, and physiological analyses reveal the potential regulatory mechanism in Tartary buckwheat under cadmium stress. 13,	Ο
191	Whole-genome sequencing of Fusarium oxysporum f. sp. Cucumerinum strain Race-4 infecting cucumber in China.	O
190	WRKY genes in black raspberry (Rubus occidentalis L.): duplicate and conquer.	0
189	Identification of long non-coding RNA-microRNA-mRNA regulatory modules and their potential roles in drought stress response in wheat (Triticum aestivum L.). 13,	O
188	Identification of RNA virus-derived RdRp sequences in publicly available transcriptomic datasets.	1
187	Characterization of lncRNAs involved in drought response in Betula platyphylla.	O

186	Divergent functions of two clades of flavodoxin in diatoms mitigate oxidative stress and iron limitation.	О
185	Chromosome-level genome assembly of the bar-headed goose (Anser indicus). 2022, 9,	О
184	Changes in functional composition and gene expression in eukaryotic plankton at the Atlantic-Arctic Polar front.	0
183	Whole genome sequencing of the fast-swimming Southern bluefin tuna (Thunnus maccoyii). 13,	0
182	Deciphering the regulatory network of miR156 in plant architecture and abiotic stress resistance of alfalfa (Medicago sativa) by transcriptome sequencing. 2022 , 189, 115828	0
181	Molecular identification and phylogenetic analysis of putative senescence associated gene 21 in Stevia rebaudiana accession MS007. 2022 , 6, 35	O
180	Structure and Mechanism of Plant DNA Methyltransferases. 2022 , 137-157	0
179	Integrative metabolome and transcriptome analyses reveals the black fruit coloring mechanism of Crataegus maximowiczii C. K. Schneid. 2023 , 194, 111-121	o
178	The combination of SMRT sequencing and Illumina sequencing highlights organ-specific and age-specific expression patterns of miRNAs in Sika Deer. 9,	0
177	Characteristics and Comparative Genomic Analysis of a Novel Virus, VarioGold, the First Bacteriophage of Variovorax. 2022 , 23, 13539	o
176	Genome-wide identification of WD40 superfamily in Cerasus humilis and functional characteristics of ChTTG1. 2022 ,	0
175	Whole-genome assembly and annotation for the little yellow croaker (Larimichthys polyactis) provide insights into the evolution of hermaphroditism and gonochorism.	О
174	Bioinformatics analysis and function prediction of NBS-LRR gene family in Broussonetia papyrifera.	0
173	Systematic Identification and Analysis of OSC Gene Family of Rosa rugosa Thunb. 2022 , 23, 13884	1
172	Deep learning in drug discovery: an integrative review and future challenges.	1
171	Constructing metagenome-assembled genomes for almost all components in a real bacterial consortium for binning benchmarking. 2022 , 23,	О
170	Age-related changes in gonadotropin-releasing hormone (GnRH) splice variants in mouse brain.	0
169	Novel insight into anthocyanin metabolism and molecular characterization of its key regulators in Camellia sasanqua.	О

168	Genome-wide Identification and Characterization of Plant-specific Transcription Factor YABBY Gene Family in Cucumber (Cucumis sativus) and its Comparison with Arabidopsis to Reveal its Role in Abiotic Stress Responses. 2022 , 3, 325-341	0
167	Interactive Analysis of Functional Residues in Protein Families.	O
166	Genome-wide identification and expression analysis of PIN gene family under phytohormone and abiotic stresses in Vitis Vinifera L	0
165	Chromosome-scale assemblies of the male and female Populus euphratica genomes reveal the molecular basis of sex determination and sexual dimorphism. 2022 , 5,	Ο
164	A widespread group of large plasmids in methanotrophic Methanoperedens archaea. 2022 , 13,	1
163	Identification of the GAPDH gene family in Citrullus lanatus and functional characteristics of ClGAPC2 in Arabidopsis thaliana.	O
162	Heterotrophic denitrification: An overlooked factor that contributes to nitrogen removal in n-DAMO mixed culture. 2023 , 216, 114802	0
161	Haplotype-phased and chromosome-level genome assembly of Puccinia polysora , a giga-scale fungal pathogen causing southern corn rust.	Ο
160	Structural and biochemical characterization of Leptospira interrogans Lsa45 reveals a penicillin-binding protein with esterase activity. 2023 , 125, 141-153	O
159	Plant invasion by Chromolaena odorata alters the soil microbiome and provides insight into the role of copiotrophs. 2023 , 26, 100157	O
158	Taxonomic and functional metagenomic profiling of microbial communities in urine sample. 2022,	O
157	Modularity of Cellulases, Xylanases, and Other Glycosyl Hydrolases Relevant for Biomass Degradation. 2022 , 1-35	O
156	Genome-Wide In Silico Identification, Structural Analysis, Promoter Analysis, and Expression Profiling of PHT Gene Family in Sugarcane Root under Salinity Stress. 2022 , 14, 15893	1
155	Genomic Analysis of the Proteasome Subunit Gene Family and Their Response to High Density and Saline-Alkali Stresses in Grass Carp. 2022 , 7, 350	O
154	Divergent and diversified proteome content across a serially acquired plastid lineage.	O
153	Genome-wide identification and expression analysis of the GRAS gene family in Dendrobium chrysotoxum. 13,	O
152	UV-B induces the expression of flavonoid biosynthetic pathways in blueberry (Vaccinium corymbosum) calli. 13,	О
151	GenomeWide identification and analysis of LEA_2 gene family in alfalfa (Medicago sativa L.) under aluminum stress. 13,	O

150	Evolutionary conservation and transcriptome analyses attribute perenniality and flowering to day-length responsive genes in bulbous barley (Hordeum bulbosum).	0
149	A large-scale benchmark study of tools for the classification of protein-coding and non-coding RNAs. 2022 , 50, 12094-12111	O
148	Predicting and Interpreting Protein Developability via Transfer of Convolutional Sequence Representation.	O
147	Impact of diet on human nutrition, immune response, gut microbiome, and cognition in an isolated and confined mission environment. 2022 , 12,	O
146	PPDP: A Data Portal of Paris polyphylla for Polyphyllin Biosynthesis and Germplasm Resource Exploration. 2022 , 14, 1057	О
145	Comparative genomics of five Valsa species gives insights on their pathogenicity evolution.	O
144	Genome-Wide Identification and Characterization of Trihelix Gene Family in Asian and African Vigna Species. 2022 , 12, 2172	O
143	Genome-wide identification and comprehensive analysis reveal potential roles of long non-coding RNAs in fruit development of southern highbush blueberry (Vaccinium corymbosum L.). 13,	O
142	In silico analysis of NHP2 membrane protein, a novel vaccine candidate present in the RD7 region of Mycobacterium tuberculosis.	O
141	The SsAtg1 Activating Autophagy Is Required for Sclerotia Formation and Pathogenicity in Sclerotinia sclerotiorum. 2022 , 8, 1314	O
140	Genome-Wide Identification of Brassica napus PEN1-LIKE Genes and Their Expression Profiling in Insect-Susceptible and Resistant Cultivars. 2022 , 44, 6385-6396	O
139	A systematic review of state-of-the-art strategies for machine learning-based protein function prediction. 2022 , 106446	O
138	Genome-Wide Analysis of Wheat GATA Transcription Factor Genes Reveals Their Molecular Evolutionary Characteristics and Involvement in Salt and Drought Tolerance. 2023 , 24, 27	1
137	Interference with orco gene expression affects host recognition in Diorhabda tarsalis. 13,	O
136	Disentangling the lipid divide: Identification of key enzymes for the biosynthesis of membrane-spanning and ether lipids in Bacteria. 2022 , 8,	O
135	Genomic, Functional and Structural Analyses Reveal Mechanisms of Evolutionary Innovation within the Sea Anemone 8 Toxin Family.	1
134	Two canonically aerobic foraminifera express distinct peroxisomal and mitochondrial metabolisms. 9,	О
133	Potential therapeutic targets for combating Mycoplasma genitalium. 2023, 13,	O

132	Genome-wide characterization and comparative analysis of the OSCA gene family and identification of its potential stress-responsive members in legumes.	O
131	A novel steroid hydroxylase from Nigrospora sphaerica exhibiting broad substrate and stero-specificity. 2022 , 106236	O
130	Syringa oblata genome provides new insights into molecular mechanism of flower color differences among individuals and biosynthesis of its flower volatiles. 13,	0
129	Transposons contribute to the functional diversification of the head, gut, and ovary transcriptomes acrossDrosophilanatural strains.	O
128	Identification and differential expression of long non-coding RNAs and their association with XIST gene during early embryonic developmental stages of Bos taurus. 2022 ,	0
127	Identification of birch lncRNAs and mRNAs responding to salt stress and characterization of functions of lncRNA.	O
126	The long non-coding RNA GhlncRNA149.1 improves cotton defense response to aphid damage as a positive regulator.	0
125	Composition and toxicity of venom produced by araneophagous white-tailed spiders (Lamponidae: Lampona sp.). 2022 , 12,	O
124	Microbiome-mediated fructose depletion restricts murine gut colonization by vancomycin-resistant Enterococcus. 2022 , 13,	0
123	Haploid-resolved and chromosome-scale genome assembly in hexa-autoploid sweetpotato (Ipomoea batatas (L.) Lam).	O
122	Reekeekee- and roodoodooviruses, two different Microviridae clades constituted by the smallest DNA phages.	0
121	CRMSS: predicting circRNA-RBP binding sites based on multi-scale characterizing sequence and structure features.	O
120	Identification and Characterization of novel long non-coding RNAs in vascular smooth cells.	0
119	Identification of genes involved in chicken follicle selection by ONT sequencing on granulosa cells. 13,	Ο
118	Mycoparasites, gut dwellers, and saprotrophs: Phylogenomic reconstructions and comparative analyses of Kickxellomycotina fungi.	0
117	The interferon stimulated gene-encoded protein HELZ2 inhibits human LINE-1 retrotransposition and LINE-1 RNA-mediated type I interferon induction. 2023 , 14,	O
116	A Cellular Platform for Production of C4Monomers.	0
115	Genomic resources enable insight into the developmental transcriptome of the blastoclad fungus, Coelomomyces lativittatus, an obligate parasite of mosquitoes and microcrustaceans.	O

114	The Aphelenchoides genomes reveal substantial horizontal gene transfers in the last common ancestor of free-living and major plant parasitic nematodes.	О
113	Multi-Omics Approaches for Breeding in Medicinal Plants. 2023 , 165-191	O
112	Endophytic fungi related to the ash dieback causal agent encode signatures of pathogenicity on European ash.	0
111	The gene regulatory network of Staphylococcus aureus ST239-SCCmecIII strain Bmb9393 and assessment of genes associated with the biofilm in diverse backgrounds. 13,	O
110	A symbiotic bacterium of Antarctic fish reveals environmental adaptability mechanisms and biosynthetic potential towards antibacterial and cytotoxic activities. 13,	O
109	Genome-wide identification and analysis of wheat LRR-RLK family genes following Chinese wheat mosaic virus infection. 13,	O
108	Genome-Wide Identification of 14-3-3 gene family reveals their diverse responses to abiotic stress by interacting with StABI5 in Potato (Solanum tuberosum L.). 13,	0
107	The genome of the oomycete Peronosclerospora sorghi, a cosmopolitan pathogen of maize and sorghum, is inflated with dispersed pseudogenes.	O
106	A Review of Basic Bioinformatic Techniques for Microbial Community Analysis in an Anaerobic Digester. 2023 , 9, 62	O
105	Genome-Wide Analysis of Aquaporin Gene Family in Triticum turgidum and Its Expression Profile in Response to Salt Stress. 2023 , 14, 202	2
104	Transcriptome analysis and gene expression analysis related to salinity-alkalinity and low temperature adaptation of Triplophysa yarkandensis. 13,	0
103	In Silico Analysis of a Drosophila Parasitoid Venom Peptide Reveals Prevalence of the Cation P olar T ation Clip Motif in Knottin Proteins. 2023 , 12, 143	O
102	Day-night cycle as a key environmental factor affecting coral-Symbiodiniaceae symbiosis. 2023 , 146, 109890	0
101	Phage-Host Prediction Using a Computational Tool Coupled with 16S rRNA Gene Amplicon Sequencing. 2023 , 15, 76	O
100	Isolation, complete genome sequencing and in silico genome mining of Burkholderia for secondary metabolites. 2022 , 22,	O
99	Phylotranscriptomic analyses of mycoheterotrophic monocots show a continuum of convergent evolutionary changes in expressed nuclear genes from three independent nonphotosynthetic lineages.	O
98	The P450 Sterol Side Chain Cleaving Enzyme (P450scc) for Digoxin Biosynthesis in the Foxglove Plant Belongs to the CYP87A Family.	О
97	The Completed Genome Data of the Pathogenic Fungus Exobasidium cylindrosporum.	O

96	Variation in heat shock protein 40 kDa relates to divergence in thermotolerance among cryptic rotifer species. 2022 , 12,	О
95	In silico analysis of NHP2 membrane protein, a novel vaccine candidate present in the RD7 region of Mycobacterium tuberculosis.	О
94	MYB pathways that regulate UV-B-induced anthocyanin biosynthesis in blueberry (Vaccinium corymbosum). 14,	О
93	Genome-wide characterization of the PP2C gene family in peanut (Arachis hypogaea L.) and the identification of candidate genes involved in salinity-stress response. 14,	О
92	Molecular characterization and phylogenetic analysis of kaurene synthase protein in Stevia rebaudiana MS007. 1-13	0
91	Regulatory mechanisms of c-di-AMP synthase (MsDisA) protein from Mycobacterium smegmatis revealed by a structure Ifunction analysis.	O
90	Genome-wide identification and transcriptome-based expression pattern of chemosensory genes in two wild silkmoths, Antheraea pernyi and Antheraea yamamai. 1-18	О
89	Cyanobacterial Bioenergetics in Relation to Cellular Growth and Productivity. 2023,	O
88	Tandem repeats in giant archaeal Borg elements undergo rapid evolution and create new intrinsically disordered regions in proteins. 2023 , 21, e3001980	О
87	DNA Double-Strand Break-Related Competitive Endogenous RNA Network of Noncoding RNA in Bovine Cumulus Cells. 2023 , 14, 290	1
86	Improved Annotation of the Peach (Prunus persica) Genome and Identification of Tissue- or Development Stage-Specific Alternative Splicing through the Integration of Iso-Seq and RNA-Seq Data. 2023 , 9, 175	О
85	Genome-Wide Characterization of the Sulfate Transporter Gene Family in Oilseed Crops: Camelina sativa and Brassica napus. 2023 , 12, 628	O
84	Large language models generate functional protein sequences across diverse families.	1
83	Omics Technologies in Environmental Microbiology and Microbial Ecology. 2023 , 433-454	O
82	Characterization and Application of EST-SSR Markers Developed from Transcriptome Sequences in Elymus breviaristatus (Poaceae: Triticeae). 2023 , 14, 302	О
81	RickettsialesIdeep evolutionary history sheds light on the emergence of intracellular lifestyles.	O
80	Impact of meltwater flow intensity on the spatiotemporal heterogeneity of microbial mats in the McMurdo Dry Valleys, Antarctica. 2023 , 3,	О
79	Genome-Wide Identification of BTB Domain-Containing Gene Family in Grapevine (Vitis vinifera L.). 2023 , 13, 252	O

78	Differential transcriptome analysis of Sporocytophaga sp. CX11 and identification of candidate genes involved in lignocellulose degradation. 2023 , 10,	0
77	Transcriptome analysis reveals the key pathways and candidate genes involved in salt stress responses in Cymbidium ensifolium leaves. 2023 , 23,	О
76	DTiGNN: Learning drug-target embedding from a heterogeneous biological network based on a two-level attention-based graph neural network. 2023 , 20, 9530-9571	0
75	Combined analysis of chromatin accessibility and gene expression profiles provide insight into Fucoxanthin biosynthesis in Isochrysis galbana under green light. 14,	Ο
74	Rie1 and Sgn1 form an RNA-binding complex that enforces the meiotic entry cell fate decision.	0
73	Full-length transcriptome profiling for fruit development in Diospyros oleifera using nanopore sequencing. 2023 , 24,	О
72	Many Families of Lids for TonB-dependent Transporters inBacteroides.	Ο
71	Genome Sequence and Assembly of 18 Fusarium Isolates from Florida Citrus under High Huanglongbing Disease Pressure and California Citrus under Low Huanglongbing Disease Pressure.	O
70	Influence of substitution model selection on protein phylogenetic tree reconstruction. 2023, 865, 147336	Ο
69	Genome-wide identification of papain-like cysteine protease family genes in cultivated peanut (Arachis hypogaea L.) and functional characterization of AhRD21B in response to chilling stress. 2023 , 209, 105272	О
68	Oat AsDA1-2D enhances heat stress tolerance and negatively regulates seed-storage globulin. 2023 , 284, 153981	0
67	Genome-wide identification and characterization of long non-coding RNA in barley roots in response to Piriformospora indica colonization. 2023 , 330, 111666	О
66	Functional characterization of a DNA-damage repair/tolerance 100 (DRT100) gene in Sedum alfredii Hance for genome stability maintenance and Cd hypertolerance. 2023 , 327, 121546	0
65	Insights into the Sulfate Transporter Gene Family and Its Expression Patterns in Durum Wheat Seedlings under Salinity. 2023 , 14, 333	3
64	Develop a preliminary core germplasm with the novel polymorphism EST-SSRs derived from three transcriptomes of colored calla lily (Zantedeschia hybrida). 14,	0
63	Genomic epidemiology of Mycobacterium avium subsp. paratuberculosis isolates from Canadian dairy herds provides evidence for multiple infection events. 14,	O
62	Identification of AHL Synthase in Desulfovibrio vulgaris Hildenborough Using an In-Silico Methodology. 2023 , 13, 364	0
61	The scalable precision medicine open knowledge engine (SPOKE): a massive knowledge graph of biomedical information. 2023 , 39,	О

60	Evidence that the PatB (CnfR) factor acts as a direct transcriptional regulator to control heterocyst development and function in the cyanobacterium Nostoc PCC 7120. 2023 , 119, 492-504	0
59	The mechanism of promoting rhizosphere nutrient turnover for arbuscular mycorrhizal fungi attributes to recruited functional bacterial assembly.	О
58	De-MISTED: Image-based classification of erroneous multiple sequence alignments using convolutional neural networks.	О
57	The genome of a vestimentiferan tubeworm (Ridgeia piscesae) provides insights into its adaptation to a deep-sea environment. 2023 , 24,	O
56	Integrated transcriptomic and metabolomic analyses reveal key metabolic pathways in response to potassium deficiency in coconut (Cocos nucifera L.) seedlings. 14,	0
55	NetSyn: genomic context exploration of protein families.	O
54	Metagenome-Assembled Genomes of Four Southern Ocean Archaea Harbor Multiple Genes Linked to Polyethylene Terephthalate and Polyhydroxybutyrate Plastic Degradation. 2023 , 12,	О
53	The EspN transcription factor is an infection-dependent regulator of the ESX-1 system inM. marinum.	О
52	De Novo Assembly and Characterization of the Transcriptome of an Omnivorous Camel Cricket (Tachycines meditationis). 2023 , 24, 4005	0
51	Transcriptome profiling reveals a global response in harmful dinoflagellate Karlodinium veneficum to naturally-occurring bacterial algicides. 10,	О
50	Chromosome-scale genome assembly of a natural diploid kiwifruit (Actinidia chinensis var. deliciosa). 2023 , 10,	0
49	The Antidepressant Sertraline Affects Cell Signaling and Metabolism in Trichophyton rubrum. 2023 , 9, 275	О
48	Effects of Maternal High-Fructose Diet on Long Non-Coding RNAs and Anxiety-like Behaviors in Offspring. 2023 , 24, 4460	О
47	In silico analysis of highly disordered human IRS1 protein 3D structure to uncover new target for Metformin to ameliorate diabetes.	O
46	In Silico Characterization of the Secretome of the Fungal Pathogen Thielaviopsis punctulata, the Causal Agent of Date Palm Black Scorch Disease. 2023 , 9, 303	О
45	Analysis of lncRNA and mRNA expression profiling in immature and mature DeZhou donkey (equine Taurus) testes.	0
44	Genome-wide identification of the auxin transporter gene families in sweet potato (Ipomoea batatas) and their expression during tuberization.	0
43	Dual domestications and origin of traits in grapevine evolution. 2023 , 379, 892-901	1

42	Pangenomic analysis identifies structural variation associated with heat tolerance in pearl millet. 2023 , 55, 507-518	0
41	Integrating Multi-Omics Analysis Reveals the Regulatory Mechanisms of White⊠iolet Mutant Flowers in Grape Hyacinth (Muscari latifolium). 2023 , 24, 5044	o
40	Transcriptome analysis and exploration of genes involved in the biosynthesis of secoiridoids in Gentiana rhodantha. 11, e14968	O
39	Chromosome-level genome assembly of Phrynocephalus forsythii using third-generation DNA sequencing and Hi-C analysis. 2023 , 30,	o
38	Genome-wide identification of bHLH transcription factors and their response to salt stress in Cyclocarya paliurus. 14,	O
37	Inference and reconstruction of the heimdallarchaeial ancestry of eukaryotes.	o
36	Genomic analysis of cultivated infant microbiomes identifiesBifidobacterium2Fucosyllactose utilization can be facilitated by co-existing species.	O
35	Biochemical Characterization of an Endoglucanase GH7 from Thermophile Thermothielavioides terrestris Expressed on Aspergillus nidulans. 2023 , 13, 582	o
34	Genome-wide characterization of trichome birefringence-like genes provides insights into fiber yield improvement. 14,	0
33	Revealing evolution of tropane alkaloid biosynthesis by analyzing two genomes in the Solanaceae family. 2023 , 14,	О
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21	Design of anArabidopsis thalianareporter line to detect heat-sensing and signaling mutants.	O
20	CsrA Shows Selective Regulation of sRNA-mRNA Networks.	O
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