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505	Similar adaptative mechanism but divergent demographic history of four sympatric desert rodents in Eurasian inland. 2023 , 6,	0
504	Integrated Transcriptome and Metabolome Provide Insights into Flavonoids Biosynthesis in 'P113', a New Purple Tea of <i>Camellia tachangensis</i>. 2023 , 1-11	0
503	Nationwide genomic surveillance reveals the prevalence and evolution of honeybee viruses in China. 2023 , 11,	o
502	Mycoparasites, gut dwellers, and saprotrophs: Phylogenomic reconstructions and comparative analyses of Kickxellomycotina fungi.	0
501	Upregulation of MAP kinase HOG1 gene of white-rot fungus Phlebia sp. MG-60 inhibits the ethanol fermentation and mycelial growth.	0
500	Knockdown of CYP9A9 increases the susceptibility to lufenuron, methoxyfenozide and a mixture of both in Spodoptera exigua.	0
499	Metavirome of 31 tick species provides a compendium of 1,801 RNA virus genomes. 2023 , 8, 162-173	О

498	From head to rootlet: comparative transcriptomic analysis of a rhizocephalan barnacle Peltogaster reticulata (Crustacea: Rhizocephala). 11, 583	О
497	Diversity of RNA viruses of three dominant tick species in North China. 9,	O
496	Auxin alleviates cadmium toxicity by increasing vacuolar compartmentalization and decreasing long-distance translocation of cadmium in Poa pratensis. 2023 , 153919	О
495	Virome analyses by next-generation sequencing (NGS) in chilli (Capsicum anuumL.) presented with diverse symptoms phenotype revealed the association of seven plant viruses.	O
494	Transcriptomic analysis of seed development in Paysonia auriculata (Brassicaceae) identifies genes involved in hydroxy fatty acid biosynthesis. 13,	О
493	The complete genome assemblies of 19 insect pests of worldwide importance to agriculture. 2023 , 105339	O
492	Liver transcriptome analysis reveals the energy regulation and functional impairment of Onychosoma sima during starvation.	О
491	Arabidopsis TRB proteins function in H3K4me3 demethylation by recruiting JMJ14.	O
490	Genomic resources enable insight into the developmental transcriptome of the blastoclad fungus, Coelomomyces lativittatus, an obligate parasite of mosquitoes and microcrustaceans.	О
489	Biased mutations and gene losses underlying diploidization of the tetraploid broomcorn millet genome.	O
488	The genome of Lyophyllum shimeji provides insight into the initial evolution of ectomycorrhizal fungal genomes.	O
487	Comparative transcriptome analyses of three Gentiana species provides signals for the molecular footprints of selection effects and the phylogenetic relationships.	O
486	Senescence in dahlia flowers is regulated by a complex interplay between flower age and floret position. 13,	О
485	Disruption of the standard kinetochore in holocentricCuscutaspecies.	O
484	The Aphelenchoides genomes reveal substantial horizontal gene transfers in the last common ancestor of free-living and major plant parasitic nematodes.	О
483	The Histone Chaperone Network Is Highly Conserved in Physarum polycephalum. 2023 , 24, 1051	O
482	RUNX1 Upregulation Causes Mitochondrial Dysfunction via Regulating the PI3K-Akt Pathway in iPSC from Patients with Down Syndrome. 2023 ,	О
481	Urate oxidase from tea microbe Colletotrichum camelliae is involved in the caffeine metabolism pathway and plays a role in fungal virulence. 9,	1

480	Comparative analysis of root anatomical structure, chemical components and differentially expressed genes between early bolting and unbolting in Peucedanum praeruptorum Dunn. 2023 , 110557	O
479	Chromosome-level genome assembly of a high-altitude-adapted frog (Rana kukunoris) from the Tibetan plateau provides insight into amphibian genome evolution and adaptation. 2023 , 20,	O
478	Adaptive evolution of carnivory inNepenthespitcher plants: a comparative transcriptomics and proteomics perspective.	0
477	Transcriptome profiling of two contrasting pigeon pea (Cajanus cajan) genotypes in response to waterlogging stress. 13,	2
476	Role of the blue light receptor gene Icwc-1 in mycelium growth and fruiting body formation of Isaria cicadae. 13,	0
475	Differentially expressed genes in head kidney of Pelteobagrus fulvidraco following Vibrio cholerae challenge. 13,	O
474	Gene Expression and Evolution in the Smalltooth Sawfish, Pristis Pectinata.	О
473	Gonad transcriptome analysis reveals the differences in gene expression related to sex-biased and reproduction of clam Cyclina sinensis. 9,	Ο
472	Revisiting the sialome of the cat flea Ctenocephalides felis. 2023 , 18, e0279070	O
471	Transcriptomic and physiological analysis of Spirodela polyrrhiza responses to sodium nitroprusside.	Ο
470	Modular transcriptional responses to environmental changes.	О
469	Iris lactea var. chinensis plant drought tolerance depends on the response of proline metabolism, transcription factors, transporters and the ROS-scavenging system. 2023 , 23,	1
468	Mechanisms of sex differentiation and sex reversal in hermaphrodite fish as revealed by the Epinephelus coioides genome.	О
467	Integrated transcriptome and proteome revealed that the declined expression of cell cycle-related genes associated with follicular atresia in geese. 2023 , 24,	O
466	Transcriptomic Analysis Provides Novel Insights into the Heat Stress-Induced Response in Codonopsis tangshen. 2023 , 13, 168	1
465	Transcriptome dynamics provides insights into divergences of photosynthesis pathway between Saccharum officinarum and Saccharum spontaneum.	O
464	Reduced effectiveness of purifying selection on new mutations in a parthenogenic terrestrial isopod (Trichoniscus pusillus).	O
463	Transcriptomic and proteomic analyses provide insights into host adaptation of a bamboo-feeding aphid. 13,	0

462	Insights from comparative transcriptome analysis in the responses of Pb-tolerant fungi Curvularia tsudae to Pb stress. 2023 , 249, 114476	О
461	Midgut transcriptomic responses to dengue and chikungunya viruses in the vectors Aedes albopictus and Aedes malayensis.	О
460	Host-microbiota interactions and responses of Metapenaeus ensis infected with decapod iridescent virus 1. 13,	О
459	A single silk and multiple pollen-expressed PMEs at the Ga1 locus modulate maize unilateral cross-incompatibility.	O
458	Screening and identification of genes associated with flight muscle histolysis of the house cricket Acheta domesticus. 13,	0
457	The genome of the oomycete Peronosclerospora sorghi, a cosmopolitan pathogen of maize and sorghum, is inflated with dispersed pseudogenes.	O
456	Natural immunity stimulation using ELICE16INDURESfi plant conditioner in field culture of soybean. 2023 , 9, e12907	1
455	Full-length transcriptome analysis provides insights into larval shell formation in Mulinia lateralis. 9,	О
454	Integrated transcriptome and proteome analyses reveal candidate genes for ginsenoside biosynthesis in Panax japonicus C. A. Meyer. 13,	0
453	Integrated comparative transcriptome and weighted gene co-expression network analysis provide valuable insights into the response mechanisms of crayfish (Procambarus clarkii) to copper stress. 2023 , 130820	О
452	Simultaneous Detection of Omicron and Other SARS-CoV-2 Variants by Multiplex PCR MassARRAY Technology.	О
451	Transcriptome analysis and gene expression analysis related to salinity-alkalinity and low temperature adaptation of Triplophysa yarkandensis. 13,	O
450	Conserved orthology in termite chemosensory gene families. 10,	О
449	Development and Characterization of Microsatellite Markers for Harpadon nehereus Based on High-Throughput Sequencing and Cross-Species Amplification in Three Myctophiformes Fishes. 2023 , 22, 181-188	O
448	Development and Characterization of SSR Markers via de Novo Transcriptome Assembly in Apocynum. hendersonii. 2023 , 20,	О
447	Nuclear Genome Sequence and Gene Expression of an Intracellular Fungal Endophyte Stimulating the Growth of Cranberry Plants. 2023 , 9, 126	О
446	Chitosan oligosaccharide induces plant resistance gene expression inPinus massoniana.	О
445	Annotation of the Turnera subulata (Passifloraceae) Draft Genome Reveals the S-Locus Evolved after the Divergence of Turneroideae from Passifloroideae in a Stepwise Manner. 2023 , 12, 286	О

444	Magnaporthe oryzae pathotype Triticum (MoT) can act as a heterologous expression system for fungal effectors with high transcript abundance in wheat. 2023 , 13,	О
443	Discovery of novel Mamastroviruses in Bactrian camels and dromedaries reveals complex recombination history.	О
442	The Integrated mRNA and miRNA Approach Reveals Potential Regulators of Flowering Time in Arundina graminifolia. 2023 , 24, 1699	О
441	Full-length transcriptome of in Medicago sativa L. roots in response to drought stress. 13,	O
440	RNA sequencing and transcriptome analyses reveal differentially expressed genes in the defensive glands of the medicinal beetle Blaps rhynchopetera.	О
439	The gyrfalcon (Falcon rusticolus) genome.	O
438	Micro and macroevolution of sea anemone venom phenotype. 2023 , 14,	1
437	Integrated transcriptomic and metabolomic analyses revealed the molecular mechanism of terpenoid formation for salicylic acid resistance in Pulsatilla chinensis callus. 13,	O
436	The venom composition and parthenogenesis mechanism of the parasitoid wasp Microctonus hyperodae, a declining biocontrol agent. 2023 , 153, 103897	О
435	Comparative transcriptional analysis of metabolic pathways and mechanisms regulating essential oil biosynthesis in four elite Cymbopogon spp 2023 , 229, 943-951	O
434	Metabolomic and transcriptomic analysis reveal high solar irradiance inhibited the melanin formation in persimmon fruit peel. 2023 , 207, 105218	1
433	Transcriptomic response to GnRH down regulation by RNA interference in clam Ruditapes philippinarum, suggest possible role in reproductive function. 2023 , 277, 111367	O
432	De novo transcriptome analysis of bagworm Metisa plana from highly infested oil palm estate in Perak revealed detoxification genes and potential insecticide targets. 2023 , 26, 102039	O
431	Dissection of the Inner Female and Male Cone Differentiation Mechanisms at Different Development Stages in Masson Pine (Pinus massoniana Lamb.) by RNA-Seq Techniques. 2022 , 16, 668-675	O
430	Transcriptomic Analysis of Ulva prolifera in Response to Salt Stress. 2023 , 15, 63	О
429	Starvation Affects the Muscular Morphology, Antioxidant Enzyme Activity, Expression of Lipid Metabolism-Related Genes, and Transcriptomic Profile of Javelin Goby (Synechogobius hasta). 2022 , 2022, 1-20	O
428	Near-chromosomal de novo assembly of Bengal tiger genome reveals genetic hallmarks of apex predation. 2022 , 12,	0
427	The Jasmine (Jasminum sambac) Genome Provides Insight into the Biosynthesis of Flower Fragrances and Jasmonates. 2022 ,	1

426	Molecular machineries of ciliogenesis, cell survival, and vasculogenesis are differentially expressed during regeneration in explants of the demosponge Halichondria panicea. 2022 , 23,	О
425	Chromosome-level assembly of triploid genome of sichuan pepper (Zanthoxylum armatum). 2022,	О
424	Isolation and characterization of 16 microsatellite loci from transcriptome-derived sequences of the topmouth culter (Culter alburnus Basilewsky). 2022 ,	0
423	Phylotranscriptomic analyses of mycoheterotrophic monocots show a continuum of convergent evolutionary changes in expressed nuclear genes from three independent nonphotosynthetic lineages.	o
422	High-quality nuclear genome and mitogenome ofBipolaris sorokinianastrain LK93, a devastating pathogen causing wheat root rot.	O
421	Resistance to white spot syndrome virus in the European shore crab is associated with suppressed virion trafficking and heightened immune responses. 13,	1
420	The redlegged earth mite draft genome provides new insights into pesticide resistance evolution and demography in its invasive Australian range.	0
419	Variation in heat shock protein 40 kDa relates to divergence in thermotolerance among cryptic rotifer species. 2022 , 12,	О
418	De-novo transcriptome assembly and analysis of lettuce plants grown under red, blue or white light. 2022 , 12,	O
417	Postglacial adaptations enabled colonization and quasi-clonal dispersal of ammonia-oxidizing archaea in modern European large lakes. 2023 , 9,	1
416	Low-level cadmium exposure induced hormesis in peppermint young plant by constantly activating antioxidant activity based on physiological and transcriptomic analyses. 14,	0
415	Physiological and Transcriptomic Response of Asiatic Hard Clam Meretrix meretrix to the Harmful Alga Heterosigma akashiwo. 2023 , 8, 67	1
414	De Novo Transcriptome Profiling of Naegleria fowleri Trophozoites and Cysts via RNA Sequencing. 2023 , 12, 174	O
413	The Pathology and Splenic Transcriptome Profiling of Trionyx sinensis Challenged with Bacillus cereus. 2023 , 8, 84	O
412	Transcriptomic Profiling Reveals Key Genes of Halophyte Apocyni Veneti Folium (Apocynum venetum L.) and Regulatory Mechanism of Salt Tolerance.	0
411	A single-cell RNA-seq analysis of early larval cell-types of the starfish, Patiria pectinifera: Insights into evolution of the chordate body plan. 2023 ,	o
410	Antibody sequences assembly method based on weighted de Bruijn graph. 2023 , 20, 6174-6190	0
409	Protein-Based Biological Materials: Molecular Design and Artificial Production.	O

408	Phylotranscriptomics Shed Light on Intrageneric Relationships and Historical Biogeography of Ceratozamia (Cycadales). 2023 , 12, 478	0
407	Identification and expression analyses of the olfactory-related genes in different tissues' transcriptome of a predacious soldier beetle, Podabrus annulatus (Coleoptera, Cantharidae).	O
406	Integrated metabolomic and transcriptomic study unveils the gene regulatory mechanisms of sugarcane growth promotion during interaction with an endophytic nitrogen-fixing bacteria. 2023 , 23,	0
405	Transcriptional Ontogeny Platform of Sex Determination/Sex Differentiation Genes in Almaco Jack Larvae.	O
404	The first homosporous lycophyte genome revealed the association between the dynamic accumulation of LTR-RTs and genome size variation.	0
403	Germline-related molecular phenotype in Metazoa: conservation and innovation highlighted by comparative transcriptomics. 2023 , 14,	O
402	Nematode gene annotation by machine-learning-assisted proteotranscriptomics enables proteome-wide evolutionary analysis. 2023 , 33, 112-128	0
401	Deep ocean water has significant physiological effects on squid Todarodes pacificus.	O
400	Phosphorus availability and planting patterns regulate soil microbial effects on plant performance in a semiarid steppe.	0
399	Best Practices for Comprehensive Annotation of Neuropeptides of Gryllus bimaculatus. 2023 , 14, 121	O
398	High-quality Fagopyrum esculentum genome provides insights into the flavonoid accumulation among different tissues and self-incompatibility.	0
397	Probing the plant transcriptomes for novel waikaviral sequences broadens the host range and genetic diversity of waikaviruses.	O
396	The MOM1 complex recruits the RdDM machinery via MORC6 to establishde novoDNA methylation.	О
395	Phylogenomic insights into the reticulate evolution of Camellia sect. Paracamellia Sealy (Theaceae).	O
394	Draft Genome Sequence of Aduncisulcus paluster, a Free-Living Microaerophilic Eukaryote Belonging to the Fornicata.	0
393	Evolutionary transcriptomics reveals longevity mostly driven by polygenic and indirect selection in mammals.	O
392	Genes related to osmoregulation and antioxidation play important roles in the response of Trollius chinensis seedlings to saline-alkali stress. 14,	0
391	Complex scaffold remodeling in plant triterpene biosynthesis. 2023 , 379, 361-368	2

390	Inversions maintain differences between migratory phenotypes of a songbird. 2023, 14,	0
389	Multi-Omic Profiling, Structural Characterization, and Potent Inhibitor Screening of Evasion-Related Proteins of a Parasitic Nematode, Haemonchus contortus, Surviving Vaccine Treatment. 2023 , 11, 411	O
388	Progress in molecular biology and translational science: Epigenetics in cardiovascular health and disease. 2023 ,	0
387	Inference of Ancient Polyploidy Using Transcriptome Data. 2023 , 47-76	O
386	Pollinator and host sharing lead to hybridization and introgression in Panamanian free-standing figs, but not in their pollinator wasps. 2023 , 13,	0
385	Drought-induced CsMYB6 interacts with CsbHLH111 to regulate anthocyanin biosynthesis in Chaenomeles speciosa. 2023 , 175,	1
384	Characterization and Application of EST-SSR Markers Developed from Transcriptome Sequences in Elymus breviaristatus (Poaceae: Triticeae). 2023 , 14, 302	0
383	RNA sequencing indicates widespread conservation of circadian clocks in marine zooplankton. 2023 , 5,	O
382	Analysis of oxidase activity and transcriptomic changes related to cutting propagation of hybrid larch. 2023 , 13,	0
381	Comparative susceptibility of SARS-CoV-2, SARS-CoV, and MERS-CoV across mammals.	O
380	Genome Assembly and Comparative Analysis of the Egg Parasitoid Wasp Trichogramma dendrolimi Shed Light on the Composition and Evolution of Olfactory Receptors and Venoms. 2023 , 14, 144	0
379	Correlated evolution of social organization and lifespan in mammals. 2023, 14,	O
378	The Effect of Trichoderma harzianum Hypovirus 1 (ThHV1) and Its Defective RNA ThHV1-S on the Antifungal Activity and Metabolome of Trichoderma koningiopsis T-51. 2023 , 9, 175	0
377	Transcriptome Sequencing of Broussonetia papyrifera Leaves Reveals Key Genes Involved in Flavonoids Biosynthesis. 2023 , 12, 563	O
376	A Zinc Finger Motif in the P1 N Terminus, Highly Conserved in a Subset of Potyviruses, Is Associated with the Host Range and Fitness of Telosma Mosaic Virus.	O
375	Improving the genome and proteome annotations of the marine model diatom Thalassiosira pseudonana using a proteogenomics strategy.	O
374	Norgestrel causes digestive gland injury in the clam Mactra veneriformis: An integrated histological, transcriptomics, and metabolomics study. 2023 , 871, 162110	0
373	Transcriptional responses to 2,4-D herbicide treatment of a Eurasian (Myriophyllum spicatum) and a hybrid (M. spicatum IM. sibiricum) genotype of watermilfoil that differ in their sensitivity to 2,4-D. 2023 , 186, 103631	O

372	Investigating the resistance responses to Alternaria brassicicola in 'Korla' fragrant pear fruit induced by a biocontrol strain Bacillus subtilis Y2. 2023 , 199, 112293	0
371	Transcriptome-based analysis reveals the key genes of sesquiterpene glycosylation in Dendrobium nobile. 43,	O
370	Short structural variation fuelled CAM evolution within an explosive bromeliad radiation.	O
369	RNA sequencing least shrew (Cryptotis parva) brainstem and gut transcripts following administration of a selective substance P neurokinin NK1 receptor agonist and antagonist expands genomics resources for emesis research. 14,	O
368	PFOS Induces Lipometabolism Change, Immune Defense, and Endocrine Disorders in Black-Spotted Frogs: Application of Transcriptome Profiling. 2023 , 15, 196	O
367	Integrative time series of cellular, humoral and molecular response revealed immunotoxicity of bifenthrin to Chinese rare minnow (Gobiocypris rarus) following Pseudomonas fluorescens challenge. 2023 , 256, 106427	O
366	Transcriptomic profiling of castes and of sexually and parthenogenetically produced reproductive females in the termite Cavitermes tuberosus. 2023 , 171, 350-360	1
365	Dynamics of annatto pigment synthesis and accumulation in seeds of Bixa orellana L. revealed by integrated chemical, anatomical, and RNA-Seq analyses.	O
364	A chromosome-level genome assembly of a model conifer plant, the Japanese cedar,Cryptomeria japonicaD. Don.	0
363	Reverse engineering environmental metatranscriptomes clarifies best practices for eukaryotic assembly. 2023 , 24,	O
362	Telomerase RNA plays a major role in the completion of the life cycle in Ustilago maydis and shares conserved domains with other Ustilaginales. 2023 , 18, e0281251	0
361	Toxicological mechanism of cadmium in the clam Ruditapes philippinarum using combined ionomic, metabolomic and transcriptomic analyses. 2023 , 323, 121286	O
360	Gossypium purpurascens genome provides insight into the origin and domestication of upland cotton. 2023 ,	0
359	Transcriptomic analysis reveals key genes and pathways corresponding to Cd and Pb in the hyperaccumulator Arabis paniculata. 2023 , 254, 114757	O
358	Effects of heat and hyposalinity on the gene expression in Acropora pruinosa larvae. 10,	0
357	The remarkably enzyme-rich venom of the Big Bend Scorpion (Diplocentrus whitei). 2023 , 226, 107080	O
356	Metatranscriptomic Sequencing Reveals Host Species as an Important Factor Shaping the Mosquito Virome. 2023 , 11,	O
355	Effect of interfering TOR signaling pathway on the biosynthesis of terpenoids in Salvia miltiorrhiza Bge. 2023 , 18,	O

354	A conserved gene regulatory network controls root epidermal cell patterning in superrosid species.	O
353	Comparative transcriptome analysis revealed genes involved in the sexual size dimorphisms and expressed sequence tag-Simple Sequence Repeat loci validation in Odorrana graminea. 11,	O
352	The Blinin Accumulation Promoted by CbMYB32 Involved in Conyza blinii Resistance to Nocturnal Low Temperature. 2023 , 24, 7143	0
351	Venomous Noodles: evolution of toxins in Nemertea through positive selection and gene duplication.	O
350	Sexual dimorphism-related gene expression analysis based on the transcriptome in Gynaephora qinghaiensis, a pest of grassland on the Qinghai-Tibet Plateau. 2023 , 102083	0
349	The little skate genome and the evolutionary emergence of wing-like fins.	O
348	Mechanisms of Phaeocystis globosa blooms in the Beibu Gulf revealed by metatranscriptome analysis. 2023 , 124, 102407	0
347	Chromosome-level genome of the bean bug Megacopta cribraria in native range, provides insights into adaptation and pest management. 2023 , 237, 123989	O
346	Combined metabolomics and transcriptomics analysis reveals the mechanism underlying blue light-mediated promotion of flavones and flavonols accumulation in Ligusticum chuanxiong Hort. microgreens. 2023 , 242, 112692	0
345	Broadening the host range and genetic diversity of waikaviruses. 2023 , 582, 106-113	O
344	Two different anti-algal control mechanisms in Microcystis aeruginosa induced by robinin or tannin rich plants. 2023 , 323, 138202	0
343	Molecular characterization of diploid YY sperm related to its developmental advantages. 2023 , 570, 739397	O
342	Jinfeng pills ameliorate premature ovarian insufficiency induced by cyclophosphamide in rats and correlate to modulating IL-17A/IL-6 axis and MEK/ERK signals. 2023 , 307, 116242	0
341	Advances in the understanding of Blattodea evolution: Insights from phylotranscriptomics and spermathecae. 2023 , 182, 107753	O
340	How does particulate matter affect plant transcriptome and microbiome?. 2023, 209, 105313	0
339	Physiological and transcriptome analysis reveals key genes and molecular basis into heterosis of kenaf (Hibiscus cannabinus L.) under drought stress. 2023 , 209, 105293	O
338	Analysis of oil synthesis pathway in Cyperus esculentus tubers and identification of oleosin and caleosin genes. 2023 , 284, 153961	0
337	The effect of acute toxicity from tributyltin on Liza haematocheila liver: Energy metabolic disturbance, oxidative stress, and apoptosis. 2023 , 258, 106506	O

336	Population genomics indicate three different modes of divergence and speciation with gene flow in the green-winged teal duck complex. 2023 , 182, 107733	0
335	Phylogenetic and functional properties of hagfish neurohypophysial hormone receptors distinct from their jawed vertebrate counterparts. 2023 , 336, 114257	0
334	Transcriptome analysis of two bloom-forming Prorocentrum species reveals physiological changes related to light and temperature. 2023 , 125, 102421	0
333	The transcriptional mechanism responding to air particulate matter in Laurus nobilis (L.). 2023 , 210, 105304	Ο
332	Integrated analysis of smRNAome, transcriptome, and degradome data to decipher microRNAs regulating costunolide biosynthesis in Saussurea lappa. 2023 , 331, 111689	0
331	Late Cenozoic history and the role of Beringia in assembling a Holarctic cestode species complex. 2023 , 183, 107775	O
330	Physiological and transcriptomic responses of two Artemisia californica populations to drought: implications for restoring drought-resilient native communities. 2023 , 43, e02466	0
329	Identification of GnRH-like peptide and its potential signaling pathway involved in the oocyte meiotic maturation in the Chinese mitten crab, Eriocheir sinensis. 2023 , 239, 124326	O
328	Legume-bacteria-soil interaction networks linked to improved plant productivity and soil fertility in intercropping systems. 2023 , 196, 116504	0
327	Transcriptome analysis reveals key metabolic pathways and gene expression involving in cell wall polysaccharides-disassembling and postharvest fruit softening in custard apple (Annona squamosa L.). 2023 , 240, 124356	0
326	Transcriptomic analysis of Mythimna separata ovaries and identification of genes involved in reproduction. 2023 , 46, 101075	0
325	Transcriptome analysis reveals dysregulated gene expression networks in Sertoli cells of cattle-yak hybrids. 2023 , 203, 33-42	O
324	Identification of 14 glutathione S-transferase genes from Lasioderma serricorne and characterization of LsGSTe1 involved in lambda-cyhalothrin detoxification. 2023 , 193, 105425	0
323	Integrated miRNA-mRNA analysis reveals the molecular mechanism in mandarin fish (Siniperca chuatsi) in response to fresh baits and artificial diets feeding. 2023 , 30, 101554	О
322	Integrated biochemical and transcriptomic analysis reveals the effects of Burkholderia sp. SRB-1 on cadmium accumulating in Chrysopogon zizanioides L. under Cd stress. 2023 , 337, 117723	0
321	Metabolomic and transcriptomic responses of Adiantum (Adiantum nelumboides) leaves under drought, half-waterlogging, and rewater conditions. 14,	O
320	Self-Healable Spider Dragline Silk Materials.	0
319	Combined Study of Transcriptome and Metabolome Reveals Involvement of Metabolites and Candidate Genes in Flavonoid Biosynthesis in Prunus avium L 2023 , 9, 463	0

318	Identification of Candidate Genes Involved in the Determinism of Pollen Grain Aperture Morphology by Comparative Transcriptome Analysis in Papaveraceae. 2023 , 12, 1570	O
317	Chromosome-level genome assembly and population genomic resource to accelerate orphan crop lablab breeding. 2023 , 14,	O
316	The evolution and structure of snake venom phosphodiesterase (svPDE) highlight its importance in venom actions. 12,	O
315	Single-cell transcriptome reveals cell division-regulated hub genes in the unicellular eukaryote Paramecium. 2023 , 89, 125978	Ο
314	Sources, bioaccumulation, and toxicity mechanisms of cadmium in Chlamys farreri. 2023, 453, 131395	0
313	The diurnal salivary glands transcriptome of Dermacentor nuttalli from the first four days of blood feeding. 2023 , 14, 102178	Ο
312	Acute hypoxia induces reduction of algal symbiont density and suppression of energy metabolism in the scleractinian coral Pocillopora damicornis. 2023 , 191, 114897	О
311	Integrated metabolomic and transcriptomic analysis of specialized metabolites and isoflavonoid biosynthesis in Sophora alopecuroides L. under different degrees of drought stress. 2023 , 197, 116595	Ο
310	The phylogeny and divergence times of leaf-mining flies (Diptera: Agromyzidae) from anchored phylogenomics. 2023 , 184, 107778	О
309	Genomics and Metabolomics: A Strategy for Elucidation of Metabolic Pathways in Medicinal Plants. 2022 , 343-360	Ο
308	Nitric oxide synthase (NOS)-dependent nitric oxide generation is involved in putrescine-induced chilling tolerance of Anthurium andraeanum. 2023 , 312, 111849	0
307	Parallel Evolution of Sex-Linked Genes across XX/XY and ZZ/ZW Sex Chromosome Systems in the Frog Glandirana rugosa. 2023 , 14, 257	Ο
306	Pine has two glutamine synthetase paralogs, GS1b.1 and GS1b.2, exhibiting distinct biochemical properties. 2023 , 113, 1330-1347	О
305	Transcriptome analysis of growth and shell color between two genetic variants of Corbicula fluminea with different shell colors. 2023 , 45, 101056	O
304	Citrus genomic resources unravel putative genetic determinants of Huanglongbing pathogenicity. 2023 , 26, 106024	O
303	Novel Proposals for FAIR, Automated, Recommendable, and Robust Workflows. 2022,	O
302	Annelid functional genomics reveal the origins of bilaterian life cycles. 2023, 615, 105-110	1
301	Heat shock protein 70 and Cathepsin B genes are involved in the thermal tolerance of Aphis gossypii.	O

300	Genome Sequencing. 2021 , 298-317	O
299	Light-Induced Flavonoid Biosynthesis in Sinopodophyllum hexandrum with High-Altitude Adaptation. 2023 , 12, 575	O
298	Mapping of quantitative trait locus reveals PsXI gene encoding xylanase inhibitor as the candidate gene for bruchid (Callosobruchus spp.) resistance in pea (Pisum sativum L.). 14,	0
297	Contaminants of emerging concern in the Maumee River and their effects on freshwater mussel physiology. 2023 , 18, e0280382	1
296	The chromosome-level genome assembly of lance asiabell (Codonopsis lanceolata), a medicinal and vegetable plant of the Campanulaceae family. 14,	О
295	Immune priming prior to pathogen exposure sheds light on the relationship between host, microbiome and pathogen in disease. 2023 , 10,	1
294	Naegleria genus pangenome reveals new structural and functional insights into the versatility of these free-living amoebae. 13,	O
293	Combined analysis of multi-omics reveals the potential mechanism of flower color and aroma formation in Macadamia integrifolia. 13,	O
292	In-situ fabrication of a three-dimensional nanopalladium network into a biocathode enhances chloramphenicol degradation. 2023 , 459, 141656	0
291	Chromosome-level genomes of multicellular algal sisters to land plants illuminate signaling network evolution.	O
290	Identification, classification and characterization of the dermonecrotic toxins in venom glands of Hottentotta saulcyi, Androctonus crassicauda and Hemiscorpius lepturus using transcriptome analysis.	О
289	Novel canonical and non-canonical viral antigens extend current targets for immunotherapy of HPV-driven cervical cancer. 2023 , 26, 106101	O
288	Whole-genome sequence of synthetically derived Brassica napus inbred cultivar Da-Ae. 2023, 13,	O
287	Develop a preliminary core germplasm with the novel polymorphism EST-SSRs derived from three transcriptomes of colored calla lily (Zantedeschia hybrida). 14,	O
286	HiMAP2 : Identifying phylogenetically informative genetic markers from diverse genomic resources.	O
285	Proteomic and Transcriptomic Responses of the Desiccation-Tolerant Moss Racomitrium canescens in the Rapid Rehydration Processes. 2023 , 14, 390	O
284	Transcriptome analysis of Saposhnikovia divaricata and mining of bolting and flowering genes. 2023 ,	О
283	Characterization of the microbiota dynamics associated with Moniliophthora roreri, causal agent of cocoa frosty pod rot disease, reveals new viral species. 13,	O

282	Chromosome-level genome assembly of goose provides insight into the adaptation and growth of local goose breeds. 2022 , 12,	Ο
281	Effects of testis testosterone deficiency on gene expression in the adrenal gland and skeletal muscle of ducks. 1-9	Ο
280	De novo transcriptome assembly from the nodal root growth zone of hydrated and water-deficit stressed maize inbred line FR697. 2023 , 13,	0
279	Differential expression of some termite neuropeptides and insulin/IGF-related hormones and their plausible functions in growth, reproduction and caste determination.	O
278	A novel insight of Picrorhiza kurroa miRNAs in human cystic fibrosis: A transcriptome-wide cross-kingdom study. 2023 , 35, 201153	0
277	Simultaneous detection of omicron and other SARS-CoV-2 variants by multiplex PCR MassARRAY technology. 2023 , 13,	1
276	Screening and Analyzing of Genes and Signaling Pathways Associated with Size Differentiation of Adult Male Prawn Macrobrachium nipponense. 2023 , 2023, 1-16	0
275	Sequences and Genome-Wide Analysis of mRNA and microRNA Expression in Tea (Camellia sinensis) Leaves in Response to Epicoccum sorghinum Infection.	O
274	Transcriptomic Analysis and Functional Gene Expression in Different Stages of Gonadal Development of Macrobrachium rosenbergii. 2023 , 8, 94	0
273	De novo transcriptome assemblies of C3 and C4 non-model grass species reveal key differences in leaf development. 2023 , 24,	Ο
272	De novo Genome Assembly of Auanema melissensis, a Trioecious Free-Living Nematode. 2023 , 54,	Ο
271	Transcriptomic analysis of polyketide synthesis in dinoflagellate, Prorocentrum lima. 2023 , 123, 102391	Ο
270	Potential of Alpha-(争Solanine as a Natural Inhibitor of Fungus Causing Leaf Spot Disease in Strawberry. 2023 , 13, 450	Ο
269	Phylotranscriptomics of Swertiinae (Gentianaceae) reveals that key floral traits are not phylogenetically correlated.	0
268	Gene expression responses of Bactrocera tryoni larvae feeding on different ripening stages of tomato fruit. 2023 , 147, 205-230	Ο
267	Woody encroachment affects multiple dimensions of ant diversity in a neotropical savanna.	0
266	MiRNA Profiling and Its Potential Roles in Rapid Growth of Velvet Antler in Gansu Red Deer (Cervus elaphus kansuensis). 2023 , 14, 424	0
265	Insights into the convergent evolution of fructan biosynthesis in angiosperms from the highly characteristic chicory genome. 2023 , 238, 1245-1262	O

264	Integration of miRNA and mRNA expression profiles in Asian spongy moth Lymantria dispar in response to cyantraniliprole. 2023 , 191, 105364	O
263	Uncovering a Complex Virome Associated with the Cacao Pathogens Ceratocystis cacaofunesta and Ceratocystis fimbriata. 2023 , 12, 287	O
262	Dissecting the genetic basis of heterosis in elite super-hybrid rice.	O
261	Absence of microbiome triggers extensive changes in the transcriptional profile of Hermetia illucens during larval ontology. 2023 , 13,	O
260	Development of unigene-derived SSR markers from RNA-seq data of Uraria lagopodioides (Fabaceae) and their application in the genus Uraria Desv. (Fabaceae). 2023 , 23,	О
259	Evaluating the Performance of Widely Used Phylogenetic Models for Gene Expression Evolution.	O
258	Molecular Regulatory Mechanism of the Iron-Ion-Promoted Asexual Sporulation of Antrodia cinnamomea in Submerged Fermentation Revealed by Comparative Transcriptomics. 2023 , 9, 235	О
257	Rickettsia parkeri hijacks tick hemocytes to manipulate cellular and humoral transcriptional responses. 14,	O
256	GF14f gene is negatively associated with yield and grain chalkiness under rice ratooning. 14,	O
255	Integrative mRNA-miRNA interaction analysis associated with the immune response of Strongylocentrotus intermedius to Vibrio harveyi infection. 2023 , 134, 108577	O
254	Genotyping of two congeneric bitterling fish species by nuclear SNP markers and the detection of hybridization in a sympatric region.	O
253	Molecular characterization of horse nettle virus A, a new member of subgroup B of the genus Nepovirus. 2023 , 168,	O
252	The genome of a vestimentiferan tubeworm (Ridgeia piscesae) provides insights into its adaptation to a deep-sea environment. 2023 , 24,	O
251	Response of the obligate halophile fungus Aspergillus loretoensis to stress salinity. 2023 , 11, 26-33	O
250	A Mitosome With Distinct Metabolism in the Uncultured Protist ParasiteParamikrocytos canceri(Rhizaria, Ascetosporea). 2023 , 15,	O
249	Identification of drought-responsive phenolic compounds and their biosynthetic regulation under drought stress in Ligularia fischeri. 14,	O
248	Physiological and Transcriptional Responses of Apocynum venetum to Salt Stress at the Seed Germination Stage. 2023 , 24, 3623	О
247	Comparative transcriptome analysis of Saposhnikovia divaricata to reveal drought and rehydration adaption strategies. 2023 , 50, 3493-3502	O

246	Development and characterization of EST-SSR markers in Rhodomyrtus tomentosa Hassk. based on transcriptome.	O
245	Physiology and transcriptome analysis of the response mechanism of Solidago canadensis to the nitrogen addition environment. 14,	Ο
244	High turnover ofde novotranscripts inDrosophila melanogaster.	O
243	A chromosome-level genome assembly of Ostrea denselamellosa provides initial insights into its evolution. 2023 , 115, 110582	O
242	Distinct regulatory networks control toxin gene expression in elapid and viperid snakes.	O
241	UDP-glycosyltransferases play a crucial role in the accumulation of alkaloids and sesquiterpene glycosides in Dendrobium nobile. 2023 , 16, 104673	O
240	Transcriptomic and metabolomic analyses provide new insights into the appropriate harvest period in regenerated bulbs of Fritillaria hupehensis. 14,	O
239	Analysis of Fowl Adenovirus 4 Transcriptome by De Novo ORF Prediction Based on Corrected Nanopore Full-Length cDNA Sequencing Data. 2023 , 15, 529	Ο
238	Transcriptome Sequencing of the Diatom Asterionellopsis thurstonii and In Silico Identification of Enzymes Potentially Involved in the Synthesis of Bioactive Molecules. 2023 , 21, 126	O
237	On the origin and evolution of RNA editing in metazoans. 2023 , 42, 112112	O
236	Differential Expression Genes of the Head Kidney and Spleen in Streptococcus iniae-Infected East Asian Fourfinger Threadfin Fish (Eleutheronema tetradactylum). 2023 , 24, 3832	0
235	Genome-Wide Identification and Expression Analysis of Calmodulin-Like Gene Family in Paspalums vaginatium Revealed Their Role in Response to Salt and Cold Stress. 2023 , 45, 1693-1711	O
234	Genomics and biochemical analyses reveal a metabolon key to 配-ODAP biosynthesis in Lathyrus sativus. 2023 , 14,	O
233	Evidence for an aquatic origin of influenza virus and the orderArticulavirales.	O
232	Transcriptome profiling reveals a global response in harmful dinoflagellate Karlodinium veneficum to naturally-occurring bacterial algicides. 10,	0
231	AMAW: automated gene annotation for non-model eukaryotic genomes. 12, 186	O
230	Comparative Transcriptome Analysis Provides Insights into the Molecular Mechanism Underlying the Effect of MeJA Treatment on the Biosynthesis of Saikosaponins in Bupleurum chinense DC 2023 , 13, 563	О
229	Liver Transcriptome Analysis Reveals Energy Regulation and Functional Impairment of Onychostoma sima During Starvation.	Ο

228	Transcriptome sequencing and gene expression analysis revealed early ovule abortion of Paeonia ludlowii. 2023 , 24,	O
227	Identification and Comparative Expression Profiles of Candidate Olfactory Receptors in the Transcriptomes of the Important Egg Parasitoid Wasp Anastatus japonicus Ashmead (Hymenoptera: Eupelmidae). 2023 , 12, 915	O
226	Pangolin genomes offer key insights and resources for the world most trafficked wild mammals.	О
225	Effect of light conditions on trophic level and gene expression of partially mycoheterotrophic orchid, Cymbidium goeringii. 2023 , 18,	O
224	Investigation of the role of TmMYB16/123 and their targets (TmMTP1/11) in the tolerance of Taxus mediato cadmium.	О
223	Ingestion of Species-Specific dsRNA Alters Gene Expression and Can Cause Mortality in the Forest Pest, Ips calligraphus. 2023 , 14, 422	O
222	Genome-Wide Identification and Expression Pattern of Cytochrome P450 Genes in the Social Aphid Pseudoregma bambucicola. 2023 , 14, 212	0
221	Transcriptome-based variations effectively untangling the intraspecific relationships and selection signals in Xinyang Maojian tea population. 14,	O
220	Evolutionary History of thePoecilia pictaSex Chromosomes. 2023 , 15,	0
219	Chromosome-scale genome assembly of a natural diploid kiwifruit (Actinidia chinensis var. deliciosa). 2023 , 10,	O
218	Genomic Epidemiology and Transmission Dynamics of Global Coxsackievirus B4. 2023 , 15, 569	O
217	Telomere-to-telomere gap-free genome assembly and chromosome segment substitution lines facilitated gene identification in wild rice.	O
216	Species boundaries and conservation implications of Cinnamomum japonicum , an endangered plant in China.	0
215	Chromosome-level genome assembly and population genomics of Mongolian racerunner (Eremias argus) provide insights into high-altitude adaptation in lizards. 2023 , 21,	O
214	Chromosome-level genome assembly of tree sparrow reveals a burst of new genes driven by segmental duplications.	O
213	Bat pluripotent stem cells reveal unusual entanglement between host and viruses. 2023 , 186, 957-974.e28	O
212	A molecular perspective on the invasibility of the southern ocean benthos: The impact of hypoxia and temperature on gene expression in South American and Antarctic Aequiyoldia bivalves. 14,	О
211	Comparative transcriptome analysis reveals the regulatory mechanisms of two tropical water lilies in response to cold stress. 2023 , 24,	O

210	Phagocytosis underpins the biotrophic lifestyle of intracellular parasites in the class Phytomyxea (Rhizaria).	O
209	A chromosome-level genome assembly for Erianthus fulvus provides insights into its biofuel potential and facilitates breeding for improvement of sugarcane. 2023 , 100562	O
208	A conserved gene regulatory network controls root epidermal cell patterning in superrosid species.	O
207	Transcriptome analysis of Ganoderma lingzhi (Agaricomycetes) response to Trichoderma hengshanicum infection. 14,	O
206	Conservation genomics reveals low connectivity among populations of threatened roseate terns (Sterna dougallii) in the Atlantic Basin.	0
205	Phylogenomics of darkling beetles (Coleoptera: Tenebrionidae) from the Atacama Desert. 11, e14848	O
204	Novel insights into plant defensin ingestion induced metabolic responses in the polyphagous insect pest Helicoverpa armigera. 2023 , 13,	O
203	Physiological and Transcriptomic Analyses Reveal the Response of Medicinal Plant Bletilla striata (Thunb. ex A. Murray) Rchb. f. via Regulating Genes Involved in the ABA Signaling Pathway, Photosynthesis, and ROS Scavenging under Drought Stress. 2023 , 9, 307	O
202	The first description of the blue swimming crab (Portunus pelagicus) transcriptome and immunological defense mechanism in response to white spot syndrome virus (WSSV). 2023 , 134, 108626	O
201	Comprehensive phylogenomic analyses reveal that order Armophorida is most closely related to class Armophorea (Protista, Ciliophora). 2023 , 182, 107737	O
200	Transcriptomic thermal plasticity underlying gonadal development in a turtle with ZZ / ZW sex chromosomes despite canalized genotypic sex determination. 2023 , 13,	O
199	Transcriptome analysis of gall oak (Quercus infectoria): De novo assembly, functional annotation and metabolic pathways analysis. 2023 , 115, 110588	O
198	Skin infectome of patients with a tick bite history. 13,	O
197	Transcriptomics explores the potential of flavonoid in non-medicinal parts of Saposhnikovia divaricata (Turcz.) Schischk. 14,	O
196	Revealing the History and Mystery of RNA-Seq. 2023, 45, 1860-1874	O
195	Full-length transcriptome sequence and SSR marker development for genetic diversity research in yellowfin seabream Acanthopagrus latus.	O
194	Microbial gene activity in straw residue amendments reveals carbon sequestration mechanisms in agricultural soils. 2023 , 179, 108994	O
193	Same same, but different: exploring the enigmatic role of the pituitary adenylate cyclase-activating polypeptide (PACAP) in invertebrate physiology.	O

192	A parasitic fungus employs mutated eIF4A to survive on rocaglate-synthesizing Aglaia plants. 12,	O
191	Comparative Transcriptome Analysis Identified Potential Genes and Transcription Factors for Flower Coloration in Kenaf (Hibiscus cannabinus L.). 2023 , 13, 715	O
190	Genome assembly of the deep-sea coralLophelia pertusa.	O
189	Full-length transcriptome sequencing reveals extreme incomplete annotation of the goat genome.	O
188	Comparative Transcriptome Analysis of the Differential Effects of Florpyrauxifen-Benzyl Treatment on Phytohormone Transduction between Florpyrauxifen-Benzyl-Resistant and -Susceptible Barnyard Grasses (Echinochloa crus-galli (L.) P. Beauv). 2023 , 13, 702	0
187	Glutathione S-transferase gene diversity and their regulation by Nrf2 in Chinese mitten crab (Eriocheir sinensis) during nitrite stress. 2023 , 864, 147324	O
186	Transcriptome and molecular regulatory mechanisms analysis of gills in the black tiger shrimp Penaeus monodon under chronic low-salinity stress. 14,	O
185	Transcriptome sequencing leads to an improved understanding of the infection mechanism of Alternaria solani in potato. 2023 , 23,	O
184	Transcriptomic responses of sponge holobionts to in situ, seasonal anoxia and hypoxia.	O
183	Deep origins of eukaryotic multicellularity revealed by the Acrasis kona genome and developmental transcriptomes.	O
182	Comparative Transcriptomic Analysis Reveals the Molecular Responses in Two Contrasting Hazelnut Varieties against Botrytis cinerea Infection. 2023 , 14, 493	O
181	Dual domestications and origin of traits in grapevine evolution. 2023 , 379, 892-901	1
180	Pangenomic analysis identifies structural variation associated with heat tolerance in pearl millet. 2023 , 55, 507-518	O
179	The enormous repetitive Antarctic krill genome reveals environmental adaptations and population insights. 2023 , 186, 1279-1294.e19	O
178	Key innovations and the diversification of Hymenoptera. 2023 , 14,	O
177	Photoreceptor genes in a trechine beetle, Trechiama kuznetsovi, living in the upper hypogean zone.	O
176	The triticale mature pollen and stigma proteomes lassembling the proteins for a productive encounter. 2023 , 278, 104867	O
175	Transcriptomics and Proteomics of Haemonchus contortus in Response to Ivermectin Treatment. 2023 , 13, 919	O

174	Metatranscriptomics and metabarcoding reveal spatiotemporal shifts in fungal communities and their activities in Chinese coastal waters.	Ο
173	A gene silencing screen uncovers diverse tools for targeted gene repression in Arabidopsis. 2023 , 9, 460-472	O
172	Cutaneous transcriptomic profiling and candidate pigment genes in the wild discus (Symphysodon spp.). 1-19	O
171	Non-negligible Effect of Native Rhizobacteria on Cooperation with Plant Growth Regulators Improve Tolerance to Cadmium: A Case Study Using Duckweed Spirodela polyrhiza as Indicating Plant.	O
170	Identification of the NA+/K+-ATPase ⊞soforms in Six Species of Poison Dart Frogs and their Sensitivity to Cardiotonic Steroids. 2023 , 49, 116-132	0
169	First insights into theAurelia auritatranscriptome response upon manipulation of its microbiome.	O
168	Integrated analysis of metabolome and transcriptome reveals key candidate genes involved in flavonoid biosynthesis in Pinellia ternata under heat stress.	0
167	LED omics in Rocket Salad (Diplotaxis tenuifolia): Comparative Analysis in Different Light-Emitting Diode (LED) Spectrum and Energy Consumption. 2023 , 12, 1203	О
166	Seasonal gene-expression signatures of delayed fertilization in Fagaceae.	0
165	Identifying Genes Associated with Female Flower Development of Phellodendron amurense Rupr. Using a Transcriptomics Approach. 2023 , 14, 661	O
164	A transcriptional activator effector of Ustilago may disregulates hyperplasia in maize during pathogen-induced tumor formation.	0
163	Post-secretory synthesis of a natural analog of iron-gall ink in the black nectar of Melianthus spp	Ο
162	Transcriptome analysis and exploration of genes involved in the biosynthesis of secoiridoids in Gentiana rhodantha. 11, e14968	0
161	Species Delimitation Under Allopatry: Genomic Divergences Within and Across Continents in Lepidoptera.	O
160	LSTrAP-denovo: Automated Generation of Transcriptome Atlases for Eukaryotic Species Without Genomes.	0
159	Contrasting Metabolisms in Green and White Leaf Sectors of Variegated Pelargonium zonaleAn Integrative Transcriptomic and Metabolomic Study. 2023 , 24, 5288	O
158	Epidermal threads reveal the origin of hagfish slime. 12,	0
157	Upregulation of tandem duplicated BoFLC1 genes is associated with the non-flowering trait in Brassica oleracea var. capitata. 2023 , 136,	O

156	Gene expression during the formation of resting spores induced by nitrogen starvation in the marine diatom Chaetoceros socialis. 2023 , 24,	Ο
155	Identification of key genes involved in flavonoid and terpenoid biosynthesis and the pathway of triterpenoid biosynthesis in Passiflora edulis. 2023 ,	Ο
154	Transcriptome Analysis During Tetrasporogenesis of Gracilariopsis lemaneiformis and Preliminary Study of the Expressions of Its Meiotic Genes. 2023 , 22, 541-554	Ο
153	Differential universal ortholog composition of Coffea arabical. sub-genomes and its contribution to regulatory networks governing essential biological processes.	Ο
152	A transcriptome-based phylogeny of Scarabaeoidea confirms the sister group relationship of dung beetles and phytophagous pleurostict scarabs (Coleoptera).	0
151	RNA-seq data science: From raw data to effective interpretation. 14,	Ο
150	Complete genome sequence of a novel variant of citrus tristeza virus infecting Chinese wild mandarin (Citrus daoxianensis S.W. He & D.F. Liu., syn. Citrus reticulata Blanco) in China.	0
149	Lipid extract derived from newly isolated Rhodotorula toruloides LAB-07 for cosmetic applications. 2023 , 21, 2009-2017	O
148	Danger Analysis: Risk-Averse on/off-Target Assessment for CRISPR Editing Without a Reference Genome.	0
147	Phylogenomics of novel ploeotid taxa contribute to the backbone of the euglenid tree.	O
146	Effects of acidification on nitrification and associated nitrous oxide emission in estuarine and coastal waters. 2023 , 14,	0
145	The Lichen Flavin-Dependent Halogenase, DnHal: Identification, Heterologous Expression and Functional Characterization.	O
144	Stochastic Processes Drive the Assembly and Metabolite Profiles of Keystone Taxa during Chinese Strong-Flavor Baijiu Fermentation. 2023 , 11,	O
143	Integrative Analysis of Metabolome and Transcriptome Reveals Molecular Insight into Metabolomic Variations during Hawthorn Fruit Development. 2023 , 13, 423	O
143		0
	Variations during Hawthorn Fruit Development. 2023, 13, 423 Low dissolved oxygen supply functions as a global regulator of the growth and metabolism of Aurantiochytrium sp. PKU#Mn16 in the early stages of docosahexaenoic acid fermentation. 2023,	
142	Variations during Hawthorn Fruit Development. 2023, 13, 423 Low dissolved oxygen supply functions as a global regulator of the growth and metabolism of Aurantiochytrium sp. PKU#Mn16 in the early stages of docosahexaenoic acid fermentation. 2023, 22, Far-Red-Light-Induced Morphology Changes, Phytohormone, and Transcriptome Reprogramming of	0

138	Comparative genomics reveals the diversification of triterpenoid biosynthesis and origin of ocotillol-type triterpenes in Panax. 2023 , 100591	О
137	Transcriptome analysis reveals defense-related genes and pathways during dodder (Cuscuta australis) parasitism on white clover (Trifolium repens). 14,	O
136	Genome assembly of the deep-sea coral Lophelia pertusa. 2023, 1-12	О
135	Predictors of sequence capture in a large-scale anchored phylogenomics project. 10,	O
134	Antiviral immune response reveals host-specific virus infections in natural ant populations. 14,	0
133	Sex matters: predator presence induces sexual dimorphism in a monomorphic prey, from stress genes to morphological defences. 2023 , 77, 304-317	О
132	Larval transcriptomes reflect the evolutionary history of plantihsect associations. 2023, 77, 519-533	О
131	Functional and Proteomic Insights into Aculeata Venoms. 2023 , 15, 224	O
130	Assessing environmental suitability of Ligusticum chuanxiong based on ecological analyses with chemical and molecular verification. 2023 , 9, e14629	О
129	New insights into the oxidative damage and antioxidant defense mechanism in Manila clams (Ruditapes philippinarum) exposed to 8:2 polyfluoroalkyl phosphate diester stress. 2023 , 106500	О
128	Transcriptome and Metabolome Profiling Provide Insights into Flavonoid Synthesis in Acanthus ilicifolius Linn. 2023 , 14, 752	О
127	De Novo Transcriptome Sequencing of Codonopsis lanceolata for Identification of Triterpene Synthase and Triterpene Acetyltransferase. 2023 , 24, 5769	О
126	A near complete genome assembly of chia assists in identification of key fatty acid desaturases in developing seeds. 14,	О
125	Meta-Transcriptomic Analysis Reveals Novel RNA Viruses in Hippocampus erectus. 2023 , 15, 772	О
124	Rickettsial DNA and a trans-splicing rRNA group I intron in the unorthodox mitogenome of the fern Haplopteris ensiformis. 2023 , 6,	О
123	Genic-SSR-based genetic diversity and population structure analysis in a global germplasm collection highlights the African origin of winged bean (Psophocarpus tetragonolobus L.).	О
122	Transcriptome Analysis Reveals the Heat Stress Response Genes by Fire Stimulation in Michelia macclurei Dandy. 2023 , 14, 610	O
121	Emergence of an ancient and pathogenic mammarenavirus. 2023 , 12,	О

120	Comparative transcriptome profiling of high and low grain-iron containing Indian barnyard millet (Echinochloa frumentacea L.) genotypes during different stages of grain development.	O
119	Biocatalytic potential of Pseudolycoriella CAZymes (Sciaroidea, Diptera) in degrading plant and fungal cell wall polysaccharides. 2023 , 26, 106449	O
118	Transcriptomic and Metabolomic Profiles Provide Insights into the Red-Stipe Symptom of Morel Fruiting Bodies. 2023 , 9, 373	0
117	Selective deployment of virulence effectors correlates with host specificity in a fungal plant pathogen. 2023 , 238, 1578-1592	O
116	A new genome assembly of an African weakly electric fish (Campylomormyrus compressirostris, Mormyridae) indicates rapid gene family evolution in Osteoglossomorpha. 2023 , 24,	O
115	Parthenocarpy-related genes induced by naphthalene acetic acid in oil palm interspecific O 🖸 [Elaeis oleifera (Kunth) Cort Elaeis guineensis Jacq.] hybrids. 14,	O
114	High-quality genome assembly and comparative genomic profiling of yellowhorn (Xanthoceras sorbifolia) revealed environmental adaptation footprints and seed oil contents variations. 14,	O
113	Different waves of postglacial recolonisation and genomic structure of bank vole populations in NE Poland.	O
112	Discovery of Brassica Yellows Virus and Porcine Reproductive and Respiratory Syndrome Virus in Diaphorina citri and Changes in Virome Due to Infection with ICa . L. asiaticus I2023, 11,	O
111	Co-segregation of recombinant chromatids maintains genome-wide heterozygosity in an asexual nematode.	O
110	Gene clustering and co-expression analysis for the identification of putative transcription factors associated with the genes of secondary metabolic pathways in Plantago ovata Forsk. and its wild allies.	O
109	Regulatory and coding sequences of TRNP1 co-evolve with brain size and cortical folding in mammals. 12,	O
108	Assembly and Analysis of Haemonchus contortus Transcriptome as a Tool for the Knowledge of Ivermectin Resistance Mechanisms. 2023 , 12, 499	O
107	Floral Development Stage-Specific Transcriptomic Analysis Reveals the Formation Mechanism of Different Shapes of Ray Florets in Chrysanthemum. 2023 , 14, 766	O
106	Elucidation of the pathway for biosynthesis of saponin adjuvants from the soapbark tree. 2023 , 379, 1252-1264	1
105	Multiple gene co-options underlie the rapid evolution of sexually deceptive flowers in Gorteria diffusa. 2023 ,	O
104	Comparative transcriptome analysis in contrasting finger millet (Eleusine coracana(L.) Gaertn) genotypes for heat stress.	O
103	Metabolic Composition and Quality Traits of Polygonatum cyrtonema Hua from Different Germplasms and Age Sections Based on Widely Targeted Metabolomics Analysis. 2023 , 24, 6077	O

102	Study on molecular mechanism of volatiles variation during Bupleurum scorzonerifolium root development based on metabolome and transcriptome analysis. 14,	0
101	Effects of Starvation on the Physiology and Liver Transcriptome of Yellowcheek (Elopichthys bambusa). 2023 , 8, 175	O
100	Effects of branched-chain amino acids on Shiraia perylenequinone production in mycelium cultures. 2023 , 22,	0
99	Intraspecific diversity in the mechanisms underlying abamectin resistance in a cosmopolitan pest.	O
98	Extensive search of genetic sex markers in Siberian (Acipenser baerii) and Atlantic (A. oxyrinchus) sturgeons. 2023 , 739517	0
97	Evidence for adaptive evolution towards high magnetic sensitivity of potential magnetoreceptor in songbirds.	О
96	A neurotransmitter histamine mediating phototransduction and photopreference in Callosobruchus maculatus.	О
95	Improved chromosomal-level genome assembly and re-annotation of leopard coral grouper. 2023 , 10,	О
94	De novo transcriptome assemblies of five major European oilseed rape insect pests. 2023 , 24,	0
93	Massive genome reduction occurred prior to the origin of coral algal symbionts.	Ο
92	DELLA functions evolved by rewiring of associated transcriptional networks. 2023 , 9, 535-543	0
91	The Torreya grandis genome illuminates the origin and evolution of gymnosperm-specific sciadonic acid biosynthesis. 2023 , 14,	O
90	QTL mapping and transcriptome analysis identify novel QTLs and candidate genes in Brassica villosa for quantitative resistance against Sclerotinia sclerotiorum. 2023 , 136,	0
89	A deeper insight into the sialome of male and female Culex quinquefasciatus mosquitoes. 2023 , 24,	O
88	Transcriptome Analysis of Ethylene Response in Chrysanthemum´moriflolium Ramat. with an Emphasis on Flowering Delay. 2023 , 9, 428	0
87	Transposable elements in the transcriptome of the velvetbean caterpillar Anticarsia gemmatalis HBner, 1818 (Lepidoptera: Erebidae).	O
86	Venomous gland transcriptome and venom proteomic analysis of the scorpion Androctonus amoreuxi reveal new peptides with anti-SARS- CoV-2 activity.	О
85	A phylogenomic approach to resolving interrelationships of polyclad flatworms, with implications for life-history evolution. 2023 , 10,	Ο

84	Arabidopsis TRB proteins function in H3K4me3 demethylation by recruiting JMJ14. 2023, 14,	0
83	The genome of Lactuca saligna , a wild relative of lettuce, provides insight into non-host resistance to the downy mildew Bremia lactucae.	O
82	Desmoglein-specific B-cell-targeted single-cell analysis revealing unique gene regulation in pemphigus patients. 2023 ,	O
81	Two haplotype-resolved genomes of highly heterozygous AAB allotriploid bananas provide insights into subgenome asymmetric evolution and banana wilt control.	O
80	RNA- Seq analysis of Taverniera cuneifolia (Roth) Ali	O
79	Transcriptome analysis reveals insight into the protective effect of N-acetylcysteine against cadmium toxicity in Ganoderma lucidum (Polyporales: Polyporaceae).	O
78	Towards high-throughput parallel imaging and single-cell transcriptomics of microbial eukaryotic plankton.	O
77	Inflorescence Trait Diversity and Genotypic Differentiation as Influenced by the Environment in Elymus nutans Griseb. from Qinghaillibet Plateau. 2023 , 13, 1004	O
76	Using metatranscriptomics to better understand the role of microbial nitrogen cycling in coastal sediment benthic flux denitrification efficiency.	O
75	Characterisation of the antiviral RNA interference response to Toscana virus in sand fly cells. 2023 , 19, e1011283	O
74	A novel eukaryotic RdRP-dependent small RNA pathway represses antiviral immunity by controlling an ERK pathway component in the black-legged tick. 2023 , 18, e0281195	0
73	RNA-seq analysis revealed considerable genetic diversity and enabled the development of specific KASP markers for Psathyrostachys huashanica. 14,	O
72	Identification and characterization of odorant-binding protein genes in the brown-winged green bug, Plautia stali.	O
71	Chromosome-Scale Genome Assembly and Triterpenoid Saponin Biosynthesis in Korean Bellflower (Platycodon grandiflorum). 2023 , 24, 6534	O
70	Novel evolved Yarrowia lipolytica strains for enhanced growth and lipid content under high concentrations of crude glycerol. 2023 , 22,	O
69	The effects of circularly polarized light on mating behavior and gene expression in Anomala corpulenta (Coleoptera: Scarabaeidae). 14,	O
68	Fascinating strategies of marine benthic organisms to cope with emerging pollutant: Titanium dioxide nanoparticles. 2023 , 121538	0
67	Roles and Benefits of Mycorrhiza. 2023 , 415-445	Ο

66	Metabolic resistance to acetolactate synthase inhibitors in Beckmannia syzigachne: identification of CYP81Q32 and its transcription regulation.	O
65	When does the female bias arise? Insights from the sex determination cascade of a flea beetle with a strongly skewed sex ratio. 2023 , 23,	o
64	Uncovering the history of recombination and population structure in western Canadian stripe rust populations through mating-type alleles.	O
63	Phylogeographic and demographic patterns reveal congruent histories in seven Amazonian White-Sand ecosystems birds.	O
62	Potential Effects of High Temperature and Heat Wave on Nanorana pleskei Based on Transcriptomic Analysis. 2023 , 45, 2937-2949	О
61	A complete gap-free diploid genome in Saccharum complex and the genomic footprints of evolution in the highly polyploid Saccharum genus. 2023 , 9, 554-571	O
60	Metagenomic study for the identification of viruses infecting soybean in Pakistan.	0
59	transXpress: a Snakemake pipeline for streamlined de novo transcriptome assembly and annotation. 2023 , 24,	o
58	Antennal transcriptomic analysis of carboxylesterases and glutathione S-transferases associated with odorant degradation in the tea gray geometrid, Ectropis grisescens (Lepidoptera, Geometridae). 14,	0
57	Transcriptomic insights into archaeal nitrification in the Amundsen Sea Polynya, Antarctica.	O
56	Comparative transcriptome analysis of juniper branches infected by Gymnosporangium spp. highlights their different infection strategies associated with cytokinins. 2023 , 24,	O
55	A high-quality chromosome-level Eutrema salsugineum genome, an extremophile plant model. 2023 , 24,	O
54	Sampling strategies for sugarcane using either clonal replicates or diverse genotypes can bias the conclusions of RNA-Seq studies. 2023 , 46,	0
53	Super-pangenome analyses highlight genomic diversity and structural variation across wild and cultivated tomato species.	o
52	Analysis of the P.1ividus sea urchin genome highlights contrasting trends of genomic and regulatory evolution in deuterostomes. 2023 , 3, 100295	O
51	Comparative Phylogenomics and Phylotranscriptomics Provide Insights into the Genetic Complexity of Nitrogen Fixing Root Nodule Symbiosis.	O
50	Functional characterization of five triterpene synthases through De-novo assembly and transcriptome analysis of Euphorbia grantiiand Euphorbia tirucalli.	О
49	Coinfection and circulation of chikungunya virus and dengue virus in pediatric patients in Myanmar, 2019. 2023 , 105129	O

48	The transcriptome of Litopenaeus vannamei in zoea larvae and adults infected by Vibrio parahaemolyticus. 10,	O
47	Comparative Transcriptomic and Proteomic Analyses Provide New Insights into the Tolerance to Cyclic Dehydration in a Lichen Phycobiont.	О
46	Establishment of a New Model Sea Anemone for Comparative Studies on Cnidarian-Algal Symbiosis. 2023 , 40,	0
45	Sensory specializations drive octopus and squid behaviour. 2023 , 616, 378-383	О
44	Metabolomics and transcriptomics strategies to reveal the mechanism of diversity of maize kernel color and quality. 2023 , 24,	O
43	Genomic and transcriptomic analysis of sacred fig (Ficus religiosa). 2023 , 24,	О
42	Complete genome sequence of zoysia mosaic virus, a novel member of the genus Poacevirus. 2023 , 168,	O
41	Integrated Metabolome and Transcriptome Analysis Reveals a Potential Mechanism for Water Accumulation Mediated Translucency in Pineapple (Ananas comosus (L.) Merr.) Fruit. 2023 , 24, 7199	О
40	Ovule Transcriptome Analysis Discloses Deregulation of Genes and Pathways in Sexual and Apomictic Limonium Species (Plumbaginaceae). 2023 , 14, 901	O
39	Transcriptome analysis reveals the molecular mechanisms of adaptation to high temperatures in Gracilaria bailinae. 14,	О
38	Transcriptome analysis of Indian freshwater pearl mussel Lamellidens marginalis to unravel the genes associated with biomineralization.	O
37	The mechanisms of optimal nitrogen conditions to accelerate flowering of Chrysanthemum vestitum under short day based on transcriptome analysis. 2023 , 153982	O
36	Comparative population genomics provide new insight into the evolutionary history and adaptive potential of World Ocean krill.	0
35	Integrated transcriptome catalog of Tenualosa ilisha as a resource for gene discovery and expression profiling. 2023 , 10,	O
34	Uniparental Inheritance and Recombination as Strategies to Avoid Competition and Combat Muller Ratchet among Mitochondria in Natural Populations of the Fungus Amanita phalloides. 2023 , 9, 476	0
33	Identification of multiple transcription factor genes potentially involved in the development of electrosensory versus mechanosensory lateral line organs.	O
32	The chromosome-level genome of Cherax quadricarinatus. 2023 , 10,	0
31	Transcriptome Analysis of Solanum Virginianum and in Silico Prediction of Antimicrobial Peptides. 2023 , 14, 1-10	О

30	Rps6ka2 enhances iMSC chondrogenic differentiation to attenuate knee osteoarthritis through articular cartilage regeneration in mice. 2023 ,	0
29	Differential gene expression patterns between the head and thorax of Gynaephora aureata are associated with high-altitude adaptation. 14,	O
28	Single worm long read sequencing reveals genome diversity in free-living nematodes.	О
27	Orb weaver aggregate glue protein composition as a mechanism for rapid evolution of material properties. 11,	O
26	Chromosome-scale genome assembly-assisted identification of Mi-9 gene in Solanum arcanum accession LA2157, conferring heat-stable resistance to Meloidogyne incognita.	O
25	The whole genome of Colletes collaris (Hymenoptera: Colletidae): an important step in comparative genomics of cellophane bees.	Ο
24	The hagfish genome and the evolution of vertebrates.	0
23	Mitochondrial Heteroplasmy and PCR Amplification Bias Lead to Wrong Species Delimitation with High Confidence in the South American and Antarctic Marine Bivalve Aequiyoldia eightsii Species Complex. 2023 , 14, 935	O
22	Subgenome-aware analyses suggest a reticulate allopolyploidization origin in three Papaver genomes. 2023 , 14,	0
21	Venom-gland transcriptomics of the Malayan pit viper (Calloselasma rhodostoma) for identification, classification, and characterization of venom proteins. 2023 , 9, e15476	O
20	De novo transcriptome sequencing and gene co-expression reveal a genomic basis for drought sensitivity and evidence of a rapid local adaptation on Atlas cedar (Cedrus atlantica). 14,	Ο
19	Inference of phylogenetic trees directly from raw sequencing reads using Read2Tree.	0
18	Gapless genome assembly of Fusarium verticillioides, a filamentous fungus threatening plant and human health. 2023 , 10,	O
17	Insights into the Molecular Basis of Huanglongbing Tolerance in Persian Lime (Citrus latifolia Tan.) through a Transcriptomic Approach. 2023 , 24, 7497	O
16	The Antimicrobial Potential and Aquaculture Wastewater Treatment Ability of Penaeidins 3a Transgenic Duckweed. 2023 , 12, 1715	O
15	In Ovo Injection of CHIR-99021 Promotes Feather Follicle Development via Modulating the Wnt Signaling Pathway and Transcriptome in Goose Embryos (Anser cygnoides). 13,	O
14	A scoping review on deep learning for next-generation RNA-Seq. data analysis. 2023, 23,	О
13	Identification and sex-specific expression of chemosensory genes in the antennal transcriptomes of Pachyrhinus yasumatsui (Coleoptera: Curculionidae). 2023 , 23,	O

12	A DBHS family member regulates male determination in the filariasis vector Armigeres subalbatus. 2023 , 14,	0
11	Transcriptomic dissection of termite gut microbiota following entomopathogenic fungal infection. 14,	О
10	Integrated transcriptome and metabolome provide insight into flavonoid variation in goji berries (Lycium barbarum L.) from different areas in China. 2023 , 199, 107722	O
9	Mitochondrial Genome Uncovered Hidden Genetic Diversity in Microdous chalmersi (Teleostei: Odontobutidae). 2023 , 8, 228	O
8	Physiological and biochemical responses of Limonium tetragonum to NaCl concentrations in hydroponic solution. 14,	O
7	Differential expression of some termite neuropeptides and insulin/IGF-related hormones and their plausible functions in growth, reproduction and caste determination. 11, e15259	o
6	A second unveiling: Haplotig masking of the eastern oyster genome improves population-level inference.	0
5	Diverse Molecular Mechanisms Underlying Microbe-Inducing Male Killing in the Moth Homona magnanima.	o
4	Exploring Toxin Genes of Myanmar Russell Viper, Daboia siamensis, through De Novo Venom Gland Transcriptomics. 2023 , 15, 309	0
3	Transcriptomic analysis of cave, surface, and hybrid samples of the isopod Asellus aquaticus and identification of chromosomal location of candidate genes for cave phenotype evolution. 2023 , 14,	o
2	Unraveling molecular mechanisms underlying low-temperature adaptation in Laguncularia racemosa. 2023 , 199, 107747	0
1	Physiology and transcriptomic analysis of endogenous hormones regulating in vitro adventitious root formation in tree peony. 2023 , 318, 112122	О