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Ultrafast and memory-efficient alignment of short DNA sequences to the human genome

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2039	Assembly algorithms for next-generation sequencing data. <b>2010</b> , 95, 315-27	764
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2030	Fast and SNP-tolerant detection of complex variants and splicing in short reads. <b>2010</b> , 26, 873-81		1457
2029	Minimizing off-target signals in RNA fluorescent in situ hybridization. <b>2010</b> , 38, e115		19
2028	A unique H3K4me2 profile marks tissue-specific gene regulation. <b>2010</b> , 20, 1493-502		91
2027	Cell-type specific analysis of translating RNAs in developing flowers reveals new levels of control. <b>2010</b> , 6, 419		136
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2021	Homoeolog-specific retention and use in allotetraploid Arabidopsis suecica depends on parent of origin and network partners. <i>Genome Biology</i> , <b>2010</b> , 11, R125	18.3	65
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663	An unusual mode of baseline translation adjusts cellular protein synthesis capacity to metabolic needs. <b>2022</b> , 41, 111467	O
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661	Integrator endonuclease drives promoter-proximal termination at all RNA polymerase II-transcribed loci. <b>2022</b> ,	O
660	NaWe pluripotent-like characteristics of non-tumorigenic Muse cells isolated from human amniotic membrane. <b>2022</b> , 12,	O
659	Small extravesicular microRNA in head and neck squamous cell carcinoma and its potential as a liquid biopsy for early detection.	1
658	HIRA loss transforms FH -deficient cells. <b>2022</b> , 8,	O
657	Genetic risk of osteoarthritis operates during human skeletogenesis.	O
656	Enhancing stability of recombinant CHO cells by CRISPR/Cas9-mediated site-specific integration into regions with distinct histone modifications. 10,	O
655	Serum extracellular vesicle MicroRNAs as candidate biomarkers for acute rejection in patients subjected to liver transplant. 13,	1
654	Expression Profile of microRNAs during Development of the Hypopharyngeal Gland in Honey Bee, Apis mellifera. <b>2022</b> , 23, 12970	O
653	Identification of tRNA-derived small RNAs and their potential roles in porcine skeletal muscle with intrauterine growth restriction. 13,	1
652	Characteristics of environmental RNAi in potato psyllid, Bactericera cockerelli (Sulc) (Hemiptera: Psylloidea: Triozidae). 13,	O
651	Supt16 haploinsufficiency causes neurodevelopment disorder by disrupting MAPK pathway in neural stem cells.	1
650	Differential Gene Expression and Metabolic Pathway Analysis of Cladophora rupestris under Pb Stress Conditions. <b>2022</b> , 19, 13910	O

649	COOBoostR: an extreme gradient boosting-based tool for robust tissue or cell-of-origin prediction of tumors.	0
648	Liver comparative transcriptome analysis reveals the mechanism of the Hainan medaka, Oryzias curvinotus, to adapt to salinity.	O
647	Identification of novel microRNAs associated with type 2 diabetes by an integrative bioinformatic analysis. <b>2022</b> , 201125	О
646	Experimental Evolution Reveals Unifying Systems-Level Adaptations but Diversity in Driving Genotypes.	1
645	Tetrabromobisphenol A effects on differentiating mouse embryonic stem cells reveals unexpected impact on immune system. 13,	O
644	Hypoxia and ER⊞ranscriptional Crosstalk Is Associated with Endocrine Resistance in Breast Cancer. <b>2022</b> , 14, 4934	o
643	Escaping antibody responses to bacteriolytic enzymes Pal and Cpl-1 by epitope scanning and engineering.	О
642	miRNome-transcriptome analysis unveils the key regulatory pathways involved in the tumorigenesis of tongue squamous cell carcinoma.	0
641	Approaches for identification and analysis of plant Circular RNAs and their role in stress responses. <b>2022</b> , 105099	0
640	Transcriptomics in serum and culture medium reveal shared and differential gene regulation in pathogenic and commensalStreptococcus suis.	0
639	Host genetic requirements for DNA release of lactococcal phage TP901 -1.	0
638	Runx2 and Runx3 differentially regulate articular chondrocytes during surgically induced osteoarthritis development. <b>2022</b> , 13,	2
637	3D genome topologies distinguish pluripotent epiblast and primitive endoderm cells in the mouse blastocyst.	О
636	Predictive Network Analysis IdentifiesJMJD6and Other Novel Key Drivers in Alzheimer Disease.	О
635	Effects of Sub-Minimum Inhibitory Concentrations of Imipenem and Colistin on Expression of Biofilm-Specific Antibiotic Resistance and Virulence Genes in Acinetobacter baumannii Sequence Type 1894. <b>2022</b> , 23, 12705	2
634	Rolling circle reverse transcription enables high fidelity nanopore sequencing of small RNA. <b>2022</b> , 17, e0275471	o
633	Potential Roles of miRNAs in Acute Rejection for Vascularized Composite Allotransplantation. Volume 15, 6021-6030	О
632	KCNQ1OT1 promotes genome-wide transposon repression by guiding RNADNA triplexes and HP1 binding.	2

631	Karyotype variation, spontaneous genome rearrangements affecting chemical insensitivity, and expression level polymorphisms in the plant pathogen Phytophthora infestans revealed using its first chromosome-scale assembly. <b>2022</b> , 18, e1010869	1
630	Genome-Wide Identification of miRNAs and Its Downstream Transcriptional Regulatory Network during Seed Maturation in Tilia tuan. <b>2022</b> , 13, 1750	O
629	RTCB Complex Regulates Stress-Induced tRNA Cleavage. <b>2022</b> , 23, 13100	O
628	Metagenomic Analysis of Gut Microbiome in Gout Patients with Different Chinese Traditional Medicine Treatments. <b>2022</b> , 2022, 1-12	O
627	Screening and identification of miRNAs regulating Tbx4/5 genes of Pampus argenteus. 10, e14300	O
626	PRC2-mediated epigenetic suppression of type I IFN-STAT2 signaling impairs antitumor immunity in luminal breast cancer.	O
625	Biphasic cell cycle defect causes impaired neurogenesis in down syndrome. 13,	1
624	Influence of the microbiome, diet and genetics on inter-individual variation in the human plasma metabolome.	3
623	Natural polymorphism of ZmICE1 contributes to amino acid metabolism that impacts cold tolerance in maize. <b>2022</b> , 8, 1176-1190	1
622	Regulation of Parietal Cell Homeostasis by Bone Morphogenetic Protein signaling. 2022,	O
621	The mitochondrial complex I proteins of Candida albicans moderate phagocytosis and the production of pro-inflammatory cytokines in murine macrophages and dendritic cells. <b>2022</b> , 36,	О
620	Genomic consequences and selection efficacy in sympatric sexual versus asexual kelps. 9,	O
619	Integrated analysis of miRNA and mRNA expression profiles in testes of Landrace and Hezuo boars. 9,	0
618	A Novel Self-Cleaving Viroid-Like RNA Identified in RNA Preparations from a Citrus Tree Is Not Directly Associated with the Plant. <b>2022</b> , 14, 2265	1
617	Identification of plant-derived microRNAs in human kidney.	O
616	Contrasting levels of hybridization across the two contact zones between two hedgehog species revealed by genome-wide SNP data. <b>2022</b> , 129, 305-315	O
615	Nitrogen-dependent binding of the transcription factor PBF1 contributes to the balance of protein and carbohydrate storage in maize endosperm.	О
614	Map-based cloning and transcriptome analysis of the more-tiller and small-grain mutant in rice. <b>2022</b> , 256,	O

613	CRISPRon/off: CRISPR/Cas9 on- and off-target gRNA design.	O
612	Non-intuitive trends of fetal fraction development related to gestational age and fetal gender, and their practical implications for non-invasive prenatal testing. <b>2022</b> , 101870	O
611	The first high-density genetic map of common cockle (Cerastoderma edule) reveals a major QTL controlling shell color variation. <b>2022</b> , 12,	O
610	Trichoderma atroviride hyphal regeneration and conidiation depend on cell-signaling processes regulated by a microRNA-like RNA. <b>2022</b> , 8,	O
609	Transcriptome Analysis of Hong Yang Kiwifruit in Response to Bactrocera dorsalis (Diptera: Tephritidae) Larval Feeding. <b>2022</b> , 57, 488-501	O
608	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
607	Multi-Organ Transcriptome Response of Lumpfish (Cyclopterus lumpus) to Aeromonas salmonicida Subspecies salmonicida Systemic Infection. <b>2022</b> , 10, 2113	1
606	Differential H3K9me2 heterochromatin levels and concordant mRNA expression in postmortem brain tissue of individuals with schizophrenia, bipolar, and controls. 13,	O
605	Circadian lncRNA ADIRF-AS1 binds PBAF and regulates renal clear cell tumorigenesis. 2022, 41, 111514	O
604	Chromosome-level genome assembly ofTorreya grandisprovides insights into the origin and evolution of gymnosperm-specific sciadonic acid biosynthesis.	O
603	Transposable element expansion and low-level piRNA silencing in grasshoppers may cause genome gigantism. <b>2022</b> , 20,	O
602	Wolbachia wAlbB inhibit dengue and Zika infection in the mosquito Aedes aegypti with an Australian background. <b>2022</b> , 16, e0010786	O
601	Comparative transcriptome analysis reveals an insight into the candidate genes involved in anthocyanin and scent volatiles biosynthesis in color changing flowers of Combretum indicum (L.) DeFilipps.	O
600	Splicing factor BUD31 promotes ovarian cancer progression through sustaining the expression of anti-apoptotic BCL2L12. <b>2022</b> , 13,	O
599	Dormant SOX9-positive cells facilitate MYC-driven recurrence of medulloblastoma.	1
598	miR766-3p and miR124-3p Dictate Drug Resistance and Clinical Outcome in HNSCC. <b>2022</b> , 14, 5273	O
597	Metagenomic analysis reveals differences in the co-occurrence and abundance of viral species in SARS-CoV-2 patients with different severity of disease. <b>2022</b> , 22,	O
596	Early suppression of antiviral host response and protocadherins by SARS-CoV-2 Spike protein in THP-1-derived macrophage-like cells. 13,	O

595	RNA structural dynamics modulate EGFR-TKIs resistance through controllingYRDCtranslation in NSCLC cells.	O
594	Epigenetic and transcriptional plasticity of myeloid cells in Cystic Fibrosis.	O
593	Towards a Flexible and Portable Workflow for Analyzing miRNA-Seq Neuropsychiatric Data: An Initial Replicability Assessment. <b>2023</b> , 31-42	O
592	The Role of Regulator Catabolite Control Protein A (CcpA) in Streptococcus agalactiae Physiology and Stress Response.	O
591	Initiation of HIV-1 Gag lattice assembly is required for cytoplasmic recognition of the viral genome packaging signal.	0
590	Genome-wide analysis of histone trimethylation reveals a global impact of bisphenol A on telomeric binding proteins and histone acetyltransferase factors: Complementing in vitro and human data from the INMA cohort	O
589	Profiling non-coding RNA expression in cerebrospinal fluid of amyotrophic lateral sclerosis patients. <b>2022</b> , 54, 3069-3078	0
588	Forced expression of the non-coding RNA miR-17~92 restores activation and function in CD28-deficient CD4+ T´cells. <b>2022</b> , 25, 105372	O
587	Canonical strigolactones are not the major determinant of tillering but important rhizospheric signals in rice. <b>2022</b> , 8,	3
586	Prophage-like gene transfer agents promote Caulobacter crescentus survival and DNA repair during stationary phase. <b>2022</b> , 20, e3001790	O
585	A gene silencing screen uncovers diverse tools for targeted gene repression in Arabidopsis.	0
584	Systemic circulating microRNA landscape in Lynch syndrome.	O
583	A comprehensive Bioconductor ecosystem for the design of CRISPR guide RNAs across nucleases and technologies. <b>2022</b> , 13,	0
582	Small Molecule Inducers of Neuroprotective miR-132 Identified by HTS-HTS in Human iPSC-derived Neurons.	O
581	CD74 as a regulator of transcription in normal B cells. <b>2022</b> , 41, 111572	O
580	Identification of MicroRNAs Related to Phytohormone Signal Transduction and Self-incompatibility of Rabbiteye Blueberry Pollen. <b>2022</b> , 147, 300-311	O
579	Mechanisms governing target search and binding dynamics of hypoxia-inducible factors. 11,	0
578	Activation of Pancreatic Acinar FXR Protects against Pancreatitis via Osgin1-Mediated Restoration of Efficient Autophagy. <b>2022</b> , 2022, 1-15	0

577	BRD9-containing non-canonical BAF complex maintains somatic cell transcriptome and acts as a barrier to human reprogramming. <b>2022</b> ,	O
576	P bodies coat germ granules to promote transgenerational gene silencing in C. elegans.	Ο
575	The two Gtsf paralogs in silkworms orthogonally activate their partner PIWI proteins for target cleavage. rna.079380.122	O
574	Transcriptional and post-transcriptional mechanisms that regulate the genetic program in Zika virus-infected macrophages. <b>2022</b> , 153, 106312	O
573	The sheep miRNAome: Characterization and distribution of miRNAs in 21 tissues. <b>2023</b> , 851, 146998	O
572	Plasma exosomal microRNA expression profiles in patients with high-altitude polycythemia. <b>2023</b> , 98, 102707	О
571	Desert plant transcriptomics and adaptation to abiotic stress. <b>2023</b> , 199-256	О
570	Recent advances in transcriptomic biomarker detection for cancer. <b>2023</b> , 453-478	Ο
569	Genome-wide QTL mapping and RNA-seq reveal the genetic variation influencing growth traits in giant grouper (Epinephelus lanceolatus). <b>2023</b> , 563, 738944	0
568	Compressed Indexes for Repetitive Textual Datasets. <b>2022</b> , 1-7	Ο
567	Analysis of the p53/microRNA Network in Cancer. <b>2022</b> , 187-228	1
566	Toxicity of nitenpyram to silkworm (Bombyx mori L.) and its potential mechanisms. 2023, 311, 137026	Ο
565	Analysis of Exosomal MicroRNA Dynamics in Response to Rhinovirus Challenge in a Longitudinal Case-Control Study of Asthma. <b>2022</b> , 14, 2444	0
564	RNA -seq and ATAC -seq analysis of CD163 + macrophage-induced progestin-insensitive endometrial cancer cells.	Ο
563	vsRNAfinder: a novel method for identifying high-confidence viral small RNAs from small RNA-Seq data.	1
562	The Characterization of Three Novel Insect-Specific Viruses Discovered in the Bean Bug, Riptortus pedestris. <b>2022</b> , 14, 2500	0
561	Transcriptome analysis of PBMCs isolated from piglets treated with a miR-124 sponge construct identified miR124/IQGAP2/Rho GTPase as a target pathway support Salmonella Typhimurium infection.	0
560	New insights into the molecular mechanism of low-temperature stratification on dormancy release and germination of Saposhnikovia divaricata seeds.	Ο

559	Abundant and cosmopolitan lineage of cyanopodoviruses lacking a DNA polymerase gene.	О
558	Placental microRNAs relate to early childhood growth trajectories.	O
557	Physiological and transcriptomic analysis of OsLHCB3 knockdown lines in rice.	O
556	MicroRNA expression profiles in response to Phytophthora infestans and Oidium neolycopersici and functional identification of sly-miR397 in tomato.	O
555	Trans-regulatory changes underpin the evolution of the Drosophila immune response. <b>2022</b> , 18, e1010453	0
554	Characterization of MxiE- and H-NS-Dependent Expression of ipaH7.8 , ospC1 , yccE , and yfdF in Shigella flexneri.	O
553	Stress-induced transcriptional readthrough into neighboring genes is linked to intron retention. <b>2022</b> , 105543	0
552	The UBP5 histone H2A deubiquitinase counteracts PRC2-mediated repression to regulate Arabidopsis development and stress responses.	O
551	Transcriptomic responses of females to consumption of nuptial food gifts as a potential mediator of sexual conflict in decorated crickets.	0
550	Reconstructing mutational lineages in breast cancer by multi-patient-targeted single-cell DNA sequencing. <b>2022</b> , 100215	O
549	Crosstalk between Thyroid Hormone and Corticosteroid Signaling Targets Cell Proliferation in Xenopus tropicalis Tadpole Liver. <b>2022</b> , 23, 13715	O
548	A Mollicutes Metagenome-Assembled Genome from the Gut of the Pteropod Limacina rangii.	O
547	Rapid Acquisition and Transmission of Drug Resistance Amongst Beijing LineageMycobacterium tuberculosisin Vietnam.	O
546	Comparative transcriptome sequencing analysis of female and male Decapterus macrosoma. 10, e14342	O
545	Negative effects of heat stress on ovarian tissue in female rabbit. 9,	O
544	Metabolomic, Lipidomic, Transcriptomic, and Metagenomic Analyses in Mice Exposed to PFOS and Fed Soluble and Insoluble Dietary Fibers. <b>2022</b> , 130,	1
543	Transcriptome analysis of differentially expressed circRNAs miRNAs and mRNAs during the challenge of coccidiosis. 13,	O
542	Genome-scale CRISPR screening in a single mouse liver. <b>2022</b> , 100217	O

541	Discovery of aphid-transmitted Rice tiller inhibition virus from native plants through metagenomic sequencing.	O
540	Phylogenomic analysis and development of molecular markers for the determination of twelve plum cultivars (Prunus, Rosaceae). <b>2022</b> , 23,	1
539	Transcriptome Sequencing Analysis of circRNA in Skeletal Muscle between Fast- and Slow-Growing Chickens at Embryonic Stages. <b>2022</b> , 12, 3166	0
538	The small RNA landscape is stable with age and resistant to loss of dFOXO signaling in Drosophila. <b>2022</b> , 17, e0273590	O
537	Cucumber STACHYOSE SYNTHASE is regulated by its cis-antisense RNA asCsSTS to balance sourceBink carbon partitioning.	0
536	A comparative atlas of single-cell chromatin accessibility in the human brain.	O
535	Systematic and benchmarking studies of pipelines for mammal WGBS data in the novel NGS platform.	0
534	HOST GENE EXPRESSION IS ASSOCIATED WITH VIRAL SHEDDING MAGNITUDE IN BLUE-WINGED TEALS (SPATULA DISCORS) INFECTED WITH LOW-PATH AVIAN INFLUENZA VIRUS. <b>2022</b> , 101909	O
533	Identification of microRNA editing sites in three subtypes of leukemia. 9,	0
532	VSGs Expressed during Natural T. b. gambiense Infection Exhibit Extensive Sequence Divergence and a Subspecies-Specific Bias towards Type B N-Terminal Domains.	O
531	KRAB family is involved in network shifts in response to osmotic stress in camels. 1-10	О
530	Multifaceted contributions ofDicer2to arbovirus transmission byAedes aegypti.	O
529	Functional characterization of diverse type I-F CRISPR-associated transposons.	0
528	Polony gels enable amplifiable DNA stamping and spatial transcriptomics of chronic pain. 2022,	1
527	Phage resistance profiling identifies new genes required for biogenesis and modification of the corynebacterial cell envelope. 11,	0
526	Human Dectin-1 deficiency impairs macrophage-mediated defense against phaeohyphomycosis. <b>2022</b> , 132,	O
525	Analysis of the chloroplast genome and phylogenetic evolution of three species of Syringa.	0
524	Inactivation of Notch4 attenuated pancreatic tumorigenesis in mice.	O

523	Mapping open chromatin by ATAC-seq in bread wheat. 13,	1
522	2cChIP-seq and 2cMeDIP-seq: The Carrier-Assisted Methods for Epigenomic Profiling of Small Cell Numbers or Single Cells. <b>2022</b> , 23, 13984	0
521	The tRNA-Cys-GCA Derived tsRNAs Suppress Tumor Progression of Gliomas via Regulating VAV2. <b>2022</b> , 2022, 1-16	О
520	Dynamic Changes of Rhizosphere Soil Microbiome and Functional Genes Involved in Carbon and Nitrogen Cycling in Chinese Fir Monoculture. <b>2022</b> , 13, 1906	O
519	A New Benzothiazolthiazolidine Derivative, 11726172, Is Active In Vitro , In Vivo , and against Nonreplicating Cells of Mycobacterium tuberculosis.	О
518	A chromosomal-scale reference genome of the New World Screwworm, Cochliomyia hominivorax.	O
517	Mode of delivery modulates the intestinal microbiota and impacts the response to vaccination. <b>2022</b> , 13,	О
516	The CUT&RUN Blacklist of Problematic Regions of the Genome.	O
515	A new cut&run low volume-urea (LoV-U) protocol optimized for transcriptional co-factors uncovers Wnt/b-catenin tissue-specific genomic targets.	1
514	A Virus-Packageable CRISPR System Identifies Host Dependency Factors Across Multiple HIV-1 Strains.	O
513	Characterization of the promoter region of the murine Catsper2 gene.	О
512	Spatially resolved gene regulatory and disease-related vulnerability map of the adult Macaque cortex. <b>2022</b> , 13,	O
511	Characterization of HCI-EC-23 a novel estrogen- and progesterone-responsive endometrial cancer cell line. <b>2022</b> , 12,	О
510	Functional characterization ofBotrytis cinereaABC transporter geneBcatrBin response to phytoalexins produced in plants belonging to families Solanaceae, Brassicaceae and Fabaceae.	O
509	Exosomal long noncoding RNAs MAGI2-AS3 and CCDC144NL-AS1 in oral squamous cell carcinoma development via the PI3K-AKT-mTOR signaling pathway. <b>2022</b> , 240, 154219	0
508	Coordinated regulation of microRNA genes in C19MC by SETDB1. <b>2022</b> , 637, 17-22	O
507	Mapping separase-mediated cleavage in situ. <b>2022</b> , 4,	О
506	Sex-determining 3D regulatory hubs revealed by genome spatial auto-correlation analysis.	1

505	Genomic selection for morphological and yield-related traits using genome-wide SNPs in oil palm. <b>2022</b> , 42,	O
504	Integration of host-pathogen functional genomics data into the chromosome-level genome assembly of turbot (Scophthalmus maximus). <b>2022</b> , 739067	o
503	srnaMapper: an optimal mapping tool for sRNA-Seq reads. <b>2022</b> , 23,	1
502	Distinct super-enhancer elements differentially control Il2ra gene expression in a cell-type specific fashion.	О
501	POLIprocesses ssDNA gaps and promotes replication fork progression in BRCA1-deficient cells. <b>2022</b> , 111716	2
500	Virome and nrEVEome diversity of Aedes albopictus mosquitoes from La Reunion Island and China. <b>2022</b> , 19,	0
499	Evolution of lmiRNAs and their targets from MITEs for rice adaptation.	О
498	Bioinformatics for Saffron-Omics and Crop Improvement. <b>2022</b> , 63-82	o
497	annotate_my_genomes: an easy-to-use pipeline to improve genome annotation and uncover neglected genes by hybrid RNA sequencing. <b>2022</b> , 11,	1
496	Letrozole treatment alters hippocampal gene expression in common marmosets (Callithrix jacchus). <b>2023</b> , 147, 105281	o
495	Temporal progress of gene expression analysis with RNA-Seq data: A review on the relationship between computational methods. <b>2023</b> , 21, 86-98	0
494	Temporal regulation of head-on transcription at replication initiation sites. <b>2023</b> , 26, 105791	o
493	Exosomal microRNAs regulate the heat stress response in sea cucumber Apostichopus japonicus. <b>2023</b> , 249, 114419	0
492	The inhibition of ecdysone signal pathway was the key of pyriproxyfen poisoning for silkworm, Bombyx mori. <b>2023</b> , 189, 105307	0
491	Sex-specific markers developed by 2b-RAD and genome sequencing reveal an XX/XY sex-determination system in mud carp (Cirrhinus molitorella). <b>2023</b> , 565, 739131	0
490	Comparative global gene expression analysis of biofilm forms of Salmonella Typhimurium ATCC 14028 and its seqA mutant. <b>2023</b> , 853, 147094	0
489	Salmonella Typhimurium induces genome-wide expression and phosphorylation changes that modulate immune response, intracellular survival and vesicle transport in infected neutrophils. <b>2023</b> , 140, 104597	0
488	Comparative transcriptomic assessment of the chemosensory receptor repertoire of Drosophila suzukii adult and larval olfactory organs. <b>2023</b> , 45, 101049	o

487	Comparative genomic analysis provides insight into the phylogeny and potential mechanisms of adaptive evolution of Sphingobacterium sp. CZ-2. <b>2023</b> , 855, 147118	O
486	Transcriptome Sequencing and Analysis of Seabuckthorn (Hippophae Sp.). <b>2022</b> , 231-246	О
485	Multi-omics analysis identifies drivers of protein phosphorylation.	О
484	Low-affinity SPL binding sites contribute to subgenome expression divergence in allohexaploid wheat.	O
483	Identification of Liver Fibrosis-Related MicroRNAs in Human Primary Hepatic Stellate Cells Using High-Throughput Sequencing. <b>2022</b> , 13, 2201	1
482	Plant MicroRNA Identification and Annotation Using Deep Sequencing Data. <b>2023</b> , 239-250	o
481	Biology and medicine in the landscape of quantum advantages. <b>2022</b> , 19,	0
480	Early-life starvation alters lipid metabolism in adults to cause developmental pathology in Caenorhabditis elegans.	o
479	Nucleotide-level linkage of transcriptional elongation and polyadenylation. 11,	0
478	Bioinformatics Analysis of miRNA Sequencing Data. <b>2023</b> , 225-237	o
477	Transcriptome analysis reveals key drought-stress-responsive genes in soybean. 13,	0
476	ZMP recruits and excludes Pol IVThediated DNA methylation in a site-specific manner. 2022, 8,	О
475	Intestinal flora induces depression by mediating the dysregulation of cerebral cortex gene expression and regulating the metabolism of stroke patients. 9,	0
474	Transcriptome Analysis and Identification of Chemosensory Genes in Baryscapus dioryctriae (Hymenoptera: Eulophidae). <b>2022</b> , 13, 1098	О
473	Two murine cytomegalovirus microRNAs target the major viral immediate early 3 gene. 2022, 103,	0
472	The virome of the invasive Asian bush mosquitoAedes japonicusin Europe.	О
471	Ribo-uORF: a comprehensive data resource of upstream open reading frames (uORFs) based on ribosome profiling.	О
470	Self-cleaving guide RNAs enable pharmacological selection of precise gene editing events in vivo. <b>2022</b> , 13,	О

469	Human papillomavirus genotyping using next generation sequencing (NGS) in cervical lesions: Genotypes by histologic grade and their relative proportion in multiple infections. <b>2022</b> , 17, e0278117	Ο
468	SMARCB1 loss creates patient-specificMYCtopologies that drive malignant rhabdoid tumor growth.	0
467	A review on bioinformatics advances in CRISPR-Cas technology.	О
466	Determining epigenetic memory in kidney proximal tubule cell derived induced pluripotent stem cells using a quadruple transgenic reprogrammable mouse. <b>2022</b> , 12,	Ο
465	The preliminary study of exosomes derived from thymosin beta 4-treated adipose-derived stem cells in fat grafting.	0
464	Intestinal proline is a potential anti-allergy factor for allergy diagnosis and therapy. 9,	O
463	Forensic age estimation from human blood using age-related microRNAs and circular RNAs markers. 13,	0
462	RNA Structural Dynamics Modulate EGFR-TKI Resistance Through Controlling YRDC Translation in NSCLC Cells. <b>2022</b> ,	1
461	ThSCSP_12: Novel Effector in Tilletia horrida That Induces Cell Death and Defense Responses in Non-Host Plants. <b>2022</b> , 23, 14752	0
460	Breast cancer plasticity is restricted by a LATS1-NCOR1 repressive axis. <b>2022</b> , 13,	O
459	Long noncoding RNA study: Genome-wide approaches. 2022,	0
458	A Comprehensive Sequencing Analysis of Testis-Born miRNAs in Immature and Mature Indigenous Wandong Cattle (Bos taurus). <b>2022</b> , 13, 2185	Ο
457	MYC multimers shield stalled replication forks from RNA polymerase. <b>2022</b> , 612, 148-155	Ο
456	IMA genome-F17. <b>2022</b> , 13,	Ο
455	miRador: a fast and precise tool for the prediction of plant miRNAs.	Ο
454	Factors governing attachment ofRhizobium leguminosarumto legume roots.	Ο
453	Identification and Functional Analysis of Long Non-Coding RNA (lncRNA) in Response to Seed Aging in Rice. <b>2022</b> , 11, 3223	0
452	Evolutionary conservation and transcriptome analyses attribute perenniality and flowering to day-length responsive genes in bulbous barley (Hordeum bulbosum).	O

451	Integrated Multi-omics Analyses of NFKB1 patients B cells points towards an up regulation of NF- <b>B</b> network inhibitors.	O
450	Wastewater genomic surveillance captures early detection of Omicron in Utah.	О
449	stepRNA: Identification of Dicer cleavage signatures and passenger strand lengths in small RNA sequences. 2,	O
448	Comparative analysis of piRNA sequences, targets and functions in nematodes. <b>2022</b> , 19, 1276-1292	O
447	Genetic variation in P-element dysgenic sterility is associated with double-strand break repair and alternative splicing of TE transcripts. <b>2022</b> , 18, e1010080	O
446	The canonical E2Fs together with RETINOBLASTOMA-RELATED are required to establish quiescence during plant development.	O
445	Multidimensional control of therapeutic human cell function with synthetic gene circuits. <b>2022</b> , 378, 1227-1234	4
444	Lab evolution, transcriptomics, and modeling reveal mechanisms of paraquat tolerance.	O
443	Differential miRNA expression profiles in the bone marrow of Beagle dogs at different stages of Toxocara canis infection. <b>2022</b> , 23,	O
442	Transposable element and host silencing activity in gigantic genomes.	O
441	HNF1B-driven three-dimensional chromatin structure for molecular classification in pancreatic cancers.	О
440	Mitochondrial PARP1 regulates NAD+-dependent poly ADP-ribosylation of mitochondrial nucleoids. <b>2022</b> , 54, 2135-2147	O
439	Irregular alignment of arbitrarily long DNA sequences on GPU.	O
438	Two vacuolar invertase inhibitors PpINHa and PpINH3 display opposite effects on fruit sugar accumulation in peach. 13,	O
437	A specific type of Argonaute phosphorylation regulates binding to microRNAs during C. elegans development. <b>2022</b> , 41, 111822	1
436	Establishment of preanalytical conditions for microRNA profile analysis of clinical plasma samples. <b>2022</b> , 17, e0278927	O
435	Search for New Participants in the Pathogenesis of High-Grade Serous Ovarian Cancer with the Potential to Be Used as Diagnostic Molecules. <b>2022</b> , 12, 2017	O
434	Systematic analysis of Baobaoqu fermentation starter for Wuliangye Baijiu by the combination of metagenomics and metabolomics. 13,	O

433	Hierarchical filtering: improving similar substring matching under edit distance.	О
432	Adaptive lifestyle of bacteria determines phage-bacteria interaction. 13,	О
431	The mechanisms of siRNA selection by plant Argonaute proteins triggering DNA methylation.	О
430	Testing the chilling- before drought-tolerance hypothesis in Pooideae grasses.	О
429	DNA-protein quasi-mapping for rapid differential gene expression analysis in non-model organisms.	O
428	Linolenic Acid-Derived Oxylipins Inhibit Aflatoxin Biosynthesis in Aspergillus flavus through Activation of Imizoquin Biosynthesis. <b>2022</b> , 70, 15928-15944	O
427	Evidence that direct inhibition of transcription factor binding is the prevailing mode of gene and repeat repression by DNA methylation. <b>2022</b> , 54, 1895-1906	O
426	The histone acetyltransferase KAT6A is recruited to unmethylated CpG islands via a DNA binding winged helix domain.	O
425	An optimized proteomics approach reveals novel alternative proteins in mouse liver development. <b>2022</b> , 100480	O
424	miR-210-3p promotes obesity-induced adipose tissue inflammation and insulin resistance by targeting SOCS1 mediated NF- <b>B</b> pathway.	О
423	Long non-coding RNAs as the regulatory hubs in rice response to salt stress. <b>2022</b> , 12,	1
422	Genome-wide distribution of histone trimethylation reveals a global impact of bisphenol A on telomeric binding proteins and histone acetyltransferase factors: a pilot study with human and in vitro data. <b>2022</b> , 14,	О
421	Efficient combinatorial targeting of RNA transcripts in single cells with Cas13 RNA Perturb-seq.	О
420	Active DNA demethylation promotes cell fate specification and the DNA damage response. <b>2022</b> , 378, 983-989	2
419	Diverse monogenic subforms of human spermatogenic failure. <b>2022</b> , 13,	1
418	LDL delivery of microbial small RNAs drives atherosclerosis through macrophage TLR8. <b>2022</b> , 24, 1701-1713	О
417	StripeDiff: Model-based algorithm for differential analysis of chromatin stripe. <b>2022</b> , 8,	О
416	TCDD induces multigenerational alterations in the expression of microRNA in the thymus through epigenetic modifications.	О

415	Single-Cell and Spatial Transcriptomics Decodes Wharton's Jelly-Derived Mesenchymal Stem Cells Heterogeneity and a Subpopulation with Wound Repair Signatures. 2204786	О
414	Interplay Between the Histone Variant H2A.Z and the Epigenome in Pancreatic Cancer. <b>2022</b> , 53, 840-858	O
413	Climate-responsive DNA methylation is involved in the biosynthesis of lignin in birch. 13,	1
412	Ehydroxybutyrate inhibits ferroptosis-mediated pancreatic damage in acute liver failure through the increase of H3K9bhb. <b>2022</b> , 41, 111847	O
411	PI3K /Akt/ CncC signaling pathway mediates response to EPN-Bt infection in Holotrichia parallela larvae.	O
410	Polyglutamine-expanded ATXN7 alters a specific epigenetic signature underlying photoreceptor identity gene expression in SCA7 mouse retinopathy. <b>2022</b> , 29,	O
409	Human JAK1 gain of function causes dysregulated myelopoeisis and severe allergic inflammation. <b>2022</b> , 7,	О
408	Abundance of Ruminococcaceae is Associated with Claudin 22 Gene Expression and Body Weight in Mice.	O
407	Pan-cancer surveys indicate cell cycle-related roles of primate-specific genes in tumors and embryonic cerebrum. <b>2022</b> , 23,	0
406	SALIENT: Ultra-Fast FPGA-based Short Read Alignment. <b>2022</b> ,	O
406 405	SALIENT: Ultra-Fast FPGA-based Short Read Alignment. 2022,  Culex Mosquito Piwi4 Is Antiviral against Two Negative-Sense RNA Viruses. 2022, 14, 2758	0
405	Culex Mosquito Piwi4 Is Antiviral against Two Negative-Sense RNA Viruses. <b>2022</b> , 14, 2758	О
405 404	Culex Mosquito Piwi4 Is Antiviral against Two Negative-Sense RNA Viruses. 2022, 14, 2758  Probiotic effects on immunity and microbiome in HIV-1 discordant patients. 13,  FBXO42activity is required to prevent mitotic arrest, spindle assembly checkpoint activation, and	0
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405 404 403 402	Culex Mosquito Piwi4 Is Antiviral against Two Negative-Sense RNA Viruses. 2022, 14, 2758  Probiotic effects on immunity and microbiome in HIV-1 discordant patients. 13,  FBXO42activity is required to prevent mitotic arrest, spindle assembly checkpoint activation, and lethality in glioblastoma and other cancers.  Host tRNA-Derived RNAs Target the 3?Untranslated Region of SARS-CoV-2. 2022, 11, 1479	0 0
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397	Modulation of RNA splicing enhances response to BCL2 inhibition in leukemia. 2022,	O
396	Histone modifications and DNA methylation act cooperatively in regulating symbiosis genes in the sea anemone Aiptasia. <b>2022</b> , 20,	O
395	The immune-related circRNA-miRNA-mRNA ceRNA regulatory network in the liver of turbot (Scophthalmus maximus L.) induced by Vibrio anguillarum. <b>2022</b> , 108506	0
394	SCONE Short Conditional intrON for conditional knockout with one-step zygote injection. <b>2022</b> , 54, 2188-2199	O
393	Orally administratedLactobacillus gasseriTM13 andLactobacillus crispatusLG55 Can Restore the Vaginal Health of Patients Recovering from Bacterial Vaginosis.	0
392	Pathogen and Antibody Identification in Children with Encephalitis in Myanmar.	O
391	CIS controls the functional polarization of GM-CSF-derived macrophages.	O
390	Comparative Analysis of mRNA and miRNA Expression between Dermal Papilla Cells and Hair Matrix Cells of Hair Follicles in Yak. <b>2022</b> , 11, 3985	Ο
389	Strobealign: flexible seed size enables ultra-fast and accurate read alignment. 2022, 23,	1
388	Investigation of MicroRNA Biomarkers in Equine Distal Interphalangeal Joint Osteoarthritis. <b>2022</b> , 23, 15526	O
387	RNAi machinery regulates nutrient metabolism and fluconazole resistance in the pathogenic fungus Cryptococcus deneoformans.	0
386	Clustering pattern and evolution characteristic of microRNAs in grass carp (Ctenopharyngodon Idella).	Ο
385	Aberrant expression of agouti signaling protein (ASIP) as a cause of monogenic severe childhood obesity. <b>2022</b> , 4, 1697-1712	0
384	Transposons contribute to the functional diversification of the head, gut, and ovary transcriptomes acrossDrosophilanatural strains.	O
383	G-quadruplexes sense natural porphyrin metabolites for regulation of gene transcription and chromatin landscapes. <b>2022</b> , 23,	0
382	Construction of a Transposon Mutant Library in the Pathogen Agrobacterium tumefaciens C58 and Identification of Genes Involved in Gall Niche Exploitation and Colonization. <b>2023</b> , 209-226	Ο
381	L-SCRaMbLE creates large-scale genome rearrangements in synthetic Sc2.0 chromosomes.	0
380	Composition and toxicity of venom produced by araneophagous white-tailed spiders (Lamponidae: Lampona sp.). <b>2022</b> , 12,	O

379	Analysis of antibiotic resistance genes in pig feces during the weaning transition using whole metagenome shotgun sequencing.	О
378	Accumulation of DNA damage alters microRNA gene transcription in Arabidopsis thaliana. <b>2022</b> , 22,	Ο
377	The complex etiology of Epilepsy: Genetic analysis and HLA association in patients in the Middle East.	О
376	Systematic identification and characterization of repressive domains in Drosophila transcription factors.	O
375	Juvenile zebrafish (Danio rerio) are able to recover from lordosis. 2022, 12,	1
374	Effects of enhanced insect feeding on the faecal microbiota and transcriptome of a family of captive common marmosets (Callithrix jacchus). <b>2022</b> , 17, e0279380	O
373	RNA binding protein PRRC2B mediates translation of specific proteins and regulates cell cycle progression.	Ο
372	Detection of horizontal sequence transfer in microorganisms in the genomic era.	Ο
371	Functional investigation of five R2R3-MYB transcription factors associated with wood development in Eucalyptus using DAP-seq-ML.	0
370	Long non-coding RNA LEENE promotes angiogenesis and ischemic recovery in diabetes models.	1
369	Comprehensive re-analysis of hairpin small RNAs in fungi reveals loci with conserved links. 11,	0
368	Genetic evidence of aberrant striatal synaptic maturation and secretory pathway alteration in a dystonia mouse model. 1,	Ο
367	In vivo PIWI slicing in mouse testes deviates from rules established in vitro. rna.079349.122	0
366	Inhibition of histone methyltransferase Smyd3 rescues NMDAR and cognitive deficits in a tauopathy mouse model. <b>2023</b> , 14,	O
365	Functional partitioning of transcriptional regulators by patterned charge blocks. 2023,	3
364	Decapping factor Dcp2 controls mRNA abundance and translation to adjust metabolism and filamentation to nutrient availability.	O
363	Space-efficient computation of parallel approximate string matching.	О
362	Ischemic Stroke Induces Skeletal Muscle Damage and Alters Transcriptome Profile in Rats. <b>2023</b> , 12, 547	O

361	The hitchhikers@uide to RNA sequencing and functional analysis.	0
360	Physiological and morphological factors affecting leaf sheath reinforcement and their contribution to lodging resistance in rice. 1-17	O
359	A central role for regulated protein stability in the control of TFE3 and MITF by nutrients. 2023, 83, 57-73.e9	0
358	A Flexible Automated Pipeline Engine for Transcript-Level Quantification from RNA-seq. <b>2022</b> , 45-54	O
357	HA-tag CD63 is a novel conditional transgenic approach to track extracellular vesicle interactions with sperm and their transfer at conception. <b>2023</b> , 13,	0
356	Micrococcus luteus-derived extracellular vesicles attenuate neutrophilic asthma by regulating miRNAs in airway epithelial cells.	Ο
355	General transcription factor TAF4 antagonizes epigenetic silencing by Polycomb to maintain intestine stem cell functions.	0
354	Altered miRNA Expression Profiles in the Serum of Beagle Dogs Experimentally Infected with Toxocara canis. <b>2023</b> , 13, 299	О
353	Integrative analysis of small non-coding RNAs predict a piRNA/miRNA-CCND1/BRAF/HRH1/ATXN3 regulatory circuit that drives oncogenesis in Glioblastoma.	0
352	Uncovering novel MHC alleles from RNA-Seq data: expanding the spectrum of MHC class I alleles in sheep. <b>2023</b> , 24,	O
351	The miR156x + p/SPL13-6 module responds to ABA, IAA, and ethylene, and SPL13-6 participates in the juvenile∃dult phase transition in Pyrus.	0
350	Genome-wide measurement of DNA replication fork directionality and quantification of DNA replication initiation and termination with Okazaki fragment sequencing.	O
349	Intron retention of an adhesion GPCR generates single transmembrane-helix isoforms to enable 7TM-adhesion GPCR function.	1
348	A metagenomic survey on Solanum tuberosum virome revealed environmental contamination of a laboratory-developed strain of SARS-CoV-2.	O
347	Mosquito vector competence for dengue is modulated by insect-specific viruses. <b>2023</b> , 8, 135-149	O
346	Determination of Mutational Timing of Colistin-Resistance Genes through Klebsiella pneumoniae Evolution. <b>2023</b> , 15, 270	O
345	DeteX: A highly accurate software for detecting SNV and InDel in single and paired NGS data in cancer research. 13,	0
344	Transcriptome analyses reveal the effects of mixed saline∃lkali stress on indoleacetic acid and cytokinins in Malus hupehensis Rehd. leaves.	O

343	Genomic resources enable insight into the developmental transcriptome of the blastoclad fungus, Coelomomyces lativittatus, an obligate parasite of mosquitoes and microcrustaceans.	0
342	Long term follow-up of colorectal cancer screening attendees identifies differences in Phascolarctobacterium spp. using 16S rRNA and metagenome sequencing.	O
341	BREVIPEDICELLUS Positively Regulates Salt-Stress Tolerance in Arabidopsis thaliana. <b>2023</b> , 24, 1054	O
340	Insights into chloroplast genome structure, intraspecific variation, and phylogeny of Cyclamen species (Myrsinoideae). <b>2023</b> , 13,	O
339	MicroRNA-eQTLs in the developing human neocortex link miR-4707-3p expression to brain size. 12,	0
338	Soya saponins and prebiotics alter intestinal functions in Ballan wrasse (Labrus bergylta). 1-46	O
337	tncRNA Toolkit: A pipeline for convenient identification of RNA (tRNA)-derived non-coding RNAs. <b>2023</b> , 10, 101991	0
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335	Integrating Analysis to Identify Differential circRNAs Involved in Goat Endometrial Receptivity. <b>2023</b> , 24, 1531	0
334	Towards understanding the mechanism of n-hexane tolerance in Synechocystis sp. PCC 6803. <b>2023</b> ,	O
333	Molecular Characterization of Three Apple Geminivirus Isolates in Crabapples Detected in Inner Mongolia, China. <b>2023</b> , 12, 195	0
332	pmartR 2.0: A Quality Control, Visualization, and Statistics Pipeline for Multiple Omics Datatypes.	O
331	Functional genomic analysis of adult and pediatric brain tumor isolates.	0
330	A virulence activator of a surface attachment protein in Burkholderia pseudomallei acts as a global regulator of other membrane-associated virulence factors. 13,	O
329	Transcriptome, Proteome, and Protein Synthesis within the Intracellular Cytomatrix. 2023, 105965	0
328	The LHX2-OTX2 transcriptional regulatory module controls retinal pigmented epithelium differentiation and underlies genetic risk for age-related macular degeneration. <b>2023</b> , 21, e3001924	0
327	Wnt/Etatenin signalling is required for pole-specific chromatin remodeling during planarian regeneration. <b>2023</b> , 14,	1
326	Analysis of microRNAs in response to cycloastragenol by small RNA sequencing in Arabidopsis thaliana.	O

325	Current advances in antiviral RNA interference in mammals.	O
324	Transcriptome analysis and gene expression analysis related to salinity-alkalinity and low temperature adaptation of Triplophysa yarkandensis. 13,	O
323	Differential Susceptibility of Fetal Retinal Pigment Epithelial Cells, hiPSC- Retinal Stem Cells, and Retinal Organoids to Zika Virus Infection. <b>2023</b> , 15, 142	1
322	Translation initiation of leaderless and polycistronic transcripts in mammalian mitochondria.	Ο
321	A transcription factor atlas of directed differentiation. <b>2023</b> , 186, 209-229.e26	1
320	Local and terminal cell differentiation mediated by the jasmonic acid-mediated autophagy evokes petal abscission in Arabidopsis thaliana.	O
319	A computational pipeline to learn gene expression predictive models from epigenetic information at enhancers or promoters. <b>2023</b> , 4, 101948	0
318	COD-FISH: Contrastive Oligonucleotide Design for Fluorescence In-Situ Hybridization to Detect Single RNA Molecules with High Specificity. <b>2022</b> ,	O
317	Serverless computing for RNA-Seq data analysis. 2022,	O
316	Pre-exposure cognitive performance variability is associated with severity of respiratory infection. <b>2022</b> , 12,	Ο
315	miR-34a Regulates Lipid Droplet Deposition in 3T3-L1 and C2C12 Cells by Targeting LEF1. <b>2023</b> , 12, 167	Ο
314	A multi-omics integrative network map of maize. <b>2023</b> , 55, 144-153	1
313	Serum-Exosome-Derived miRNAs Serve as Promising Biomarkers for HCC Diagnosis. <b>2023</b> , 15, 205	O
312	Resistance to white spot syndrome virus in the European shore crab is associated with suppressed virion trafficking and heightened immune responses. 13,	1
311	The gold-ringed octopus (Amphioctopus fangsiao) 'genome and cerebral single-nucleus transcriptomes provide insights into the evolution of karyotype and neural novelties. <b>2022</b> , 20,	0
310	Characterizing Relevant MicroRNA Editing Sites in Parkinson Disease. <b>2023</b> , 12, 75	O
309	Multi-omics gut microbiome signatures in obese women: role of diet and uncontrolled eating behavior. <b>2022</b> , 20,	1
308	Expansion of ventral foregut is linked to changes in the enhancer landscape for organ-specific differentiation.	Ο

307	Using the Gut Microbiome to Assess Stocking Efforts of the Endangered Pallid Sturgeon, Scaphirhynchus albus. <b>2023</b> , 13, 309	Ο
306	Histone deacetylation regulates de novo shoot regeneration.	O
305	Characterizing microRNA editing and mutation sites in Autism Spectrum Disorder. 15,	0
304	Initiation of HIV-1 Gag lattice assembly is required for recognition of the viral genome packaging signal. 12,	O
303	Defining the contribution of microRNA-specific slicing Argonautes in animals.	0
302	The miR-430 locus with extreme promoter density forms a transcription body during the minor wave of zygotic genome activation. <b>2023</b> , 58, 155-170.e8	O
301	Polymorphic inverted repeats near coding genes impact chromatin topology and phenotypic traits in Arabidopsis thaliana. <b>2023</b> , 42, 112029	0
300	Epigenomic charting and functional annotation of risk loci in renal cell carcinoma. 2023, 14,	Ο
299	Chromatin landscape governing murine epidermal differentiation. 2023,	Ο
298	Genomic analysis of an ultrasmall freshwater green alga, Medakamo hakoo. 2023, 6,	Ο
297	ETV6 dependency in Ewing sarcoma by antagonism of EWS-FLI1-mediated enhancer activation.	Ο
296	Aligner-D: Leveraging In-DRAM Computing to Accelerate DNA Short Read Alignment. 2023, 1-1	Ο
295	Multiplepalsgene modules control a balance between immunity and development inCaenorhabditis elegans.	Ο
294	Hypomethylation in MTNR1B: a novel epigenetic marker for atherosclerosis profiling using stenosis radiophenotype and blood inflammatory cells. <b>2023</b> , 15,	Ο
293	The coordinated regulation of early meiotic stages is dominated by non-coding RNAs and stage-specific transcription in wheat.	0
292	Characteristics and functions of DNA N(6)-methyladenine in embryonic chicken muscle development. <b>2023</b> , 102528	O
291	Quantitative Comparison of Multiple Chromatin Immunoprecipitation-Sequencing (ChIP-seq) Experiments with spikChIP. <b>2023</b> , 55-72	0
290	KSHV infection of endothelial precursor cells with lymphatic characteristics as a novel model for translational Kaposi⊠ sarcoma studies. <b>2023</b> , 19, e1010753	Ο

289	DOT-1.1 (DOT1L) deficiency in C. elegans leads to small RNA-dependent gene activation. <b>2023</b> , 3, 100080	О
288	CONSTANS alters the circadian clock inArabidopsis thaliana.	O
287	Identification of a tsRNA Contributor to Impaired Diabetic Wound Healing via High Glucose-Induced Endothelial Dysfunction. Volume 16, 285-298	O
286	RUNX1 is required in granulocyte-monocyte progenitors to attenuate inflammatory cytokine production by neutrophils.	O
285	Sensitized piRNA reporter identifies multiple RNA processing factors involved in piRNA-mediated gene silencing.	O
284	The ribose methylation enzyme FTSJ1 has a conserved role in neuron morphology and learning performance. <b>2023</b> , 6, e202201877	O
283	miR-203 drives breast cancer cell differentiation.	0
282	Systematic and benchmarking studies of pipelines for mammal WGBS data in the novel NGS platform. <b>2023</b> , 24,	O
281	Feeding Asian honeybee queens with European honeybee royal jelly alters body color and expression of related coding and non-coding RNAs. 14,	O
280	A modular CRISPR screen identifies individual and combination pathways contributing to HIV-1 latency. <b>2023</b> , 19, e1011101	1
279	Purified regenerating retinal neurons reveal regulatory role of DNA methylation-mediated Na+/K+-ATPase in murine axon regeneration. <b>2023</b> , 6,	0
278	DNA Double-Strand Break-Related Competitive Endogenous RNA Network of Noncoding RNA in Bovine Cumulus Cells. <b>2023</b> , 14, 290	1
277	Molecular characterization of extracellular vesicles derived from follicular fluid of women with and without PCOS: integrating analysis of differential miRNAs and proteins reveals vital molecules involving in PCOS.	0
276	DEtail-seq is an ultra-efficient and convenient method for meiotic DNA break profiling in multiple organisms.	O
275	Trem2 H157Y increases soluble TREM2 production and reduces amyloid pathology. <b>2023</b> , 18,	1
274	How Many Sirtuin Genes Are Out There? Evolution of Sirtuin Genes in Vertebrates With a Description of a New Family Member. <b>2023</b> , 40,	O
273	Patterns of stress response to foreign eggs by a rejecter host of an obligate avian brood parasite. <b>2023</b> , 13,	0
272	Model-driven experimental design workflow expands understanding of regulatory role of Nac in Escherichia coli. <b>2023</b> , 5,	O

271	Allosteric autoregulation of DNA binding via a DNA-mimicking protein domain: a biophysical study of ZNF410DNA interaction using small angle X-ray scattering.	О
270	ciRS-7-miR7 regulate ischemia induced neuronal death via glutamatergic signaling.	O
269	Deep-learning optimized DEOCSU suite provides an iterable pipeline for accurate ChIP-exo peak calling.	0
268	A New Insight into MYC Action: Control of RNA Polymerase II Methylation and Transcription Termination. <b>2023</b> , 11, 412	O
267	In Vivo Dissection of Chamber-Selective Enhancers Reveals Estrogen-Related Receptor as a Regulator of Ventricular Cardiomyocyte Identity.	1
266	A Comprehensive Investigation of Genomic Variants in Prostate Cancer Reveals 30 Putative Regulatory Variants. <b>2023</b> , 24, 2472	O
265	Methods to improve the accuracy of next-generation sequencing. 11,	0
264	Costimulatory domains direct distinct fates of CAR-driven T cell dysfunction.	O
263	The catalytic activity of microRNA Argonautes plays a modest role in microRNA star strand cleavage inC. elegans.	O
262	KDM6 demethylases mediate EWSR1-FLI1-driven oncogenic transformation in Ewing Sarcoma.	O
261	Human zygotic genome activation is initiated from paternal genome. <b>2023</b> , 9,	O
260	Influenza A virus modulation ofStreptococcus pneumoniaeinfection using ex vivo transcriptomics in a human primary lung epithelial cell model reveals differential host glycoconjugate uptake and metabolism.	O
259	Exon architecture controls mRNA m 6 A suppression and gene expression.	O
258	Advancing Microbe Detection for Lower Respiratory Tract Infection Diagnosis and Management with Metagenomic Next-Generation Sequencing. Volume 16, 677-694	O
257	Bioinformatic analysis for age prediction using epigenetic clocks: Application to fisheries management and conservation biology. 10,	O
256	Identification of Conserved and Novel MicroRNAs with their Targets in Garden Pea (Pisum Sativum L.) Leaves by High-Throughput Sequencing. <b>2023</b> , 17, 117793222311627	O
255	The interaction between the histone acetyltransferase complex Hat1-Hat2 and transcription factor AmyR provides a molecular brake to regulate amylase gene expression. <b>2023</b> , 119, 471-491	О
254	Quantitative analysis of high-throughput biological data.	O

253	A dual-activity topoisomerase complex promotes both transcriptional activation and repression in response to starvation. <b>2023</b> , 51, 2415-2433	О
252	S-adenosylmethionine synthases specify distinct H3K4me3 populations and gene expression patterns during heat stress. 12,	O
251	Characterization of De Novo Promoter Variants in Autism Spectrum Disorder with Massively Parallel Reporter Assays. <b>2023</b> , 24, 3509	О
250	Production, purification, characterization and application of two novel endoglucanases from buffalo rumen metagenome. <b>2023</b> , 14,	Ο
249	Enhancer-promoter interactions are reconfigured through the formation of long-range multiway chromatin hubs as mouse ES cells exit pluripotency.	0
248	Spliceosome component Usp39 contributes to hepatic lipid homeostasis through the regulation of lipophagy.	O
247	Antitumor T-cell function requires CPEB4-mediated adaptation to chronic endoplasmic reticulum stress.	0
246	Global identification of direct SWI/SNF targets reveals compensation by EP400.	O
245	MiRNA-Seq reveals key MicroRNAs involved in fat metabolism of sheep liver. 14,	О
244	Transcriptomic analysis reveals key genes and pathways corresponding to Cd and Pb in the hyperaccumulator Arabis paniculata. <b>2023</b> , 254, 114757	O
243	An efficient CRISPRCas12a promoter editing system for crop improvement.	О
242	Predicting the effects of cultivation condition on gene regulation in Escherichia coli by using deep learning. <b>2023</b> ,	O
241	3D genome organization drives gene expression in trypanosomes.	О
240	Chromosomal positioning and epigenetic architecture influence DNA methylation patterns triggered by galactic cosmic radiation.	O
239	ETV4 mediates dosage-dependent prostate tumor initiation and cooperates with p53 loss to generate prostate cancer. <b>2023</b> , 9,	О
238	Genetic markers associated with divergent selection against the parasite Marteilia cochillia in common cockle (Cerastoderma edule) using transcriptomics and population genomics data. 10,	Ο
237	Translatomics and physiological analyses of the detoxification mechanism of green alga Chlamydomonas reinhardtii to cadmium toxicity. <b>2023</b> , 448, 130990	0
236	The cotton miR530-SAP6 module activated by systemic acquired resistance mediates plant defense against Verticillium dahliae. <b>2023</b> , 330, 111647	O

235	Protocol for performing pooled CRISPR-Cas9 loss-of-function screens. 2023, 4, 102201	O
234	Polycomb safeguards imaginal disc specification through control of the Vestigial-Scalloped complex.	O
233	Scalable Text Index Construction. <b>2022</b> , 252-284	0
232	Short-term feeding of defatted bovine colostrum mitigates inflammation in the gut via changes in metabolites and microbiota in a chicken animal model. <b>2023</b> , 5,	O
231	The endothelial-enriched lncRNA LINC00607 mediates angiogenic function. 2023, 118,	O
230	SMC5/6 complex-mediated SUMOylation stimulates DNAprotein cross-link repair in Arabidopsis. <b>2023</b> , 35, 1532-1547	O
229	Characterization and microRNA Expression Analysis of Serum-Derived Extracellular Vesicles in Severe Liver Injury from Chronic HBV Infection. <b>2023</b> , 13, 347	O
228	mRNA ageing shapes the Cap2 methylome in mammalian mRNA. <b>2023</b> , 614, 358-366	O
227	Unstable EBV latency drives inflammation in multiple sclerosis patient derived spontaneous B cells.	O
226	Glucose deprivation promotes pseudo-hypoxia and de-differentiation in lung adenocarcinoma.	O
225	Reanalysis of ribosome profiling datasets reveals a function of rocaglamide A in perturbing the dynamics of translation elongation via eIF4A. <b>2023</b> , 14,	O
224	Histone H2A deubiquitinases in the transcriptional programs of development and hematopoiesis: a consolidated analysis. <b>2023</b> , 157, 106384	O
223	Identification of determinants for entering into a viable but nonculturable state in Vibrio alginolyticus by Tn-seq. <b>2023</b> , 107, 1813-1827	O
222	Exosomes of adipose-tissue-derived stem cells over-expressing Neat1 promote wound healing by sponging miR-17-5p and inducing autophagy protein Ulk1. Publish Ahead of Print,	O
221	Molecular characterization of human cytomegalovirus infection with single-cell transcriptomics. <b>2023</b> , 8, 455-468	O
220	microRNAs profiling of small extracellular vesicles from midbrain tissue of Parkinson⊠ disease. 16,	O
219	NFATc2-dependent epigenetic downregulation of the TSC2/Beclin-1 pathway is involved in neuropathic pain induced by oxaliplatin. <b>2023</b> , 19, 174480692311582	О
218	Epistasis between promoter activity and coding mutations shapes gene evolvability. <b>2023</b> , 9,	O

217	Extracellular vesicles and high-density lipoproteins: Exercise and oestrogen-responsive small RNA carriers. <b>2023</b> , 12, 12308	0
216	Cell-specific and shared enhancers control a high-density multi-gene locus active in mammary and salivary glands.	O
215	A Virus-Packageable CRISPR System Identifies Host Dependency Factors Co-Opted by Multiple HIV-1 Strains. <b>2023</b> , 14,	0
214	Cell-specific and shared enhancers control a high-density multi-gene locus active in mammary and salivary glands.	O
213	A cytokine-responsive promoter is required for distal enhancer function mediating the hundreds-fold increase in milk protein gene expression during lactation.	0
212	Excess PrPCinhibits muscle cell differentiation via miRNA-enhanced liquid $f I$ quid phase separation implicated in myopathy.	Ο
211	Transgenerational inheritance of acquired epigenetic signatures at CpG islands in mice. 2023, 186, 715-731.	e19 <u>1</u>
210	A cytokine-responsive promoter is required for distal enhancer function mediating the hundreds-fold increase in milk protein gene expression during lactation.	O
209	Aberrant association of chromatin with nuclear periphery induced by Rif1 leads to mitotic defect. <b>2023</b> , 6, e202201603	0
208	Characterisation of the Upper Respiratory Tract Virome of Feedlot Cattle and Its Association with Bovine Respiratory Disease. <b>2023</b> , 15, 455	Ο
207	Single-molecule footprinting identifies context-dependent regulation of enhancers by DNA methylation. <b>2023</b> , 83, 787-802.e9	0
206	NFATc1 Is a Central Mediator of EGFR-Induced ARID1A Chromatin Dissociation During Acinar Cell Reprogramming. <b>2023</b> , 15, 1219-1246	Ο
205	Framing Apache Spark in life sciences. <b>2023</b> , 9, e13368	Ο
204	The piRNA cluster torimochi is an expanding transposon in cultured silkworm cells. 2023, 19, e1010632	Ο
203	A novel HERC4-dependent glue degrader targeting STING.	Ο
202	CRISPR-Cas9-Mediated Mutation of Methyltransferase METTL4 Results in Embryonic Defects in Silkworm Bombyx mori. <b>2023</b> , 24, 3468	Ο
201	Transcription factor SOX15 regulates stem cell pluripotency and promotes neural fate during differentiation by activating the neurogenic gene Hes5. <b>2023</b> , 299, 102996	0
200	DNA methylation trajectories during innate and adaptive immune responses of human B lymphocytes.	O

199	Strand specificity of ribonucleotide excision repair in Escherichia coli. 2023, 51, 1766-1782	О
198	Circulating Extracellular Vesicles in Human Cardiorenal Syndrome Promote Renal Injury.	О
197	HyperVR: a hybrid deep ensemble learning approach for simultaneously predicting virulence factors and antibiotic resistance genes. <b>2023</b> , 5,	0
196	RNPS1 stabilizes NAT10 protein to facilitate translation in cancer via tRNA ac4C modification.	o
195	Light-Responsive MicroRNAs in Human Retinal Tissue are Differentially Regulated by Distinct Wavelengths of Light.	О
194	Aberrant activation of Wnt/ECatenin signaling pathway drives the expression of poor prognosis-associated microRNAs in adrenocortical cancer with a major impact on miR-139-5p and its host gene PDE2A.	O
193	Viral but not bacterial community succession is characterized by extreme turnover shortly after rewetting dry soils.	0
192	Clustering pattern and evolution characteristic of microRNAs in grass carp (Ctenopharyngodon idella). <b>2023</b> , 24,	O
191	Electric-Inducive Microbial Interactions in a Thermophilic Anaerobic Digester Revealed by High-Throughput Sequencing of Micron-Scale Single Flocs. <b>2023</b> , 57, 4367-4378	O
190	Reproducible evaluation of transposable element detectors with McClintock 2 guides accurate inference of Ty insertion patterns in yeast.	o
189	Genomic profiling of HIV-1 integration in microglia cells links viral integration to the topologically associated domains. <b>2023</b> , 42, 112110	0
188	PeGRF6-PeGIF1 complex regulates cell proliferation in the leaf of Phalaenopsis equestris. <b>2023</b> , 196, 683-694	O
187	Evaluation of the antidermatophytic activity of potassium salts of N-acylhydrazinecarbodithioates and their aminotriazole-thione derivatives.	0
186	Characterization of Histone Modifications in Late-Stage Rotator Cuff Tendinopathy. <b>2023</b> , 14, 496	o
185	Promiscuous splicing-derived hairpins are dominant substrates of tailing-mediated defense of miRNA biogenesis in mammals. <b>2023</b> , 42, 112111	0
184	Transcriptomic profiling reveals candidate allelopathic genes in rice responsible for interactions with barnyardgrass. 14,	o
183	Transcriptional Profiling Supports the Notochordal Origin of Chordoma and Its Dependence on a TGFB1-TBXT Network. <b>2023</b> , 193, 532-547	0
182	Ultra-small bacteria and archaea exhibit genetic flexibility towards groundwater oxygen content, and adaptations for attached or planktonic lifestyles. <b>2023</b> , 3,	O

181	CRISPR screens identify novel regulators of cFLIP dependency and ligand-independent, TRAIL-R1-mediated cell death.	0
180	Evolutionary History of thePoecilia pictaSex Chromosomes. <b>2023</b> , 15,	О
179	Identification and profiling of microRNAs during yakl testicular development. 2023, 19,	О
178	Critical Role of the Transcription Factor AKNA in T-Cell Activation: An Integrative Bioinformatics Approach. <b>2023</b> , 24, 4212	O
177	Interleukin-27-dependent transcriptome signatures during neonatal sepsis. 14,	0
176	Approaches for sRNA Analysis of Human RNA-Seq Data: Comparison, Benchmarking. <b>2023</b> , 24, 4195	o
175	Screening and Analysis of Key Transcription Factors of Yili Goose Sperm Motility miRNAs-mRNAs.	О
174	Metagenomes from Coastal Sediments of Kuwait: Insights into the Microbiome, Metabolic Functions and Resistome. <b>2023</b> , 11, 531	1
173	Cloning of an Albino Mutation of Arabidopsis thaliana Using Mapping-by-Sequencing. 2023, 24, 4196	O
172	Not1 and Not4 inversely determine mRNA solubility that sets the dynamics of co-translational events. <b>2023</b> , 24,	O
171	NFATc1 induction by an intronic enhancer restricts NKT Lell formation. 2023, 26, 106234	0
170	The potential role of serum extracellular vesicle derived small RNAs in AML research as non-invasive biomarker. <b>2023</b> , 5, 1691-1705	O
169	Genome assembly and genetic dissection of a prominent drought-resistant maize germplasm. <b>2023</b> , 55, 496-506	0
168	A Satellite-Free Centromere in Equus przewalskii Chromosome 10. <b>2023</b> , 24, 4134	0
167	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
166	Comparison between articular chondrocytes and mesenchymal stromal cells for the production of articular cartilage implants. 11,	0
165	3? UTR is critical for viral RNA accumulation of jasmine virus H. <b>2023</b> , 5,	0
164	Dual-Uptake Mode of the Antibiotic Phazolicin Prevents Resistance Acquisition by Gram-Negative Bacteria.	O

163	Stress Response in Entamoeba histolytica Is Associated with Robust Processing of tRNA to tRNA Halves.	O
162	Pan-genotypic probe-based enrichment to improve efficiency of Hepatitis B virus sequencing.	O
161	SETD2 regulates chromatin accessibility and transcription to suppress lung tumorigenesis. 2023, 8,	О
160	choros: correction of sequence-based biases for accurate quantification of ribosome profiling data.	O
159	GLIS3 regulates transcription of thyroid hormone biosynthetic genes in coordination with other thyroid transcription factors. <b>2023</b> , 13,	O
158	Community-wide collaboration is a must to reinstall trust in bioinformatics solutions and biomedical interpretation. <b>2023</b> , 20,	O
157	Acquired radioresistance in EMT6 mouse mammary carcinoma cell line is mediated by CTLA-4 and PD-1 through JAK/STAT/PI3K pathway. <b>2023</b> , 13,	O
156	Regulatory mechanism of MeGI on sexuality in Diospyros oleifera. 14,	O
155	Biofilm Reactor Performance and Shifts of Microbial Community during the Start-Up and Operation Phase of MBBRs at 8 °C: Effect of Exogenous Quorum Sensing Bacteria. <b>2023</b> , 3, 804-816	O
154	Deviating Alternative Splicing as a Molecular Subtype of Microsatellite Stable Colorectal Cancer. <b>2023</b> ,	O
153	Transposable element and host silencing activity in gigantic genomes. 11,	O
152	Comparative analysis of two kinds of garlic seedings: qualities and transcriptional landscape. <b>2023</b> , 24,	O
151	MicroRNA transcriptomics in liver of the freeze-tolerant gray tree frog (Dryophytes versicolor) indicates suppression of energy-expensive pathways. <b>2023</b> , 41, 309-320	O
150	Pro-inflammatory polarization and colorectal cancer modulate alternative and intronic polyadenylation in primary human macrophages.	O
149	Characterization of volatile organic compounds in grafted tomato plants upon potyvirus necrotic infection. <b>2023</b> ,	O
148	Revealing the History and Mystery of RNA-Seq. <b>2023</b> , 45, 1860-1874	O
147	Translational landscape in human early neural fate determination. 2023, 150,	0
146	Differential Expression of miRNAs Involved in Response to Candidatus Liberibacter asiaticus Infection in Mexican Lime at Early and Late Stages of Huanglongbing Disease. <b>2023</b> , 12, 1039	O

145	The Effect of Human and Bovine Milk Osteopontin on Intestinal Caco-2 Cells: A Transcriptome Comparison. <b>2023</b> , 15, 1166	1
144	Mapping Nucleosome Location Using FS-Seq. <b>2023</b> , 21-38	O
143	Simultaneous Single-Cell Profiling of the Transcriptome and Accessible Chromatin Using SHARE-seq. <b>2023</b> , 187-230	0
142	In vitroreconstitution of chromatin domains.	O
141	Expression analysis and targets prediction of microRNAs in OGD/R treated astrocyte-derived exosomes by smallRNA sequencing. <b>2023</b> , 115, 110594	О
140	Genome-wide hydroxymethylation profiles in liver of female Nile tilapia with distinct growth performance. <b>2023</b> , 10,	O
139	Intergenerational Inheritance of Hepatic Steatosis in a Mouse Model of Childhood Obesity: Potential Involvement of Germ-Line microRNAs. <b>2023</b> , 15, 1241	0
138	Trypanosoma cruzi dysregulates expression profile of piRNAs in primary human cardiac fibroblasts during early infection phase. 13,	Ο
137	Network of miR396-mRNA in Tissue Differentiation in Moso Bamboo (Phyllostachys edulis). <b>2023</b> , 12, 1103	0
136	Fluctuations in chromatin state at regulatory loci occur spontaneously under relaxed selection and are associated with epigenetically inherited variation in C. elegans gene expression. <b>2023</b> , 19, e1010647	O
135	BaM-seq and TBaM-seq, highly multiplexed and targeted RNA-seq protocols for rapid, low-cost library generation from bacterial samples. <b>2023</b> , 5,	O
134	Chromatin opening ability of pioneer factor Pax7 depends on unique isoform and C-terminal domain.	O
133	Chromatin Accessibility and Pioneer Factor FOXA1 Shape Glucocorticoid Receptor Action in Prostate Cancer.	О
132	MicroRNA172b-5p/trehalose-6-phosphate synthase module stimulates trehalose synthesis and microRNA172b-3p/AP2-like module accelerates flowering in barley upon drought stress. 14,	O
131	Long noncoding RNA AL109754.1 Regulates Myeloid Dendritic Cell Differentiation and Potentiates TLR signaling.	0
130	Genomic transcription factor binding site selection is edited by the chromatin remodeling factor CHD4.	O
129	Song features correlate with male reproductive success and avian malaria infection in a promiscuous songbird with female-only parental care.	0
128	Microbiota epigenetically direct tuft cell differentiation to control type 2 immunity.	Ο

127	Enhancing HIV-1 latency reversal through regulating the elongating RNA Pol II pause-release by a small-molecule disruptor of PAF1C. <b>2023</b> , 9,	0
126	Plastome variations reveal the distinct evolutionary scenarios of plastomes in the subfamily Cereoideae (Cactaceae). <b>2023</b> , 23,	O
125	Blocking Abundant RNA Transcripts by High-Affinity Oligonucleotides during Transcriptome Library Preparation. <b>2023</b> , 25,	0
124	The nucleolar aberrancies that drive ribosome impairment induced by RNA binding proteins are hallmarks of aging.	O
123	Inhibition of Nonsense-Mediated Decay Induces Nociceptive Sensitization through Activation of the Integrated Stress Response. <b>2023</b> , 43, 2921-2933	O
122	RiboGalaxy: A Galaxy-based Web Platform for Ribosome Profiling Data Processing №023 Update. <b>2023</b> , 168043	O
121	Inference and reconstruction of the heimdallarchaeial ancestry of eukaryotes.	O
120	Transcriptional and metabolic responses of apple to different potassium environments. 14,	O
119	Tn-seq identifies Ralstonia solanacearum genes required for tolerance of plant immunity induced by exogenous salicylic acid.	0
118	Whole-Genome-Sequence-Based Evolutionary Analyses of HoBi-like Pestiviruses Reveal Insights into Their Origin and Evolutionary History. <b>2023</b> , 15, 733	O
117	Disentangling the Potential Functions of miRNAs in the Synthesis of Terpenoids during the Development of Cinnamomum burmannii Leaves. <b>2023</b> , 14, 555	0
116	MicroRNA Profiling of Self-Renewing Human Neural Stem Cells Reveals Novel Sets of Differentially Expressed microRNAs During Neural Differentiation In Vitro.	Ο
115	Impaired ATF3 Signaling Involves SNAP25 in SOD1 Mutant ALS Patients.	0
114	Batf stabilizes Th17 cell development via impaired Stat5 recruitment of Ets1-Runx1 complexes. <b>2023</b> , 42,	O
113	Small Molecule Regulators of microRNAs Identified by High-Throughput Screen Coupled with High-Throughput Sequencing.	0
112	Mycobacterial RNase E cleaves with a distinct sequence preference and controls the degradation rates of mostMycolicibacterium smegmatismRNAs.	O
111	Perturbomics of tumor-infiltrating NK cells.	0
110	Far-Red-Light-Induced Morphology Changes, Phytohormone, and Transcriptome Reprogramming of Chinese Kale (Brassica alboglabra Bailey). <b>2023</b> , 24, 5563	O

109	Rational design of immune gene therapy combinations viain vivoCRISPR activation screen of tumor microenvironment modulators.	O
108	Tonic repression of collagen I by the bradykinin receptor 2 in skin fibroblasts. <b>2023</b> , 118, 110-128	О
107	Chromatin profiling identifies transcriptional readthrough as a conserved mechanism for piRNA biogenesis in mosquitoes. <b>2023</b> , 42, 112257	0
106	Unlocking the genome of perch From genes to ecology and back again.	О
105	Antiviral immune response reveals host-specific virus infections in natural ant populations. 14,	О
104	Pharmacogenomic and Statistical Analysis. <b>2023</b> , 305-330	O
103	The MicroRNA Ame-Bantam-3p Controls Larval Pupal Development by Targeting the Multiple Epidermal Growth Factor-like Domains 8 Gene (megf8) in the Honeybee, Apis mellifera. <b>2023</b> , 24, 5726	0
102	Transcriptomes reveal microRNAs and mRNAs in different photoperiods influencing cashmere growth in goat. <b>2023</b> , 18, e0282772	O
101	TXNIP loss expands Myc-dependent transcriptional programs by increasing Myc genomic binding. <b>2023</b> , 21, e3001778	O
100	Polygenic pathogen networks control of host and pathogen transcriptional plasticity in the Arabidopsis-Botrytis pathosystem.	O
99	Hierarchy and networks in the transcriptional response of Mycobacterium abscessusto antibiotics.	О
98	De Novo Transcriptome Sequencing of Codonopsis lanceolata for Identification of Triterpene Synthase and Triterpene Acetyltransferase. <b>2023</b> , 24, 5769	O
97	Stress-sensitive dynamics of miRNAs and Elba1 in Drosophila embryogenesis.	О
96	Ectodermal Wnt signaling, cell fate determination, and polarity of the skate gill arch skeleton. 12,	0
95	Propagated Circulating Tumor Cells Uncover the Potential Role of NFB, EMT, and TGFIsignaling Pathways and COP1 in Metastasis. <b>2023</b> , 15, 1831	0
94	Enhancers display constrained sequence flexibility and context-specific modulation of motif function. <b>2023</b> , 33, 346-358	Ο
93	RNA sequencing-based exploration of the effects of far-red light on microRNAs involved in the shade-avoidance response of D. officinale. 11, e15001	0
92	miRNome profiling reveals differential miRNAs associated with embryogenic potential in the somatic embryogenesis of Araucaria angustifolia.	O

91	Multi-omics analysis identifies drivers of protein phosphorylation. <b>2023</b> , 24,	O
90	Cocktails of NSAIDs and 17Æthinylestradiol at Environmentally Relevant Doses in Drinking Water Alter Puberty Onset in Mice Intergenerationally. <b>2023</b> , 24, 5890	O
89	Genome-resolved metagenomics of milk microbiomes reveals the influence of maternal dietary fiber on neonatal inheritance of immunoregulatory traits.	О
88	A transcriptionally distinct subset of influenza-specific effector memory B cells predicts long-lived antibody responses to vaccination in humans. <b>2023</b> , 56, 847-863.e8	O
87	An unknown essential function of tRNA splicing endonuclease is linked to the integrated stress response and intron debranching.	O
86	Assembly and Analysis of Haemonchus contortus Transcriptome as a Tool for the Knowledge of Ivermectin Resistance Mechanisms. <b>2023</b> , 12, 499	O
85	Floral Development Stage-Specific Transcriptomic Analysis Reveals the Formation Mechanism of Different Shapes of Ray Florets in Chrysanthemum. <b>2023</b> , 14, 766	O
84	Improving RNA Fusion Call Confidence and Reliability in Molecular Diagnostic Testing. 2023,	O
83	The Cytomegalovirus M35 Protein Modulates Transcription ofIfnb1and Other IRF3-Driven Genes by Direct Promoter Binding.	O
82	Bacteriophage antidefense genes that neutralize TIR and STING immune responses. <b>2023</b> , 42, 112305	O
81	Preparation of therapy-grade extracellular vesicles from adipose tissue to promote diabetic wound healing. 11,	О
80	Multiple gene co-options underlie the rapid evolution of sexually deceptive flowers in Gorteria diffusa. <b>2023</b> ,	O
79	Genetic dissection of the pluripotent proteome through multi-omics data integration. 2023, 3, 100283	O
78	Comparative transcriptome analysis in contrasting finger millet (Eleusine coracana(L.) Gaertn) genotypes for heat stress.	O
77	High-Resolution Genomic Profiling of Liver Cancer Links Etiology With Mutation and Epigenetic Signatures. <b>2023</b> ,	O
76	ExosomePurity: tumour purity deconvolution in serum exosomes based on miRNA signatures.	O
75	A comprehensive map of hotspots of de novo telomere addition inSaccharomyces cerevisiae.	0
74	Discovery of aphid-transmitted Rice tiller inhibition virus from native plants through metagenomic sequencing. <b>2023</b> , 19, e1011238	O

73	U1 snRNP increases RNA Pol II elongation rate to enable synthesis of long genes. 2023, 83, 1264-1279.e10	О
72	The Expression Pattern of tRNA-Derived Small RNAs in Adult Drosophila and the Function of tRF-Trp-CCA-014-H3C4 Network Analysis. <b>2023</b> , 24, 6169	O
71	tsRNA Landscape and Potential Function Network in Subcutaneous and Visceral Pig Adipose Tissue. <b>2023</b> , 14, 782	О
70	Cbp1-Cren7 chromatinization of CRISPR arrays favours transcription from leader-over cryptic promoters.	O
69	The Torreya grandis genome illuminates the origin and evolution of gymnosperm-specific sciadonic acid biosynthesis. <b>2023</b> , 14,	О
68	Characterization of stilbene synthase genes by comparative genome sequencing of Vitis flexuosa with high contents of stilbene compounds to Vitis vinifera genome.	O
67	Rewired m6A epitranscriptomic networks link mutant p53 to neoplastic transformation. 2023, 14,	0
66	Comparative chloroplast genomics reveals the phylogeny and the adaptive evolution of Begonia in China.	O
65	High-throughput miRNA sequencing and identification of a novel ICE1-targeting miRNA in response to low temperature stress in Eucalyptus camaldulensis.	O
64	Comprehensive analysis of microRNA and metabolic profiles in bovine seminal plasma of different semen quality. 10,	O
63	Sterile faecal filtrate transplantation alters phage-microbe dynamics in individuals with metabolic syndrome: a double blind, randomised, placebo-controlled clinical trial assessing efficacy and safety.	0
62	A role for N6-methyldeoxyadenosine inC. elegansmitochondrial genome regulation.	O
61	Arabidopsis mRNA decay landscape shaped by XRN 5?-3? exoribonucleases.	0
60	Using metatranscriptomics to better understand the role of microbial nitrogen cycling in coastal sediment benthic flux denitrification efficiency.	Ο
59	Inferring Gene Regulatory Networks from RNA-seq Data Using Kernel Classification. 2023, 12, 518	О
58	Baicalein-corrected gut microbiota may underlie the amelioration of memory and cognitive deficits in APP/PS1 mice. 14,	0
57	Novel Transcriptomic Interactomes of Noncoding RNAs in the Heart under Altered Thyroid Hormonal States. <b>2023</b> , 24, 6560	O
56	Sequencing of the Pituitary Transcriptome after GnRH Treatment Uncovers the Involvement of lncRNA-m23b/miR-23b-3p/CAMK2D in FSH Synthesis and Secretion. <b>2023</b> , 14, 846	Ο

55	Nuclei on the Rise: When Nuclei-Based Methods Meet Next-Generation Sequencing. 2023, 12, 1051	0
54	Light-activated macromolecular phase separation modulates transcription by reconfiguring chromatin interactions. <b>2023</b> , 9,	O
53	Temporal colonization of the gut microbiome in neonatalBos taurusat single nucleotide resolution.	O
52	Early microbial intervention reduces diarrhea while improves later milk production in newborn calves.	O
51	RIF1 regulates replication origin activity and early replication timing in B cells.	O
50	Distinct transcriptomic and epigenomic modalities underpin human memory T cell subsets and their activation potential. <b>2023</b> , 6,	O
49	The miRNA Landscape of Lacrimal Glands in a Murine Model of Autoimmune Dacryoadenitis. <b>2023</b> , 64, 1	0
48	Human Adult Astrocyte Extracellular Vesicle Transcriptomics Study Identifies Specific RNAs Which Are Preferentially Secreted as EV Luminal Cargo. <b>2023</b> , 14, 853	O
47	Functionally distinct promoter classes initiate transcription via different mechanisms reflected in focused versus dispersed initiation patterns.	0
46	The mechanisms of siRNA selection by plant Argonaute proteins triggering DNA methylation.	O
45	Multiplexed protein stability (MPS) profiling of terminal degrons using fluorescent timer libraries in Saccharomyces cerevisiae. <b>2023</b> ,	O
44	Small RNA sequencing of circulating small extracellular vesicles microRNAs in patients with amyotrophic lateral sclerosis. <b>2023</b> , 13,	O
43	Exploring body weight-influencing gut microbiota by elucidating the association with diet and host gene expression. <b>2023</b> , 13,	0
42	tRF-Gln-CTG-026 ameliorates liver injury by alleviating global protein synthesis. <b>2023</b> , 8,	O
41	Germline-encoded amino acidBinding motifs drive immunodominant public antibody responses. <b>2023</b> , 380,	0
40	Identification of MicroRNAs Regulating Clostridium perfringens Type C Infection in the Spleen of Diarrheic Piglets. <b>2023</b> , 45, 3193-3207	O
39	DNA ultra-sensitive quantification, a technology for studying HIV unintegrated linear DNA. <b>2023</b> , 100443	0
38	The histone demethylase Kdm3 prevents auto-immune piRNAs production in Drosophila. 2023, 9,	O

37	Amniogenesis in Human Amniotic Sac Embryoids after Exposures to Organophosphate Flame Retardants. <b>2023</b> , 131,	О
36	Modeling neurodevelopmental disorder-associatedhAGO1mutations inC. elegansArgonauteALG-1.	Ο
35	Chromosome-Level Genome Assembly of the Blue Mussel Mytilus chilensis Reveals Molecular Signatures Facing the Marine Environment. <b>2023</b> , 14, 876	0
34	The methylation landscape of giga-genome and the epigenetic timer of age in Chinese pine. <b>2023</b> , 14,	Ο
33	Bombyx Vasa sequesters transposon mRNAs in nuage via phase separation requiring RNA binding and self-association. <b>2023</b> , 14,	O
32	Intracellular Cytomatrix, Immobilized Biocatalysis, Matrix Micromechanics and The Warburg Effect: Entanglement of Two Age-Old Mysteries of the Normal and Malignant Cell.	O
31	Transcriptome Analysis of Natural Killer Cells in Response to Newcastle Disease Virus Infected Hepatocellular Carcinoma Cells. <b>2023</b> , 14, 888	О
30	Comparative Analysis of Bioactive Compounds in Two Globe Artichoke Ecotypes Sanitized and Non-Sanitized from Viral Infections. <b>2023</b> , 12, 1600	Ο
29	Small vault RNA1-2 modulates expression of cell membrane proteins through nascent RNA silencing. <b>2023</b> , 6, e202302054	О
28	Exosomes derived from human umbilical cord mesenchymal stem cells alleviate Parkinson disease and neuronal damage through inhibition of microglia. <b>2023</b> , 18, 2291	Ο
27	Long-Term Transcriptomic Changes and Cardiomyocyte Hyperpolyploidy after Lactose Intolerance in Neonatal Rats. <b>2023</b> , 24, 7063	О
26	Excessive serine from the bone marrow microenvironment impairs megakaryopoiesis and thrombopoiesis in Multiple Myeloma. <b>2023</b> , 14,	Ο
25	Fob1-dependent condensin recruitment and loop extrusion on yeast chromosome III. 2023, 19, e1010705	O
24	Early transcriptomic signatures and biomarkers of renal damage due to prolonged exposure to embedded metal.	O
23	The mechanisms of optimal nitrogen conditions to accelerate flowering of Chrysanthemum vestitum under short day based on transcriptome analysis. <b>2023</b> , 153982	0
22	Dynamic changes in P300 enhancers and enhancer-promoter contacts control mouse cardiomyocyte maturation. <b>2023</b> ,	O
21	The initiation and maintenance of CHH methylation and its effects on gene expression are unique in maize.	О
20	A comparative BmicsDpproach for prediction of candidate Strongyloides stercoralis diagnostic coproantigens. <b>2023</b> , 17, e0010777	O

19	Interplay Between Superworm and its Gut Microbiome in Facilitating Polyethylene Biodegradation by Host Transcriptomic Analysis: Insights from Xenobiotic Metabolism.	0
18	Nucleosome reorganisation in breast cancer tissues.	O
17	Low-density lipoprotein receptorfielated protein 1 (LRP1) as an auxiliary host factor for RNA viruses. <b>2023</b> , 6, e202302005	О
16	Epigenetic Control of Translation Checkpoint and Tumor Progression via RUVBL1-EEF1A1 Axis.	O
15	Oncogenic CDK13 mutations impede nuclear RNA surveillance. 2023, 380,	O
14	satmut_utils: a simulation and variant calling package for multiplexed assays of variant effect. <b>2023</b> , 24,	O
13	Large-scale long terminal repeat insertions produced a significant set of novel transcripts in cotton.	0
12	Identification of miRNAs Involved in Male Fertility and Pollen Development in Brassica oleracea var. capitata L. by High-Throughput Sequencing. <b>2023</b> , 9, 515	Ο
11	A scoping review on deep learning for next-generation RNA-Seq. data analysis. 2023, 23,	0
10	MyBrain-Seq: A Pipeline for MiRNA-Seq Data Analysis in Neuropsychiatric Disorders. <b>2023</b> , 11, 1230	O
9	CasKAS: direct profiling of genome-wide dCas9 and Cas9 specificity using ssDNA mapping. <b>2023</b> , 24,	О
8	ORFeus: A Computational Method to Detect Programmed Ribosomal Frameshifts and Other Non-Canonical Translation Events.	O
7	Novel Chromatin Insulating Activities Uncovered upon Eliminating Known Insulatorsin vivo.	O
6	Competition between transcription and loop extrusion modulates promoter and enhancer dynamics.	0
5	De novo transcriptomes of six calanoid copepods (Crustacea): a resource for the discovery of novel genes. <b>2023</b> , 10,	О
4	Genetic and physical localization of a major susceptibility gene to Pyrenophora teres f. maculata in barley. <b>2023</b> , 136,	O
3	Alternative splicing decouples local from global PRC2 activity.	О
2	Development and applications of the Oil Palm 78K Infinium HD SNP Array for linkage analysis and chromosome scanning. <b>2023</b> , 318, 112104	O

Dissimilar gene repertoires of Dickeya solani involved in the colonization of lesions and roots of Solanum tuberosum. 14,

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