Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 11, 2025

University of Missouri-Columbia DNA Core Facility

RRID:SCR_017778
Type: Tool

Proper Citation

University of Missouri-Columbia DNA Core Facility (RRID:SCR_017778)

Resource Information

URL: https://dnacore.missouri.edu/

Proper Citation: University of Missouri-Columbia DNA Core Facility (RRID:SCR_017778)

Description: Core research facility providing genomic services that include next generation sequencing , single cell sequencing, metagenomic, targeted amplicon sequencing, and Sanger sequencing.

Abbreviations: DNACF

Synonyms: DNA Core Facility

Resource Type: core facility, access service resource, service resource

Keywords: Genomic, DNA, Illumina, sequencing, Sanger, fragment, analysis, 10x Genomics, Core Marketplace

Funding:

Availability: Open

Resource Name: University of Missouri-Columbia DNA Core Facility

Resource ID: SCR_017778

Alternate IDs: ABRF_363

Record Creation Time: 20220129T080336+0000

Record Last Update: 20250411T060000+0000

Ratings and Alerts

No rating or validation information has been found for University of Missouri-Columbia DNA Core Facility.

No alerts have been found for University of Missouri-Columbia DNA Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 18 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Katz ML, et al. (2024) Beta-mannosidosis in a domestic cat associated with a missense variant in MANBA. Gene, 893, 147941.

Young SM, et al. (2023) Fecal Dysbiosis and Inflammation in Intestinal-Specific Cftr Knockout Mice on Regimens Preventing Intestinal Obstruction. bioRxiv : the preprint server for biology.

Boersma MR, et al. (2022) ODORANT1 targets multiple metabolic networks in petunia flowers. The Plant journal : for cell and molecular biology, 109(5), 1134.

Cho SH, et al. (2022) Activation of the plant mevalonate pathway by extracellular ATP. Nature communications, 13(1), 450.

Chávez Montes RA, et al. (2022) A comparative genomics examination of desiccation tolerance and sensitivity in two sister grass species. Proceedings of the National Academy of Sciences of the United States of America, 119(5).

Duong HN, et al. (2022) Cyclic nucleotide-gated ion channel 6 is involved in extracellular ATP signaling and plant immunity. The Plant journal : for cell and molecular biology, 109(6), 1386.

Kim JH, et al. (2022) Utilization of Plant Architecture Genes in Soybean to Positively Impact Adaptation to High Yield Environments. Frontiers in plant science, 13, 891587.

Sangket U, et al. (2022) bestDEG: a web-based application automatically combines various tools to precisely predict differentially expressed genes (DEGs) from RNA-Seq data. PeerJ, 10, e14344.

Ramšak Ž, et al. (2021) RNA Sequencing Analyses for Deciphering Potato Molecular Responses. Methods in molecular biology (Clifton, N.J.), 2354, 57.

Mullegama SV, et al. (2021) Transcriptome analysis of MBD5-associated neurodevelopmental disorder (MAND) neural progenitor cells reveals dysregulation of autism-associated genes. Scientific reports, 11(1), 11295.

Silva AT, et al. (2021) To dry perchance to live: Insights from the genome of the desiccation-tolerant biocrust moss Syntrichia caninervis. The Plant journal : for cell and molecular biology, 105(5), 1339.

Zheng N, et al. (2020) CRISPR/Cas9-Based Gene Editing Using Egg Cell-Specific Promoters in Arabidopsis and Soybean. Frontiers in plant science, 11, 800.

Guerrero-Sanchez VM, et al. (2020) Specific Protein Database Creation from Transcriptomics Data in Nonmodel Species: Holm Oak (Quercus ilex L.). Methods in molecular biology (Clifton, N.J.), 2139, 57.

Schultz JC, et al. (2019) A galling insect activates plant reproductive programs during gall development. Scientific reports, 9(1), 1833.

Nielsen SKD, et al. (2019) De novo transcriptome assembly of the cubomedusa Tripedalia cystophora, including the analysis of a set of genes involved in peptidergic neurotransmission. BMC genomics, 20(1), 175.

Costa MD, et al. (2017) A footprint of desiccation tolerance in the genome of Xerophyta viscosa. Nature plants, 3, 17038.

De León KB, et al. (2017) Unintended Laboratory-Driven Evolution Reveals Genetic Requirements for Biofilm Formation by Desulfovibrio vulgaris Hildenborough. mBio, 8(5).

du Toit Z, et al. (2017) Mitochondrial genomes of African pangolins and insights into evolutionary patterns and phylogeny of the family Manidae. BMC genomics, 18(1), 746.