Resource Summary Report

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University of California Davis DNA Technologies and Expression Analysis Core Facility

RRID:SCR_017740
Type: Tool

Proper Citation

University of California Davis DNA Technologies and Expression Analysis Core Facility (RRID:SCR_017740)

Resource Information

URL: https://dnatech.genomecenter.ucdavis.edu/

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Description: Core at Genome Center provides high throughput sequencing, genotyping, and microarray services, training and consultation. Uses liquid handling robots to minimize sample handling variation and to provide fast turnaround times.

Synonyms: DNA Technologies and Expression Analysis Core at the UC Davis Genome Center

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

Keywords: ABRF, USEDit, sequencing, genotyping, microarray, service, training, consultation,

Funding:

Availability: Open

Resource Name: University of California Davis DNA Technologies and Expression Analysis Core Facility

Resource ID: SCR_017740

Alternate IDs: ABRF_197

Alternate URLs: https://coremarketplace.org/?FacilityID=197&citation=1

Record Creation Time: 20220129T080336+0000

Record Last Update: 20250418T055514+0000

Ratings and Alerts

No rating or validation information has been found for University of California Davis DNA Technologies and Expression Analysis Core Facility.

No alerts have been found for University of California Davis DNA Technologies and Expression Analysis Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Zaccaron AZ, et al. (2024) Transcriptome analysis of two isolates of the tomato pathogen Cladosporium fulvum, uncovers genome-wide patterns of alternative splicing during a host infection cycle. PLoS pathogens, 20(12), e1012791.

Emami AJ, et al. (2022) Altered canalicular remodeling associated with femur fracture in mice. Journal of orthopaedic research : official publication of the Orthopaedic Research Society, 40(4), 891.

Diner RE, et al. (2021) Pathogenic Vibrio Species Are Associated with Distinct Environmental Niches and Planktonic Taxa in Southern California (USA) Aquatic Microbiomes. mSystems, 6(4), e0057121.

Lehman PW, et al. (2021) Covariance of Phytoplankton, Bacteria, and Zooplankton Communities Within Microcystis Blooms in San Francisco Estuary. Frontiers in microbiology, 12, 632264.

Curtasu MV, et al. (2020) Obesity-Related Metabolome and Gut Microbiota Profiles of Juvenile Göttingen Minipigs-Long-Term Intake of Fructose and Resistant Starch. Metabolites, 10(11).

Wright ME, et al. (2020) Genome Sequence of Lactiplantibacillus plantarum ATCC 202195, a Probiotic Strain That Reduces Sepsis and Other Infections during Early Infancy. Microbiology resource announcements, 9(39).

Arbour TJ, et al. (2020) Diverse Microorganisms in Sediment and Groundwater Are Implicated in Extracellular Redox Processes Based on Genomic Analysis of Bioanode Communities. Frontiers in microbiology, 11, 1694.

Kable ME, et al. (2020) The Znt7-null mutation has sex dependent effects on the gut microbiota and goblet cell population in the mouse colon. PloS one, 15(9), e0239681.

Dillon ML, et al. (2020) Energetic and Environmental Constraints on the Community Structure of Benthic Microbial Mats in Lake Fryxell, Antarctica. FEMS microbiology ecology, 96(2).

Dillon ML, et al. (2020) Environmental control on the distribution of metabolic strategies of benthic microbial mats in Lake Fryxell, Antarctica. PloS one, 15(4), e0231053.

Jin J, et al. (2020) Toxic effects of fluridone on early developmental stages of Japanese Medaka (Oryzias latipes). The Science of the total environment, 700, 134495.

Dhanapal AP, et al. (2013) Association genetics of chilling injury susceptibility in peach (Prunus persica (L.) Batsch) across multiple years. 3 Biotech, 3(6), 481.