Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Mar 28, 2024

UniGene

RRID:SCR_004405

Type: Tool

Proper Citation

UniGene (RRID:SCR_004405)

Resource Information

URL: http://www.ncbi.nlm.nih.gov/unigene

Proper Citation: UniGene (RRID:SCR_004405)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on January 11, 2023. Web tool for an organized view of the transcriptome. Collection of the computationally identified transcripts from the same locus. Information on protein similarities, gene expression, cDNA clones, and genomic location. System for automatically partitioning GenBank sequences into a non redundant set of gene oriented clusters.

Abbreviations: UniGene

Synonyms: NCBI UniGene, Organized View of the Transcriptome, UniGene

Resource Type: data or information resource, service resource, database

Keywords: colleciton, data, information, organized, view, transcriptome, locus, protein, similarity, gene, expression,

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: UniGene

Resource ID: SCR 004405

Alternate IDs: nlx 41571, OMICS 01663

Alternate URLs: http://www.ncbi.nlm.nih.gov/sites/entrez?db=unigene

Ratings and Alerts

No rating or validation information has been found for UniGene.

No alerts have been found for UniGene.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1136 mentions in open access literature.

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

Zhang X, et al. (2024) Physiological and Transcriptome Responses of Pinus massoniana Seedlings Inoculated by Various Ecotypes of the Ectomycorrhizal Fungus Cenococcum geophilum during the Early Stage of Drought Stress. Journal of fungi (Basel, Switzerland), 10(1).

Han B, et al. (2024) Integrated multi-omics reveal gut microbiota-mediated bile acid metabolism alteration regulating immunotherapy responses to anti-?4?7-integrin in Crohn's disease. Gut microbes, 16(1), 2310894.

Santos LGC, et al. (2024) SpliceProt 2.0: A Sequence Repository of Human, Mouse, and Rat Proteoforms. International journal of molecular sciences, 25(2).

Weickhardt S, et al. (2024) Sex- and region-specific cortical and hippocampal whole genome transcriptome profiles from control and APP/PS1 Alzheimer's disease mice. PloS one, 19(2), e0296959.

Yadollahi Farsani M, et al. (2024) Deregulation of miR-1245b-5p and miR-92a-3p and their potential target gene, GATA3, in epithelial-mesenchymal transition pathway in breast cancer. Cancer reports (Hoboken, N.J.), 7(2), e1955.

Chen CC, et al. (2023) A combined bioinformatics and experimental approach identifies RMI2 as a Wnt/?-catenin signaling target gene related to hepatocellular carcinoma. BMC cancer, 23(1), 1025.

- , et al. (2023) Translation of Monoclonal Antibodies Pharmacokinetics from Animal to Human Using Physiologically Based Modeling in Open Systems Pharmacology (OSP) Suite: A Retrospective Analysis of Bevacizumab. Pharmaceutics, 15(8).
- , et al. (2023) Deacetylation induced nuclear condensation of HP1? promotes multiple myeloma drug resistance. Nature communications, 14(1), 1290.

Han YS, et al. (2023) Transcriptome analysis of Haemaphysalis flava female using Illumina

- HiSeq 4000 sequencing: de novo assembly, functional annotation and discovery of SSR markers. Parasites & vectors, 16(1), 367.
- Wei Z, et al. (2023) Crop rotation and native microbiome inoculation restore soil capacity to suppress a root disease. Nature communications, 14(1), 8126.
- Ayoub CA, et al. (2023) Identification of gene networks mediating regional resistance to tauopathy in late-onset Alzheimer's disease. PLoS genetics, 19(3), e1010681.
- , et al. (2023) Time-of-day defines NAD+ efficacy to treat diet-induced metabolic disease by synchronizing the hepatic clock in mice. Nature communications, 14(1), 1685.
- , et al. (2023) FvbHLH1 Regulates the Accumulation of Phenolic Compounds in the Yellow Cap of Flammulina velutipes. Journal of fungi (Basel, Switzerland), 9(11).
- , et al. (2023) Comparative transcriptome profiling to unravel the key molecular signalling pathways and drought adaptive plasticity in shoot borne root system of sugarcane. Scientific reports, 13(1), 12853.
- , et al. (2023) Multi-omics analysis of fecal microbiota transplantation's impact on functional constipation and comorbid depression and anxiety. BMC microbiology, 23(1), 389.
- , et al. (2023) The Identification of Potent, Selective, and Brain Penetrant PI5P4K? Inhibitors as In Vivo-Ready Tool Molecules. Journal of medicinal chemistry, 66(1), 804.
- , et al. (2023) Insight into the Molecular Mechanism of Flower Color Regulation in Rhododendron latoucheae Franch: A Multi-Omics Approach. Plants (Basel, Switzerland), 12(16).
- Zhang T, et al. (2023) Increased Tolerance of Massion's pine to Multiple-Toxic-Metal Stress Mediated by Ectomycorrhizal Fungi. Plants (Basel, Switzerland), 12(18).
- , et al. (2023) Predicting congenital renal tract malformation genes using machine learning. Scientific reports, 13(1), 13204.
- , et al. (2022) Novel genome sequence of Chinese cavefish (Triplophysa rosa) reveals pervasive relaxation of natural selection in cavefish genomes. Molecular ecology, 31(22), 5831.