Resource Summary Report

Generated by FDI Lab - SciCrunch.org on May 21, 2025

gene Expression Analysis Resource

RRID:SCR_017467
Type: Tool

Proper Citation

gene Expression Analysis Resource (RRID:SCR_017467)

Resource Information

URL: https://umgear.org/

Proper Citation: gene Expression Analysis Resource (RRID:SCR_017467)

Description: Portal for visualization and analysis of multi omic data in public and private domains. Enables upload, visualization and analysis of scRNA-seq data.

Abbreviations: gEAR

Synonyms: gene Expression Analysis Resource

Resource Type: data or information resource, service resource, software resource, portal, analysis service resource, production service resource

Keywords: Visualization, analysis, multi, omic, data, upload, scRNA-seq, BRAIN Initiative

Funding: NIMH MH114788;
NIDCD R01 DC013817;
NIMH R24 MH114815;
Hearing Health Foundation (Hearing Restoration Project)

Availability: Restricted

Resource Name: gene Expression Analysis Resource

Resource ID: SCR_017467

Record Creation Time: 20220129T080335+0000

Record Last Update: 20250521T061709+0000

Ratings and Alerts

No rating or validation information has been found for gene Expression Analysis Resource.

No alerts have been found for gene Expression Analysis Resource.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 68 mentions in open access literature.

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

Yalcouyé A, et al. (2025) Whole-exome sequencing reveals known and candidate genes for hearing impairment in Mali. HGG advances, 6(1), 100391.

Underhill A, et al. (2025) MYO7A is required for the functional integrity of the mechanoelectrical transduction complex in hair cells of the adult cochlea. Proceedings of the National Academy of Sciences of the United States of America, 122(1), e2414707122.

Iyer S, et al. (2024) The BRAIN Initiative data-sharing ecosystem: Characteristics, challenges, benefits, and opportunities. eLife, 13.

Bhatt IS, et al. (2024) A genome-wide association study reveals a polygenic architecture of speech-in-noise deficits in individuals with self-reported normal hearing. Scientific reports, 14(1), 13089.

Cepeda AP, et al. (2024) Proteomic Analysis Reveals the Composition of Glutamatergic Organelles of Auditory Inner Hair Cells. Molecular & cellular proteomics : MCP, 23(2), 100704.

Niazi A, et al. (2024) Microvilli regulate the release modes of alpha-tectorin to organize the domain-specific matrix architecture of the tectorial membrane. bioRxiv : the preprint server for biology.

Wang Y, et al. (2024) Single-cell atlas comparison across vertebrates reveals auditory cell evolution and mechanisms for hair cell regeneration. Communications biology, 7(1), 1648.

Gwilliam K, et al. (2024) A cell type-specific approach to elucidate the role of miR-96 in inner ear hair cells. Frontiers in audiology and otology, 2.

Zafeer MF, et al. (2024) Human Organoids for Rapid Validation of Gene Variants Linked to Cochlear Malformations. Research square.

Gansemer BM, et al. (2024) Spiral ganglion neuron degeneration in aminoglycoside-deafened rats involves innate and adaptive immune responses not requiring complement. Frontiers in molecular neuroscience, 17, 1389816.

Chen SP, et al. (2024) A genome-wide association study identifies novel loci of vertigo in an Asian population-based cohort. Communications biology, 7(1), 1034.

Polesskaya O, et al. (2024) Genome-wide association study for age-related hearing loss in CFW mice. bioRxiv : the preprint server for biology.

Chatterjee P, et al. (2023) GIPC3 couples to MYO6 and PDZ domain proteins and shapes the hair cell apical region. bioRxiv : the preprint server for biology.

Lewis MA, et al. (2023) Accurate phenotypic classification and exome sequencing allow identification of novel genes and variants associated with adult-onset hearing loss. PLoS genetics, 19(11), e1011058.

Qiu X, et al. (2023) The tetraspan LHFPL5 is critical to establish maximal force sensitivity of the mechanotransduction channel of cochlear hair cells. Cell reports, 42(3), 112245.

Escalera-Balsera A, et al. (2023) Rare Deletions or Large Duplications Contribute to Genetic Variation in Patients with Severe Tinnitus and Meniere Disease. Genes, 15(1).

Hui D, et al. (2023) Gene burden analysis identifies genes associated with increased risk and severity of adult-onset hearing loss in a diverse hospital-based cohort. PLoS genetics, 19(1), e1010584.

Boussaty EC, et al. (2023) Selective loss of specific subsets of hair cell and spiral ganglion cell types in an outbred mouse model of age-related hearing loss. bioRxiv : the preprint server for biology.

Krey JF, et al. (2023) Control of stereocilia length during development of hair bundles. PLoS biology, 21(4), e3001964.

Roux I, et al. (2023) CHD7 variants associated with hearing loss and enlargement of the vestibular aqueduct. Human genetics, 142(10), 1499.