Resource Summary Report

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

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

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

Availability: Restricted

Resource Name: gene Expression Analysis Resource

Resource ID: SCR_017467

Record Creation Time: 20220129T080335+0000

Record Last Update: 20260829T182600+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 91 mentions in open access literature.

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

Jang SH, et al. (2026) Gene supplementation with precise transgene expression rescues hearing loss in a mouse model with an Mpzl2 East Asian founder variant. Molecular therapy : the journal of the American Society of Gene Therapy, 34(1), 216.

Underhill A, et al. (2026) Myosin 7a is required for maintaining the transducing stereocilia and for force transmission to the MET channel during cochlear hair cell development. The Journal of physiology, 604(5), 2152.

Shi Z, et al. (2026) Genome-wide analysis implicates inner ear development in Ménière's disease. medRxiv : the preprint server for health sciences.

Ahmed S, et al. (2026) Distinct cochlear cell types associated with genetic susceptibility to sensory and metabolic hearing loss in older adults from the CLSA. bioRxiv : the preprint server for biology.

Sakamoto S, et al. (2026) Single-Cell Profiling of the Developing Organ of Corti Identifies Etv4/5/1 as Key Regulators of Pillar Cell Identity. bioRxiv : the preprint server for biology.

Mukhopadhyay M, et al. (2026) Persistence of vestibular function in the absence of glutamatergic transmission from hair cells. Scientific reports, 16(1).

Cheng H, et al. (2026) A Cross-Species Single-Cell Atlas Reveals Conserved Regulatory Networks and Candidate Hearing Loss Genes in the Cochlea. Genes, 17(4).

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

Belyantseva IA, et al. (2025) Taperin bundles F-actin at stereocilia pivot points enabling optimal lifelong mechanosensitivity. The Journal of cell biology, 224(8).

Matern MS, et al. (2025) A developmental atlas of mouse vestibular-like inner ear organoids. iScience, 28(2), 111817.

Nadar-Ponniah PT, et al. (2025) Preclinical Models to Study the Molecular Pathophysiology of Meniere's Disease: A Pathway to Gene Therapy. Journal of clinical

medicine, 14(5).

Ramzan M, et al. (2025) Carboxypeptidase D deficiency causes hearing loss amenable to treatment. The Journal of clinical investigation, 135(23).

Wu F, et al. (2025) AAVR Expression is Essential for AAV Vector Transduction in Sensory Hair Cells. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(29), e2408873.

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.

Cornejo-Sanchez DM, et al. (2025) Mendelian non-syndromic and syndromic hearing loss genes contribute to presbycusis. European journal of human genetics : EJHG, 33(6), 758.

Zafeer MF, et al. (2025) Human organoids for rapid validation of gene variants linked to cochlear malformations. Human genetics, 144(4), 375.

Hu SW, et al. (2025) PAM-flexible adenine base editing rescues hearing loss in a humanized MPZL2 mouse model harboring an East Asian founder mutation. Nature communications, 16(1), 7186.

Chen J, et al. (2024) A new mutation of Sgms1 causes gradual hearing loss associated with a reduced endocochlear potential. Hearing research, 451, 109091.

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.

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