

Resource Summary Report

Generated by [dkNET](#) on Aug 6, 2026

Gene Expression Ontology

RRID:SCR_010326

Type: Tool

Proper Citation

Gene Expression Ontology (RRID:SCR_010326)

Resource Information

URL: <http://purl.bioontology.org/ontology/GEXO>

Proper Citation: Gene Expression Ontology (RRID:SCR_010326)

Description: An application ontology for the domain of gene expression. The ontology integrates fragments of GO and MI with data from GOA, IntAct, UniProt, NCBI, KEGG and orthology relations.

Abbreviations: GEXO

Resource Type: data or information resource, ontology, controlled vocabulary

Keywords: obo

Resource Name: Gene Expression Ontology

Resource ID: SCR_010326

Alternate IDs: nlx_157413

Record Creation Time: 20220129T080258+0000

Record Last Update: 20260806T054523+0000

Ratings and Alerts

No rating or validation information has been found for Gene Expression Ontology.

No alerts have been found for Gene Expression Ontology.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Hu YQ, et al. (2025) Using proteomics and single-cell sequencing to analyze the pathogenesis of recurrent implantation failure associated with uterine natural killer cells. Archives of gynecology and obstetrics, 312(3), 885.

Yang X, et al. (2025) Identification of biomarkers associated with mitochondrial dysfunction and programmed cell death in chronic obstructive pulmonary disease via transcriptomics. Frontiers in genetics, 16, 1567173.

Soudy M, et al. (2025) Sex-dependent molecular landscape of Alzheimer's disease revealed by large-scale single-cell transcriptomics. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(2), e14476.

Gao C, et al. (2025) Regulation of reactive oxygen species and the role of mitochondrial apoptotic-related genes in rheumatoid arthritis. Scientific reports, 15(1), 2165.

Ali M, et al. (2025) Temporal transcriptomic changes in the THY-Tau22 mouse model of tauopathy display cell type- and sex-specific differences. Acta neuropathologica communications, 13(1), 93.

Ali M, et al. (2024) Single cell transcriptome analysis of the THY-Tau22 mouse model of Alzheimer's disease reveals sex-dependent dysregulations. Cell death discovery, 10(1), 119.