

Resource Summary Report

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Entrez GEO Profiles

RRID:SCR_004584

Type: Tool

Proper Citation

Entrez GEO Profiles (RRID:SCR_004584)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/sites/entrez?db=geo>

Proper Citation: Entrez GEO Profiles (RRID:SCR_004584)

Description: The GEO Profiles database stores gene expression profiles derived from curated GEO DataSets. Each Profile is presented as a chart that displays the expression level of one gene across all Samples within a DataSet. Experimental context is provided in the bars along the bottom of the charts making it possible to see at a glance whether a gene is differentially expressed across different experimental conditions. Profiles have various types of links including internal links that connect genes that exhibit similar behaviour, and external links to relevant records in other NCBI databases. GEO Profiles can be searched using many different attributes including keywords, gene symbols, gene names, GenBank accession numbers, or Profiles flagged as being differentially expressed.

Synonyms: GEO Profiles, Gene Expression Omnibus Profiles

Resource Type: data or information resource, database

Keywords: gold standard

Resource Name: Entrez GEO Profiles

Resource ID: SCR_004584

Alternate IDs: nlx_57723

Alternate URLs: <http://www.ncbi.nlm.nih.gov/geo/>

Record Creation Time: 20220129T080225+0000

Record Last Update: 20260821T193737+0000

Ratings and Alerts

No rating or validation information has been found for Entrez GEO Profiles.

No alerts have been found for Entrez GEO Profiles.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2400 mentions in open access literature.

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

Ding C, et al. (2026) Glioblastoma-Secreted C1QL1 Orchestrates Tumor Microtube Expansion and Neural Synaptic Pruning to Drive Malignant Synapse Formation and Recurrence. *Cancer discovery*, 16(6), 1176.

Wang P, et al. (2025) Temozolomide promotes glioblastoma stemness expression through senescence-associated reprogramming via HIF1 α /HIF2 α regulation. *Cell death & disease*, 16(1), 317.

Guo Y, et al. (2025) Luteolin Alleviates Inflammation Induced by Staphylococcus aureus in Bovine Mammary Epithelial Cells by Attenuating NF- κ B and MAPK Activation. *Veterinary sciences*, 12(2).

Zhang S, et al. (2025) Exploring the hepatic-ophthalmic axis through immune modulation and cellular dynamics in diabetic retinopathy and non-alcoholic fatty liver disease. *Human genomics*, 19(1), 19.

Xu X, et al. (2025) Association Between Circulating Cytokines and Endometriosis: A Mendelian Randomization Study. *Journal of cellular and molecular medicine*, 29(7), e70532.

Hu S, et al. (2025) Identification of a deubiquitinating gene-related signature in ovarian cancer using integrated transcriptomic analysis and machine learning framework. *Discover oncology*, 16(1), 510.

Zheng Q, et al. (2025) Analysis and validation of hub genes for atherosclerosis and AIDS and immune infiltration characteristics based on bioinformatics and machine learning. *Scientific reports*, 15(1), 12316.

Lin Z, et al. (2025) Identification of the disulfidptosis-related key gene CD2AP as a potential biomarker and new therapeutic target for LUAD patients by comprehensive multi-omics analysis. *Discover oncology*, 16(1), 515.

Yu H, et al. (2025) Exosome-mediated effects of BRCA1 on cardiovascular artery disease. *Cell biology and toxicology*, 41(1), 59.

Mo J, et al. (2025) Diagnostic value of C-reactive protein/ albumin ratio and TMTC1 in intracranial atherosclerotic stenosis in patients with acute cerebral infarction. *Scientific reports*, 15(1), 8653.

Gao X, et al. (2025) Combined analysis of single-cell and bulk transcriptome sequencing data identifies critical glycolysis genes in idiopathic pulmonary arterial hypertension. *Journal of translational medicine*, 23(1), 373.

Quaye A, et al. (2025) Turkey B Cell Transcriptome Profile During Turkey Hemorrhagic Enteritis Virus (THEV) Infection Highlights Upregulated Apoptosis and Breakdown Pathways That May Mediate Immunosuppression. *Viruses*, 17(3).

Deng C, et al. (2025) Multi-omics analysis identifies diagnostic circulating biomarkers and potential therapeutic targets, revealing IQGAP1 as an oncogene in gastric cancer. *NPJ precision oncology*, 9(1), 105.

Zhang J, et al. (2025) A novel tertiary lymphoid structure-associated signature accurately predicts patient prognosis and facilitates the selection of personalized treatment strategies for HNSCC. *Frontiers in immunology*, 16, 1551844.

Huo Z, et al. (2025) Identification and validation of hub m7G-related genes and infiltrating immune cells in osteoarthritis based on integrated computational and bioinformatics analysis. *BMC musculoskeletal disorders*, 26(1), 333.

Chan-On W, et al. (2025) ANGPTL4 suppresses progression and improves cisplatin sensitivity in cervical cancer. *Scientific reports*, 15(1), 14217.

Liu X, et al. (2025) Integrating single-cell sequencing and transcriptome analysis to unravel the mechanistic role of sialylation-related genes in sepsis-induced acute respiratory distress syndrome. *Frontiers in immunology*, 16, 1528769.

He X, et al. (2025) CDT1 is a Potential Therapeutic Target for the Progression of NAFLD to HCC and the Exacerbation of Cancer. *Current genomics*, 26(3), 225.

Al-Lamee H, et al. (2025) Transcriptional Profiling of SSEA-1+ Endometrial Epithelial Progenitor Cells Highlights Their Role in Endometrial Regeneration, Remodeling, and Homeostasis. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 39(9), e70578.

Chen Z, et al. (2025) Integrative analysis of crosstalk genes and diagnostic biomarkers in lupus-associated osteoporosis. *International journal of immunopathology and pharmacology*, 39, 3946320251331842.