

Resource Summary Report

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Gene Expression Omnibus (GEO)

RRID:SCR_005012

Type: Tool

Proper Citation

Gene Expression Omnibus (GEO) (RRID:SCR_005012)

Resource Information

URL: <https://www.ncbi.nlm.nih.gov/geo/>

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Description: Functional genomics data repository supporting MIAME-compliant data submissions. Includes microarray-based experiments measuring the abundance of mRNA, genomic DNA, and protein molecules, as well as non-array-based technologies such as serial analysis of gene expression (SAGE) and mass spectrometry proteomic technology. Array- and sequence-based data are accepted. Collection of curated gene expression DataSets, as well as original Series and Platform records. The database can be searched using keywords, organism, DataSet type and authors. DataSet records contain additional resources including cluster tools and differential expression queries.

Abbreviations: GEO

Synonyms: Gene Expression Omnibus (GEO), Entrez GEO DataSets, Gene Expression Data Sets, Gene Expression Omnibus, GEO, NCBI GEO DataSets, GEO DataSets, Gene Expression Omnibus DataSets

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

Defining Citation: [PMID:23193258](#), [PMID:21097893](#), [PMID:18940857](#), [PMID:17160034](#), [PMID:17099226](#), [PMID:16939800](#), [PMID:16888359](#), [PMID:15608262](#), [PMID:11752295](#)

Keywords: gold standard, genomics, data, repository, microarray, mRNA, DNA, protein, analysis, SAGE, mass spectrometry, dataset

Funding: National Library of Medicine

Resource Name: Gene Expression Omnibus (GEO)

Resource ID: SCR_005012

Alternate IDs: r3d100010283, nif-0000-00142, nlx_96903, OMICS_01030, SCR_007303

Alternate URLs: <http://www.ncbi.nlm.nih.gov/sites/entrez?db=gds>,
<http://www.ncbi.nlm.nih.gov/geo/>, <https://doi.org/10.17616/R33P44>

Old URLs: <http://www.ncbi.nlm.nih.gov/gds>

Record Creation Time: 20220129T080227+0000

Record Last Update: 20260729T044108+0000

Ratings and Alerts

No rating or validation information has been found for Gene Expression Omnibus (GEO).

No alerts have been found for Gene Expression Omnibus (GEO).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11944 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Safari M, et al. (2026) Combined HDAC and eIF4A inhibition: A novel epigenetic therapy for pancreatic ductal adenocarcinoma. Drug resistance updates : reviews and commentaries in antimicrobial and anticancer chemotherapy, 84, 101312.

Cao Z, et al. (2026) Study on the mechanism of PSENEN in modulating cisplatin resistance in NSCLC through stromal cell interactions. International immunopharmacology, 169, 116037.

Guo C, et al. (2026) NFAT mediates pro-tumorigenic inflammation in cancer-associated fibroblasts in pancreatic ductal adenocarcinoma. Cell reports, 45(1), 116849.

Zhang G, et al. (2026) Ubiquitylation-oxaliplatin-related prognosis signature reveals the landscapes of immune responses, cell communication, and therapeutic sensitivity for colorectal cancer. Anti-cancer drugs, 37(1), 67.

Nayak S, et al. (2026) Discovery of BMS-986365, a First-in-Class Dual Androgen Receptor Ligand-Directed Degradar and Antagonist, for the Treatment of Advanced Prostate Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(1), 224.

Dong YP, et al. (2026) GluN2A-NMDA receptor inhibition disinhibits the prefrontal cortex, reduces forced swim immobility, and impairs sensorimotor gating. Acta pharmacologica Sinica, 47(1), 53.

- Wen Q, et al. (2026) Identification and Validation of the Prognostic Value of PTTG1-Related Genes in Hepatocellular Carcinoma by Mendelian Randomization and Single-Cell Transcriptome Analysis. *Iranian journal of biotechnology*, 24(1), e4221.
- Yang C, et al. (2026) SF3A2: a promising therapeutic target and predictive biomarker for immunotherapy in colorectal cancer. *International journal of medical sciences*, 23(1), 177.
- Thakur M, et al. (2026) DDR1 Regulates Femoral Arterial Calcification in Lower-Extremity Artery Disease Through NF-Kappa B Activation. *Acta physiologica (Oxford, England)*, 242(1), e70146.
- Lin JH, et al. (2026) YAP/TEAD-activated TAG synthesis and peroxidation in lipid droplets confer ROS resistance in cancer stem cells. *Redox biology*, 89, 103968.
- Chen S, et al. (2026) Single-Cell and Machine Learning Analysis Reveal Novel Inflammatory Macrophage Subtypes and Biomarkers in Periodontitis. *International dental journal*, 76(1), 103983.
- Pan Y, et al. (2026) Selective autophagic degradation of glycolytic activator PFKFB3 contributes to maintaining intestinal epithelial barrier in inflammatory bowel disease. *International journal of molecular medicine*, 57(2).
- Wang H, et al. (2026) Ubiquitin D Correlates with Disease Severity and T Cell Infiltration in Cholestasis: Evidence from Integrated Bioinformatics and Experimental Analyses. *International journal of medical sciences*, 23(1), 350.
- Bi R, et al. (2026) Integrin inhibition facilitates fibrocartilaginous transformation in connective tissue in osteoarthritis. *Science advances*, 12(1), eady4112.
- Hu YM, et al. (2026) Elevated Tumor-Associated Androgen Receptor Activity Correlates with Poor Immune Infiltration and Immunotherapy Response across Cancer Types. *Cancer research communications*, 6(1), 17.
- Liu D, et al. (2026) Age-Dependent KLK8 Upregulation Contributes to Elevated Susceptibility to Ventilator-Induced Lung Injury in the Elderly Mice. *Aging cell*, 25(1), e70304.
- Xiong H, et al. (2026) Unveiling shared PANoptosis mechanisms in LUAD and osteoarthritis via bioinformatics and machine learning. *Translational oncology*, 63, 102586.
- Liu Y, et al. (2026) Identification and Analysis of PANoptosis Associated with Coronary Artery Disease Using Integrated Bioinformatics Methods. *Iranian journal of biotechnology*, 24(1), e4080.
- Chen K, et al. (2026) Liquid?liquid phase separation of PHLDB2 promotes oral squamous cell carcinoma metastasis through regulating epithelial mesenchymal transition and PIK3CA expression. *Molecular medicine reports*, 33(1).
- Panagopoulou M, et al. (2026) ?ovel methylation biomarkers in liquid biopsy and classifying biosignatures for the clinical management of breast cancer. *Breast cancer research : BCR*, 28(1), 1.