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, storage service resource, data or information resource, data repository, database

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

Availability: Free, Freely available

Resource Name: Gene Expression Omnibus (GEO)

Resource ID: SCR_005012

Alternate IDs: 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/

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

Record Creation Time: 20220129T080227+0000

Record Last Update: 20250426T055742+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 11294 mentions in open access literature.

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

Sasaki M, et al. (2025) Efficacy of CBP/p300 Dual Inhibitors against Derepression of KREMEN2 in cBAF-Deficient Cancers. Cancer research communications, 5(1), 24.

Zhou N, et al. (2025) Proteomic patterns associated with ketamine response in major depressive disorders. Cell biology and toxicology, 41(1), 26.

Yang H, et al. (2025) Gram-Negative Microflora Dysbiosis Facilitates Tumor Progression and Immune Evasion by Activating the CCL3/CCL5-CCR1-MAPK-PD-L1 Pathway in Esophageal Squamous Cell Carcinoma. Molecular cancer research : MCR, 23(1), 71.

Kim YH, et al. (2024) Integrative Multi-omics Analysis Reveals Different Metabolic Phenotypes Based on Molecular Characteristics in Thyroid Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(4), 883.

Li T, et al. (2024) N6-methyladenosine-associated genetic variants in NECTIN2 and HPCAL1 are risk factors for abdominal aortic aneurysm. iScience, 27(4), 109419.

Dietrich C, et al. (2024) INX-315, a Selective CDK2 Inhibitor, Induces Cell Cycle Arrest and Senescence in Solid Tumors. Cancer discovery, 14(3), 446.

Barravecchia I, et al. (2024) Modeling Molecular Pathogenesis of Idiopathic Pulmonary Fibrosis-Associated Lung Cancer in Mice. Molecular cancer research : MCR, 22(3), 295.

Roy Chaudhuri T, et al. (2024) Dual-Hit Strategy for Therapeutic Targeting of Pancreatic Cancer in Patient-Derived Xenograft Tumors. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(7), 1367.

Zhao K, et al. (2024) Integrated Transcriptomics and Proteomics Identified CMPK1 as a Potential Biomarker for Type 2 Diabetes Mellitus. Diabetes, metabolic syndrome and obesity : targets and therapy, 17, 2923.

Cao Y, et al. (2024) Inferring Characteristics of the Tumor Immune Microenvironment of Patients with HNSCC from Single-Cell Transcriptomics of Peripheral Blood. Cancer research communications, 4(9), 2335.

Dong B, et al. (2024) NK Receptor Signaling Lowers TCR Activation Threshold, Enhancing Selective Recognition of Cancer Cells by TAA-Specific CTLs. Cancer immunology research, 12(10), 1421.

Salloom RJ, et al. (2024) Targeting heme degradation pathway augments prostate cancer cell sensitivity to docetaxel-induced apoptosis and attenuates migration. Frontiers in oncology, 14, 1431362.

Umeda D, et al. (2024) Hypoxia drives the formation of lung micropapillary adenocarcinoma-like structure through hypoxia-inducible factor-1?. Scientific reports, 14(1), 31642.

Zhang L, et al. (2024) SRSF3 suppresses RCC tumorigenesis and progression via regulating SP4 alternative splicing. Biochimica et biophysica acta. Molecular cell research, 1871(8), 119841.

Ishida CT, et al. (2024) SREBP-Dependent Regulation of Lipid Homeostasis Is Required for Progression and Growth of Pancreatic Ductal Adenocarcinoma. Cancer research communications, 4(9), 2539.

Stutheit-Zhao EY, et al. (2024) Early Changes in Tumor-Naive Cell-Free Methylomes and Fragmentomes Predict Outcomes in Pembrolizumab-Treated Solid Tumors. Cancer discovery, 14(6), 1048.

Cheung A, et al. (2024) Anti-EGFR Antibody-Drug Conjugate Carrying an Inhibitor Targeting CDK Restricts Triple-Negative Breast Cancer Growth. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(15), 3298.

Luck C, et al. (2024) The Capicua C1 Domain Is Required for Full Activity of the CIC::DUX4 Fusion Oncoprotein. Cancer research communications, 4(12), 3099.

Wang Q, et al. (2024) Galectin-3 induces pathogenic immunosuppressive macrophages through interaction with TREM2 in lung cancer. Journal of experimental & clinical cancer research : CR, 43(1), 224.

Tian M, et al. (2024) CAR T-cells targeting FGFR4 and CD276 simultaneously show potent antitumor effect against childhood rhabdomyosarcoma. Nature communications, 15(1), 6222.