Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Mar 28, 2024

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/

Proper Citation: Gene Expression Omnibus (GEO) (RRID:SCR_005012)

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: data repository, storage service resource, service resource, data or information resource, 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 Agency: 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

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 11190 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Goodale A, et al. (2023) Transcriptional Antagonism by CDK8 Inhibition Improves Therapeutic Efficacy of MEK Inhibitors. Cancer research, 83(2), 285.

Flümann R, et al. (2023) An Aged/Autoimmune B-cell Program Defines the Early Transformation of Extranodal Lymphomas. Cancer discovery, 13(1), 216.

Young MN, et al. (2023) Kinase Inhibitor Pulldown Assay Identifies a Chemotherapy Response Signature in Triple-negative Breast Cancer Based on Purine-binding Proteins. Cancer research communications, 3(8), 1551.

, et al. (2023) Activin A-Mediated Polarization of Cancer-Associated Fibroblasts and Macrophages Confers Resistance to Checkpoint Immunotherapy in Skin Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research, 29(17), 3498.

Rodig SJ, et al. (2023) Targeting KDM2A Enhances T-cell Infiltration in NSD1-Deficient Head and Neck Squamous Cell Carcinoma. Cancer research, 83(16), 2645.

Nakamura S, et al. (2023) Tertiary lymphoid structures correlate with enhancement of antitumor immunity in esophageal squamous cell carcinoma. British journal of cancer, 129(8), 1314.

Wu Y, et al. (2023) FOXA1 Reprogramming Dictates Retinoid X Receptor Response in ESR1-Mutant Breast Cancer. Molecular cancer research : MCR, 21(6), 591.

Zhu Y, et al. (2023) Targeting the chromatin effector Pygo2 promotes cytotoxic T cell responses and overcomes immunotherapy resistance in prostate cancer. Science immunology, 8(81), eade4656.

, et al. (2023) Comprehensive analysis of autophagy-related clusters and individual risk model for immunotherapy response prediction in gastric cancer. Frontiers in oncology, 13, 1105778.

Tran GB, et al. (2023) Caffeine supplementation and FOXM1 inhibition enhance the antitumor effect of statins in neuroblastoma. Cancer research.

, et al. (2023) Mouse models of human multiple myeloma subgroups. Proceedings of the National Academy of Sciences of the United States of America, 120(10), e2219439120.

Xiao Y, et al. (2023) Targeted MDM2 Degradation Reveals a New Vulnerability for p53-Inactivated Triple-Negative Breast Cancer. Cancer discovery, 13(5), 1210.

Zhang J, et al. (2023) Single-cell analysis reveals the COL11A1+ fibroblasts are cancer-specific fibroblasts that promote tumor progression. Frontiers in pharmacology, 14, 1121586.

, et al. (2023) Establishment of a prognostic model based on m6A regulatory factors and stemness of hepatocellular carcinoma using RNA-seq data and scRNA-seq data. Journal of cancer research and clinical oncology, 149(14), 12881.

Wilkening RV, et al. (2023) Identifying genetic determinants of Streptococcus pyogenes-host interactions in a murine intact skin infection model. Cell reports, 42(11), 113332.

Block MS, et al. (2023) Methylation Signature Implicated in Immuno-Suppressive Activities in Tubo-Ovarian High-Grade Serous Carcinoma. Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology, 32(4), 542.

, et al. (2023) BET Inhibitors Target the SCLC-N Subtype of Small-Cell Lung Cancer by Blocking NEUROD1 Transactivation. Molecular cancer research : MCR, 21(2), 91.

Evans RJ, et al. (2023) Endo180 (MRC2) Antibody-Drug Conjugate for the Treatment of Sarcoma. Molecular cancer therapeutics, 22(2), 240.

García-Rodríguez JL, et al. (2023) Spatial Profiling of Circular RNAs in Cancer Reveals High Expression in Muscle and Stromal Cells. Cancer research, 83(20), 3340.

Li X, et al. (2023) Integrated single cell and bulk sequencing analysis identifies tumor reactive CXCR6+ CD8 T cells as a predictor of immune infiltration and immunotherapy outcomes in hepatocellular carcinoma. Frontiers in oncology, 13, 1099385.