

Resource Summary Report

Generated by SPARC SAWG on Aug 15, 2026

GenePattern

RRID:SCR_003201

Type: Tool

Proper Citation

GenePattern (RRID:SCR_003201)

Resource Information

URL: <http://www.broadinstitute.org/cancer/software/genepattern>

Proper Citation: GenePattern (RRID:SCR_003201)

Description: A powerful genomic analysis platform that provides access to hundreds of tools for gene expression analysis, proteomics, SNP analysis, flow cytometry, RNA-seq analysis, and common data processing tasks. A web-based interface provides easy access to these tools and allows the creation of multi-step analysis pipelines that enable reproducible in silico research.

Abbreviations: GenePattern

Resource Type: data processing software, software application, data analysis software, software resource

Defining Citation: [PMID:16642009](#)

Keywords: gene expression, analysis, genomic, pattern, proteomics, silico, snp, workflow, analysis pipeline, flow cytometry, rna-seq, data processing, bio.tools

Funding: NCI ;
NIGMS

Availability: Free, Freely available

Resource Name: GenePattern

Resource ID: SCR_003201

Alternate IDs: biotools:genepattern, OMICS_01855, nif-0000-30654

Alternate URLs: <https://bio.tools/genepattern>

Record Creation Time: 20220129T080217+0000

Ratings and Alerts

No rating or validation information has been found for GenePattern.

No alerts have been found for GenePattern.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1135 mentions in open access literature.

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

Mukherjee S, et al. (2026) A single Citrobacter rodentium infection in Pink1 knockout and wild-type mice leads to regional blood-brain-barrier perturbation and limited microglial activation without dopamine neuron axon terminal loss. PLoS pathogens, 22(6), e1014315.

Sato K, et al. (2026) Aberrant Hippo-YAP/TEAD Signaling Drives Malignant Transcriptional Reprogramming in External Auditory Canal Squamous Cell Carcinoma. Cancer research communications, 6(2), 260.

Bharadwaj S, et al. (2026) Computationally Derived Spatial Immune Signature Identifies Trastuzumab Responders in HER2+ Breast Cancer: NSABP B-41 Clinical Trial Validation. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(12), 2508.

Miyamoto T, et al. (2026) Chemotherapy induces an IL1?-dependent neutrophil recruitment and activation that promote chemoresistance in metastatic ovarian cancer. Journal for immunotherapy of cancer, 14(6).

Barcelo J, et al. (2026) Pan-cancer analysis reveals Rho kinase addiction as a vulnerability of de-differentiated cancer cells. iScience, 29(6), 116031.

Kim JK, et al. (2026) Loss of ABCA3 disrupts lipid balance and leads to AMPK-dependent suppression of SREBP1 in glioblastoma stem cells. Oncogene, 45(15), 1357.

Bassiouni R, et al. (2026) Integrated Single-Cell Whole-Genome Sequencing and Spatial Transcriptomics Reveal Intratumoral Heterogeneity in Ovarian Cancer. Cancer research communications, 6(5), 1020.

Hu C, et al. (2026) Identification and validation of an 11-kinase signature that predicts chemo- and radiosensitivity in gastric cancer. EBioMedicine, 125, 106154.

Han S, et al. (2026) RUNX1-deficiency drives immune-active ER+ mammary tumorigenesis through activation of interferon signaling. *bioRxiv : the preprint server for biology*.

Blaszczyk GJ, et al. (2026) Age and Maturation Stage Linked Consequences of Fibrinogen on Human Oligodendroglia. *Journal of neuroscience research*, 104(3), e70120.

A M, et al. (2026) Irisin ameliorates obesity and insulin resistance via adipose tissue IL-33 and regulatory T cells. *Nature metabolism*, 8(4), 885.

Ma P, et al. (2026) Integrated single-cell and bulk RNA sequencing analysis identifies a pyroptosis related prognostic model for predicting prognosis and therapeutic response in intrahepatic cholangiocarcinoma. *Discover oncology*, 17(1).

Li X, et al. (2026) Activated ATF6 γ is a hepatic tumour driver restricting immunosurveillance. *Nature*, 651(8106), 796.

Wang R, et al. (2026) SLC26A2 as a key regulator and therapeutic target in hepatocellular carcinoma: evidence from pan-cancer and mechanistic studies. *Human genomics*, 20(1).

Chen G, et al. (2026) Pan-Cancer Analysis of a Depression-Related Gene Signature Identifies an Immunosuppressive Tumor Microenvironment and Links to Immunotherapy Response in Breast Cancer. *Breast cancer (Dove Medical Press)*, 18, 578930.

Adan-Villaescusa E, et al. (2026) Histone methyl-transferase G9a inhibition boosts the efficacy of immune checkpoint inhibitors in experimental hepatocellular carcinoma. *Cell reports. Medicine*, 7(4), 102717.

Hellkamp M, et al. (2026) Targeting metabolic dependencies to reverse chemoradiotherapy resistance in colorectal cancer. *Journal of experimental & clinical cancer research : CR*, 45(1).

Magan M, et al. (2026) Plasma COL3A1 propeptide as a promising prognostic marker in oral squamous cell carcinoma. *Scientific reports*, 16(1).

Wei HK, et al. (2026) Tumour-brain crosstalk restrains cancer immunity via a sensory-sympathetic axis. *Nature*, 650(8103), 1007.

Cheng S, et al. (2026) Integrative single-cell and machine learning framework reveals prognostic fibroblast subtypes and constructs a fibroblast-related risk signature in lung adenocarcinoma. *Scientific reports*, 16(1).