

Resource Summary Report

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GenePattern

RRID:SCR_003201

Type: Tool

Proper Citation

GenePattern (RRID:SCR_003201)

Resource Information

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

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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, data analysis software, software application, 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 1078 mentions in open access literature.

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

Gou X, et al. (2026) Identification of a Two-Gene Biomarker Correlated with Sensitivity to Combined PARP7 Inhibition and AHR Activation in Cancer Cells. Cancer research communications, 6(1), 5.

Mesropian A, et al. (2025) E7386 Enhances Lenvatinib's Antitumor Activity in Preclinical Models and Human Hepatocellular Carcinoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(23), 5037.

Yonesaka K, et al. (2025) Chromosomal Instability Is Associated with cGAS-STING Activation in EGFR-TKI Refractory Non-Small-Cell Lung Cancer. Cells, 14(6).

Graziani V, et al. (2025) SLC7A11 protects amoeboid-disseminating cancer cells from oxidative stress. Cell reports, 44(7), 115939.

Laplane P, et al. (2025) Effect of Mismatch repair deficiency on metastasis occurrence in a syngeneic mouse model. Neoplasia (New York, N.Y.), 62, 101145.

Chen C, et al. (2025) Developing and validating a prognostic disulfidptosis-related signature for glioblastoma: predicting radioresistance and synergistic effect with immunotherapy. Journal of cancer research and clinical oncology, 151(3), 112.

Jin J, et al. (2025) Role of ADME genes in breast cancer prognosis: an analysis of risk scoring models based on multi-omics data. Frontiers in oncology, 15, 1582862.

Hou S, et al. (2025) Integrated multi-omics and machine learning reveal an immunogenic cell death-related signature for prognostic stratification and therapeutic optimization in colorectal cancer. Frontiers in immunology, 16, 1606874.

Mello RM, et al. (2025) BMAL1 and ARNT enable circadian HIF2?? responses in clear cell renal cell carcinoma. Nature communications, 16(1), 5834.

Guan X, et al. (2025) Integrating multi-omics data to optimize immunotherapy in endometrial cancer: a comprehensive study. *Discover oncology*, 16(1), 1161.

Frey A, et al. (2025) Targeting an essential viral oncoprotein with an IL-7-enhanced mRNA vaccine induces durable immunity to Merkel cell carcinoma. *Cell reports*, 44(10), 116359.

Yan P, et al. (2025) Molecular Subtypes and Risk Prediction Model Based on Malignant Cell Differentiation Trajectories in Breast Cancer. *Journal of cellular and molecular medicine*, 29(15), e70680.

Zhang H, et al. (2025) Novel radiation-derived gene blueprint stratifying patients with breast cancer. *Discover oncology*, 16(1), 1691.

Rogg M, et al. (2025) Arp2/3-dependent regulation of ciliogenesis governs adaptive distal tubular epithelial cell states in kidney disease. *Science advances*, 11(48), eady1623.

Weber M, et al. (2025) Transcriptomic and proteomic profiling identifies feline fibrosarcoma as clinically amenable model for aggressive sarcoma subtypes. *Neoplasia* (New York, N.Y.), 60, 101104.

Smahel M, et al. (2025) Spatial immune heterogeneity in a mouse tumor model after immunotherapy. *Cancer science*, 116(3), 622.

Cao Q, et al. (2025) Tumor microenvironment and drug resistance in lung adenocarcinoma: molecular mechanisms, prognostic implications, and therapeutic strategies. *Discover oncology*, 16(1), 238.

Frederick MI, et al. (2025) Targeting FEN1/EXO1 to enhance efficacy of PARP inhibition in triple-negative breast cancer. *Translational oncology*, 54, 102337.

Chen N, et al. (2025) KMO-driven metabolic reconfiguration and its impact on immune cell infiltration in nasopharyngeal carcinoma: a new avenue for immunotherapy. *Cancer immunology, immunotherapy : CII*, 74(3), 75.

Tang S, et al. (2025) T-bet+CD8+ T cells govern anti-PD-1 responses in microsatellite-stable gastric cancers. *Nature communications*, 16(1), 3905.