

Resource Summary Report

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Broad Institute GDAC Firehose

RRID:SCR_026267

Type: Tool

Proper Citation

Broad Institute GDAC Firehose (RRID:SCR_026267)

Resource Information

URL: <https://gdac.broadinstitute.org/>

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Description: Born of the desire to systematize analyses from The Cancer Genome Atlas pilot and scale their execution to the dozens of remaining diseases to be studied, GDAC Firehose now sits atop terabytes of analysis-ready TCGA data and reliably executes thousands of pipelines per month.

Resource Type: topical portal, data or information resource, portal

Keywords: systematize analyses from The Cancer Genome Atlas pilot, GDAC Firehose, analysis-ready TCGA data,

Availability: Free, Freely available

Resource Name: Broad Institute GDAC Firehose

Resource ID: SCR_026267

Record Creation Time: 20250110T053324+0000

Record Last Update: 20260801T191334+0000

Ratings and Alerts

No rating or validation information has been found for Broad Institute GDAC Firehose.

No alerts have been found for Broad Institute GDAC Firehose.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 73 mentions in open access literature.

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

Hwang TI, et al. (2026) Thrombospondin-4 drives lymphangiogenesis through cooperation with VEGF-C in human bladder cancer. *International journal of medical sciences*, 23(1), 204.

Li S, et al. (2026) Unveiling Alternative Splicing in HPV-Negative HNSCC: Links to Tumorigenesis and Immune Landscape. *International dental journal*, 76(1), 103857.

Ying L, et al. (2025) Predicting immunotherapy prognosis and targeted therapy sensitivity of colon cancer based on a CAF-related molecular signature. *Scientific reports*, 15(1), 6387.

Ku J, et al. (2025) Identification of a unique subpopulation of mucosal fibroblasts in colorectal cancer with tumor-restraining characteristics. *Molecules and cells*, 48(10), 100263.

Vis DJ, et al. (2025) Whole genome sequencing of 378 prostate cancer metastases reveals tissue selectivity for mismatch deficiency with potential therapeutic implications. *Genome medicine*, 17(1), 24.

Rahmati R, et al. (2025) Identification of novel diagnostic and prognostic microRNAs in sarcoma on TCGA dataset: bioinformatics and machine learning approach. *Scientific reports*, 15(1), 7521.

Zhou L, et al. (2025) MRAS: Master Regulator Analysis of Alternative Splicing. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(21), e2414493.

Bhattacharya A, et al. (2025) Transcriptional pattern enriched for synaptic signaling is associated with shorter survival of patients with high-grade serous ovarian cancer. *eLife*, 13.

Wu Q, et al. (2025) TRIM29 upregulation contributes to chemoresistance in triple negative breast cancer via modulating S100P- β -catenin axis. *Cell communication and signaling : CCS*, 23(1), 244.

Tan CY, et al. (2025) Amogel: a multi-omics classification framework using associative graph neural networks with prior knowledge for biomarker identification. *BMC bioinformatics*, 26(1), 94.

Krauß D, et al. (2025) EGFR controls transcriptional and metabolic rewiring in KRASG12D colorectal cancer. *EMBO molecular medicine*, 17(6), 1355.

Choi WY, et al. (2025) The offonome reveals on and off states of gene expression near the detection limit of RNA-seq. *Scientific reports*, 15(1), 43141.

Vats P, et al. (2025) Long noncoding RNA TMPO-AS1 upregulates chromosomal passenger complex expression to promote cell proliferation in lung cancer via sponging

microRNA let-7b-5p. Cell division, 20(1), 24.

Manasa P, et al. (2025) Characterization of RNF144B and PPP2R2A identified by a novel approach using TCGA data in ovarian cancer. Scientific reports, 15(1), 5414.

Hu Y, et al. (2025) Deep learning-driven survival prediction in pan-cancer studies by integrating multimodal histology-genomic data. Briefings in bioinformatics, 26(2).

Thomsen MT, et al. (2025) The olfactory receptor OR51E2 regulates prostate cancer aggressiveness and modulates STAT3 in prostate cancer cells and in xenograft tumors. BMC cancer, 25(1), 535.

Boyd SS, et al. (2025) AMEND 2.0: module identification and multi-omic data integration with multiplex-heterogeneous graphs. BMC bioinformatics, 26(1), 39.

Haghshenas Z, et al. (2025) Identification of BCL11A, NTN5, and OGN as Diagnosis Biomarker of Papillary Renal Cell Carcinomas by Bioinformatic Analysis. Journal of kidney cancer and VHL, 12(1), 12.

Meng X, et al. (2025) Plac1+ Tumor Cell-Treg Interplay Supports Tumorigenesis and Progression of Head and Neck Cancer. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(17), e2417312.

Lawrence SS, et al. (2025) Interferon- γ /Janus Kinase 1/STAT1 Signaling Represses Forkhead Box A1 and Drives a Basal Transcriptional State in Muscle-Invasive Bladder Cancer. The American journal of pathology, 195(5), 1013.