

Resource Summary Report

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Genomics of Drug Sensitivity in Cancer

RRID:SCR_011956

Type: Tool

Proper Citation

Genomics of Drug Sensitivity in Cancer (RRID:SCR_011956)

Resource Information

URL: <http://www.cancerrxgene.org/>

Proper Citation: Genomics of Drug Sensitivity in Cancer (RRID:SCR_011956)

Description: A genomics database project is an academic research program to identify molecular features of cancers that predict response to anti-cancer drugs.

Abbreviations: Genomics of Drug Sensitivity in Cancer

Resource Type: database, data or information resource

Keywords: compound, gene, molecule, drug, FASEB list

Related Condition: Cancer

Funding: Wellcome Trust

Resource Name: Genomics of Drug Sensitivity in Cancer

Resource ID: SCR_011956

Alternate IDs: OMICS_01581

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260807T042750+0000

Ratings and Alerts

No rating or validation information has been found for Genomics of Drug Sensitivity in Cancer.

No alerts have been found for Genomics of Drug Sensitivity in Cancer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2388 mentions in open access literature.

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

Zhang M, et al. (2026) A self-adaptive and versatile tool for eliminating multiple undesirable variations from large-scale transcriptomes. *Nature biomedical engineering*, 10(3), 413.

Tong Y, et al. (2026) Pan-cancer analysis of the oncogenic role of SRY-related high-mobility group box protein B5 in human tumors. *Experimental and therapeutic medicine*, 31(2), 32.

Cai H, et al. (2026) The role of PLOD family genes in liver hepatocellular carcinoma: from mechanisms to therapeutic potential. *BMC cancer*, 26(1), 172.

Li X, et al. (2026) MUC14 suppresses lung adenocarcinoma via integrin β 8? 6/PI3K/AKT/MAPK modulating cisplatin response and immunity. *Scientific reports*, 16(1).

Kim C, et al. (2026) Predicting condition-aware drug-induced transcriptional responses via a latent diffusion model. *Bioinformatics (Oxford, England)*, 42(4).

Lian X, et al. (2026) Identification and validation of a sphingolipid metabolism-related prognostic signature for predicting prognosis and immune microenvironment-related characteristics in ovarian cancer. *Translational cancer research*, 15(3), 153.

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).

Xiao T, et al. (2026) Lactylation-related genes signature panel in hepatocellular carcinoma reveals the prognostic and therapeutic optimization. *Molecular & cellular oncology*, 13(1), 2621475.

Zhang X, et al. (2026) INHBA: a mitochondrial-related pan-cell death gene associated with the prognosis and immunity of OSCC. *Scientific reports*, 16(1).

Dai K, et al. (2026) IGSF9 promotes immunotherapy resistance in colon cancer by orchestrating an immunosuppressive tumor microenvironment and enables combinatorial targeting strategies. *Biochemistry and biophysics reports*, 45, 102478.

Lee J, et al. (2026) NetG2P: Network-based genotype-to-phenotype transformation identifies key signaling crosstalk for prognosis in pan-cancer study. *BMC biology*, 24(1).

Han K, et al. (2026) A study on the role of cuproptosis-related immune checkpoint genes in non-small cell lung cancer. *Medicine*, 105(3), e47163.

Shu Y, et al. (2026) ACT001 synergizes with temozolomide-based chemoradiotherapy to cure refractory glioblastoma by targeting TNF-CXCL10-CD8⁺ T-cell immunity. *Frontiers in pharmacology*, 17, 1745656.

Chen B, et al. (2026) Charting cell-type-specific positive genetic interaction at single-cell resolution for lung adenocarcinoma. *NPJ precision oncology*, 10(1).

Zhou P, et al. (2026) Comprehensive analysis of PANoptosis-related molecular subtypes and prognostic model development of clear cell renal cell carcinoma. *Discover oncology*, 17(1).

He D, et al. (2026) Analysis of the transcriptomic and metabolomic landscape of prostate cancer with different anatomical origins using snFLARE-seq and mxFRIZNGRND. *Nature communications*, 17(1).

Xia P, et al. (2026) Identification of programmed cell death-related subtypes reveals immune heterogeneity and therapeutic divergence in colon cancer. *Theranostics*, 16(9), 4821.

Niu Y, et al. (2026) Functional genomics integration of glycolysis-related gene networks reveals prognostic biomarkers and immune microenvironment regulation in breast cancer. *Scientific reports*, 16(1).

Qin H, et al. (2026) Cuproptosis-associated PDHA1 promotes sarcoma progression and immunotherapy responsiveness via the E2F1-PD-L1 axis: a multi-omics and clinical validation study. *NPJ precision oncology*, 10(1).

Han C, et al. (2026) Comprehensive analysis of liquid-liquid phase separation-related genes in osteosarcoma: implications for prognosis, immune infiltration and drug sensitivity. *Translational cancer research*, 15(2), 94.