Resource Summary Report

Generated by Kravitz on Sep 10, 2026

CancerResource

RRID:SCR_011945
Type: Tool

Proper Citation

CancerResource (RRID:SCR_011945)

Resource Information

URL: http://data-analysis.charite.de/care/

Proper Citation: CancerResource (RRID:SCR_011945)

Description: Comprehensive database of cancer relevant proteins and compound interactions supported by experimental knowledge.Knowledgebase for drug-target relationships related to cancer as well as for supporting information or experimental data.

Resource Type: data or information resource, database

Defining Citation: PMID:20952398

Keywords: compound, drug, target gene, cancer relevant proteins, compound interactions, drug-target relationships, bio.tools

Related Condition: Cancer

Funding: DFG ;
European Union ;
Federal Ministry of Education and Research BMBF ;
International Research Training Group IRTG

Availability: Free, Freely available

Resource Name: CancerResource

Resource ID: SCR_011945

Alternate IDs: biotools:cancerresource, OMICS_01576

Alternate URLs: https://bio.tools/cancerresource

Old URLs: http://bioinf-data.charite.de/cancerresource/index.php?site=home

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260905T133201+0000

Ratings and Alerts

No rating or validation information has been found for CancerResource.

No alerts have been found for CancerResource.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at Kravitz .

Zhang S, et al. (2025) The role and application of bioinformatics techniques and tools in drug discovery. Frontiers in pharmacology, 16, 1547131.

Venkatachalam P, et al. (2019) Modulation of Bax and Bcl-2 genes by secondary metabolites produced by Penicillium rubens JGIPR9 causes the apoptosis of cancer cell lines. Mycology, 12(2), 69.

Deivendran S, et al. (2017) Metastasis-associated protein 1 is an upstream regulator of DNMT3a and stimulator of insulin-growth factor binding protein-3 in breast cancer. Scientific reports, 7, 44225.

Hamed M, et al. (2015) Integrative network-based approach identifies key genetic elements in breast invasive carcinoma. BMC genomics, 16 Suppl 5(Suppl 5), S2.

Kaushik A, et al. (2015) Gene Network Rewiring to Study Melanoma Stage Progression and Elements Essential for Driving Melanoma. PloS one, 10(11), e0142443.