Resource Summary Report

Generated by dkNET on Apr 16, 2025

canSAR

RRID:SCR_006794
Type: Tool

Proper Citation

canSAR (RRID:SCR_006794)

Resource Information

URL: https://cansar.icr.ac.uk/

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Description: canSAR is an integrated database that brings together biological, chemical, pharmacological (and eventually clinical) data. Its goal is to integrate this data and make it accessible to cancer research scientists from multiple disciplines, in order to help with hypothesis generation in cancer research and support translational research. This cancer research and drug discovery resource was developed to utilize the growing publicly available biological annotation, chemical screening, RNA interference screening, expression, amplification and 3D structural data. Scientists can, in a single place, rapidly identify biological annotation of a target, its structural characterization, expression levels and protein interaction data, as well as suitable cell lines for experiments, potential tool compounds and similarity to known drug targets. canSAR has, from the outset, been completely use-case driven which has dramatically influenced the design of the back-end and the functionality provided through the interfaces. The Web interface provides flexible, multipoint entry into canSAR. This allows easy access to the multidisciplinary data within, including target and compound synopses, bioactivity views and expert tools for chemogenomic, expression and protein interaction network data.

Abbreviations: canSAR

Resource Type: database, data analysis service, data or information resource, service resource, analysis service resource, production service resource

Defining Citation: PMID:22013161

Keywords: molecular target, expression, cell line, compound, molecule, protein, structure, ligand, drug, 3d, genomics, 3d complex, bioactivity, protein affinity, cell line sensitivity,

pathway, annotation, bio.tools, FASEB list

Related Condition: Cancer

Funding: Cancer Research UK C309/A8274

Availability: CanSAR is freely available to all cancer researchers. By using canSAR you are agreeing to the Terms of Use, Https://cansar.icr.ac.uk/cansar/terms-of-use/

Resource Name: canSAR

Resource ID: SCR_006794

Alternate IDs: biotools:cansar, nlx_149410

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

Record Creation Time: 20220129T080238+0000

Record Last Update: 20250416T063446+0000

Ratings and Alerts

No rating or validation information has been found for canSAR.

No alerts have been found for canSAR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 47 mentions in open access literature.

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

Bapat J, et al. (2024) CASC4/GOLM2 drives high grade serous carcinoma anoikis resistance through the recycling of EGFR. Cancer gene therapy, 31(2), 300.

Wang B, et al. (2024) A bird's eye view of the potential role of NFKBIA in pan-cancer. Heliyon, 10(10), e31204.

López-Cortés A, et al. (2024) Unraveling druggable cancer-driving proteins and targeted drugs using artificial intelligence and multi-omics analyses. Scientific reports, 14(1), 19359.

Kinnersley B, et al. (2024) Analysis of 10,478 cancer genomes identifies candidate driver

genes and opportunities for precision oncology. Nature genetics, 56(9), 1868.

Zhou Q, et al. (2024) Vemurafenib induces senescence in acute myeloid leukemia and myelodysplastic syndrome by activating the HIPPO signaling pathway: implications for potential targeted therapy. Biology direct, 19(1), 6.

Neeb A, et al. (2024) Thio-2 Inhibits Key Signaling Pathways Required for the Development and Progression of Castration-resistant Prostate Cancer. Molecular cancer therapeutics, 23(6), 791.

Zhu WZ, et al. (2023) An autophagy-related gene prognostic index predicting biochemical recurrence, metastasis, and drug resistance for prostate cancer. Asian journal of andrology, 25(2), 208.

Zhang Y, et al. (2023) Identification of the H3K36me3 reader LEDGF/p75 in the pancancer landscape and functional exploration in clear cell renal cell carcinoma. Computational and structural biotechnology journal, 21, 4134.

Candido MF, et al. (2023) Drugging Hijacked Kinase Pathways in Pediatric Oncology: Opportunities and Current Scenario. Pharmaceutics, 15(2).

Acar A, et al. (2023) Pan-Cancer Analysis of the COVID-19 Causal Gene SLC6A20. ACS omega, 8(14), 13153.

Beach C, et al. (2023) Improving radiotherapy in immunosuppressive microenvironments by targeting complement receptor C5aR1. The Journal of clinical investigation, 133(23).

Aftab F, et al. (2023) An intrinsic purine metabolite AICAR blocks lung tumour growth by targeting oncoprotein mucin 1. British journal of cancer, 128(9), 1647.

Sun W, et al. (2023) Catalytic domain-dependent and -independent transcriptional activities of the tumour suppressor histone H3K27 demethylase UTX/KDM6A in specific cancer types. Epigenetics, 18(1), 2222245.

Pons G, et al. (2023) Analysis of Cancer Genomic Amplifications Identifies Druggable Collateral Dependencies within the Amplicon. Cancers, 15(6).

Griger J, et al. (2023) An integrated cellular and molecular model of gastric neuroendocrine cancer evolution highlights therapeutic targets. Cancer cell, 41(7), 1327.

Sivapatham S, et al. (2022) Currently available molecular analyses for personalized tumor therapy (Review). Biomedical reports, 17(6), 95.

Zhang WC, et al. (2022) MicroRNA-21 guide and passenger strand regulation of adenylosuccinate lyase-mediated purine metabolism promotes transition to an EGFR-TKI-tolerant persister state. Cancer gene therapy, 29(12), 1878.

Mitsopoulos C, et al. (2021) canSAR: update to the cancer translational research and drug discovery knowledgebase. Nucleic acids research, 49(D1), D1074.

Mygland L, et al. (2021) Identification of response signatures for tankyrase inhibitor treatment in tumor cell lines. iScience, 24(7), 102807.

Katopodis P, et al. (2021) p38? - MAPK11 and its role in female cancers. Journal of ovarian research, 14(1), 84.