Resource Summary Report

Generated by NIF on Apr 22, 2025

Cancer3D

RRID:SCR_013755
Type: Tool

Proper Citation

Cancer3D (RRID:SCR_013755)

Resource Information

URL: http://cancer3d.org

Proper Citation: Cancer3D (RRID:SCR_013755)

Description: Database that allows for the exploration of cancer on somatic missense mutations from the Cancer Genome Atlas and Cancer Cell Line Encyclopedia. The site maps proteins and mutations using 3D models and is an interface to the algorithms e-Driver and e-Drug allowing for the prediction of novel cancer drivers or drug biomarkers.

Resource Type: data or information resource, database

Defining Citation: PMID:25392415

Keywords: database, cancer, somatic missense mutations, e-Driver, e-Drug

Related Condition: cancer

Funding: HFSP RGP0027/2011;
NGMS GM101457

Availability: free, public

Resource Name: Cancer3D

Resource ID: SCR_013755

Record Creation Time: 20220129T080317+0000

Record Last Update: 20250422T055747+0000

Ratings and Alerts

No rating or validation information has been found for Cancer3D.

No alerts have been found for Cancer3D.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Hao W, et al. (2025) Advances in predicting breast cancer driver mutations: Tools for precision oncology (Review). International journal of molecular medicine, 55(1).

Sedova M, et al. (2019) Cancer3D 2.0: interactive analysis of 3D patterns of cancer mutations in cancer subsets. Nucleic acids research, 47(D1), D895.

Nussinov R, et al. (2019) Review: Precision medicine and driver mutations: Computational methods, functional assays and conformational principles for interpreting cancer drivers. PLoS computational biology, 15(3), e1006658.

Zhang Z, et al. (2019) A survey and evaluation of Web-based tools/databases for variant analysis of TCGA data. Briefings in bioinformatics, 20(4), 1524.

Solomon O, et al. (2016) G23D: Online tool for mapping and visualization of genomic variants on 3D protein structures. BMC genomics, 17(1), 681.

Tian R, et al. (2015) Computational methods and resources for the interpretation of genomic variants in cancer. BMC genomics, 16 Suppl 8(Suppl 8), S7.

Porta-Pardo E, et al. (2015) A Pan-Cancer Catalogue of Cancer Driver Protein Interaction Interfaces. PLoS computational biology, 11(10), e1004518.