Resource Summary Report

Generated by dkNET on Apr 30, 2025

CHASM/SNV-Box

RRID:SCR_006445
Type: Tool

Proper Citation

CHASM/SNV-Box (RRID:SCR_006445)

Resource Information

URL: http://wiki.chasmsoftware.org/index.php/Main_Page

Proper Citation: CHASM/SNV-Box (RRID:SCR_006445)

Description: CHASM is a method that predicts the functional significance of somatic missense mutations observed in the genomes of cancer cells, allowing mutations to be prioritized in subsequent functional studies, based on the probability that they give the cells a selective survival advantage. SNV-Box is a database of pre-computed features of all possible amino acid substitutions at every position of the annotated human exome. Users can rapidly retrieve features for a given protein amino acid substitution for use in machine learning.

Abbreviations: CHASM/SNV-Box

Synonyms: CHASM / SNV-Box, Cancer-specific High-throughput Annotation of Somatic Mutations

Resource Type: database, data or information resource, software resource

Related Condition: Cancer

Funding: NCI CA152432;
NCI CA135866;
NSF DBI0845275

Availability: Acknowledgement requested, Free, Non-commercial

Resource Name: CHASM/SNV-Box

Resource ID: SCR_006445

Alternate IDs: OMICS_00127

Record Creation Time: 20220129T080236+0000

Record Last Update: 20250430T055441+0000

Ratings and Alerts

No rating or validation information has been found for CHASM/SNV-Box.

No alerts have been found for CHASM/SNV-Box.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Tsang H, et al. (2017) Resources for Interpreting Variants in Precision Genomic Oncology Applications. Frontiers in oncology, 7, 214.

Wooller SK, et al. (2017) Bioinformatics in translational drug discovery. Bioscience reports, 37(4).

Krishnan VG, et al. (2012) Predicting cancer drivers: are we there yet? Genome medicine, 4(11), 88.