

# Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

## 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](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:** data or information resource, software resource, database

**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:** 20260731T042724+0000

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## Ratings and Alerts

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

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

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

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.