Resource Summary Report

Generated by NIF on Apr 9, 2025

SomaticCall

RRID:SCR_001196
Type: Tool

Proper Citation

SomaticCall (RRID:SCR_001196)

Resource Information

URL: http://www.broadinstitute.org/science/programs/genome-biology/computational-rd/somaticcall-manual

Proper Citation: SomaticCall (RRID:SCR_001196)

Description: Software program that finds single-base differences (substitutions) between sequence data from tumor and matched normal samples. It is designed to be highly stringent, so as to achieve a low false positive rate. It takes as input a BAM file for each sample, and produces as output a list of differences (somatic mutations). Note: This software package is no longer supported and information on this page is provided for archival purposes only.

Abbreviations: SomaticCall

Resource Type: software resource

Keywords: somatic mutation, substitution, sequence, bam, mutation

Related Condition: Tumor, Cancer, Normal

Funding:

Resource Name: SomaticCall

Resource ID: SCR_001196

Alternate IDs: OMICS_02155

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250214T182931+0000

Ratings and Alerts

No rating or validation information has been found for SomaticCall.

No alerts have been found for SomaticCall.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.