

Resource Summary Report

Generated by [NIF](#) on Oct 20, 2026

SomaticSniper

RRID:SCR_005108

Type: Tool

Proper Citation

SomaticSniper (RRID:SCR_005108)

Resource Information

URL: <http://gmt.genome.wustl.edu/somatic-sniper/current/>

Proper Citation: SomaticSniper (RRID:SCR_005108)

Description: Software program to identify single nucleotide positions that are different between tumor and normal (or, in theory, any two bam files). It takes a tumor bam and a normal bam and compares the two to determine the differences. It outputs a file in a format very similar to Samtools consensus format. It uses the genotype likelihood model of MAQ (as implemented in Samtools) and then calculates the probability that the tumor and normal genotypes are different. This probability is reported as a somatic score. The somatic score is the Phred-scaled probability (between 0 to 255) that the Tumor and Normal genotypes are not different where 0 means there is no probability that the genotypes are different and 255 means there is a probability of $1 - 10^{-(255/-10)}$ that the genotypes are different between tumor and normal. This is consistent with how the SAM format reports such probabilities. It is currently available as source code via github or as a Debian APT package.

Abbreviations: SomaticSniper

Resource Type: software resource

Defining Citation: [PMID:22155872](#)

Related Condition: Cancer, Tumor, Normal

Availability: Acknowledgement requested

Resource Name: SomaticSniper

Resource ID: SCR_005108

Alternate IDs: OMICS_00092

Record Creation Time: 20220129T080228+0000

Record Last Update: 20261017T202605+0000

Ratings and Alerts

No rating or validation information has been found for SomaticSniper.

No alerts have been found for SomaticSniper.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.