Resource Summary Report

Generated by <u>NIF</u> on May 16, 2025

SNAPE-pooled

RRID:SCR_003476 Type: Tool

Proper Citation

SNAPE-pooled (RRID:SCR_003476)

Resource Information

URL: https://code.google.com/p/snape-pooled/

Proper Citation: SNAPE-pooled (RRID:SCR_003476)

Description: Software that computes the probability distribution for the frequency of the minor allele in a certain population, at a certain position in the genome.

Synonyms: snape-pooled: Computes the minor allele frequency spectrum in pooled DNA (sequenced) samples

Resource Type: software resource

Defining Citation: PMID:22992255

Keywords: standalone software

Funding:

Availability: GNU General Public License, v3

Resource Name: SNAPE-pooled

Resource ID: SCR_003476

Alternate IDs: OMICS_05820

Record Creation Time: 20220129T080219+0000

Record Last Update: 20250420T014144+0000

Ratings and Alerts

No rating or validation information has been found for SNAPE-pooled.

No alerts have been found for SNAPE-pooled.

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 <u>NIF</u>.

Frey LA, et al. (2022) Phenotypic variation and quantitative trait loci for resistance to southern anthracnose and clover rot in red clover. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 135(12), 4337.

Ergon Å, et al. (2022) Identification of loci controlling timing of stem elongation in red clover using genotyping by sequencing of pooled phenotypic extremes. Molecular genetics and genomics : MGG, 297(6), 1587.

Kapun M, et al. (2021) Drosophila Evolution over Space and Time (DEST): A New Population Genomics Resource. Molecular biology and evolution, 38(12), 5782.

Ferretti L, et al. (2020) Pervasive within-host recombination and epistasis as major determinants of the molecular evolution of the foot-and-mouth disease virus capsid. PLoS pathogens, 16(1), e1008235.

Ferretti L, et al. (2018) Within-Host Recombination in the Foot-and-Mouth Disease Virus Genome. Viruses, 10(5).

Verwimp C, et al. (2018) Temporal changes in genetic diversity and forage yield of perennial ryegrass in monoculture and in combination with red clover in swards. PloS one, 13(11), e0206571.

Eierman LE, et al. (2014) Transcriptomic analysis of candidate osmoregulatory genes in the eastern oyster Crassostrea virginica. BMC genomics, 15(1), 503.