

Resource Summary Report

Generated by T1D on Aug 1, 2026

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](https://pubmed.ncbi.nlm.nih.gov/22992255/)

Keywords: standalone software

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: 20260725T190540+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 8 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Fischer NM, et al. (2025) Two distinct host-specialized fungal species cause white-nose disease in bats. *Nature*, 642(8069), 1034.

Ergon ??, 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.

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.

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.