

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 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](#)

**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:** 20260905T132504+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 [PRECISE-TBI](#) .

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.