

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

[ngsRelate](#)

RRID:SCR_016588

Type: Tool

Proper Citation

ngsRelate (RRID:SCR_016588)

Resource Information

URL: <https://github.com/ANGSD/ngsRelate>

Proper Citation: ngsRelate (RRID:SCR_016588)

Description: Software tool for estimating pairwise relatedness from next-generation sequencing data.

Synonyms: ngsRelateV2

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [PMID:26323718](#)

Keywords: estimating, pairwise, relatedness, next, generation, sequencing, data, bio.tools, bio.tools

Funding: Danish Council for Independent Research ;
Danish National Research Foundation

Availability: Free, Available for download, Freely available

Resource Name: ngsRelate

Resource ID: SCR_016588

Alternate IDs: biotools:ngsRelateV2, biotools:ngsrelate

Alternate URLs: <https://bio.tools/ngsRelateV2>, <https://bio.tools/ngsrelate>

Old URLs: <http://www.popgen.dk/software/index.php?title=NgsRelate&oldid=694>

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260905T133007+0000

Ratings and Alerts

No rating or validation information has been found for ngsRelate.

No alerts have been found for ngsRelate.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Srivastava R, et al. (2023) Genealogical Analyses of 3 Cultivated and 1 Wild Specimen of *Vitis vinifera* from Greece. *Genome biology and evolution*, 15(12).

Gopalakrishnan S, et al. (2022) The population genomic legacy of the second plague pandemic. *Current biology : CB*, 32(21), 4743.

Brace S, et al. (2022) Genomes from a medieval mass burial show Ashkenazi-associated hereditary diseases pre-date the 12th century. *Current biology : CB*, 32(20), 4350.

Yaka R, et al. (2021) Variable kinship patterns in Neolithic Anatolia revealed by ancient genomes. *Current biology : CB*, 31(11), 2455.

Ning C, et al. (2021) Ancient genome analyses shed light on kinship organization and mating practice of Late Neolithic society in China. *iScience*, 24(11), 103352.

Hangh??j K, et al. (2019) Fast and accurate relatedness estimation from high-throughput sequencing data in the presence of inbreeding. *GigaScience*, 8(5).