

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

ANCESTRY

RRID:SCR_009121

Type: Tool

Proper Citation

ANCESTRY (RRID:SCR_009121)

Resource Information

URL: <http://ciil.case.edu:3000>

Proper Citation: ANCESTRY (RRID:SCR_009121)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented September 22, 2016. Software application that provides an easy to use web-based user interface to compute individual ancestry estimates using the Maximum Likelihood Estimation method. This website also allows registered users to manage genotype and marker/allele frequency files. Registration is optional.

Abbreviations: ANCESTRY

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, ruby on rails, fortran, web-based

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: ANCESTRY

Resource ID: SCR_009121

Alternate IDs: nlx_154224

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260727T040444+0000

Ratings and Alerts

No rating or validation information has been found for ANCESTRY.

No alerts have been found for ANCESTRY.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Hu S, et al. (2025) Fine-scale population structure and widespread conservation of genetic effect sizes between human groups across traits. Nature genetics, 57(2), 379.

Foltz SM, et al. (2024) Somatic mutation phasing and haplotype extension using linked-reads in multiple myeloma. bioRxiv : the preprint server for biology.

Edge MD, et al. (2020) Attacks on genetic privacy via uploads to genealogical databases. eLife, 9.