

Resource Summary Report

Generated by SPARC SAWG on Sep 14, 2026

RELATIVEFINDER

RRID:SCR_009356

Type: Tool

Proper Citation

RELATIVEFINDER (RRID:SCR_009356)

Resource Information

URL: <http://genome.sph.umich.edu/wiki/RelativeFinder>

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Description: Software program for checking relationships between pairs of individuals. There are many excellent programs that carry out similar tasks. Some of the unique features in relativeFinder are the batch mode options, that allow large jobs to be divided into many smaller jobs (suitable for deployment on a compute cluster environment), and the flexibility of the underlying Merlin engine, which allows relative finder to handle large pedigrees and consider a variety of alternate relationships -- including potential relationships specified by the user on the fly. (entry from Genetic Analysis Software)

Abbreviations: RELATIVEFINDER

Resource Type: software application, software resource

Keywords: gene, genetic, genomic

Resource Name: RELATIVEFINDER

Resource ID: SCR_009356

Alternate IDs: nlx_154571

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260912T200245+0000

Ratings and Alerts

No rating or validation information has been found for RELATIVEFINDER.

No alerts have been found for RELATIVEFINDER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Stuart PE, et al. (2015) Genome-wide Association Analysis of Psoriatic Arthritis and Cutaneous Psoriasis Reveals Differences in Their Genetic Architecture. American journal of human genetics, 97(6), 816.

Lange LA, et al. (2014) Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. American journal of human genetics, 94(2), 233.