

Resource Summary Report

Generated by [kravitz2](#) on Sep 17, 2026

RELPAIR

RRID:SCR_009358

Type: Tool

Proper Citation

RELPAIR (RRID:SCR_009358)

Resource Information

URL: <http://csg.sph.umich.edu/boehnke/relpair.php>

Proper Citation: RELPAIR (RRID:SCR_009358)

Description: Software program that infers the relationships of pairs of individuals based on genetic marker data, either within families or across an entire sample. (entry from Genetic Analysis Software)

Abbreviations: RELPAIR

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, fortran77, ms-windows, (95), unix

Resource Name: RELPAIR

Resource ID: SCR_009358

Alternate IDs: nlx_154573

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260912T200245+0000

Ratings and Alerts

No rating or validation information has been found for RELPAIR.

No alerts have been found for RELPAIR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Hou X, et al. (2026) Genetic legacy and recent cross of two ancient lineages underlie the rebound of the world's rarest primate. *Science advances*, 12(7), eadw3298.

Fortes-Lima CA, et al. (2021) Complex genetic admixture histories reconstructed with Approximate Bayesian Computation. *Molecular ecology resources*, 21(4), 1098.

Masi S, et al. (2021) No evidence for female kin association, indications for extragroup paternity, and sex-biased dispersal patterns in wild western gorillas. *Ecology and evolution*, 11(12), 7634.

Hossain S, et al. (2019) The Interplay of Diet Quality and Alzheimer's Disease Genetic Risk Score in Relation to Cognitive Performance Among Urban African Americans. *Nutrients*, 11(9).

Sethuraman A, et al. (2018) Estimating Genetic Relatedness in Admixed Populations. *G3 (Bethesda, Md.)*, 8(10), 3203.

Glusman G, et al. (2017) Ultrafast Comparison of Personal Genomes via Precomputed Genome Fingerprints. *Frontiers in genetics*, 8, 136.

Chou WC, et al. (2016) A combined reference panel from the 1000???Genomes and UK10K projects improved rare variant imputation in European and Chinese samples. *Scientific reports*, 6, 39313.

Messina F, et al. (2016) Spatially Explicit Models to Investigate Geographic Patterns in the Distribution of Forensic STRs: Application to the North-Eastern Mediterranean. *PloS one*, 11(11), e0167065.

Chen H, et al. (2016) Exome Sequencing and Gene Prioritization Correct Misdiagnosis in a Chinese Kindred with Familial Amyloid Polyneuropathy. *Scientific reports*, 6, 26362.

Gazal S, et al. (2015) High level of inbreeding in final phase of 1000 Genomes Project. *Scientific reports*, 5, 17453.

Palomba G, et al. (2015) Genome-wide association study of susceptibility loci for breast cancer in Sardinian population. *BMC cancer*, 15, 383.

Pemberton TJ, et al. (2010) Inference of unexpected genetic relatedness among individuals in HapMap Phase III. *American journal of human genetics*, 87(4), 457.

Casselbrant ML, et al. (2009) Otitis media: a genome-wide linkage scan with evidence of susceptibility loci within the 17q12 and 10q22.3 regions. *BMC medical genetics*, 10, 85.

Murphy A, et al. (2009) PRKCA: a positional candidate gene for body mass index and asthma. *American journal of human genetics*, 85(1), 87.

Cox LA, et al. (2006) A second-generation genetic linkage map of the baboon (*Papio hamadryas*) genome. *Genomics*, 88(3), 274.