

Resource Summary Report

Generated by [NIF](#) on Aug 31, 2026

Genetic Analysis Package

RRID:SCR_003006

Type: Tool

Proper Citation

Genetic Analysis Package (RRID:SCR_003006)

Resource Information

URL: <http://cran.r-project.org/web/packages/gap/>

Proper Citation: Genetic Analysis Package (RRID:SCR_003006)

Description: GAP is designed as an integrated package for genetic data analysis of both population and family data. Currently, it contains functions for sample size calculations of both population-based and family-based designs, classic twin models, probability of familial disease aggregation, kinship calculation, some statistics in linkage analysis, and association analysis involving one or more genetic markers including haplotype analysis with or without environmental covariates.

Synonyms: GAP

Resource Type: software resource

Keywords: genetic, analysis, package, data, population, family, calculation, family, disease, aggregation, kinship, environmental, covariate, haplotype, marker

Resource Name: Genetic Analysis Package

Resource ID: SCR_003006

Alternate IDs: nif-0000-30271

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260829T182119+0000

Ratings and Alerts

No rating or validation information has been found for Genetic Analysis Package.

No alerts have been found for Genetic Analysis Package.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Koutnikova H, et al. (2009) Identification of the UBP1 locus as a critical blood pressure determinant using a combination of mouse and human genetics. PLoS genetics, 5(8), e1000591.