

# Resource Summary Report

Generated by [ASWG](#) on Aug 10, 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/>

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**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:** 20260808T185751+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](#)

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

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.