Resource Summary Report

Generated by PRECISE-TBI on Jul 31, 2026

R/GAP

RRID:SCR_009364
Type: Tool

Proper Citation

R/GAP (RRID:SCR_009364)

Resource Information

URL: http://www.mrc-epid.cam.ac.uk/~jinghua.zhao/r-progs.htm

Proper Citation: R/GAP (RRID:SCR_009364)

Description: An integrated software 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 ACE/ADE/AE/CE 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 (entry from Genetic Analysis Software)

Abbreviations: R/GAP

Synonyms: R/Genetic Analysis Package

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, r

Resource Name: R/GAP

Resource ID: SCR_009364

Alternate IDs: nlx_154583

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260731T042808+0000

Ratings and Alerts

No rating or validation information has been found for R/GAP.

No alerts have been found for R/GAP.

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 PRECISE-TBI .

Halvorsen M, et al. (2020) Increased burden of ultra-rare structural variants localizing to boundaries of topologically associated domains in schizophrenia. Nature communications, 11(1), 1842.