

Resource Summary Report

Generated by SPARC SAWG on Sep 16, 2026

ACT

RRID:SCR_009033

Type: Tool

Proper Citation

ACT (RRID:SCR_009033)

Resource Information

URL: <http://www.epigenetic.org/Linkage/act.html>,

Proper Citation: ACT (RRID:SCR_009033)

Description: Software application that contains the following modules: ibd, calculates the proportion of gene shared identical by descent for a nuclear family; ibdn, (modified program of ERPA), which implements a method for assessing increased-allele sharing between all pairs of affected relatives within a pedigree; multic, multivariate analysis for complex traits; ml, estimation of variance components using maximum likelihood; ql, estimation of variance components using quasi likelihood; relcov, generates first degree relationship coefficients for extended families; sim2s, the simulation program that was used to test ACT; cage, Cohort Analysis for Genetic Epidemiology; gh: GeneHunter, heavily modified to assist multipoint calculation using multic; TDT: TDT programs written in SAS; gcc and f77 compilers are necessary. Executable programs are included for compatible operating systems, i.e., Solaris2.6. (entry from Genetic Analysis Software)

Abbreviations: ACT

Synonyms: Analysis of Complex Traits

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, fortran77, c++, unix, solaris 2.4

Resource Name: ACT

Resource ID: SCR_009033

Alternate IDs: nlx_153997

Old URLs: <http://www.epigenetic.org/Linkage/act.tar.gz>

Record Creation Time: 20220129T080250+0000

Record Last Update: 20260912T200239+0000

Ratings and Alerts

No rating or validation information has been found for ACT.

No alerts have been found for ACT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.