

# Resource Summary Report

Generated by [NIF](#) on Sep 1, 2026

## LRTAE

RRID:SCR\_009265

Type: Tool

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### Proper Citation

LRTAE (RRID:SCR\_009265)

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### Resource Information

**URL:** <http://ftp://linkage.rockefeller.edu/software/lrtae/>

**Proper Citation:** LRTAE (RRID:SCR\_009265)

**Description:** Software application to compute a likelihood ratio test statistic that increases power to detect genetic association in the presence of phenotype, genotype, and/or haplotype misclassification errors. In addition, the program produces asymptotically unbiased estimates of frequency parameters. (entry from Genetic Analysis Software)

**Abbreviations:** LRTAE

**Synonyms:** Likelihood Ratio Test Allowing for Errors

**Resource Type:** software application, software resource

**Keywords:** gene, genetic, genomic, c, ms-windows, unix, solaris, linux

**Resource Name:** LRTAE

**Resource ID:** SCR\_009265

**Alternate IDs:** nlx\_154443

**Record Creation Time:** 20220129T080252+0000

**Record Last Update:** 20260829T183057+0000

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### Ratings and Alerts

No rating or validation information has been found for LRTAE.

No alerts have been found for LRTAE.

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### 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 [NIF](#) .

Levenstien MA, et al. (2006) Are molecular haplotypes worth the time and expense? A cost-effective method for applying molecular haplotypes. PLoS genetics, 2(8), e127.