

# Resource Summary Report

Generated by [NIF](#) on Sep 11, 2026

## MUTAGENESYS

RRID:SCR\_009309

Type: Tool

### Proper Citation

MUTAGENESYS (RRID:SCR\_009309)

### Resource Information

**URL:** <http://magnet.c2b2.columbia.edu/mutagenesys/>

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**Description:** Software application that uses genome-wide genotype data to estimate disease susceptibility. Our system integrates three data sources: HapMap, whole-genome marker correlation data, and OMIM database. It accepts SNP data of individuals as query input and delivers disease susceptibility hypotheses even if the original set of typed SNPs is incomplete. (entry from Genetic Analysis Software)

**Abbreviations:** MUTAGENESYS

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

**Keywords:** gene, genetic, genomic

**Resource Name:** MUTAGENESYS

**Resource ID:** SCR\_009309

**Alternate IDs:** nlx\_154499

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

**Record Last Update:** 20260905T133249+0000

### Ratings and Alerts

No rating or validation information has been found for MUTAGENESYS.

No alerts have been found for MUTAGENESYS.

### Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.