

# Resource Summary Report

Generated by ASWG on Aug 4, 2026

## MKGST

RRID:SCR\_009295

Type: Tool

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### Proper Citation

MKGST (RRID:SCR\_009295)

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### Resource Information

**URL:** <http://www.uni-kiel.de/medinfo/mitarbeiter/krawczak/download/index.html>

**Proper Citation:** MKGST (RRID:SCR\_009295)

**Description:** Software application (entry from Genetic Analysis Software)

**Abbreviations:** MKGST

**Synonyms:** including ASP (power calculator for gene mapping using a sibpair design), with given infants or parent-infant duos), child and putative father), MUTPROF/MUTCOMP (comparison of mutation profiles), Michael Krawczak's Genetics Software Tools, typed at single locus DNA markers, PATERN (calculation of paternity probabilities from the multilocus DNA profiles of trios, comparing specific types of simple hypotheses regarding the familial relationships involved), ASPSHARE (rapid calculation of the expected ibd sharing at the trait locus, FINDSIRE (identify mothers or sires by means of the comparison of a large number of potential parents, EASYPAT (calculation of likelihood ratios for single locus data, comprising mother, based upon the model)

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

**Keywords:** gene, genetic, genomic

**Resource Name:** MKGST

**Resource ID:** SCR\_009295

**Alternate IDs:** nlx\_154486

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

**Record Last Update:** 20260801T191048+0000

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### Ratings and Alerts

No rating or validation information has been found for MKGST.

No alerts have been found for MKGST.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Vyletal P, et al. (2007) Diversity of cystathionine beta-synthase haplotypes bearing the most common homocystinuria mutation c.833T>C: a possible role for gene conversion. Human mutation, 28(3), 255.

Knight J, et al. (2004) A survey of current software for genetic power calculations. Human genomics, 1(3), 225.