

# Resource Summary Report

Generated by [dkNET](#) on Aug 12, 2026

## MSG

RRID:SCR\_004161

Type: Tool

### Proper Citation

MSG (RRID:SCR\_004161)

### Resource Information

**URL:** <http://genomics.princeton.edu/AndolfattoLab/MSG.html>

**Proper Citation:** MSG (RRID:SCR\_004161)

**Description:** A pipeline of scripts to assign ancestry to genomic segments using next-gen sequence data. This method can identify recombination breakpoints in a large number of individuals simultaneously at a resolution sufficient for most mapping purposes, such as quantitative trait locus (QTL) mapping and mapping of induced mutations.

**Abbreviations:** MSG

**Synonyms:** Multiplexed shotgun genotyping, Multiplexed shotgun genotyping (MSG), MSG: Multiplexed Shotgun Genotyping

**Resource Type:** software resource

**Defining Citation:** [PMID:21233398](#)

**Keywords:** next generation sequencing, genotyping, genetic mapping, ancestry, genome

**Resource Name:** MSG

**Resource ID:** SCR\_004161

**Alternate IDs:** OMICS\_01551

**Record Creation Time:** 20220129T080223+0000

**Record Last Update:** 20260808T185812+0000

### Ratings and Alerts

No rating or validation information has been found for MSG.

No alerts have been found for MSG.

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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 [dkNET](#) .

Zhang L, et al. (2018) A compartmentalized signaling network mediates crossover control in meiosis. eLife, 7.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.