# **Resource Summary Report**

Generated by dkNET on Apr 29, 2025

## **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

**Funding:** 

Resource Name: MSG

Resource ID: SCR\_004161

Alternate IDs: OMICS 01551

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

**Record Last Update:** 20250420T014210+0000

### **Ratings and Alerts**

No rating or validation information has been found for MSG.

No alerts have been found for MSG.

### Data and Source Information

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at <u>dkNET</u>.

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.