

# Resource Summary Report

Generated by SPARC SAWG on Sep 18, 2026

## MULTIMAP

RRID:SCR\_007168

Type: Tool

### Proper Citation

MULTIMAP (RRID:SCR\_007168)

### Resource Information

**URL:** <http://compgen.rutgers.edu/multimap.shtml>

**Proper Citation:** MULTIMAP (RRID:SCR\_007168)

**Description:** Software program for automated construction of genetic maps (entry from Genetic Analysis Software)

**Abbreviations:** MULTIMAP

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

**Keywords:** gene, genetic, genomic, lisp, unix, (sun/compaq-alpha/hp..), bio.tools

**Resource Name:** MULTIMAP

**Resource ID:** SCR\_007168

**Alternate IDs:** biotools:multimap, nlx\_154013

**Alternate URLs:** <https://bio.tools/multimap>

**Old URLs:** <http://compgen.rutgers.edu/Multimap/>

**Record Creation Time:** 20220129T080240+0000

**Record Last Update:** 20260912T200236+0000

### Ratings and Alerts

No rating or validation information has been found for MULTIMAP.

No alerts have been found for MULTIMAP.

### Data and Source Information

## Usage and Citation Metrics

We found 31 mentions in open access literature.

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

Li M, et al. (2026) SpatialCOC: an integrative framework for spatial continuous mapping and cross-omics correction in spatial multi-omics data. *Nature communications*, 17(1).

Ren J, et al. (2026) Optimal transport for label transfer in single-cell multi-omics integration. *Briefings in bioinformatics*, 27(3).

Naqing F, et al. (2026) Benchmarking component choices for unpaired single cell RNA and epigenomic integration. *Genome biology*, 27(1).

Torres-Cano A, et al. (2025) Spatially organized cellular communities shape functional tissue architecture in the pancreas. *Science advances*, 11(46), eadx5791.

Liu T, et al. (2025) SuperGLUE facilitates an explainable training framework for multi-modal data analysis. *Cell reports methods*, 5(9), 101167.

González-Velasco O, et al. (2025) Identifying similar populations across independent single cell studies without data integration. *NAR genomics and bioinformatics*, 7(2), lqaf042.

Dias Mirandela M, et al. (2024) Two-factor authentication underpins the precision of the piRNA pathway. *Nature*, 634(8035), 979.

Samaran J, et al. (2024) scConfluence: single-cell diagonal integration with regularized Inverse Optimal Transport on weakly connected features. *Nature communications*, 15(1), 7762.

Qayoom A, et al. (2024) A novel approach for credit card fraud transaction detection using deep reinforcement learning scheme. *PeerJ. Computer science*, 10, e1998.

Quiñones I, et al. (2024) Unveiling the neuroplastic capacity of the bilingual brain: insights from healthy and pathological individuals. *Brain structure & function*, 229(9), 2187.

Ghazanfar S, et al. (2024) Stabilized mosaic single-cell data integration using unshared features. *Nature biotechnology*, 42(2), 284.

Zhang Z, et al. (2023) scMoMaT jointly performs single cell mosaic integration and multi-modal bio-marker detection. *Nature communications*, 14(1), 384.

Cao K, et al. (2022) A unified computational framework for single-cell data integration with optimal transport. *Nature communications*, 13(1), 7419.

Geng S, et al. (2022) Oscillatory dynamics underlying noun and verb production in highly proficient bilinguals. *Scientific reports*, 12(1), 764.

Quiñones I, et al. (2021) What Can Glioma Patients Teach Us about Language (Re)Organization in the Bilingual Brain: Evidence from fMRI and MEG. *Cancers*, 13(11).

Straub SCK, et al. (2020) Enabling evolutionary studies at multiple scales in Apocynaceae through Hyb-Seq. *Applications in plant sciences*, 8(11), e11400.

Varando G, et al. (2018) MultiMap: A Tool to Automatically Extract and Analyse Spatial Microscopic Data From Large Stacks of Confocal Microscopy Images. *Frontiers in neuroanatomy*, 12, 37.

Palti Y, et al. (2015) Detection and Validation of QTL Affecting Bacterial Cold Water Disease Resistance in Rainbow Trout Using Restriction-Site Associated DNA Sequencing. *PloS one*, 10(9), e0138435.

Frydman M, et al. (2014) Automating risk analysis of software design models. *TheScientificWorldJournal*, 2014, 805856.

Goldstein O, et al. (2010) Exonic SINE insertion in STK38L causes canine early retinal degeneration (erd). *Genomics*, 96(6), 362.