

Resource Summary Report

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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: nlx_154013, biotools:multimap

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

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

Record Creation Time: 20220129T080240+0000

Record Last Update: 20260727T040429+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 27 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

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

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.

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

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.

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

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.

Raveendran M, et al. (2006) Designing new microsatellite markers for linkage and population genetic analyses in rhesus macaques and other nonhuman primates. Genomics, 88(6), 706.

Cox LA, et al. (2006) A second-generation genetic linkage map of the baboon (*Papio hamadryas*) genome. Genomics, 88(3), 274.

Swinburne JE, et al. (2006) Single linkage group per chromosome genetic linkage map for the horse, based on two three-generation, full-sibling, crossbred horse reference families. Genomics, 87(1), 1.

Rogers J, et al. (2006) An initial genetic linkage map of the rhesus macaque (*Macaca mulatta*) genome using human microsatellite loci. Genomics, 87(1), 30.