## **Resource Summary Report**

Generated by NIF on Apr 25, 2025

# MCL

RRID:SCR\_024109 Type: Tool

**Proper Citation** 

MCL (RRID:SCR\_024109)

## **Resource Information**

URL: https://micans.org/mcl/

Proper Citation: MCL (RRID:SCR\_024109)

**Description:** Software tool as general purpose cluster algorithm for both weighted and unweighted networks. Unsupervised cluster algorithm for graphs based on simulation of stochastic flow in graphs. Cluster algorithm for graphs.

Synonyms: , Markov Cluster Algorithm, MCL, mcl

Resource Type: software library, software toolkit, software resource

Defining Citation: PMID:22144159

**Keywords:** cluster algorithm for graphs, general purpose cluster algorithm, weighted and unweighted networks, graphs, simulation of stochastic flow in graphs,

#### Funding:

Availability: Free, Available for download, Freely available,

Resource Name: MCL

Resource ID: SCR\_024109

Alternate URLs: https://sources.debian.org/src/mcl/

License: GNU General Public License, version 3.

Record Creation Time: 20230824T050212+0000

## **Ratings and Alerts**

No rating or validation information has been found for MCL.

No alerts have been found for MCL.

## Data and Source Information

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 7 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Sundararajan R, et al. (2025) Loss of correlated proteasomal subunit expression selectively promotes the 20SHigh state which underlies luminal breast tumorigenicity. Communications biology, 8(1), 55.

Bisht MS, et al. (2024) Genome of the most noxious weed water hyacinth (Eichhornia crassipes) provides insights into plant invasiveness and its translational potential. iScience, 27(9), 110698.

Denoeud F, et al. (2024) Evolutionary genomics of the emergence of brown algae as key components of coastal ecosystems. Cell, 187(24), 6943.

Rubert DP, et al. (2023) Efficient gene orthology inference via large-scale rearrangements. Algorithms for molecular biology : AMB, 18(1), 14.

Wang X, et al. (2023) QTG-Miner aids rapid dissection of the genetic base of tassel branch number in maize. Nature communications, 14(1), 5232.

Yildirim A, et al. (2023) Evaluating the role of the nuclear microenvironment in gene function by population-based modeling. Nature structural & molecular biology, 30(8), 1193.

Najle SR, et al. (2023) Stepwise emergence of the neuronal gene expression program in early animal evolution. Cell, 186(21), 4676.