

Resource Summary Report

Generated by [dkNET](#) on Aug 26, 2026

MUMmerGPU

RRID:SCR_001200

Type: Tool

Proper Citation

MUMmerGPU (RRID:SCR_001200)

Resource Information

URL: <http://sourceforge.net/apps/mediawiki/mummergpu/index.php?title=MUMmerGPU>

Proper Citation: MUMmerGPU (RRID:SCR_001200)

Description: Software tool as high throughput DNA sequence alignment program that runs on nVidia G80-class GPUs. Aligns sequences in parallel on video card to accelerate widely used serial CPU program MUMmer.

Abbreviations: MUMmerGPU

Synonyms: High-throughput sequence alignment using Graphics Processing Units

Resource Type: data processing software, software application, software resource

Defining Citation: [PMID:20161021](#)

Keywords: parallel computation 4, high-throughput sequencing, sequence alignment, dna, graphics processing unit

Funding: NIGMS R01 GM083873;
NLM R01 LM006845

Availability: Free, Available for download, Freely available

Resource Name: MUMmerGPU

Resource ID: SCR_001200

Alternate IDs: OMICS_02151

License: Artistic License

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260821T193621+0000

Ratings and Alerts

No rating or validation information has been found for MUMmerGPU.

No alerts have been found for MUMmerGPU.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Chen MS, et al. (2020) De novo genome assembly and Hi-C analysis reveal an association between chromatin architecture alterations and sex differentiation in the woody plant *Jatropha curcas*. *GigaScience*, 9(2).

Wang W, et al. (2020) The draft nuclear genome assembly of *Eucalyptus pauciflora*: a pipeline for comparing de novo assemblies. *GigaScience*, 9(1).

Khan HS, et al. (2020) Identification of scavenger receptor B1 as the airway microfold cell receptor for *Mycobacterium tuberculosis*. *eLife*, 9.

Todd RT, et al. (2019) Genome plasticity in *Candida albicans* is driven by long repeat sequences. *eLife*, 8.

Hamilton EP, et al. (2016) Structure of the germline genome of *Tetrahymena thermophila* and relationship to the massively rearranged somatic genome. *eLife*, 5.