

# Resource Summary Report

Generated by T1D on Jul 29, 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>

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**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:** software application, software resource, data processing software

**Defining Citation:** [PMID:20161021](#)

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

**Funding:** NLM R01 LM006845;  
NIGMS R01 GM083873

**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:** 20260727T040300+0000

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## Ratings and Alerts

No rating or validation information has been found for MUMmerGPU.

No alerts have been found for MUMmerGPU.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 5 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#).

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.