

# Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 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 resource, software application, 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:** 20260731T042606+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 [kravitz2](#) .

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

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).

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.