

Resource Summary Report

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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: 20260905T133036+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 [RRID](#) .

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.