

Resource Summary Report

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CUDASW++

RRID:SCR_008862

Type: Tool

Proper Citation

CUDASW++ (RRID:SCR_008862)

Resource Information

URL: <http://cudasw.sourceforge.net/>

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Description: CUDASW++ is a bioinformatics software for Smith-Waterman protein database searches that takes advantage of the massively parallel CUDA architecture of NVIDIA Tesla GPUs to perform sequence searches 10x-50x faster than NCBI BLAST. In this algorithm, we deeply explore the SIMT (Single Instruction, Multiple Thread) and virtualized SIMD (Single Instruction, Multiple Data) abstractions to achieve fast speed. This algorithm has been fully tested on Tesla C1060, Tesla C2050, GeForce GTX 280 and GTX 295 graphics cards, and has been incorporated to NVIDIA Tesla Bio Workbench. * Operating System: Linux * Programming language: CUDA and C * Other requirements: CUDA SDK and Toolkits 2.0 or higher

Abbreviations: CUDASW++

Synonyms: CUDASW++ (Smith Waterman)

Resource Type: software resource, source code

Defining Citation: [PMID:19416548](#), [PMID:20370891](#)

Keywords: smith-waterman, bioinformatics, protein, protein database, sequence, simt, simd, bio.tools

Availability: Open-source

Resource Name: CUDASW++

Resource ID: SCR_008862

Alternate IDs: nlx_149212, biotools:cudasw

Alternate URLs: <https://bio.tools/cudasw>

Record Creation Time: 20220129T080249+0000

Record Last Update: 20260905T133329+0000

Ratings and Alerts

No rating or validation information has been found for CUDASW++.

No alerts have been found for CUDASW++.

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 [Kravitz](#) .

Zong P, et al. (2024) TSTA: thread and SIMD-based trapezoidal pairwise/multiple sequence-alignment method. GigaByte (Hong Kong, China), 2024, gigabyte141.

Huang LT, et al. (2015) Improving the Mapping of Smith-Waterman Sequence Database Searches onto CUDA-Enabled GPUs. BioMed research international, 2015, 185179.

Liu Y, et al. (2013) CUDASW++ 3.0: accelerating Smith-Waterman protein database search by coupling CPU and GPU SIMD instructions. BMC bioinformatics, 14, 117.

Liu Y, et al. (2010) CUDASW++2.0: enhanced Smith-Waterman protein database search on CUDA-enabled GPUs based on SIMT and virtualized SIMD abstractions. BMC research notes, 3, 93.

Liu Y, et al. (2009) CUDASW++: optimizing Smith-Waterman sequence database searches for CUDA-enabled graphics processing units. BMC research notes, 2, 73.