Scalable Nucleotide Alignment Program

RRID:SCR_005501
Type: Tool

Proper Citation

Scalable Nucleotide Alignment Program (RRID:SCR_005501)

Resource Information

URL: http://snap.cs.berkeley.edu/

Description: A sequence aligner software program that is 10-100x faster and simultaneously more accurate than existing tools like BWA, Bowtie2 and SOAP2. It runs on commodity x86 processors, and supports a rich error model that lets it cheaply match reads with more differences from the reference than other tools. This gives SNAP up to 2x lower error rates than existing tools and lets it match larger mutations that they may miss. SNAP also natively reads BAM, FASTQ, or gzipped FASTQ, and natively writes SAM or BAM, with built-in sorting, duplicate marking, and BAM indexing.

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Resource Type: Resource, software resource

Keywords: windows, linux, os x

Resource ID: SCR_005501

Parent Organization: University of California; Berkeley; USA

Availability: Apache License, 2, Acknowledgement requested

Website Status: Last checked up

Alternate IDs: OMICS_00687

Abbreviations: SNAP
No rating or validation information has been found for Scalable Nucleotide Alignment Program.

No alerts have been found for Scalable Nucleotide Alignment Program.

**Data and Source Information**

**Source:** SciCrunch Registry

**Usage and Citation Metrics**

We found 64 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [scicrunch](http://scicrunch).


Lantican DV, et al. (2019) Genome Sequence Assembly of Dwarf Coconut (L. 'Catigan Green Dwarf') Provides Insights into Genomic Variation Between Coconut Types and Related Palm Species. G3 (Bethesda, Md.), 9(8), 2377-2393.


Baschal EE, et al. (2018) Idiopathic Scoliosis Families Highlight Actin-Based and Microtubule-Based Cellular Projections and Extracellular Matrix in Disease Etiology. G3 (Bethesda, Md.), 8(8), 2663-2672.