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/

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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.

Abbreviations: SNAP

Synonyms: SNAP - Scalable Nucleotide Alignment Program

Resource Type: software resource

Keywords: windows, linux, os x

Availability: Apache License, 2, Acknowledgement requested

Resource Name: Scalable Nucleotide Alignment Program

Resource ID: SCR_005501

Alternate IDs: OMICS_00687

Alternate URLs: https://sources.debian.org/src/snap-aligner/
Ratings and Alerts

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 112 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.


Tandonnet S, et al. (2023) A chromosomal-scale reference genome of the New World Screwworm, Cochliomyia hominivorax. DNA research : an international journal for rapid publication of reports on genes and genomes, 30(1).


Sethuraman A, et al. (2022) Genome of the parasitoid wasp Dinocampus coccinellae reveals
extensive duplications, accelerated evolution, and independent origins of thelytokous parthenogeny and solitary behavior. G3 (Bethesda, Md.), 12(3).

Liedtke HC, et al. (2022) Chromosome-level assembly, annotation and phylome of Pelobates cultripes, the western spadefoot toad. DNA research : an international journal for rapid publication of reports on genes and genomes, 29(3).


Bieker VC, et al. (2022) Uncovering the genomic basis of an extraordinary plant invasion. Science advances, 8(34), eabo5115.


Pickett BD, et al. (2022) Genome assembly of the roundjaw bonefish (Albula glossodonta), a vulnerable circumtropical sportfish. GigaByte (Hong Kong, China), 2022, gigabyte44.

