

Resource Summary Report

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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/>

Proper Citation: Scalable Nucleotide Alignment Program (RRID:SCR_005501)

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/>

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260725T190604+0000

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 119 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Wang TY, et al. (2025) Chromosome-Level Genome Assembly of the Loach Goby *Rhyacichthys aspro* Offers Insights Into Gobioidae Evolution. *Molecular ecology resources*, 25(7), e14110.

Cho H, et al. (2025) Chromosome-level genome assembly and improved annotation of onion genome (*Allium cepa* L.). *Scientific data*, 12(1), 336.

Jung Sun K, et al. (2025) Chromosome-level genome assembly of *Bienertia sinuspersici*, Single-cell-C4 plant. *Scientific data*, 12(1), 1563.

Mallik R, et al. (2025) Investigating the Impact of Whole-Genome Duplication on Transposable Element Evolution in Teleost Fishes. *Genome biology and evolution*, 17(1).

Snead AA, et al. (2025) Embryonic thermal environments drive plasticity in gene expression. *Fish physiology and biochemistry*, 51(3), 111.

Luecke D, et al. (2024) Highly contiguous genome assembly of *Drosophila prolongata*-a model for evolution of sexual dimorphism and male-specific innovations. *G3 (Bethesda, Md.)*, 14(10).

Luecke D, et al. (2024) Highly Contiguous Genome Assembly of *Drosophila prolongata* - a Model for Evolution of Sexual Dimorphism and Male-specific Innovations. *bioRxiv : the preprint server for biology*.

Utomo C, et al. (2024) Whole-genome sequencing of *Ganoderma boninense*, the causal agent of basal stem rot disease in oil palm, via combined short- and long-read sequencing. *Scientific reports*, 14(1), 10520.

Zimmermann B, et al. (2023) Topological structures and syntenic conservation in sea anemone genomes. *Nature communications*, 14(1), 8270.

Lee IHT, et al. (2023) The genome and sex-dependent responses to temperature in the common yellow butterfly, *Eurema hecabe*. *BMC biology*, 21(1), 200.

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).

Mallik R, et al. (2023) A chromosome-level genome assembly of longnose gar, *Lepisosteus osseus*. *G3 (Bethesda, Md.)*, 13(7).

Chaudhary R, et al. (2023) Sequencing of *Camelina neglecta*, a diploid progenitor of the hexaploid oilseed *Camelina sativa*. *Plant biotechnology journal*, 21(3), 521.

Ketchum RN, et al. (2022) A Chromosome-level Genome Assembly of the Highly Heterozygous Sea Urchin *Echinometra* sp. EZ Reveals Adaptation in the Regulatory Regions of Stress Response Genes. *Genome biology and evolution*, 14(10).

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).

Law STS, et al. (2022) Chromosomal-level reference genome of the moth *Heortia vitessoides* (Lepidoptera: Crambidae), a major pest of agarwood-producing trees. *Genomics*, 114(4), 110440.

Barnard-Kubow KB, et al. (2022) Genetic Variation in Reproductive Investment Across an Ephemerality Gradient in *Daphnia pulex*. *Molecular biology and evolution*, 39(6).

Dong Y, et al. (2022) Parental legacy versus regulatory innovation in salt stress responsiveness of allopolyploid cotton (*Gossypium*) species. *The Plant journal : for cell and molecular biology*, 111(3), 872.

Sork VL, et al. (2022) High-quality genome and methylomes illustrate features underlying evolutionary success of oaks. *Nature communications*, 13(1), 2047.