

# Resource Summary Report

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## Scalable Nucleotide Alignment Program

RRID:SCR\_005501

Type: Tool

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### Proper Citation

Scalable Nucleotide Alignment Program (RRID:SCR\_005501)

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### 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:** 20260815T182315+0000

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### 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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 124 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [NIF](#) .

Oliveira AGG, et al. (2026) Seasonal and Source-Associated Microbiome Dynamics in Brazilian Drinking Water. *Microbial ecology*, 89(1).

Marková S, et al. (2026) Chromosome-level genome of the bank vole (*Clethrionomys glareolus*): a resource for eco-evo-disease research. *Scientific data*, 13(1).

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*.

Zhai X, et al. (2024) A chromosome level genome assembly of *Pseudoroegneria libanotica* reveals a key Kcs gene involves in the cuticular wax elongation for drought resistance. *BMC genomics*, 25(1), 253.

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).

Hundsdoerfer AK, et al. (2023) High-quality haploid genomes corroborate 29 chromosomes and highly conserved synteny of genes in Hyles hawkmoths (Lepidoptera: Sphingidae). *BMC genomics*, 24(1), 443.

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

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

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).