Resource Summary Report

Generated by RRID on Apr 18, 2025

NextGenMap

RRID:SCR_005488
Type: Tool

Proper Citation

NextGenMap (RRID:SCR_005488)

Resource Information

URL: http://cibiv.github.io/NextGenMap/

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Description: A mapping program for Next Generation Sequencing reads that is more than twice as fast as BWA, while achieving a mapping sensitivity similar to Stampy or Bowtie2. NextGenMap uses a memory efficient index structure (hash table) to store the positions of all 13-mers present in the reference genome. This index enables a quick identification of potential mapping regions for every read. Unlike other methods, NextGenMap dynamically determines for each read individually how many of the potential mapping regions have to be evaluated by a pairwise sequence alignment. Moreover, NextGenMap uses fast SIMD instructions (SSE) to accelerate the alignment calculations on the CPU. If available NextGenMap calculates the alignments on the GPU (using OpenCL/CUDA) resulting in a runtime reduction of another 20 - 50 %, depending on the underlying data set.

Abbreviations: NGM

Synonyms: Nextgenmap - A mapping method for Next Generation Sequencing reads

Resource Type: software resource

Keywords: next-generation sequencing

Funding:

Resource Name: NextGenMap

Resource ID: SCR_005488

Alternate IDs: OMICS_00672

Record Creation Time: 20220129T080230+0000

Record Last Update: 20250410T065300+0000

Ratings and Alerts

No rating or validation information has been found for NextGenMap.

No alerts have been found for NextGenMap.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 146 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Owens GL, et al. (2025) Shared Selection and Genetic Architecture Drive Strikingly Repeatable Evolution in Long-Term Experimental Hybrid Populations. Molecular biology and evolution, 42(1).

Woronowicz KC, et al. (2024) Phylogenomic analysis of the Lake Kronotskoe species flock of Dolly Varden charr reveals genetic and developmental signatures of sympatric radiation. bioRxiv : the preprint server for biology.

Villegas LI, et al. (2024) Parthenogenomics: Insights on mutation rates and nucleotide diversity in parthenogenetic Panagrolaimus nematodes. Ecology and evolution, 14(1), e10831.

Müller J, et al. (2024) A novel approach for in vivo DNA footprinting using short double-stranded cell-free DNA from plasma. Genome research, 34(8), 1185.

Becker A, et al. (2024) Identification of CRTH2 as a New PPAR?-Target Gene in T Cells Suggested CRTH2 Dependent Conversion of Th2 Cells as Therapeutic Concept in COVID-19 Infection. ImmunoTargets and therapy, 13, 595.

Dogantzis KA, et al. (2024) Accurate Detection of scutellata-Hybrids (Africanized Bees) Using a SNP-Based Diagnostic Assay. Ecology and evolution, 14(11), e70554.

Li H, et al. (2024) Novel Mito-Nuclear Combinations Facilitate the Global Invasion of a Major Agricultural Crop Pest. Advanced science (Weinheim, Baden-Wurttemberg, Germany),

11(34), e2305353.

Glaser-Schmitt A, et al. (2024) Pervasive tissue-, genetic background-, and allele-specific gene expression effects in Drosophila melanogaster. PLoS genetics, 20(8), e1011257.

Ferraioli S, et al. (2024) LAP2alpha facilitates myogenic gene expression by preventing nucleoplasmic lamin A/C from spreading to active chromatin regions. Nucleic acids research, 52(19), 11500.

Taylor BA, et al. (2024) Population genomics of the invasive Northern Giant Hornet Vespa mandarinia in North America and across its native range. Scientific reports, 14(1), 10803.

Sigeman H, et al. (2024) The rate of W chromosome degeneration across multiple avian neo-sex chromosomes. Scientific reports, 14(1), 16548.

Ward CM, et al. (2024) Recombination, admixture and genome instability shape the genomic landscape of Saccharomyces cerevisiae derived from spontaneous grape ferments. PLoS genetics, 20(3), e1011223.

Bitencourt T, et al. (2024) Integrated multi-omics identifies pathways governing interspecies interaction between A. fumigatus and K. pneumoniae. Communications biology, 7(1), 1496.

Shivarathri R, et al. (2024) The Candida auris Hog1 MAP kinase is essential for the colonization of murine skin and intradermal persistence. mBio, 15(11), e0274824.

Huang HY, et al. (2024) Alternations in inflammatory macrophage niche drive phenotypic and functional plasticity of Kupffer cells. Nature communications, 15(1), 9337.

Hashiguchi Y, et al. (2024) Draft Genome of Akame (Lates Japonicus) Reveals Possible Genetic Mechanisms for Long-Term Persistence and Adaptive Evolution with Low Genetic Diversity. Genome biology and evolution, 16(8).

Fraser R, et al. (2024) Evidence for a Novel X Chromosome in Termites. Genome biology and evolution, 16(12).

Moström MJ, et al. (2023) Protective effect of pre-existing natural immunity in a nonhuman primate reinfection model of congenital cytomegalovirus infection. PLoS pathogens, 19(10), e1011646.

Hartwig C, et al. (2023) From Gut to Blood: Spatial and Temporal Pathobiome Dynamics during Acute Abdominal Murine Sepsis. Microorganisms, 11(3).

Zuber J, et al. (2023) Genome-Wide DNA Changes Acquired by Candida albicans Caspofungin-Adapted Mutants. Microorganisms, 11(8).