

Resource Summary Report

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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

Resource Name: NextGenMap

Resource ID: SCR_005488

Alternate IDs: OMICS_00672

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260801T190259+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 167 mentions in open access literature.

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

Georgiou K, et al. (2025) MyoD1 localization at the nuclear periphery is mediated by association of WFS1 with active enhancers. *Nature communications*, 16(1), 2614.

Robertson C, et al. (2025) Spiral phyllotaxis predicts left-right asymmetric growth and style deflection in mirror-image flowers of *Cyanella alba*. *Nature communications*, 16(1), 3695.

Nowicki M, et al. (2025) HPV-KITE: sequence analysis software for rapid HPV genotype detection. *Briefings in bioinformatics*, 26(2).

Adhikari TB, et al. (2025) Genome-wide association study identifies quantitative trait loci associated with resistance to *Verticillium dahliae* race 3 in tomato. *The plant genome*, 18(4), e70132.

Krüger A, et al. (2025) Plasma-treated water applied as a foliar spray promotes root growth in barley. *BMC plant biology*, 25(1), 1210.

Xue H, et al. (2025) The Genomic Basis of the Tristylous Floral Polymorphism: Evidence for a Role of Gene Duplications in a Region of Restricted Recombination. *Molecular biology and evolution*, 42(8).

Curaudeau M, et al. (2025) Squirrel reservoirs of monkeypox virus are sister species separated by the Sanaga River (Cameroon), as are the two main viral clades. *One health* (Amsterdam, Netherlands), 21, 101157.

Yang X, et al. (2025) Lineage-specific targets of positive selection in three leaf beetles correspond with defence capacity against their shared parasitoid wasp. *Heredity*, 134(9), 567.

Müller JM, et al. (2025) Halfpipe: a tool for analyzing metabolic labeling RNA-seq data to quantify RNA half-lives. *NAR genomics and bioinformatics*, 7(1), lqaf006.

Brenman-Suttner DB, et al. (2025) Exploring the genetics of social behaviour in *C. calcarata*. *Scientific reports*, 15(1), 5580.

Shang R, et al. (2025) Separable roles for Microprocessor and its cofactors ERH and SAFB1/2 during microRNA cluster assistance. *bioRxiv : the preprint server for biology*.

Selmoni O, et al. (2025) Global coral genomic vulnerability explains recent reef losses. *bioRxiv : the preprint server for biology*.

Wijnants S, et al. (2025) *Candida albicans* Hxk1 influences expression of metabolic- and virulence-related genes. *mSphere*, 10(10), e0039525.

Yang Q, et al. (2025) The NEXT complex regulates H3K27me3 levels to affect cancer progression by degrading G4/U-rich lncRNAs. *Nucleic acids research*, 53(4).

Owens GL, et al. (2025) A trans-species cytoplasmic polymorphism is associated with seed shape and aridity across multiple species of sunflowers. *Proceedings of the National Academy of Sciences of the United States of America*, 122(31), e2410943122.

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).

Li S, et al. (2025) Development of vascularized adipose organoids from PBMSCs and their application in evaluating Celastrol's effects. *Adipocyte*, 14(1), 2548787.

Glaser-Schmitt A, et al. (2025) Expression of De Novo Open Reading Frames in Natural Populations of *Drosophila melanogaster*. *Journal of experimental zoology. Part B, Molecular and developmental evolution*, 344(7), 415.

Taylor BA, et al. (2025) Multi-Omic Analysis Reveals Population Differentiation and Signatures of Social Evolution in *Tetragonula Stingless Bees*. *Molecular ecology*, 34(13), e17823.

Huang K, et al. (2025) Inversions contribute disproportionately to parallel genomic divergence in dune sunflowers. *Nature ecology & evolution*, 9(2), 325.