

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 12, 2026

NextGenMap

RRID:SCR_005488

Type: Tool

Proper Citation

NextGenMap (RRID:SCR_005488)

Resource Information

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

Proper Citation: NextGenMap (RRID:SCR_005488)

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: 20260912T195626+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 179 mentions in open access literature.

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

Cameron DP, et al. (2026) MYC modulates TOP2A diffusion to promote substrate detection and activity. *Nature communications*, 17(1).

Shang R, et al. (2026) Separable roles for Microprocessor and its cofactors, ERH and SAFB1/2, during microRNA cluster assistance. *Genes & development*, 40(7-8), 517.

Li ML, et al. (2026) G4-Ligand-Directed PROTACs Unveil DR1 as a Novel Ligand-Co-Binding G4-Protein and Reshape G4-Dependent Transcription. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(27), e23819.

Shultz RR, et al. (2026) Eye can see clearly now: Identifying the locus associated with a white-eye mutation in honey bees (*Apis mellifera*). *Insect molecular biology*, 35(2), 209.

Feng MW, et al. (2026) P-bodies act as dynamic control hubs for RNA processing and storage. *The Journal of biological chemistry*, 302(3), 111273.

Davies BE, et al. (2026) A Chromosome-level Assembly and Functional Genomic Resources for the Model Annelid *Capitella teleta*. *Genome biology and evolution*, 18(3).

Lange T, et al. (2026) Urinary Exosomal miRNAs as Non-Invasive Biomarkers Linked to Podocyte Morphometry in CKD. *Cells*, 15(7).

Glaser-Schmitt A, et al. (2026) Conservation and divergence of sex-biased gene expression across 50 million years of *Drosophila* evolution. *Molecular biology and evolution*, 43(4).

Cho A, et al. (2026) Aerobic sister lineage of breviate has gene-rich mitochondrial genomes. *Current biology : CB*, 36(6), 1481.

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).

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

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.

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).

Selmoni O, et al. (2025) Global coral genomic vulnerability explains recent reef losses. *Nature communications*, 17(1), 896.

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.

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).

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.