

Resource Summary Report

Generated by T1D on Aug 2, 2026

GMAP

RRID:SCR_008992

Type: Tool

Proper Citation

GMAP (RRID:SCR_008992)

Resource Information

URL: <http://research-pub.gene.com/gmap/>

Proper Citation: GMAP (RRID:SCR_008992)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented August 29, 2016. A software program for mapping and aligning cDNA sequences to a genome. The program maps and aligns a single sequence with minimal startup time and memory requirements, and provides fast batch processing of large sequence sets. The program generates accurate gene structures, even in the presence of substantial polymorphisms and sequence errors, without using probabilistic splice site models. Methodology underlying the program includes a minimal sampling strategy for genomic mapping, oligomer chaining for approximate alignment, sandwich DP for splice site detection, and microexon identification with statistical significance testing.

Abbreviations: GMAP

Resource Type: image analysis software, alignment software, source code, software application, software resource, data processing software

Defining Citation: [PMID:15728110](#)

Keywords: mrna, est sequence, expressed sequence tag, sequence, cdna sequence, genome, cdna, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GMAP

Resource ID: SCR_008992

Alternate IDs: OMICS_15072, biotools:gmap, nlx_152505

Alternate URLs: <https://bio.tools/gmap>, <https://sources.debian.org/src/gmap/>

Record Creation Time: 20220129T080250+0000

Record Last Update: 20260801T190341+0000

Ratings and Alerts

No rating or validation information has been found for GMAP.

No alerts have been found for GMAP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 594 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Chen H, et al. (2025) Chromosome-level genome assembly of *Pinus massoniana* provides insights into conifer adaptive evolution. *GigaScience*, 14.

Hemara LM, et al. (2025) Identification and Characterization of Innate Immunity in *Actinidia melanandra* in Response to *Pseudomonas syringae* pv. *actinidiae*. *Plant, cell & environment*, 48(2), 1037.

Yu Y, et al. (2025) Combined transcriptome and whole genome sequencing analyses reveal candidate drug-resistance genes of *Eimeria tenella*. *iScience*, 28(1), 111592.

Willemsen A, et al. (2025) Novel High-Quality *Amoeba* Genomes Reveal Widespread Codon Usage Mismatch Between Giant Viruses and Their Hosts. *Genome biology and evolution*, 17(1).

Liang H, et al. (2025) Wnt/ERK/CDK4/6 activation in the partial EMT state coordinates mammary cancer stemness with self-renewal and inhibition of differentiation. *British journal of cancer*, 133(7), 986.

Ksouri N, et al. (2025) Mapping the genomic landscape of *Prunus* spp. with PrunusMap. *Horticulture research*, 12(2), uhae301.

Wang R, et al. (2025) Chromosome-level genome assembly of *Malus niedzwetzkyana*, the mother of Rosybloom crabapple. *Scientific data*, 12(1), 211.

Grandi N, et al. (2025) HERV Modulation in Colorectal Carcinoma Patients: A Snapshot of Endogenous Retroviral Transcriptome. *Journal of medical virology*, 97(3), e70249.

Huang C, et al. (2025) Impacts of parental genomic divergence in non-syntenic regions on cotton heterosis. *Journal of advanced research*, 73, 15.

Naktang C, et al. (2025) Chromosome-level assemblies of two hexaploid bamboos, *Thyrsostachys oliveri* and *Thyrsostachys siamensis*, provide a foundation for functional and comparative genomics studies. *GigaScience*, 14.

Zhang S, et al. (2025) Collinearity-based Assembly Correction Tool GUI: Software for collinearity-based genome assembly correction. *G3* (Bethesda, Md.), 15(2).

Wang F, et al. (2025) Haplotype-resolved genome of a papaya provides insights into the geographical origin and evolution of Citrus. *Journal of integrative plant biology*, 67(2), 276.

Li C, et al. (2025) Near complete genome assembly of Yadong trout (*Salmo trutta*). *Scientific data*, 12(1), 74.

Ndoja A, et al. (2025) COP1 Deficiency in BRAFV600E Melanomas Confers Resistance to Inhibitors of the MAPK Pathway. *Cells*, 14(13).

Zou X, et al. (2025) Chromosome-level genome assembly of the pine wood nematode carrier *Arhopalus unicolor*. *Scientific data*, 12(1), 111.

Shippy TD, et al. (2024) Diaci v3.0: chromosome-level assembly, de novo transcriptome, and manual annotation of *Diaphorina citri*, insect vector of Huanglongbing. *GigaScience*, 13.

Wang X, et al. (2024) Chromosome level genome assembly and transcriptome analysis of E11 cells infected by tilapia lake virus. *Fish & shellfish immunology*, 148, 109505.

Lu Y, et al. (2024) Whole-genome sequencing of the invasive golden apple snail *Pomacea canaliculata* from Asia reveals rapid expansion and adaptive evolution. *GigaScience*, 13.

Póti Á, et al. (2024) Mutational profile of the regenerative process and de novo genome assembly of the planarian *Schmidtea polychroa*. *Nucleic acids research*, 52(4), 1779.

Long Q, et al. (2024) Population comparative genomics discovers gene gain and loss during grapevine domestication. *Plant physiology*, 195(2), 1401.