GMAP
RRID:SCR_008992
Type: Tool

Proper Citation

GMAP (RRID:SCR_008992)

Resource Information

URL: http://www.gene.com/share/gmap

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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.

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

References: PMID:15728110

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

Parent Organization: Genentech

Availability: THIS RESOURCE IS NO LONGER IN SERVICE, documented August 29, 2016.

Website Status: Last checked down
Abbreviations: GMAP

Resource Name: GMAP

Resource ID: SCR_008992

Alternate IDs: nlx_152505, biotools:gmap

Alternate URLs: https://bio.tools/gmap

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 285 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.


Huang L, et al. (2020) Genome assembly provides insights into the genome evolution and


