

Resource Summary Report

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GSNAP

RRID:SCR_005483

Type: Tool

Proper Citation

GSNAP (RRID:SCR_005483)

Resource Information

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

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Description: Software to align single and paired end reads as short as 14 nt and of arbitrarily long length. Can detect short and long distance splicing, including interchromosomal splicing, in individual reads, using probabilistic models or database of known splice sites. Permits SNP-tolerant alignment to reference space of all possible combinations of major and minor alleles, and can align reads from bisulfite-treated DNA for study of methylation state.

Abbreviations: GSNAP

Synonyms: Genomic Short-read Nucleotide Alignment Program

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

Defining Citation: [PMID:20147302](#)

Keywords: next-generation sequencing, bio.tools, FASEB list

Resource Name: GSNAP

Resource ID: SCR_005483

Alternate IDs: OMICS_00665, biotools:gsnap

Alternate URLs: <https://bio.tools/gsnap>

Record Creation Time: 20220129T080230+0000

Record Last Update: 20261017T203133+0000

Ratings and Alerts

No rating or validation information has been found for GSNAP.

No alerts have been found for GSNAP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.