Resource Summary Report

Generated by RRID on Apr 28, 2025

G-Mo.R-Se

RRID:SCR_005273
Type: Tool

Proper Citation

G-Mo.R-Se (RRID:SCR_005273)

Resource Information

URL: http://www.genoscope.cns.fr/externe/gmorse/

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Description: Software aimed at using RNA-Seq short reads to build de novo gene models. First, candidate exons are built directly from the positions of the reads mapped on the genome (without any ab initio assembly of the reads), and all the possible splice junctions between those exons are tested against unmapped reads : the testing of junctions is directed by the information available in the RNA-Seq dataset rather than a priori knowledge about the genome. Exons can thus be chained into stranded gene models.

Abbreviations: G-Mo.R-Se

Synonyms: Gene MOdeling using RNA-Seq, G-Mo.R-Se: Gene MOdeling using RNA-Seq

Resource Type: software resource

Keywords: bio.tools, bio.tools

Funding:

Resource Name: G-Mo.R-Se

Resource ID: SCR_005273

Alternate IDs: OMICS_01259, biotools:g-mo.r-se, biotools:gmorse

Alternate URLs: https://bio.tools/g-mo.r-se, https://bio.tools/gmorse

Record Creation Time: 20220129T080229+0000

Record Last Update: 20250420T014247+0000

Ratings and Alerts

No rating or validation information has been found for G-Mo.R-Se.

No alerts have been found for G-Mo.R-Se.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Oshlack A, et al. (2010) From RNA-seq reads to differential expression results. Genome biology, 11(12), 220.