Resource Summary Report

Generated by NIF on May 4, 2025

HMMSplicer

RRID:SCR_013315
Type: Tool

Proper Citation

HMMSplicer (RRID:SCR_013315)

Resource Information

URL: http://derisilab.ucsf.edu/index.php?software=105

Proper Citation: HMMSplicer (RRID:SCR_013315)

Description: An accurate and efficient algorithm for discovering canonical and non-canonical splice junctions in short read datasets.

Abbreviations: HMMSplicer

Resource Type: software resource

Funding:

Resource Name: HMMSplicer

Resource ID: SCR_013315

Alternate IDs: OMICS_01241

Record Creation Time: 20220129T080315+0000

Record Last Update: 20250420T014640+0000

Ratings and Alerts

No rating or validation information has been found for HMMSplicer.

No alerts have been found for HMMSplicer.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Wilson IW, et al. (2019) Genetic Diversity and Gene Family Expansions in Members of the Genus Entamoeba. Genome biology and evolution, 11(3), 688.

Ilik IA, et al. (2017) A mutually exclusive stem-loop arrangement in roX2 RNA is essential for X-chromosome regulation in Drosophila. Genes & development, 31(19), 1973.

Min F, et al. (2015) Survey of Programs Used to Detect Alternative Splicing Isoforms from Deep Sequencing Data In Silico. BioMed research international, 2015, 831352.