

Resource Summary Report

Generated by [NIF](#) on Aug 30, 2026

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

Resource Name: HMMSplicer

Resource ID: SCR_013315

Alternate IDs: OMICS_01241

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260829T182433+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 4 mentions in open access literature.

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

Gujarati S, et al. (2026) Differential expression of mitochondria-associated genes in clinical samples of Plasmodium falciparum showing severe manifestations. BMC genomics, 27(1).

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.