

Resource Summary Report

Generated by [RRID](#) on Aug 2, 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: 20260801T190447+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 [RRID](#) .

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.