

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## HMMSplicer

RRID:SCR\_013315

Type: Tool

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### Proper Citation

HMMSplicer (RRID:SCR\_013315)

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### 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:** 20260905T132734+0000

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### Ratings and Alerts

No rating or validation information has been found for HMMSplicer.

No alerts have been found for HMMSplicer.

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### Data and Source Information

**Source:** [SciCrunch Registry](#)

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### Usage and Citation Metrics

We found 4 mentions in open access literature.

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

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.