

Resource Summary Report

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SpliceMap

RRID:SCR_009650

Type: Tool

Proper Citation

SpliceMap (RRID:SCR_009650)

Resource Information

URL: <http://www.stanford.edu/group/wonglab/SpliceMap/>

Proper Citation: SpliceMap (RRID:SCR_009650)

Description: A de novo splice junction discovery and alignment tool.

Abbreviations: SpliceMap

Resource Type: software resource

Defining Citation: [PMID:25577377](#), [PMID:20371516](#)

Keywords: bio.tools

Resource Name: SpliceMap

Resource ID: SCR_009650

Alternate IDs: OMICS_01252, biotools:splicemap

Alternate URLs: <https://bio.tools/splicemap>

Record Creation Time: 20220129T080254+0000

Record Last Update: 20260801T190410+0000

Ratings and Alerts

No rating or validation information has been found for SpliceMap.

No alerts have been found for SpliceMap.

Data and Source Information

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Higuchi S, et al. (2023) BCL7B, a SWI/SNF complex subunit, orchestrates cancer immunity and stemness. BMC cancer, 23(1), 811.

Andrieux G, et al. (2023) Spatially resolved transcriptomic profiles reveal unique defining molecular features of infiltrative 5ALA-metabolizing cells associated with glioblastoma recurrence. Genome medicine, 15(1), 48.

Ma T, et al. (2021) Genome-Wide Analysis of Light-Regulated Alternative Splicing in *Artemisia annua* L. Frontiers in plant science, 12, 733505.

Iraola-Guzmán S, et al. (2020) Target Enrichment Enables the Discovery of lncRNAs with Somatic Mutations or Altered Expression in Paraffin-Embedded Colorectal Cancer Samples. Cancers, 12(10).

Walter Costa MB, et al. (2019) SSS-test: a novel test for detecting positive selection on RNA secondary structure. BMC bioinformatics, 20(1), 151.

Aeschimann F, et al. (2019) let-7 coordinates the transition to adulthood through a single primary and four secondary targets. Life science alliance, 2(2).

Glinsky G, et al. (2018) Single cell expression analysis of primate-specific retroviruses-derived HPAT lincRNAs in viable human blastocysts identifies embryonic cells co-expressing genetic markers of multiple lineages. Heliyon, 4(6), e00667.

Mochizuki M, et al. (2017) Polo-Like Kinase 2 is Dynamically Regulated to Coordinate Proliferation and Early Lineage Specification Downstream of Yes-Associated Protein 1 in Cardiac Progenitor Cells. Journal of the American Heart Association, 6(10).

Daum JM, et al. (2017) The formation of the light-sensing compartment of cone photoreceptors coincides with a transcriptional switch. eLife, 6.

Colombo DF, et al. (2017) Binding of high mobility group A proteins to the mammalian genome occurs as a function of AT-content. PLoS genetics, 13(12), e1007102.

Däster S, et al. (2017) Induction of hypoxia and necrosis in multicellular tumor spheroids is associated with resistance to chemotherapy treatment. Oncotarget, 8(1), 1725.

Schuieler S, et al. (2016) The exon quantification pipeline (EQP): a comprehensive approach to the quantification of gene, exon and junction expression from RNA-seq data. Nucleic acids research, 44(16), e132.

Miki TS, et al. (2016) XRN2 Autoregulation and Control of Polycistronic Gene Expression in *Caenorhabditis elegans*. PLoS genetics, 12(9), e1006313.

Wang J, et al. (2016) A novel long intergenic noncoding RNA indispensable for the cleavage of mouse two-cell embryos. *EMBO reports*, 17(10), 1452.

Zhang Q, et al. (2016) Involvement of Alternative Splicing in Barley Seed Germination. *PloS one*, 11(3), e0152824.

Hirt C, et al. (2015) Bioreactor-engineered cancer tissue-like structures mimic phenotypes, gene expression profiles and drug resistance patterns observed "in vivo". *Biomaterials*, 62, 138.

Tasnim M, et al. (2015) Accurate inference of isoforms from multiple sample RNA-Seq data. *BMC genomics*, 16 Suppl 2(Suppl 2), S15.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. *Database : the journal of biological databases and curation*, 2015.

Li JW, et al. (2014) Transcriptome sequencing of Chinese and Caucasian population identifies ethnic-associated differential transcript abundance of heterogeneous nuclear ribonucleoprotein K (hnRNPK). *Genomics*, 103(1), 56.

Tan MH, et al. (2013) RNA sequencing reveals a diverse and dynamic repertoire of the *Xenopus tropicalis* transcriptome over development. *Genome research*, 23(1), 201.