

Resource Summary Report

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ASprofile

RRID:SCR_001833

Type: Tool

Proper Citation

ASprofile (RRID:SCR_001833)

Resource Information

URL: <http://ccb.jhu.edu/software/ASprofile/>

Proper Citation: ASprofile (RRID:SCR_001833)

Description: A suite of programs for extracting, quantifying and comparing alternative splicing (AS) events from RNA-seq data.

Abbreviations: ASprofile

Resource Type: software resource

Defining Citation: [PMID:24555089](#)

Keywords: alternative splicing event, rna-seq, alternative splicing

Funding: NHGRI R01-HG006677

Availability: Free, Available for download, Freely available

Resource Name: ASprofile

Resource ID: SCR_001833

Alternate IDs: OMICS_01942

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260801T190137+0000

Ratings and Alerts

No rating or validation information has been found for ASprofile.

No alerts have been found for ASprofile.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 37 mentions in open access literature.

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

Wang C, et al. (2025) RBM15-mediated metabolic reprogramming boosts immune response in colorectal cancer. *Frontiers in immunology*, 16, 1515568.

Li AM, et al. (2025) Dissection of genetic basis underlying heat stress response of Apis cerana. *BMC genomics*, 26(1), 512.

Zhang C, et al. (2022) Genome-wide identification, evolution analysis of cytochrome P450 monooxygenase multigene family and their expression patterns during the early somatic embryogenesis in Dimocarpus longan Lour. *Gene*, 826, 146453.

Cheng Y, et al. (2022) Molecular mechanism of atractylon in the invasion and migration of hepatic cancer cells based on high-throughput sequencing. *Molecular medicine reports*, 25(4).

Teng L, et al. (2021) The pan-cancer lncRNA PLANE regulates an alternative splicing program to promote cancer pathogenesis. *Nature communications*, 12(1), 3734.

Li Y, et al. (2021) Role of intestinal extracellular matrix-related signaling in porcine epidemic diarrhea virus infection. *Virulence*, 12(1), 2352.

Hu Z, et al. (2021) Skeletal Muscle Transcriptome Analysis of Hanzhong Ma Duck at Different Growth Stages Using RNA-Seq. *Biomolecules*, 11(2).

Duan M, et al. (2021) Analyses of transcriptomes and the first complete genome of *Leucocalocybe mongolica* provide new insights into phylogenetic relationships and conservation. *Scientific reports*, 11(1), 2930.

Long X, et al. (2021) BRLF1-dependent viral and cellular transcriptomes and transcriptional regulation during EBV primary infection in B lymphoma cells. *Genomics*, 113(4), 2591.

Zhao C, et al. (2021) De novo full length transcriptome analysis of *Arachis glabrata* provides insights into gene expression dynamics in response to biotic and abiotic stresses. *Genomics*, 113(3), 1579.

Li T, et al. (2021) Single-molecule real-time transcript sequencing of developing cotton anthers facilitates genome annotation and fertility restoration candidate gene discovery. *Genomics*, 113(6), 4245.

Batool R, et al. (2020) Synergistic Effect of *Beauveria bassiana* and *Trichoderma asperellum* to Induce Maize (*Zea mays* L.) Defense against the Asian Corn Borer, *Ostrinia*

furnacalis (Lepidoptera, Crambidae) and Larval Immune Response. International journal of molecular sciences, 21(21).

Fan Y, et al. (2020) Dynamic Transcriptome Analysis Reveals Uncharacterized Complex Regulatory Pathway Underlying Dose IBA-Induced Embryogenic Redifferentiation in Cotton. International journal of molecular sciences, 21(2).

Zou C, et al. (2020) Long non-coding RNAs in the alkaline stress response in sugar beet (*Beta vulgaris* L.). BMC plant biology, 20(1), 227.

An X, et al. (2020) Effects of miR-101-3p on goat granulosa cells in vitro and ovarian development in vivo via STC1. Journal of animal science and biotechnology, 11, 102.

Tong X, et al. (2020) Comparative transcriptome analysis revealed genes involved in the fruiting body development of *Ophiocordyceps sinensis*. PeerJ, 8, e8379.

Chen B, et al. (2020) Systematic Identification of Hub Genes in Placenta Accreta Spectrum Based on Integrated Transcriptomic and Proteomic Analysis. Frontiers in genetics, 11, 551495.

Zhang Z, et al. (2020) Identification and Characterization of Hypothalamic Alternative Splicing Events and Variants in Ovine Fecundity-Related Genes. Animals : an open access journal from MDPI, 10(11).

Zhang NN, et al. (2020) Transcriptome sequencing analysis of mono-ADP-ribosylation in colorectal cancer cells. Oncology reports, 43(5), 1413.

Ding Y, et al. (2020) Alternative splicing in tea plants was extensively triggered by drought, heat and their combined stresses. PeerJ, 8, e8258.