

Resource Summary Report

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TransDecoder

RRID:SCR_017647

Type: Tool

Proper Citation

TransDecoder (RRID:SCR_017647)

Resource Information

URL: <https://github.com/TransDecoder/TransDecoder>

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Description: Software tool to identify candidate coding regions within transcript sequences, such as those generated by de novo RNA-Seq transcript assembly using Trinity, or constructed based on RNA-Seq alignments to genome using Tophat and Cufflinks. Starts from FASTA or GFF file. Can scan and retain open reading frames (ORFs) for homology to known proteins by using BlastP or Pfam search and incorporate results into obtained selection. Predictions can then be visualized by using genome browser such as IGV.

Synonyms: , Find Coding Regions Within Transcripts

Resource Type: data processing software, software application, software resource, standalone software

Keywords: Identify, candidate, coding, region, transcript, sequence, de novo, RNAseq, assembly, alignment, genome, open, reading, frame, homology, protein, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: TransDecoder

Resource ID: SCR_017647

Alternate IDs: biotools:transDecoder, OMICS_10852

Alternate URLs: <https://bio.tools/TransDecoder>,
<https://sources.debian.org/src/transdecoder/>,
<https://github.com/TransDecoder/TransDecoder/wiki>

License: BSD 3-clause "New" or "Revised" License

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260912T200106+0000

Ratings and Alerts

No rating or validation information has been found for TransDecoder.

No alerts have been found for TransDecoder.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1572 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Wu X, et al. (2026) Locus-Specific Human Endogenous Retrovirus ERVK18 Expression Indicates an Inflamed Microenvironment and Favorable Immunotherapy Outcome in Small Cell Lung Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(11), 2214.

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

Dersch L, et al. (2026) Vector venom: venomomics of *Aedes albopictus* reveals a large enzyme repertoire and novel cecropins with activity against *E. coli*. *npj drug discovery*, 3(1).

Chen Y, et al. (2026) Benchmarking Software for DDA-PASEF Immunopeptidomics. *Molecular & cellular proteomics : MCP*, 25(4), 101492.

Ollivier R, et al. (2026) Pea transcriptional and phytohormonal responses to adapted and non-adapted aphid biotypes at early stages of infestation. *Scientific reports*, 16(1).

Zhang JL, et al. (2026) Opposing insulin signals underlie the same developmental switch across hemipteran insects. *Science advances*, 12(7), eaea4413.

Grau J, et al. (2026) Improved reconstruction of transcripts and coding sequences from RNA-seq data. *Nucleic acids research*, 54(4).

Zegers JMS, et al. (2026) Systems acclimation to osmotic stress in zygnematophyte cells. *Nature communications*, 17(1), 755.

Zhao Q, et al. (2026) Multi-omics analyses of *Dracocephalum moldavica* L. reveal two flavonoid glycosyltransferases in tilianin biosynthesis. *BMC genomics*, 27(1), 208.

Xin G, et al. (2026) The chromosome-scale genome assembly, annotation of *Bischofia polycarpa* (H. Lév.) Airy Shaw, Phyllanthaceae. *Scientific data*, 13(1).

Mohn RA, et al. (2026) Origin of subgenomes in the circumboreal, allopolyploid, carnivorous plant *Drosera anglica*. *American journal of botany*, 113(3), e70170.

Morihara N, et al. (2026) Functional Annotation Workflow for Fungal Transcriptomes. *Journal of fungi* (Basel, Switzerland), 12(2).

Liu Y, et al. (2026) A high-quality chromosome-level genome assembly of the endangered species *Magnolia amoena*. *Scientific data*, 13(1).

Strowbridge N, et al. (2026) Skin Colour in Salamanders Is Modulated by Both Epitranscriptomic Methylation and Gene Expression. *Molecular ecology*, 35(6), e70302.

Niu Y, et al. (2026) Chromosome-level genome assembly of the blackchin tilapia (*Sarotherodon melanotheron*). *Scientific data*, 13(1).

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing *Cobitis*. *GigaScience*, 15.

Wu Y, et al. (2026) Telomere-to-telomere gapless genome assembly of *Siniperca scherzeri*. *Scientific data*, 13(1).

Chen L, et al. (2026) Integrative utilization of genomic resources for improved phylogenetic resolution in *Sonerileae* (Melastomataceae). *American journal of botany*, 113(6), e70216.

Wang K, et al. (2026) Melatonin Enhances Thermal Resilience and Extends Worker Lifespan in *Apis cerana* via Redox-Metabolic Reprogramming. *Insects*, 17(4).

Li Y, et al. (2026) Haplotype-resolved chromosomal-level genome assembly of *Chrysaora achlyos* (black sea nettle). *Scientific data*, 13(1).