

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: software application, standalone software, software resource, data processing 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: 20260729T044435+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 1309 mentions in open access literature.

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

Hirase S, et al. (2026) Ancestral Origin and Structural Characteristics of Non-Syntenic Homologous Chromosomes in Abalones (*Haliotis*). *Molecular ecology resources*, 26(1), e70057.

Ren L, et al. (2025) Genomes reveal pervasive distant hybridization in nature among cyprinid fishes. *GigaScience*, 14.

Sun YS, et al. (2025) Convergent musk biosynthesis across host and microbiota in musk deer and muskrat. *Zoological research*, 46(3), 505.

Jiang M, et al. (2025) The telomere-to-telomere gap-free reference genome and taxonomic reassessment of *Siniperca roulei*. *GigaScience*, 14.

Johnson SR, et al. (2025) Computational scoring and experimental evaluation of enzymes generated by neural networks. *Nature biotechnology*, 43(3), 396.

Cao S, et al. (2025) *Lactuca* super-pangenome provides insights into lettuce genome evolution and domestication. *Nature communications*, 16(1), 7257.

Hu Y, et al. (2025) Evolutionary history of magnoliid genomes and benzyloisoquinoline alkaloid biosynthesis. *Nature communications*, 16(1), 4039.

Zeng Y, et al. (2025) Chromosome-level genomes of Arctic and Antarctic mosses: *Aulacomnium turgidum* and *Polytrichastrum alpinum*. *Scientific data*, 12(1), 705.

Gong W, et al. (2025) A chromosome-level genome assembly and annotation of *Cercis chuniana* (Fabaceae). *Scientific data*, 12(1), 1163.

Chen X, et al. (2025) Chromosome-level genome assembly of the vegetable leafminer *Liriomyza sativae* (Diptera: Agromyzidae). *Scientific data*, 12(1), 1393.

Zhang M, et al. (2025) Telomere-to-telomere genome assembly uncovers Wolbachia-driven recurrent male bottleneck effect and selection in a sawfly. *Communications biology*, 8(1), 1211.

Gomaa F, et al. (2025) Array of metabolic pathways in a kleptoplastidic foraminiferan protist supports chemoautotrophy in dark, euxinic seafloor sediments. *The ISME journal*, 19(1).

Vysakh VG, et al. (2025) De novo transcriptome assembly of the *Perna viridis*: A novel invertebrate model for ecotoxicological studies. *Scientific data*, 12(1), 147.

Chang CY, et al. (2025) Chromosome number variation and phylogenetic divergence of East Asian *Cirsium* sect. *Onotrophe* subsect. *Nipponocirsium* (Compositae), with a new species from Taiwan. *Botanical studies*, 66(1), 8.

Dai Y, et al. (2025) The chromosome-scale assembly of the *Salvia plebeia* genome provides insight into the biosynthesis and regulation of rosmarinic acid. *Plant biotechnology journal*, 23(5), 1507.

Brown T, et al. (2025) Chromosome-scale genome assembly reveals how repeat elements shape non-coding RNA landscapes active during newt limb regeneration. *Cell genomics*, 5(2), 100761.

Xie YJ, et al. (2025) Phylotranscriptomics resolved phylogenetic relationships and divergence time between 20 golden camellia species. *Scientific reports*, 15(1), 699.

Pratt CJ, et al. (2025) *Anaeromyces corallioides*, sp. nov., a new anaerobic gut fungus from the faeces of cattle. *International journal of systematic and evolutionary microbiology*, 75(3).

Jiang L, et al. (2025) Chromosome-level genome assembly and annotation of pawak croaker (*Pennahia pawak*). *Scientific data*, 12(1), 412.

Lenhart A, et al. (2025) Worker Survival and Egg Production-But Not Transcriptional Activity-Respond to Queen Number in the Highly Polygynous, Invasive Ant *Tapinoma magnum*. *Molecular ecology*, 34(6), e17679.