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 resource, software application, data processing software, standalone software

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

Funding:

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

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Record Last Update: 20250411T055953+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 1068 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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

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.

Hosaka AJ, et al. (2025) Allotetraploid nature of a wild potato species, Solanum stoloniferum Schlechtd. et Bché., as revealed by whole-genome sequencing. The Plant journal : for cell and molecular biology, 121(1), e17158.

Yu X, et al. (2025) Super pan-genome reveals extensive genomic variations associated with phenotypic divergence in Actinidia. Molecular horticulture, 5(1), 4.

Liu J, et al. (2025) Chromosome-level genome assembly of the seasonally polyphenic scorpionfly (Panorpa liui). Scientific data, 12(1), 22.

Li L, et al. (2025) A Chromosomal-level genome assembly and annotation of fat greenling (Hexagrammos otakii). Scientific data, 12(1), 78.

Öztoprak H, et al. (2025) Chromosome-scale genome dynamics reveal signatures of independent haplotype evolution in the ancient asexual mite Platynothrus peltifer. Science advances, 11(4), eadn0817.

Li C, et al. (2025) Near complete genome assembly of Yadong trout (Salmo trutta). Scientific data, 12(1), 74.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, Protosalanx chinensis. GigaScience, 14.

Hermawaty D, et al. (2025) De novo transcriptome assembly and analysis during agarwood induction in Gyrinops versteegii Gilg. seedling. Scientific reports, 15(1), 2977.

Liu C, et al. (2025) A chromosome-scale genome assembly of the pioneer plant Stylosanthes angustifolia: insights into genome evolution and drought adaptation. GigaScience, 14.

Zhao Q, et al. (2025) Near telomere-to-telomere genome assemblies of Silkie Gallus gallus and Mallard Anas platyrhynchos restored the structure of chromosomes and "missing" genes in birds. Journal of animal science and biotechnology, 16(1), 9.

Zou X, et al. (2025) Chromosome-level genome assembly of the pine wood nematode carrier Arhopalus unicolor. Scientific data, 12(1), 111.

Chen Y, et al. (2025) An improved chromosome-level genome assembly and annotation of Hong Kong catfish (Clarias fuscus). Scientific data, 12(1), 193.

Ding R, et al. (2025) Chromosome-Level Genome Assembly and Whole-Genome Resequencing Revealed Contrasting Population Genetic Differentiation of Black Bream (Megalobrama skolkovii) (Teleostei: Cyprinidae) Allopatric and Sympatric to Its Kin Species. Ecology and evolution, 15(1), e70874.

Choi S, et al. (2025) Chromosome-level genome assembly of Salvia sclarea. Scientific data, 12(1), 14.

Liu Z, et al. (2025) Genome architecture of the allotetraploid wild grass Aegilops ventricosa reveals its evolutionary history and contributions to wheat improvement. Plant communications, 6(1), 101131.

Ma C, et al. (2025) Chromosome-level Genome Assembly and Annotation of the Arctic Moss Ptychostomum knowltonii. Genome biology and evolution, 17(1).

Qiu S, et al. (2025) Functional evolution and diversification of CYP82D subfamily members have shaped flavonoid diversification in the genus Scutellaria. Plant communications, 6(1), 101134.