Resource Summary Report

Generated by NIF on Apr 18, 2025

UTRome.org

RRID:SCR_005878
Type: Tool

Proper Citation

UTRome.org (RRID:SCR_005878)

Resource Information

URL: http://www.utrome.org

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Description: This database is intended as a comprehensive resource for UTR (Untranslated Region) biology in C. elegans. The database provides detailed information on UTR structures for all protein-coding mRNAs, and includes annotations extracted from other databases (such as WormBase and PicTar) as well as new annotations generated as part of the NYU UTRome project (including preliminary characterization of UTR clones, USTs (UTR sequence tags), curated sequences, and computational and experimental analysis of functional elements). Examples of functional elements within UTRs include predicted and validated microRNA (miRNA) binding sites (responsible for post-transcriptional gene regulation), putative consensus signals for polyA addition, and predicted secondary structures (which may influence the biological activity of UTRs). The UTRome project is part of the ModEncode Consortium, an NIH initiative to characterize at a genomic scale functional sequence elements encoded in the worm (C. elegans) and fly (D. melanogaster) genomes. UTRs are important portions of mRNAs required for post-transcriptional regulation by interacting with proteins or non-coding RNAs (e.g. microRNAs). To study the role of UTRs we are building a UTR database for C. elegans.

Synonyms: UTRome

Resource Type: database, data or information resource

Funding:

Resource Name: UTRome.org

Resource ID: SCR_005878

Alternate IDs: nif-0000-03620

Record Creation Time: 20220129T080233+0000

Record Last Update: 20250412T055010+0000

Ratings and Alerts

No rating or validation information has been found for UTRome.org.

No alerts have been found for UTRome.org.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Murari E, et al. (2024) A comprehensive analysis of 3'UTRs in Caenorhabditis elegans. Nucleic acids research, 52(13), 7523.

Steber HS, et al. (2019) The C. elegans 3' UTRome v2 resource for studying mRNA cleavage and polyadenylation, 3'-UTR biology, and miRNA targeting. Genome research, 29(12), 2104.

Blazie SM, et al. (2017) Alternative Polyadenylation Directs Tissue-Specific miRNA Targeting in Caenorhabditis elegans Somatic Tissues. Genetics, 206(2), 757.

Tamburino AM, et al. (2013) A compendium of Caenorhabditis elegans RNA binding proteins predicts extensive regulation at multiple levels. G3 (Bethesda, Md.), 3(2), 297.

Ahmed F, et al. (2011) Mining Functional Elements in Messenger RNAs: Overview, Challenges, and Perspectives. Frontiers in plant science, 2, 84.

Merritt C, et al. (2010) Transgenic solutions for the germline. WormBook : the online review of C. elegans biology, 1.