Resource Summary Report

Generated by NIF on May 25, 2025

Transterm

RRID:SCR_008244
Type: Tool

Proper Citation

Transterm (RRID:SCR_008244)

Resource Information

URL: http://mrna.otago.ac.nz/

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Description: Database that provides access to mRNA sequences and associated regulatory elements that were processed from Genbank. These mRNA sequences include complete genomes, which are divided into 5-prime UTRs, 3-prime UTRs, initiation sequences, termination regions and full CDS sequences. This data can be searched for a range of properties including specific mRNA sequences, mRNA motifs, codon usage, RSCU values, information content, etc.

Resource Type: data or information resource, database

Defining Citation: DOI:10.1186/gb-2007-8-2-r22

Keywords: element, gene, 3' utr, 5' utr, codon, genome, genomic, initiation, motif, mrna, nucleotide sequences, transcriptional regulator sites, transcription factors databases, region, regulatory, rna sequence, species, termination

Funding:

Availability: Public

Resource Name: Transterm

Resource ID: SCR_008244

Alternate IDs: nif-0000-21399, OMICS_06165

Alternate URLs: https://sources.debian.org/src/transtermhp/

Old URLs: http://uther.otago.ac.nz/Transterm.html

Record Creation Time: 20220129T080246+0000

Record Last Update: 20250525T032328+0000

Ratings and Alerts

No rating or validation information has been found for Transterm.

No alerts have been found for Transterm.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Pita T, et al. (2023) Identification of Burkholderia cenocepacia non-coding RNAs expressed during Caenorhabditis elegans infection. Applied microbiology and biotechnology, 107(11), 3653.

Menendez-Gil P, et al. (2020) Differential evolution in 3'UTRs leads to specific gene expression in Staphylococcus. Nucleic acids research, 48(5), 2544.

Cridge AG, et al. (2018) Eukaryotic translational termination efficiency is influenced by the 3' nucleotides within the ribosomal mRNA channel. Nucleic acids research, 46(4), 1927.

Rossi CC, et al. (2016) A computational strategy for the search of regulatory small RNAs in Actinobacillus pleuropneumoniae. RNA (New York, N.Y.), 22(9), 1373.

Nikolaichik Y, et al. (2016) SigmoID: a user-friendly tool for improving bacterial genome annotation through analysis of transcription control signals. PeerJ, 4, e2056.

Lee BP, et al. (2016) Functional characterisation of ADIPOQ variants using individuals recruited by genotype. Molecular and cellular endocrinology, 428, 49.

Hammerl JA, et al. (2016) Analysis of the First Temperate Broad Host Range Brucellaphage (BiPBO1) Isolated from B. inopinata. Frontiers in microbiology, 7, 24.

Arnold WK, et al. (2016) RNA-Seq of Borrelia burgdorferi in Multiple Phases of Growth Reveals Insights into the Dynamics of Gene Expression, Transcriptome Architecture, and Noncoding RNAs. PloS one, 11(10), e0164165.

Bardina C, et al. (2016) Genomics of Three New Bacteriophages Useful in the Biocontrol of Salmonella. Frontiers in microbiology, 7, 545.

Xiao Y, et al. (2015) Genome-Wide Transcriptional Profiling of Clostridium perfringens SM101 during Sporulation Extends the Core of Putative Sporulation Genes and Genes Determining Spore Properties and Germination Characteristics. PloS one, 10(5), e0127036.

Jäckel C, et al. (2015) Campylobacter group II phage CP21 is the prototype of a new subgroup revealing a distinct modular genome organization and host specificity. BMC genomics, 16(1), 629.

Sass AM, et al. (2015) Genome-wide transcription start site profiling in biofilm-grown Burkholderia cenocepacia J2315. BMC genomics, 16, 775.

Schroeder CL, et al. (2015) Bacterial small RNAs in the Genus Rickettsia. BMC genomics, 16, 1075.

Miranda H, et al. (2013) Co-expression analysis, proteomic and metabolomic study on the impact of a Deg/HtrA protease triple mutant in Synechocystis sp. PCC 6803 exposed to temperature and high light stress. Journal of proteomics, 78, 294.

Hamby SE, et al. (2011) A meta-analysis of single base-pair substitutions in translational termination codons ('nonstop' mutations) that cause human inherited disease. Human genomics, 5(4), 241.

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

Crawford DJ, et al. (1999) Indirect regulation of translational termination efficiency at highly expressed genes and recoding sites by the factor recycling function of Escherichia coli release factor RF3. The EMBO journal, 18(3), 727.