Resource Summary Report

Generated by kravitz2 on Sep 18, 2026

RiboTaper

RRID:SCR_018880
Type: Tool

Proper Citation

RiboTaper (RRID:SCR_018880)

Resource Information

URL: https://ohlerlab.mdc-berlin.de/software/RiboTaper_126/

Proper Citation: RiboTaper (RRID:SCR_018880)

Description: Software tool as analysis pipeline for ribosome profiling experiments, which exploits triplet periodicity of ribosomal footprints to call translated regions. Statistical approach that identifies translated regions on basis of characteristic three nucleotide periodicity of Ribo-seq data.

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

Defining Citation: PMID:26657557

Keywords: Ribo-seq data, analysis, ribosome profiling experiment, triplet periodicity, ribosomal footprint, translated region, three nucleotide periodicity, data, ribosome profiling, bio.tools

Funding: Berlin Institute for Medical Systems Biology ;
NIGMS R01 GM104962

Availability: Free, Freely available

Resource Name: RiboTaper

Resource ID: SCR_018880

Alternate IDs: biotools:ribotaper

Alternate URLs: https://bioconda.github.io/recipes/ribotaper/README.html, https://bio.tools/ribotaper

License: GPL

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260912T195906+0000

Ratings and Alerts

No rating or validation information has been found for RiboTaper.

No alerts have been found for RiboTaper.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Zhang T, et al. (2025) Small open reading frame-encoded microproteins in cancer: identification, biological functions and clinical significance. Molecular cancer, 24(1), 105.

Balakrishnan A, et al. (2025) Unlocking the secrets of the immunopeptidome: MHC molecules, ncRNA peptides, and vesicles in immune response. Frontiers in immunology, 16, 1540431.

Ding Z, et al. (2024) Exploring the potential of large language model-based chatbots in challenges of ribosome profiling data analysis: a review. Briefings in bioinformatics, 26(1).

Xiao Y, et al. (2024) Long non-coding RNA-encoded micropeptides: functions, mechanisms and implications. Cell death discovery, 10(1), 450.

Chothani SP, et al. (2022) A high-resolution map of human RNA translation. Molecular cell, 82(15), 2885.

Gaertner B, et al. (2020) A human ESC-based screen identifies a role for the translated lncRNA LINC00261 in pancreatic endocrine differentiation. eLife, 9.

Weber R, et al. (2020) 4EHP and GIGYF1/2 Mediate Translation-Coupled Messenger RNA Decay. Cell reports, 33(2), 108262.

Lim CS, et al. (2018) The exon-intron gene structure upstream of the initiation codon predicts translation efficiency. Nucleic acids research, 46(9), 4575.