

Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

[ANNOgesic](#)

RRID:SCR_016326

Type: Tool

Proper Citation

ANNOgesic (RRID:SCR_016326)

Resource Information

URL: <https://github.com/Sung-Huan/ANNOgesic>

Proper Citation: ANNOgesic (RRID:SCR_016326)

Description: Software tool for bacterial/archaeal RNA-Seq based genome annotations. Used for integrating, detecting, predicting, and grouping RNA-Seq data.

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

Keywords: bacterial, archaeal, RNA, sequencing, data, analysis, genome, annotation, statistic, visualization, protein, interaction, prediction, grouping, go, ontology, gene, differential, circular

Availability: Free, Freely available, Available for download

Resource Name: ANNOgesic

Resource ID: SCR_016326

License: Internet Systems Consortium License, Simplified BSD License

License URLs: <http://annogesic.readthedocs.io/en/latest/index.html>

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260905T132807+0000

Ratings and Alerts

No rating or validation information has been found for ANNOgesic.

No alerts have been found for ANNOgesic.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Ryan D, et al. (2024) An expanded transcriptome atlas for *Bacteroides thetaiotaomicron* reveals a small RNA that modulates tetracycline sensitivity. *Nature microbiology*, 9(4), 1130.

Wu W, et al. (2024) The functional small RNA interactome reveals targets for the vancomycin-responsive sRNA RsaOI in vancomycin-tolerant *Staphylococcus aureus*. *mSystems*, 9(4), e0097123.

Wei G, et al. (2022) High-Resolution Small RNAs Landscape Provides Insights into Alkane Adaptation in the Marine Alkane-Degrader *Alcanivorax dieselolei* B-5. *International journal of molecular sciences*, 23(24).

Mediati DG, et al. (2022) RNase III-CLASH of multi-drug resistant *Staphylococcus aureus* reveals a regulatory mRNA 3'UTR required for intermediate vancomycin resistance. *Nature communications*, 13(1), 3558.

Chen L, et al. (2021) The bioinformatics toolbox for circRNA discovery and analysis. *Briefings in bioinformatics*, 22(2), 1706.

Ryan D, et al. (2020) A high-resolution transcriptome map identifies small RNA regulation of metabolism in the gut microbe *Bacteroides thetaiotaomicron*. *Nature communications*, 11(1), 3557.

Michaux C, et al. (2020) Single-Nucleotide RNA Maps for the Two Major Nosocomial Pathogens *Enterococcus faecalis* and *Enterococcus faecium*. *Frontiers in cellular and infection microbiology*, 10, 600325.

Yu SH, et al. (2018) ANNOgesic: a Swiss army knife for the RNA-seq based annotation of bacterial/archaeal genomes. *GigaScience*, 7(9).

Remes B, et al. (2017) An RpoHI-Dependent Response Promotes Outgrowth after Extended Stationary Phase in the Alphaproteobacterium *Rhodobacter sphaeroides*. *Journal of bacteriology*, 199(14).

Dingemans J, et al. (2016) Effect of Shear Stress on *Pseudomonas aeruginosa* Isolated from the Cystic Fibrosis Lung. *mBio*, 7(4).