Resource Summary Report

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ANNOgesic

RRID:SCR_016326
Type: Tool

Proper Citation

ANNOgesic (RRID:SCR_016326)

Resource Information

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

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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 toolkit, software resource, software application, standalone software

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

Funding:

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: 20250329T061140+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 FDI Lab - SciCrunch.org.

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).