Resource Summary Report

Generated by RRID on Apr 28, 2025

CanSNPer

RRID:SCR_001980
Type: Tool

Proper Citation

CanSNPer (RRID:SCR_001980)

Resource Information

URL: https://github.com/adrlar/CanSNPer

Proper Citation: CanSNPer (RRID:SCR_001980)

Description: Software that is a hierarchical genotype classifier of clonal pathogens.

Resource Type: software resource

Defining Citation: PMID:24574113

Keywords: python, bio.tools

Funding:

Availability: GNU General Public License, v3

Resource Name: CanSNPer

Resource ID: SCR_001980

Alternate IDs: biotools:cansnper, OMICS_03706

Alternate URLs: https://bio.tools/cansnper

Record Creation Time: 20220129T080210+0000

Record Last Update: 20250420T014047+0000

Ratings and Alerts

No rating or validation information has been found for CanSNPer.

No alerts have been found for CanSNPer.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Kellgren T, et al. (2024) Completed genome and emergence scenario of the multidrug-resistant nosocomial pathogen Staphylococcus epidermidis ST215. BMC microbiology, 24(1), 215.

Antwerpen M, et al. (2024) New Insights into the Phylogeny of the A.Br.161 ("A.Br.Heroin") Clade of Bacillus anthracis. Pathogens (Basel, Switzerland), 13(7).

Linde J, et al. (2023) Comparison of Illumina and Oxford Nanopore Technology for genome analysis of Francisella tularensis, Bacillus anthracis, and Brucella suis. BMC genomics, 24(1), 258.

Braun P, et al. (2022) In-Depth Analysis of Bacillus anthracis 16S rRNA Genes and Transcripts Reveals Intra- and Intergenomic Diversity and Facilitates Anthrax Detection. mSystems, 7(1), e0136121.

Braun P, et al. (2022) Reoccurring Bovine Anthrax in Germany on the Same Pasture after 12 Years. Journal of clinical microbiology, 60(3), e0229121.

Neubert K, et al. (2021) Testing assembly strategies of Francisella tularensis genomes to infer an evolutionary conservation analysis of genomic structures. BMC genomics, 22(1), 822.

Kittl S, et al. (2020) First European report of Francisella tularensis subsp. holarctica isolation from a domestic cat. Veterinary research, 51(1), 109.

Kevin M, et al. (2020) Phylogeography and Genetic Diversity of Francisella tularensis subsp. holarctica in France (1947-2018). Frontiers in microbiology, 11, 287.

Linde J, et al. (2020) Genotyping of Francisella tularensis subsp. holarctica from Hares in Germany. Microorganisms, 8(12).

Myrtennäs K, et al. (2020) Genetic Traces of the Francisella tularensis Colonization of Spain, 1998-2020. Microorganisms, 8(11).

Janse I, et al. (2018) Environmental Surveillance of Zoonotic Francisella tularensis in the Netherlands. Frontiers in cellular and infection microbiology, 8, 140.

Wittwer M, et al. (2018) Population Genomics of Francisella tularensis subsp. holarctica and its Implication on the Eco-Epidemiology of Tularemia in Switzerland. Frontiers in cellular and infection microbiology, 8, 89.

Busch A, et al. (2018) Revisiting Francisella tularensis subsp. holarctica, Causative Agent of Tularemia in Germany With Bioinformatics: New Insights in Genome Structure, DNA Methylation and Comparative Phylogenetic Analysis. Frontiers in microbiology, 9, 344.

Busch A, et al. (2017) High-Quality Draft Genome Sequence of Francisella tularensis subsp. holarctica Strain 08T0073 Isolated from a Wild European Hare. Genome announcements, 5(12).

Dwibedi C, et al. (2016) Long-range dispersal moved Francisella tularensis into Western Europe from the East. Microbial genomics, 2(12), e000100.

Myrtennäs K, et al. (2016) Introduction and persistence of tularemia in Bulgaria. Infection ecology & epidemiology, 6, 32838.