

Resource Summary Report

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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

Availability: Free, Available for download, Freely available

Resource Name: CanSNPer

Resource ID: SCR_001980

Alternate IDs: biotools:cansnper, OMICS_03706

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

License: GNU General Public License, v3

Record Creation Time: 20220129T080210+0000

Record Last Update: 20260801T190140+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 18 mentions in open access literature.

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

Nothdurfter S, et al. (2025) Epidemiology of Tularemia among Humans and Animals, Baden-Wuerttemberg, Germany, 2012-2022. *Emerging infectious diseases*, 31(4), 678.

Podowski JC, et al. (2025) Genomic reconstruction of *Bacillus anthracis* from complex environmental samples enables high-throughput identification and lineage assignment in Pakistan. *Microbial genomics*, 11(6).

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).

Myrtenäs 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.

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.

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. (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.

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