

Resource Summary Report

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Parsnp

RRID:SCR_024153

Type: Tool

Proper Citation

Parsnp (RRID:SCR_024153)

Resource Information

URL: <https://harvest.readthedocs.io/en/latest/content/parsnp.html>

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Description: Software to align the core genome of hundreds to thousands of bacterial genomes. Input can be both draft assemblies and finished genomes, and output includes variant (SNP) calls, core genome phylogeny and multi-alignments. Parsnp leverages contextual information provided by multi-alignments surrounding SNP sites for filtration/cleaning, in addition to existing tools for recombination detection/filtration and phylogenetic reconstruction.

Synonyms: parsnp

Resource Type: software library, software resource, software toolkit

Defining Citation: [PMID:25410596](#)

Keywords: align core genome, bacterial genomes,

Availability: Free, Available for download, Freely available,

Resource Name: Parsnp

Resource ID: SCR_024153

Alternate IDs: OMICS_21461

Alternate URLs: <https://sources.debian.org/src/parsnp/>, <https://github.com/marbl/parsnp>

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260829T182902+0000

Ratings and Alerts

No rating or validation information has been found for Parsnp.

No alerts have been found for Parsnp.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 54 mentions in open access literature.

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

Xie S, et al. (2026) Toxin gene profiles, antibiotic resistance, and genetic diversity of *Clostridium perfringens* from food-producing animals: a whole-genome sequencing study with implications for food safety. *Current research in food science*, 12, 101460.

Chudejova K, et al. (2026) One-year multicenter surveillance of Fosfomycin resistance Enterobacterales: the rise of FosA3-producing *P. mirabilis*. *Current research in microbial sciences*, 10, 100582.

Li G, et al. (2026) Emergence of a carbapenem-resistant *Klebsiella pneumoniae* ST15-KL19 clone with elevated virulence potential in a tertiary hospital in China. *Frontiers in cellular and infection microbiology*, 16, 1745492.

Xu Z, et al. (2026) The nucleoid-associated protein subunit HupA positively regulates the Pqs system and pyocyanin production in *Pseudomonas aeruginosa*. *Applied and environmental microbiology*, 92(4), e0242525.

Rossi L, et al. (2025) Epidemiology and Genomic Characterization of Trichophyton mentagrophytes over a Period of 4 Years in Northern Italy. *Journal of fungi (Basel, Switzerland)*, 11(8).

Zhang Y, et al. (2025) Emerging Mobile Colistin Resistance Gene Mcr-1 and Mcr-10 in Enterobacteriaceae Isolates From Urban Sewage in China. *Infection and drug resistance*, 18, 1035.

Chan Y-X, et al. (2025) Antimicrobial susceptibility and genomic characterization of *Lactococcus formosensis*, *Lactococcus garvieae*, and *Lactococcus petauri* in Hong Kong. *Microbiology spectrum*, 13(10), e0010125.

Okada K, et al. (2025) First recorded food-borne outbreak of gastroenteritis caused by enteroinvasive *Escherichia coli* serotype O8:H19 in Thailand. *European journal of clinical microbiology & infectious diseases* : official publication of the European Society of Clinical Microbiology, 44(3), 733.

Adesoji AT, et al. (2025) *Serratia nevei* in Nigeria: First Report and Global Distribution. *Microorganisms*, 13(12).

Nagpala MJM, et al. (2025) Genomic characterization of antimicrobial-resistant *Salmonella enterica* in chicken meat from wet markets in Metro Manila, Philippines. *Frontiers in microbiology*, 16, 1496685.

Fayad S, et al. (2025) Evidence of transmission and dissemination of diverse blaNDM-5-producing *Escherichia coli* clones between refugee and host communities and their environment: a multicenter cross-sectional study. *Applied and environmental microbiology*, 91(12), e0162525.

Adams JRG, et al. (2025) High-risk clonal groups of avian pathogenic *Escherichia coli* (APEC) demonstrate heterogeneous phenotypic characteristics in vitro and in vivo. *Virulence*, 16(1), 2546682.

Peng R, et al. (2025) Community gut colonization by tet(X4)-positive multidrug-resistant *Escherichia coli* in healthy individuals from urban residents in Shenzhen, China. *Frontiers in cellular and infection microbiology*, 15, 1667196.

AbdulHak A, et al. (2025) The genomic configurations driving antimicrobial resistance and virulence in colistin resistant *Pseudomonas aeruginosa* from an Egyptian Tertiary Oncology Hospital. *PLOS global public health*, 5(8), e0004976.

Guo Y, et al. (2025) Research Note: Isolation and genomic characterization of *Avibacterium paragallinarum* from the Hubei Province, China. *Poultry science*, 104(10), 105514.

Shahimi NH, et al. (2025) Draft genome sequence data of *Klebsiella pneumoniae* subsp. *pneumoniae* B36336, a multidrug-resistant strain isolated from a human bloodstream infection. *Data in brief*, 61, 111744.

Zhu W, et al. (2025) Genomic Characterization of Intestinal Colonizing *Pseudomonas* *juntendi* Strains Harboring bla VIM-2. *Infection and drug resistance*, 18, 6501.

Grist LF, et al. (2025) Global phylogenomic analysis of *Staphylococcus pseudintermedius* reveals genomic and prophage diversity in multidrug-resistant lineages. *Microbial genomics*, 11(3).

Wang Y, et al. (2025) A global atlas and drivers of antimicrobial resistance in *Salmonella* during 1900-2023. *Nature communications*, 16(1), 4611.

Ayoub H, et al. (2025) Genomic insights into *Brucella melitensis* in India: stability of ST8 and the role of virulence genes in regional adaptations. *Microbiology spectrum*, 13(6), e0264724.