

# Resource Summary Report

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## Parsnp

RRID:SCR\_024153

Type: Tool

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### Proper Citation

Parsnp (RRID:SCR\_024153)

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### Resource Information

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

**Proper Citation:** Parsnp (RRID:SCR\_024153)

**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:** 20260728T043707+0000

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### Ratings and Alerts

No rating or validation information has been found for Parsnp.

No alerts have been found for Parsnp.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 39 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [nidm-terms](#) .

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.

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.

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.

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

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

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.

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.

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.

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.

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).

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.

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

Jiang Y, et al. (2024) Persistent Colonization of Ciprofloxacin-Resistant and Extended-Spectrum ??-Lactamase (ESBL)-Producing Salmonella enterica Serovar Kentucky ST198 in a Patient with Inflammatory Bowel Disease. *Infection and drug resistance*, 17, 1459.

Ge Q, et al. (2024) Detection of antimicrobial resistance in Glaesserella parasuis in South China using whole-genome sequencing. *Frontiers in microbiology*, 15, 1532743.

Meijs AP, et al. (2024) Human carriage of ESBL/pAmpC-producing Escherichia coli and Klebsiella pneumoniae in relation to the consumption of raw or undercooked vegetables, fruits, and fresh herbs. *Microbiology spectrum*, 12(2), e0284923.

Rhoads DD, et al. (2024) Molecular Genomic Analyses of Enterococcus cecorum from Sepsis Outbreaks in Broilers. *Microorganisms*, 12(2).

Mattioni Marchetti V, et al. (2024) Enterobacter asburiae ST229: an emerging carbapenemases producer. *Scientific reports*, 14(1), 6220.

Cave R, et al. (2024) Expansion of pneumococcal serotype 23F and 14 lineages with genotypic changes in capsule polysaccharide locus and virulence gene profiles post introduction of pneumococcal conjugate vaccine in Blantyre, Malawi. *Microbial genomics*, 10(6).

Gong X, et al. (2024) Genomic insight into the diversity of Glaesserella parasuis isolates from 19 countries. *mSphere*, 9(9), e0023124.