

Resource Summary Report

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Enterobase

RRID:SCR_019019

Type: Tool

Proper Citation

Enterobase (RRID:SCR_019019)

Resource Information

URL: <http://enterobase.warwick.ac.uk/>

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Description: Integrated software environment that supports identification of global population structures within several bacterial genera that include pathogens. Web service for analyzing and visualizing genomic variation within bacteria. Genome database to enable to identify, analyse, quantify and visualise genomic variation within bacterial genera including Salmonella, Escherichia/Shigella, Clostridioides, Vibrio, Yersinia, Helicobacter, Moraxella.

Resource Type: web service, software resource, data access protocol, data or information resource, database

Keywords: Bacteria, pathogen, genome, Illumina short read, genotype, core genome multilocus, sequence typing, cgMLST, cgMLST sequence, bacterial strain mapping, visualizing genomic variation, bio.tools, FASEB list

Funding: Biotechnology and Biological Sciences Research Council ; Wellcome Trust

Availability: Restricted

Resource Name: Enterobase

Resource ID: SCR_019019

Alternate IDs: biotools:Enterobase

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

License URLs: <https://enterobase.readthedocs.io/en/latest/enterobase-terms-of-use.html>

Record Creation Time: 20220129T080343+0000

Ratings and Alerts

No rating or validation information has been found for EnteroBase.

No alerts have been found for EnteroBase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 233 mentions in open access literature.

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

An H, et al. (2025) Genomic and virulent characterization of a duck-associated *Salmonella* serovar Potsdam from China. *Poultry science*, 104(1), 104646.

Gabor CE, et al. (2025) Characterization of *Shigella flexneri* serotype 6 strains from geographically diverse low- and middle-income countries. *mBio*, 16(1), e0221024.

Gray HA, et al. (2025) Genomic epidemiology of extended-spectrum beta-lactamase-producing *Escherichia coli* from humans and a river in Aotearoa New Zealand. *Microbial genomics*, 11(1).

Zhao K, et al. (2025) IS15DIV-flanked composite transposon harboring bla NDM-5 in multidrug-resistant *Salmonella* Typhimurium. *iScience*, 28(2), 111720.

Fernandes IdA, et al. (2025) TccP4: a novel effector identified in the *Escherichia albertii* strain 1551-2 required for attaching and effacing lesion formation on infected Nck-null cells. *Microbiology spectrum*, 13(3), e0205524.

Yin H, et al. (2025) Virulence Potential of ESBL-Producing *Escherichia coli* Isolated during the Perinatal Period. *American journal of perinatology*, 42(6), 822.

Metz F, et al. (2025) Functional and intricate interaction network connecting *Helicobacter pylori* Cag type 4 secretion system surface proteins with outer membrane proteins HopQ and HopZ. *microLife*, 6, uqaf027.

Rocha VGP, et al. (2025) *Escherichia coli* Sequence Type 131-H22 in Parrots from Illegal Pet Trade, Brazil, 2024. *Emerging infectious diseases*, 31(10), 2025.

Dyer NP, et al. (2025) EnteroBase in 2025: exploring the genomic epidemiology of bacterial pathogens. *Nucleic acids research*, 53(D1), D757.

Aldaz N, et al. (2025) In Silico Detection of Virulence Genes in Whole-Genome Sequences of Extra-Intestinal Pathogenic *Escherichia coli* (ExPEC) Documented in

Countries of the Andean Community. *Current issues in molecular biology*, 47(3).

Gichure J, et al. (2025) Exploring the Genetic Diversity, Virulence and Antimicrobial Resistance of Diarrhoeagenic *Escherichia coli* From Southern Africa Using Whole-Genome Data. *Public health challenges*, 4(3), e70098.

Wu J, et al. (2025) Genome analysis of colistin-resistant *Salmonella* isolates from human sources in Guizhou of southwestern China, 2019-2023. *Frontiers in microbiology*, 16, 1498995.

Li Y, et al. (2025) Potential links between human bloodstream infection by *Salmonella enterica* serovar Typhimurium and international transmission to Colombia. *PLoS neglected tropical diseases*, 19(1), e0012801.

Kaingu J, et al. (2025) Phenotypic markers misclassify isolates of *Salmonella* Typhimurium as *S. Typhi*, but were correctly identified by whole genome sequencing during a septicemia study in western Kenya. *PLOS global public health*, 5(10), e0004773.

van den Berg OE, et al. (2025) Ongoing increase in autochthonous *Salmonella* Enteritidis infections, the Netherlands, June 2023 to June 2025. *Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin*, 30(30).

Jin Q-Y, et al. (2025) Population structure of *Helicobacter pylori* and antibiotic resistance-associated variants in a high-risk area of gastric cancer. *Journal of clinical microbiology*, 63(5), e0003325.

Shin E, et al. (2025) Emergence of Distinct *Salmonella enterica* Serovar Enteritidis Lineage since 2020, South Korea. *Emerging infectious diseases*, 31(7), 1386.

Smaoui F, et al. (2025) Molecular epidemiology of a multidrug-resistant *Shigella sonnei* outbreak in Tunisia (2022-2023) using whole-genome sequencing. *Microbial genomics*, 11(3).

Tambassi M, et al. (2025) *Salmonella* pathogenicity Island 1 undergoes decay in serovars adapted to swine and poultry. *Microbiology spectrum*, 13(1), e0264324.

Al Fadhli AH, et al. (2025) *Salmonella enterica* serotypes causing infection in Kuwait during 2018-2021, determined by multi-locus sequence typing or whole genome sequencing. *Microbiology spectrum*, 13(5), e0224824.