

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/>

Proper Citation: Enterobase (RRID:SCR_019019)

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

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 [RRID](#) .

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

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

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

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.

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).

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

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.

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.

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.

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.

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.

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

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).

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.

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.

Sroithongkham P, et al. (2025) IncN-R plasmid co-integration contributing to extensive drug resistance in *Escherichia coli* isolated from a canine prostatic abscess. *Microbiology spectrum*, 13(9), e0079025.

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.

Ruzickova M, et al. (2025) The presence of multiple variants of IncF plasmid alleles in a single genome sequence can hinder accurate replicon sequence typing using in silico pMLST tools. *mSystems*, 10(5), e0101024.