

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 access protocol, data or information resource, 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 317 mentions in open access literature.

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

Kahler A, et al. (2026) Large-volume sampling for improved characterization of microbial contamination in agricultural waters: a case study from southeastern U.S. produce farms. *Journal of water and health*, 24(2), 176.

de Larminat J, et al. (2026) Hemolytic Uremic Syndrome Outbreak in Adults and Shiga Toxin-Producing *Escherichia coli* Negative for Locus of Enterocyte Effacement, France, 2025. *Emerging infectious diseases*, 32(4), 592.

Lin SX, et al. (2026) Characteristics of *Escherichia coli* ST131 strains isolated from dogs and cats with urinary tract infections in a teaching hospital in Taiwan. *PloS one*, 21(5), e0350088.

Ruzickova M, et al. (2026) From ecology to evolution: plasmid- and colicin-mediated persistence of antibiotic-resistant *Escherichia coli* in gulls. *mSystems*, 11(2), e0166325.

Korves-Wilm AM, et al. (2026) Antimicrobial resistance of commensal and extended-spectrum ??-lactamase/AmpC-producing *Escherichia coli* in organic meat chicken farms. *Poultry science*, 105(4), 106559.

Ota Y, et al. (2026) Whole-Genome Sequence Analysis of Shiga Toxin-Producing *Escherichia coli* Isolated from Livestock Animals in Ghana. *Microorganisms*, 14(1).

Gaino R, et al. (2026) Global Clones of *Escherichia coli* CTX-M-15/ST10 and CTX-M-65/ST683 Isolated from Brazilian Recreational Freshwater. *Current microbiology*, 83(4).

Liu B, et al. (2026) Prevalence and whole genome sequencing analysis of *Salmonella* isolated from a homebred chicken farm in Jiangsu province. *Frontiers in veterinary science*, 13, 1769606.

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.

Nisbet AM, et al. (2026) The typhoid Mary legacy: Genomic epidemiology uncovers contemporary carriage dynamics across two decades of enteric fever surveillance in England and Wales. *PLoS neglected tropical diseases*, 20(4), e0014177.

Ivanova M, et al. (2026) Human-associated NDM-5-producing multidrug-resistant *Escherichia coli* detected in retail beef and pork in Hungary, 2021. *Frontiers in bioinformatics*, 6, 1793862.

Schiaffino F, et al. (2026) Robust Performance of Culture, qPCR, and Genomic Approaches for *Shigella* Serotyping in a Pediatric Surveillance Cohort. *medRxiv : the preprint server for health sciences*.

Hong Y-P, et al. (2026) Epidemiology and genomics of azithromycin-resistant extensively drug-resistant *Salmonella enterica* serovar Typhimurium in Taiwan. *Antimicrobial agents and chemotherapy*, 70(4), e0133425.

Mbwana JR, et al. (2026) Molecular characterisation of extended-Spectrum-Beta-lactamase-producing *Klebsiella pneumoniae* among children and chicken in the rural Korogwe District, Tanzania. *One health (Amsterdam, Netherlands)*, 23, 101472.

Roer L, et al. (2026) Genomic characterization and sub-clustering of *Escherichia coli* clonal complex 38 reveal host associated genetic markers. *Communications medicine*, 6(1).

Verschuuren TD, et al. (2026) Extended-spectrum beta-lactamase-producing *Escherichia coli* and *Klebsiella pneumoniae* from human carriage, the human-polluted environment, and food: Molecular epidemiology of two prospective cohorts in five European metropolitan areas. *PloS one*, 21(1), e0337346.

Valverde G, et al. (2026) An ancient genome of *Streptococcus pyogenes* from a pre-Columbian Bolivian mummy. *Nature communications*, 17(1).

Guitart-Matas J, et al. (2026) CTX-M variants on the move: Tracking resistance in *Escherichia coli* and *Klebsiella* spp. across humans, livestock and wildlife in Western Uganda. *One health (Amsterdam, Netherlands)*, 22, 101407.

Adriaansens DL, et al. (2026) The role of contaminated eggshells used in poultry feed in a diffuse nationwide outbreak of *Salmonella Enteritidis*, the Netherlands, 2023 to 2025. *Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin*, 31(9).

Krug C, et al. (2026) Nationwide outbreak of Shiga toxin-producing *Escherichia coli* infections associated with frozen pizzas, France, 2022. *Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin*, 31(8).