Resource Summary Report

Generated by NIF on May 4, 2025

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

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

Record Last Update: 20250503T060829+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 192 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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

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).

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

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

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

Rigden DJ, et al. (2025) The 2025 Nucleic Acids Research database issue and the online molecular biology database collection. Nucleic acids research, 53(D1), D1.

Bogaerts B, et al. (2025) Galaxy @ Sciensano: a comprehensive bioinformatics portal for genomics-based microbial typing, characterization, and outbreak detection. BMC genomics,

Malaure C, et al. (2024) Early-Onset Infection Caused by Escherichia coli Sequence Type 1193 in Late Preterm and Full-Term Neonates. Emerging infectious diseases, 30(1), 20.

Recacha E, et al. (2024) Impact of suppression of the SOS response on protein expression in clinical isolates of Escherichia coli under antimicrobial pressure of ciprofloxacin. Frontiers in microbiology, 15, 1379534.

Chudejova K, et al. (2024) Genomic characterization of ST38 NDM-5-producing Escherichia coli isolates from an outbreak in the Czech Republic. Antimicrobial agents and chemotherapy, 68(6), e0013324.

Manikandan R, et al. (2024) First report on whole genome sequencing and comparative genomics of Salmonella enterica serovar Abortusequi isolated from Donkey in India. Scientific reports, 14(1), 23455.

Buczkowska M, et al. (2024) Linking epidemiological and genomic data in cases of enteric fever in England to inform clinical management and public health action. The Journal of antimicrobial chemotherapy, 79(8), 1811.

Du C, et al. (2024) Molecular serotyping of diarrheagenic Escherichia coli with a MeltArray assay reveals distinct correlation between serotype and pathotype. Gut microbes, 16(1), 2401944.

Jacqueline C, et al. (2024) Non-toxigenic cases of Vibrio cholerae in Spain from 2012 to 2022. Microbial genomics, 10(12).

Che M, et al. (2024) Comparison of IncK-blaCMY-2 Plasmids in Extended-Spectrum Cephalosporin-Resistant Escherichia coli Isolated from Poultry and Humans in Denmark, Finland, and Germany. Antibiotics (Basel, Switzerland), 13(4).

Tchesnokova V, et al. (2024) Gut resident Escherichia coli profile predicts the eighteenmonth probability and antimicrobial susceptibility of urinary tract infections. medRxiv: the preprint server for health sciences.

Merrick R, et al. (2024) A genetically related cluster of Salmonella Typhimurium cases in humans associated with ruminant livestock and related food chains, United Kingdom, August 2021-December 2022. Epidemiology and infection, 152, e89.

Ba X, et al. (2024) Global emergence of a hypervirulent carbapenem-resistant Escherichia coli ST410 clone. Nature communications, 15(1), 494.

Yu X-J, et al. (2024) Modulation of Salmonella virulence by a novel SPI-2 injectisome effector that interacts with the dystrophin-associated protein complex. mBio, 15(7), e0112824.