

Resource Summary Report

Generated by [NIF](#) on Sep 19, 2026

Xbase

RRID:SCR_002537

Type: Tool

Proper Citation

Xbase (RRID:SCR_002537)

Resource Information

URL: <http://www.xbase.ac.uk/>

Proper Citation: Xbase (RRID:SCR_002537)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on January 13, 2026. Database aimed at helping laboratory-based bacteriologists make best use of bacterial genome sequence data, with a particular emphasis on comparative genomics. The latest version, xBASE 2.0, now provides comprehensive coverage of all bacterial genomes and features an updated modularized backend and an improved user interface, which includes a taxonomy browser and a powerful full-text search facility. There are 2082 genomes in the database, 1062 complete and 1020 incomplete xSites: * coliBASE - a genome resource for the E. coli research community * campyDB - a genome resource for the Campylobacter research community * MycoDB - a genome resource for the Mycobacteria research community * RhizoDB - a genome resource for the Rhizobia research community * FtBASE - a genome resource for the Francisella research community * ClostriDB - a genome resource for the Clostridiales research community If you use xBASE in your work, please cite: xBASE2: a comprehensive resource for comparative bacterial genomics. Chaudhuri RR, Loman NJ, Snyder LA, Bailey CM, Stekel DJ, Pallen MJ. Nucleic Acids Res. 2008 Jan;36(Database issue):D543-6. Epub 2007 Nov 5. PMID: 17984072 This work is supported by the BBSRC, grant number BBE0111791, awarded to MJP and DJS.

Resource Type: data or information resource, database

Defining Citation: [PMID:17984072](#)

Keywords: prokaryote

Funding: BBSRC

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Xbase

Resource ID: SCR_002537

Alternate IDs: nif-0000-21423

Record Creation Time: 20220129T080214+0000

Record Last Update: 20260912T200126+0000

Ratings and Alerts

No rating or validation information has been found for Xbase.

No alerts have been found for Xbase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Janganan TK, et al. (2020) Architecture and Self-Assembly of Clostridium sporogenes and Clostridium botulinum Spore Surfaces Illustrate a General Protective Strategy across Spore Formers. mSphere, 5(4).

Hornsey M, et al. (2018) Effects of In vivo Emergent Tigecycline Resistance on the Pathogenic Potential of Acinetobacter baumannii. Scientific reports, 8(1), 4234.

Vitko NP, et al. (2016) Expanded Glucose Import Capability Affords Staphylococcus aureus Optimized Glycolytic Flux during Infection. mBio, 7(3).

Sharma G, et al. (2016) Complete Genome Sequence and Comparative Genomics of a Novel Myxobacterium Myxococcus hansupus. PloS one, 11(2), e0148593.

Benjak A, et al. (2016) Genomic and transcriptomic analysis of the streptomycin-dependent Mycobacterium tuberculosis strain 18b. BMC genomics, 17, 190.

Lange A, et al. (2016) Extensive Mobilome-Driven Genome Diversification in Mouse Gut-Associated Bacteroides vulgatus mpk. Genome biology and evolution, 8(4), 1197.

Xu K, et al. (2015) Genome comparison provides molecular insights into the phylogeny of the reassigned new genus Lysinibacillus. BMC genomics, 16(1), 140.

Bianconi I, et al. (2015) Comparative genomics and biological characterization of sequential Pseudomonas aeruginosa isolates from persistent airways infection. BMC genomics, 16, 1105.

Soo RM, et al. (2015) Back from the dead; the curious tale of the predatory cyanobacterium *Vampirovibrio chlorellavorus*. *PeerJ*, 3, e968.

Sant'Anna FH, et al. (2015) Analysis of three genomes within the thermophilic bacterial species *Caldanaerobacter subterraneus* with a focus on carbon monoxide dehydrogenase evolution and hydrolase diversity. *BMC genomics*, 16, 757.

Bertin Y, et al. (2014) The gluconeogenesis pathway is involved in maintenance of enterohaemorrhagic *Escherichia coli* O157:H7 in bovine intestinal content. *PloS one*, 9(6), e98367.

Ogunremi D, et al. (2014) High resolution assembly and characterization of genomes of Canadian isolates of *Salmonella Enteritidis*. *BMC genomics*, 15(1), 713.

Feeney M, et al. (2014) Designing PCR primers painlessly. *Journal of microbiology & biology education*, 15(1), 28.

De la Cruz MA, et al. (2013) A toxin-antitoxin module of *Salmonella* promotes virulence in mice. *PLoS pathogens*, 9(12), e1003827.

McLean JS, et al. (2013) Genome of the pathogen *Porphyromonas gingivalis* recovered from a biofilm in a hospital sink using a high-throughput single-cell genomics platform. *Genome research*, 23(5), 867.

Cota I, et al. (2012) STM2209-STM2208 (*opvAB*): a phase variation locus of *Salmonella enterica* involved in control of O-antigen chain length. *PloS one*, 7(5), e36863.

Halachev MR, et al. (2011) Calculating orthologs in bacteria and Archaea: a divide and conquer approach. *PloS one*, 6(12), e28388.