

Resource Summary Report

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Gubbins

RRID:SCR_016131

Type: Tool

Proper Citation

Gubbins (RRID:SCR_016131)

Resource Information

URL: <https://sanger-pathogens.github.io/gubbins/>

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Description: Software application as an algorithm that iteratively identifies loci containing elevated densities of base substitutions while concurrently constructing a phylogeny based on the putative point mutations outside of these regions. It is used for phylogenetic analysis of genome sequences and generating highly accurate reconstructions under realistic models of short-term bacterial evolution., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: Gubbins: Genealogies Unbiased By recombInations In Nucleotide Sequences

Resource Type: software application, data analysis software, sequence analysis software, software resource, data processing software

Defining Citation: [PMID:25414349](#)

Keywords: rapid, phylogenetic, analysis, large, sample, recombinant, bacteria, whole, genome, sequence, loci, elevated, densities, base, substitution, mutation, outside, region, evolution, alignment

Funding: Wellcome Trust 098051

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Gubbins

Resource ID: SCR_016131

Alternate IDs: OMICS_14386

Alternate URLs: <https://sources.debian.org/src/gubbins/>

License: GNU

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260729T044414+0000

Ratings and Alerts

No rating or validation information has been found for Gubbins.

No alerts have been found for Gubbins.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 602 mentions in open access literature.

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

Sia CM, et al. (2025) Distinct adaptation and epidemiological success of different genotypes within *Salmonella enterica* serovar Dublin. *eLife*, 13.

Michels R, et al. (2025) Clinical relevance of *Staphylococcus saccharolyticus* detection in human samples: a retrospective cohort study. *Infection*, 53(1), 145.

Gawor J, et al. (2025) ICESp1109, a Novel Hybrid Integrative Conjugative Element of Macrolide-Resistant *Streptococcus pyogenes* Serotype M77 Collected Between 2003 and 2017 in Poland. *The Journal of infectious diseases*, 231(3), e521.

Gallichan S, et al. (2025) Optimized methods for the targeted surveillance of extended-spectrum beta-lactamase-producing *Escherichia coli* in human stool. *Microbiology spectrum*, 13(1), e0105824.

van Hal SJ, et al. (2025) *Neisseria meningitidis* Serogroup Y Sequence Type 1466 and Urogenital Infections. *Emerging infectious diseases*, 31(1), 86.

Wu S, et al. (2025) The clinical impact and dissemination of carbapenemase-producing *Enterobacter*: a genome-based study in China. *Microbiology spectrum*, 13(9), e0116625.

Brangsch H, et al. (2025) Comparative genomics of *Mycobacterium avium* subsp. *hominissuis* strains within a group of captive lowland tapirs. *PloS one*, 20(4), e0320499.

Zhang F, et al. (2025) Tracking international and regional dissemination of the KPC/NDM co-producing *Klebsiella pneumoniae*. *Nature communications*, 16(1), 5574.

Lebreton F, et al. (2025) High genetic relatedness between multidrug resistant bacteria before and after the 2022 invasion of Ukraine. *Genome medicine*, 17(1), 74.

Tan Z, et al. (2025) Origin of *Neisseria meningitidis* clonal complex 4821. *Emerging microbes & infections*, 14(1), 2515461.

Bednarczyk L, et al. (2025) Phenotypic and genetic heterogeneity of *Acinetobacter baumannii* in the course of an animal chronic infection. *Microbial genomics*, 11(2).

Rubio M, et al. (2025) Non-tuberculous mycobacteria isolates from patients with chronic pulmonary disease and no epidemiological relationship show sequence clusters through whole-genome sequencing. *Frontiers in microbiology*, 16, 1549030.

Hrala M, et al. (2025) Whole genome sequences of nine *Typhlocyba equigenitalis* strains isolated in the Czech Republic between 1982-2021: Molecular dating suggests a common ancestor at the time of Roman Empire. *PloS one*, 20(1), e0315946.

Ngomtcho SCH, et al. (2025) Continued T12 transmission and shared antibiotic resistance during 2018-2023 *Vibrio cholerae* outbreaks in Cameroon. *PLOS global public health*, 5(2), e0003763.

Hawkey J, et al. (2025) Genomic diversity of clinically relevant bacterial pathogens from an acute care hospital in Suva, Fiji. *JAC-antimicrobial resistance*, 7(3), dlaf058.

Kebenei CK, et al. (2025) Environmental persistence of nontyphoidal *Salmonella* in an urban informal settlement in Nairobi, Kenya. *PloS one*, 20(4), e0321760.

Furstenau TN, et al. (2025) High-throughput targeted amplicon screening tool for characterizing intrahost diversity in *Staphylococcus aureus* directly from sample. *Microbial genomics*, 11(6).

Ross TA, et al. (2025) *Enterococcus lactis* is ecologically and genetically distinct from the major opportunistic pathogen *Enterococcus faecium*. *Microbial genomics*, 11(6).

Anderson T, et al. (2025) Characterization of *Staphylococcus argenteus* in Christchurch, New Zealand, and comparison to global strains. *Access microbiology*, 7(7).

Wang Q, et al. (2025) A strain defined as a novel species in the *Acinetobacter* genus co-harboring chromosomal associated tet(X3) and plasmid associated bla NDM-1 from a beef cattle farm in Hebei, China. *Frontiers in cellular and infection microbiology*, 15, 1594982.