

Resource Summary Report

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

Clonalframe

RRID:SCR_016060

Type: Tool

Proper Citation

Clonalframe (RRID:SCR_016060)

Resource Information

URL: <http://www.xavierdidelot.xtreemhost.com/clonalframe.htm>

Proper Citation: Clonalframe (RRID:SCR_016060)

Description: Software package for the inference of bacterial microevolution using multilocus sequence data. It is used to identify the clonal relationships between the members of a sample, while also estimating the chromosomal position of homologous recombination events that have disrupted the clonal inheritance.

Synonyms: ClonalFrameML

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

Defining Citation: [DOI:10.1534/genetics.106.063305](https://doi.org/10.1534/genetics.106.063305)

Keywords: analysis, sequence, inference, bacteria, microevolution, multilocus, clonal, sample, chromosome, homologous, recombination, disrupted, inheritance, DNA, genome

Funding: Wellcome Trust

Availability: Free, Available for download

Resource Name: Clonalframe

Resource ID: SCR_016060

Alternate IDs: OMICS_14623

Alternate URLs: <https://github.com/xavierdidelot/ClonalFrameML>,
<https://sources.debian.org/src/clonalframe/>

License: GNU General Public License

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260819T044431+0000

Ratings and Alerts

No rating or validation information has been found for Clonalframe.

No alerts have been found for Clonalframe.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 407 mentions in open access literature.

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

She Q, et al. (2026) Rapid dissemination of Staphylococcus aureus in the neonatal intensive care unit is associated with invasive infection. Nature communications, 17(1).

Yuan X, et al. (2026) Genetic Adaptation of Mesorhizobium Symbionts Associated With Caragana in Northern China Deserts. Ecology and evolution, 16(2), e73134.

Ko S, et al. (2026) Genome co-adaptation and the evolution of methicillin resistant Staphylococcus aureus. Genome biology, 27(1).

Zhang T, et al. (2026) Genomic survey uncovers the emergence of a multidrug-resistant dominant lineage in Proteus mirabilis populations. npj antimicrobials and resistance, 4(1).

Yoshizawa S, et al. (2026) One Health genomic insights into environmental and animal reservoirs of community-associated Clostridioides difficile in Japan. Applied and environmental microbiology, 92(6), e0039726.

Yu XA, et al. (2026) Genome-wide sweeps create ecological units in the human gut microbiome. Nature, 655(8121), 202.

Yin Z, et al. (2026) Insights into novel diagnostic assay development, antimicrobial resistance, and pathogenicity in Proteus mirabilis through pan-genome analysis. Applied and environmental microbiology, 92(3), e0189825.

Hariharan J, et al. (2026) Biogeographical and phylogenetic constraints on horizontal gene transfer and genome evolution in Streptomyces. Microbiology spectrum, 14(2), e0295825.

Sharma P, et al. (2026) Putative azithromycin resistance mutations in Chlamydia trachomatis are globally distributed but arose before azithromycin was discovered. Antimicrobial agents and chemotherapy, 70(3), e0170825.

Griffin A, et al. (2026) Transport of the abundant intestinal amino acid glutamine by the enteric pathogen *Campylobacter jejuni* occurs via GutA (Cj0903), an AGCS family transporter. *Microbiology* (Reading, England), 172(1).

Chen D, et al. (2026) Analysis of mobile genetic elements carrying *mcr* genes in clinical *Leclercia* spp. isolates. *BMC microbiology*, 26(1).

Zhang X, et al. (2026) Within-host diversity and phased variant analysis reveal structures and recombination of *Helicobacter pylori* subpopulations in stomach. *GigaScience*, 15.

Fang C, et al. (2026) Fourteen-year genomic surveillance of pediatric invasive *Streptococcus pneumoniae*: genomic and pan-genomic characterization. *BMC microbiology*, 26(1).

Yano H, et al. (2026) Giant linear plasmids in *Mycobacterium avium* harbour a tRNA array unit. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 33(1).

Rouxel C, et al. (2026) Exploration of geographical population structure of *Anaplasma phagocytophilum*: Insights from 12 newly sequenced European human and bovine genome assemblies. *Current research in parasitology & vector-borne diseases*, 9, 100393.

Bull EM, et al. (2026) Pathological convergence of a bacterial plant pathogen is associated with the horizontal transfer of an effector-containing mobile element. *BMC genomics*, 27(1).

Mota-Merlo M, et al. (2026) Diversity of enzymes for exopolysaccharide synthesis in the fructophilic honeybee symbiont *Apilactobacillus kunkeei*. *BMC microbiology*, 26(1), 62.

Monteith W, et al. (2026) Everything is everywhere but *Escherichia coli* adapts to different niches. *The ISME journal*, 20(1).

Webster J, et al. (2026) Buscogeny: A BUSCO leveraged phylogenomic tree builder. *International microbiology : the official journal of the Spanish Society for Microbiology*, 29(2), 255.

Maldonado N, et al. (2026) A matched case-control study on *Escherichia coli* factors contributing to sepsis and septic shock in bacteraemic patients. *Communications medicine*, 6(1), 104.