Resource Summary Report

Generated by <u>dkNET</u> on May 23, 2025

ClonalOrigin

RRID:SCR_016061 Type: Tool

Proper Citation

ClonalOrigin (RRID:SCR_016061)

Resource Information

URL: https://github.com/xavierdidelot/clonalorigin

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Description: Software package for comparative analysis of the sequences of a sample of bacterial genomes in order to reconstruct the recombination events that have taken place in their ancestry.

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

Defining Citation: PMID:20923983, DOI:10.1534/genetics.110.120121

Keywords: comparative, analysis, sequence, bacteria, genome, reconstruct, recombination, events, ancestry, bayesian

Funding: Wellcome Trust WT082930MA; National Science Foundation DBI-0630765; Science Foundation of Ireland 05/FE1/B882

Availability: Free, Available for download

Resource Name: ClonalOrigin

Resource ID: SCR_016061

Alternate IDs: OMICS_18881

Alternate URLs: https://sources.debian.org/src/clonalorigin/

License: GNU General Public Licence

Record Creation Time: 20220129T080328+0000

Record Last Update: 20250523T055145+0000

Ratings and Alerts

No rating or validation information has been found for ClonalOrigin.

No alerts have been found for ClonalOrigin.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Kupczok A, et al. (2018) Rates of Mutation and Recombination in Siphoviridae Phage Genome Evolution over Three Decades. Molecular biology and evolution, 35(5), 1147.

Hoetzinger M, et al. (2017) Genomic divergence and cohesion in a species of pelagic freshwater bacteria. BMC genomics, 18(1), 794.

Lassalle F, et al. (2015) GC-Content evolution in bacterial genomes: the biased gene conversion hypothesis expands. PLoS genetics, 11(2), e1004941.

Revez J, et al. (2014) Genome analysis of Campylobacter jejuni strains isolated from a waterborne outbreak. BMC genomics, 15(1), 768.

Mortimer TD, et al. (2014) Genomic signatures of distributive conjugal transfer among mycobacteria. Genome biology and evolution, 6(9), 2489.

Kivistö RI, et al. (2014) Evolution and comparative genomics of Campylobacter jejuni ST-677 clonal complex. Genome biology and evolution, 6(9), 2424.

Cadillo-Quiroz H, et al. (2012) Patterns of gene flow define species of thermophilic Archaea. PLoS biology, 10(2), e1001265.

Didelot X, et al. (2012) Impact of homologous and non-homologous recombination in the genomic evolution of Escherichia coli. BMC genomics, 13, 256.