

Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

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: data analysis software, data processing software, sequence 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: National Science Foundation DBI-0630765;
Science Foundation of Ireland 05/FE1/B882;
Wellcome Trust WT082930MA

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: 20260912T200018+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 [SPARC SAWG](#) .

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.

Hoetzing 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.

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

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

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

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

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