

Resource Summary Report

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CGAT

RRID:SCR_005550

Type: Tool

Proper Citation

CGAT (RRID:SCR_005550)

Resource Information

URL: <http://mbgd.genome.ad.jp/CGAT/>

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Description: A comparative genome analysis tool for detailed comparison of closely related bacterial-sized genomes. It visualizes precomputed pairwise genome alignments on both dotplot and alignment viewers. Users can add information on this alignment, such as existence of tandem repeats or interspersed repetitive sequences and changes in codon usage bias, to facilitate interpretation of the observed genomic changes. Besides visualization functionalities, it also provides a general framework to process genome-scale alignments using various existing alignment programs. CGAT employs a client-server architecture, which consists of AlignmentViewer (client; a Java application) and DataServer (a set of Perl scripts). The DataServer package contains data construction scripts and CGI scripts and the AlignmentViewer program visualizes the alignment data obtained from the server thorough the HTTP protocol.

Abbreviations: CGAT

Synonyms: CGAT - A Comparative Genome Analysis Tool, Comparative Genome Analysis Tool

Resource Type: software resource

Defining Citation: [PMID:17062155](#)

Keywords: genome, alignment, visualizing, evolution, dotplot

Resource Name: CGAT

Resource ID: SCR_005550

Alternate IDs: OMICS_00930

Record Creation Time: 20220129T080231+0000

Ratings and Alerts

No rating or validation information has been found for CGAT.

No alerts have been found for CGAT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Litschko C, et al. (2025) Transition transferases prime bacterial capsule polymerization. Nature chemical biology, 21(1), 120.

Uchiyama I, et al. (2006) CGAT: a comparative genome analysis tool for visualizing alignments in the analysis of complex evolutionary changes between closely related genomes. BMC bioinformatics, 7, 472.