Resource Summary Report

Generated by NIF on Apr 21, 2025

GASiC

RRID:SCR_006765
Type: Tool

Proper Citation

GASiC (RRID:SCR_006765)

Resource Information

URL: http://sourceforge.net/projects/gasic/

Proper Citation: GASiC (RRID:SCR_006765)

Description: A method to correct read alignment results for the ambiguities imposed by similarities of genomes.

Abbreviations: GASiC

Synonyms: GASiC - Genome Abundance Similarity Correction, Genome Abundance Similarity Correction

Resource Type: software resource

Defining Citation: PMID:22941661, DOI:10.1093/nar/gks803

Keywords: metagenome, genome, sequence, python

Funding:

Availability: BSD License

Resource Name: GASiC

Resource ID: SCR_006765

Alternate IDs: OMICS_01437

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

Record Creation Time: 20220129T080238+0000

Record Last Update: 20250420T014347+0000

Ratings and Alerts

No rating or validation information has been found for GASiC.

No alerts have been found for GASiC.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Zhang X, et al. (2023) Expansion of Betatorquevirus and/or Gammatorquevirus in Patients with Severe Clinical Outcomes of the Liver Diseases. Viruses, 15(8).

Fischer M, et al. (2017) Abundance estimation and differential testing on strain level in metagenomics data. Bioinformatics (Oxford, England), 33(14), i124.

Lindner MS, et al. (2015) Metagenomic profiling of known and unknown microbes with microbeGPS. PloS one, 10(2), e0117711.