

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 8, 2026

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

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: 20260808T185901+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 [SPARC SAWG](#) .

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.