

# Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

## [GASiC](#)

RRID:SCR\_006765

Type: Tool

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### Proper Citation

GASiC (RRID:SCR\_006765)

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### 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:** 20260905T132600+0000

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### Ratings and Alerts

No rating or validation information has been found for GASiC.

No alerts have been found for GASiC.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [RRID](#) .

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.