

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 7, 2026

GASSST

RRID:SCR_004413

Type: Tool

Proper Citation

GASSST (RRID:SCR_004413)

Resource Information

URL: <http://www.irisa.fr/symbiose/projects/gassst/>

Proper Citation: GASSST (RRID:SCR_004413)

Description: Software that finds global alignments of short DNA sequences against large DNA banks. It is able to perform fast gapped alignments and works well for both short and longer reads. It has been tested for reads up to 500bp.

Abbreviations: GASSST

Synonyms: GASSST : Global Alignment Short Sequence Search Tool, Global Alignment Short Sequence Search Tool

Resource Type: software resource

Defining Citation: [PMID:20739310](#)

Keywords: bio.tools

Availability: CeCILL license, v2

Resource Name: GASSST

Resource ID: SCR_004413

Alternate IDs: biotools:gassst, OMICS_00663

Alternate URLs: <https://bio.tools/gassst>

Record Creation Time: 20220129T080224+0000

Record Last Update: 20260905T132519+0000

Ratings and Alerts

No rating or validation information has been found for GASSST.

No alerts have been found for GASSST.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Xuan B, et al. (2021) Draft genome of the Korean smelt *Hypomesus nipponensis* and its transcriptomic responses to heat stress in the liver and muscle. *G3* (Bethesda, Md.), 11(9).

Alser M, et al. (2021) Technology dictates algorithms: recent developments in read alignment. *Genome biology*, 22(1), 249.

Bush SJ, et al. (2021) Generalizable characteristics of false-positive bacterial variant calls. *Microbial genomics*, 7(8).

You I, et al. (2020) Genome-based species-specific primers for rapid identification of six species of *Lactobacillus acidophilus* group using multiplex PCR. *PloS one*, 15(3), e0230550.

Li G, et al. (2020) Genome-wide identification and analysis of highly specific CRISPR/Cas9 editing sites in pepper (*Capsicum annuum* L.). *PloS one*, 15(12), e0244515.

Xu J, et al. (2017) Altered expression profiles of microRNA families during de-etiolation of maize and rice leaves. *BMC research notes*, 10(1), 108.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. *Database : the journal of biological databases and curation*, 2015.