

# Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](#) on Apr 29, 2025

## SOAP3

RRID:SCR\_005502

Type: Tool

### Proper Citation

SOAP3 (RRID:SCR\_005502)

### Resource Information

**URL:** <http://soap.genomics.org.cn/soap3.html>

**Proper Citation:** SOAP3 (RRID:SCR\_005502)

**Description:** THIS RESOURCE IS NO LONGER IN SERVICE. Documented on April 12,2024. GPU-based software for aligning short reads with a reference sequence. It can find all alignments with k mismatches, where k is chosen from 0 to 3.

**Abbreviations:** SOAP3

**Resource Type:** data processing software, software resource, software application

**Defining Citation:** [PMID:22285832](#)

**Keywords:** gpu/cuda, next generation sequencing, alignment, short read, gpu

**Funding:**

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** SOAP3

**Resource ID:** SCR\_005502

**Record Creation Time:** 20220129T080230+0000

**Record Last Update:** 20250429T055005+0000

### Ratings and Alerts

No rating or validation information has been found for SOAP3.

No alerts have been found for SOAP3.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 7 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](#).

Gattoni G, et al. (2022) Genomic study and lipidomic bioassay of *Leeuwenhoekiella parthenopeia*: A novel rare biosphere marine bacterium that inhibits tumor cell viability. *Frontiers in microbiology*, 13, 1090197.

Patil G, et al. (2015) Soybean (*Glycine max*) SWEET gene family: insights through comparative genomics, transcriptome profiling and whole genome re-sequence analysis. *BMC genomics*, 16(1), 520.

Liang C, et al. (2014) Global small RNA analysis in fast-growing *Arabidopsis thaliana* with elevated concentrations of ATP and sugars. *BMC genomics*, 15, 116.

Manconi A, et al. (2014) GPU-BSM: a GPU-based tool to map bisulfite-treated reads. *PloS one*, 9(5), e97277.

Dolled-Filhart MP, et al. (2013) Computational and bioinformatics frameworks for next-generation whole exome and genome sequencing. *TheScientificWorldJournal*, 2013, 730210.

Jia B, et al. (2013) NeSSM: a Next-generation Sequencing Simulator for Metagenomics. *PloS one*, 8(10), e75448.

Kumar S, et al. (2012) SNP Discovery through Next-Generation Sequencing and Its Applications. *International journal of plant genomics*, 2012, 831460.