

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 12, 2026

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 application, software resource

Defining Citation: [PMID:22285832](#)

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

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SOAP3

Resource ID: SCR_005502

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260912T200056+0000

Ratings and Alerts

No rating or validation information has been found for SOAP3.

No alerts have been found for SOAP3.

Data and Source Information

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

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.