

Resource Summary Report

Generated by [NIF](#) on Aug 20, 2026

SOAPfusion

RRID:SCR_000079

Type: Tool

Proper Citation

SOAPfusion (RRID:SCR_000079)

Resource Information

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

Proper Citation: SOAPfusion (RRID:SCR_000079)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on August 22,2022. An open source software tool for fusion discovery with paired-end RNA-Seq reads. The tool follows a different strategy by finding fusions directly and verifying them, differentiating it from all other existing tools by finding the candidate regions and searching for the fusions afterwards.

Abbreviations: SOAPfusion

Resource Type: software resource

Defining Citation: [PMID:24123671](#)

Keywords: software, open source, free, RNA, sequencing, data, computing, research, analysis, rna-seq, candidate regions, bio.tools

Funding: Guangdong Innovative Research Team Program ;
General Research Fund of the Hong Kong Government

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SOAPfusion

Resource ID: SCR_000079

Alternate IDs: OMICS_01358, biotools:soapfusion

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

Record Creation Time: 20220129T080159+0000

Record Last Update: 20260815T182140+0000

Ratings and Alerts

No rating or validation information has been found for SOAPfusion.

No alerts have been found for SOAPfusion.

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 [NIF](#) .

Parada CM, et al. (2025) Growth-dependent concentration gradient of the oscillating Min system in Escherichia coli. The Journal of cell biology, 224(2).

Latysheva NS, et al. (2016) Discovering and understanding oncogenic gene fusions through data intensive computational approaches. Nucleic acids research, 44(10), 4487.

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