

Resource Summary Report

Generated by [NIF](#) on Sep 1, 2026

SOAPaligner/soap2

RRID:SCR_005503

Type: Tool

Proper Citation

SOAPaligner/soap2 (RRID:SCR_005503)

Resource Information

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

Proper Citation: SOAPaligner/soap2 (RRID:SCR_005503)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on April 12,2024. Updated version of SOAP software for short oligonucleotide alignment that features in super fast and accurate alignment for huge amounts of short reads generated by Illumina/Solexa Genome Analyzer., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: SOAPaligner, SOAP2

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

Defining Citation: [PMID:19497933](#), [DOI:10.1093/bioinformatics/btn025](#)

Keywords: next generation sequencing, alignment, short read, oligonucleotide, single-read, pair-end, resequencing, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SOAPaligner/soap2

Resource ID: SCR_005503

Alternate IDs: biotools:soap2

Alternate URLs: <https://bio.tools/soap2>, <https://sources.debian.org/src/soapaligner/>

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260829T182841+0000

Ratings and Alerts

No rating or validation information has been found for SOAPaligner/soap2.

No alerts have been found for SOAPaligner/soap2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 325 mentions in open access literature.

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

Yu L, et al. (2026) Identification of a novel CLCN2 homozygous variant in a man with leukoencephalopathy and infertility: a case report and literature review. *Frontiers in genetics*, 17, 1761205.

Cen C, et al. (2025) Impact of Habitat Transformation on Soil Microbial Diversity and Functionality in Karst Mountainous Parks: A Comparative Study of Remnant Forests and Artificial Green Spaces. *Ecology and evolution*, 15(8), e72021.

Chen H, et al. (2025) Chromosome-level genome assembly of *Pinus massoniana* provides insights into conifer adaptive evolution. *GigaScience*, 14.

Cao Y, et al. (2025) KDM2B and its peptides promote the stem cells from apical papilla mediated nerve injury repair in rats by intervening EZH2 function. *Cell proliferation*, 58(2), e13756.

Xiao J, et al. (2025) Mechanistic insights from metagenomics into the early-stage quality improvement of licorice under partial replacement of chemical by organic fertilizers. *Frontiers in plant science*, 16, 1613771.

Chugh RM, et al. (2025) Modulation of β -Catenin promotes WNT expression in macrophages and mitigates intestinal injury. *Cell communication and signaling : CCS*, 23(1), 78.

Chen H, et al. (2025) Structural characteristics of intestinal microbiota of domestic ducks with different body sizes. *Poultry science*, 104(4), 104930.

Li J, et al. (2024) Genome-wide study of drought tolerance traits in wild jujube. *BMC plant biology*, 24(1), 1000.

Wang Y, et al. (2024) *Stenotrophomonas maltophilia* uses a c-di-GMP module to sense the mammalian body temperature during infection. *PLoS pathogens*, 20(9), e1012533.

Zhang W, et al. (2024) SETMAR Facilitates the Differentiation of Thyroid Cancer by Regulating SMARCA2-Mediated Chromatin Remodeling. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 11(32), e2401712.

Huo Y, et al. (2024) GhCTSF1, a short PPR protein with a conserved role in chloroplast development and photosynthesis, participates in intron splicing of *rpoC1* and *ycf3-2* transcripts in cotton. *Plant communications*, 5(6), 100858.

Zhao S, et al. (2024) The role of halophyte-induced saline fertile islands in soil microbial biogeochemical cycling across arid ecosystems. *Communications biology*, 7(1), 1061.

Li X, et al. (2024) Autographiviridae phage HH109 uses capsular polysaccharide for infection of *Vibrio alginolyticus*. *iScience*, 27(9), 110695.

Fraser R, et al. (2024) Evidence for a Novel X Chromosome in Termites. *Genome biology and evolution*, 16(12).

Liang J, et al. (2024) Metagenomic analysis of core differential microbes between traditional starter and Round-Koji-mechanical starter of Chi-flavor Baijiu. *Frontiers in microbiology*, 15, 1390899.

Cui X, et al. (2024) The histone methyltransferase SUV420H2 regulates brown and beige adipocyte thermogenesis. *JCI insight*, 9(11).

Du HY, et al. (2023) Analysis of the Properties of 44 ABC Transporter Genes from Biocontrol Agent *Trichoderma asperellum* ACCC30536 and Their Responses to Pathogenic *Alternaria alternata* Toxin Stress. *Current issues in molecular biology*, 45(2), 1570.

Liu Z, et al. (2023) Simulated spaceflight-induced cardiac remodeling is modulated by gut microbial-derived trimethylamine N-oxide. *iScience*, 26(12), 108556.

Gattoni G, et al. (2023) Biosynthetic gene profiling and genomic potential of the novel photosynthetic marine bacterium *Roseibaca domitiana*. *Frontiers in microbiology*, 14, 1238779.

Zhang Y, et al. (2023) Genome-Wide Identification of the NRT1 Family Members and Their Expression under Low-Nitrate Conditions in Chinese Cabbage (*Brassica rapa* L. ssp. *pekinensis*). *Plants (Basel, Switzerland)*, 12(22).