

Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

SOAP

RRID:SCR_000689

Type: Tool

Proper Citation

SOAP (RRID:SCR_000689)

Resource Information

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

Proper Citation: SOAP (RRID:SCR_000689)

Description: Software package that provides full solution to next generation sequencing data analysis consisting of an alignment tool (SOAPaligner/soap2), a re-sequencing consensus sequence builder (SOAPSnp), an indel finder (SOAPindel), a structural variation scanner (SOAPSv), a de novo short reads assembler (SOAPdenovo), and a GPU-accelerated alignment tool for aligning short reads with a reference sequence. (SOAP3/GPU)., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: SOAP,

Synonyms: SOAP: short oligonucleotide alignment program, Short Oligonucleotide Analysis Package

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

Defining Citation: [PMID:18227114](#)

Keywords: gene, genetic, genomic, next generation sequencing, alignment, short read, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SOAP

Resource ID: SCR_000689

Alternate IDs: nlx_154652, biotools:soap

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

Record Creation Time: 20220129T080203+0000

Record Last Update: 20260805T044012+0000

Ratings and Alerts

No rating or validation information has been found for SOAP.

No alerts have been found for SOAP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 402 mentions in open access literature.

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

Chen L, et al. (2022) Antimicrobial Biosynthetic Potential and Phylogenetic Analysis of Culturable Bacteria Associated with the Sponge *Ophlitaspongia* sp. from the Yellow Sea, China. *Marine drugs*, 20(10).

Duckett DJ, et al. (2021) Genomic Resources for the North American Water Vole (*Microtus richardsoni*) and the Montane Vole (*Microtus montanus*). *GigaByte* (Hong Kong, China), 2021, gigabyte19.

Mu W, et al. (2020) The draft genome assembly of the critically endangered *Nyssa yunnanensis*, a plant species with extremely small populations endemic to Yunnan Province, China. *GigaByte* (Hong Kong, China), 2020, gigabyte4.

Yang P, et al. (2019) Genome sequence of the Chinese white wax scale insect *Ericerus pela*: the first draft genome for the Coccidae family of scale insects. *GigaScience*, 8(9).

Farré M, et al. (2019) A near-chromosome-scale genome assembly of the gemsbok (*Oryx gazella*): an iconic antelope of the Kalahari desert. *GigaScience*, 8(2).

Mays HL, et al. (2018) Genomic Analysis of Demographic History and Ecological Niche Modeling in the Endangered Sumatran Rhinoceros *Dicerorhinus sumatrensis*. *Current biology : CB*, 28(1), 70.

Wang Z, et al. (2018) Genome-wide analysis of long non-coding RNAs in *Catalpa bungei* and their potential function in floral transition using high-throughput sequencing. *BMC genetics*, 19(1), 86.

Prommer HU, et al. (2018) Chronic kidney disease induces a systemic microangiopathy, tissue hypoxia and dysfunctional angiogenesis. *Scientific reports*, 8(1), 5317.

Ke M, et al. (2018) Leukemia inhibitory factor regulates marmoset induced pluripotent stem cell proliferation via a PI3K/Akt-dependent Tbx3 activation pathway. *International journal of molecular medicine*, 42(1), 131.

Árnason Ú, et al. (2018) Whole-genome sequencing of the blue whale and other rorquals finds signatures for introgressive gene flow. *Science advances*, 4(4), eaap9873.

Hultin E, et al. (2018) Viremia preceding multiple sclerosis: Two nested case-control studies. *Virology*, 520, 21.

Hu Y, et al. (2018) Genome-wide DNA methylation analysis in jejunum of *Sus scrofa* with intrauterine growth restriction. *Molecular genetics and genomics : MGG*, 293(4), 807.

Wang A, et al. (2018) Species Identification of *Conyza bonariensis* Assisted by Chloroplast Genome Sequencing. *Frontiers in genetics*, 9, 374.

Du L, et al. (2018) Identification of candidate chemosensory genes in *Mythimna separata* by transcriptomic analysis. *BMC genomics*, 19(1), 518.

Wang L, et al. (2018) Comparative microRNA-seq Analysis Depicts Candidate miRNAs Involved in Skin Color Differentiation in Red Tilapia. *International journal of molecular sciences*, 19(4).

Li X, et al. (2018) Silkworm Pupa Protein Hydrolysate Induces Mitochondria-Dependent Apoptosis and S Phase Cell Cycle Arrest in Human Gastric Cancer SGC-7901 Cells. *International journal of molecular sciences*, 19(4).

Yi S, et al. (2018) Characterization of Population Genetic Structure of red swamp crayfish, *Procambarus clarkii*, in China. *Scientific reports*, 8(1), 5586.

Chen JY, et al. (2018) Comparative genomics reveals cotton-specific virulence factors in flexible genomic regions in *Verticillium dahliae* and evidence of horizontal gene transfer from *Fusarium*. *The New phytologist*, 217(2), 756.

Liu P, et al. (2018) Next generation sequencing based pathogen analysis in a patient with neurocysticercosis: a case report. *BMC infectious diseases*, 18(1), 113.

Yu Y, et al. (2018) Use of Next Generation Sequencing and Synergy Susceptibility Testing in Diagnosis and Treatment of Carbapenem-Resistant *Klebsiella pneumoniae* Blood Stream Infection. *Case reports in infectious diseases*, 2018, 3295605.