

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 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:** software application, software resource, data processing software

**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:** 20260727T040251+0000

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## Ratings and Alerts

No rating or validation information has been found for SOAP.

No alerts have been found for SOAP.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 402 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [nidm-terms](#).

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.

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.

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).

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

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.

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.