# **Resource Summary Report**

Generated by dkNET on Apr 18, 2025

# SOAP

RRID:SCR\_000689

Type: Tool

## **Proper Citation**

SOAP (RRID:SCR\_000689)

### Resource Information

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

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**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).

Abbreviations: SOAP,

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

Package

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

**Defining Citation: PMID:18227114** 

**Keywords:** gene, genetic, genomic, next generation sequencing, alignment, short read,

bio.tools

**Funding:** 

Availability: Acknowledgement requested

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:** 20250416T063226+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 dkNET.

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.

Ke M, et al. (2018) Leukemia inhibitory factor regulates marmoset induced pluripotent stem cell proliferation via a PI3K/?Akt?dependent Tbx?3 activation pathway. International journal of molecular medicine, 42(1), 131.

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

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.

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.

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

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.

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.

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

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

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).

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).

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.

Huang Z, et al. (2018) Glimepiride treatment in a patient with type A insulin resistance syndrome due to a novel heterozygous missense mutation in the insulin receptor gene. Journal of diabetes investigation, 9(5), 1075.