

Resource Summary Report

Generated by [NIF](#) on Aug 10, 2026

SOAPdenovo-Trans

RRID:SCR_013268

Type: Tool

Proper Citation

SOAPdenovo-Trans (RRID:SCR_013268)

Resource Information

URL: <http://soap.genomics.org.cn/SOAPdenovo-Trans.html>

Proper Citation: SOAPdenovo-Trans (RRID:SCR_013268)

Description: A de novo transcriptome assembler basing on the SOAPdenovo framework, adapt to alternative splicing and different expression level among transcripts., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: SOAPdenovo-Trans

Resource Type: software resource

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SOAPdenovo-Trans

Resource ID: SCR_013268

Alternate IDs: OMICS_01324

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260808T190009+0000

Ratings and Alerts

No rating or validation information has been found for SOAPdenovo-Trans.

No alerts have been found for SOAPdenovo-Trans.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 170 mentions in open access literature.

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

Wu W, et al. (2025) Brochosomes as an antireflective camouflage coating for leafhoppers. *eLife*, 13.

Li D, et al. (2025) Revealing that artificial reproduction promotes increased genetic diversity between generations in *Carpinus putoensis*. *Frontiers in plant science*, 16, 1494694.

Cui J, et al. (2025) High-alcohol-producing *Klebsiella pneumoniae* aggravates lung injury by affecting neutrophils and the airway epithelium. *Cell reports. Medicine*, 6(1), 101886.

He RS, et al. (2025) Construction of the graph genomes of *Takifugu* provides novel insights into the genomic mechanisms of population structure and migratory traits. *BMC biology*, 23(1), 195.

Saldarriaga-Córdoba M, et al. (2024) Unveiling Novel Kunitz- and Waprin-Type Toxins in the *Micrurus mipartitus* Coral Snake Venom Gland: An In Silico Transcriptome Analysis. *Toxins*, 16(5).

Ndotono EW, et al. (2024) Mitogenomic profiling and gut microbial analysis of the newly identified polystyrene-consuming lesser mealworm in Kenya. *Scientific reports*, 14(1), 21370.

Johnston CR, et al. (2024) First draft reference genome and annotation of the alternative oil species *Physaria fendleri*. *G3 (Bethesda, Md.)*, 14(9).

Lindsey CR, et al. (2024) Fossil-calibrated molecular clock data enable reconstruction of steps leading to differentiated multicellularity and anisogamy in the Volvocine algae. *BMC biology*, 22(1), 79.

Hoepner CM, et al. (2024) Proteotranscriptomics of the Most Popular Host Sea Anemone *Entacmaea quadricolor* Reveals Not All Toxin Genes Expressed by Tentacles Are Recruited into Its Venom Arsenal. *Toxins*, 16(2).

Andradi-Brown C, et al. (2024) A novel computational pipeline for var gene expression augments the discovery of changes in the *Plasmodium falciparum* transcriptome during transition from in vivo to short-term in vitro culture. *eLife*, 12.

Ashwood LM, et al. (2023) Genomic, functional and structural analyses elucidate evolutionary innovation within the sea anemone 8 toxin family. *BMC biology*, 21(1), 121.

Xie B, et al. (2022) Dynamic genetic differentiation drives the widespread structural and functional convergent evolution of snake venom proteinaceous toxins. *BMC biology*, 20(1), 4.

Liu H, et al. (2022) The reference genome and organelle genomes of wasabi (*Eutrema japonicum*). *Frontiers in genetics*, 13, 1048264.

Zhang L, et al. (2022) Evolution of toll-like receptor gene family in amphibians. International journal of biological macromolecules, 208, 463.

Lim L, et al. (2022) Analysis of Transcriptome Difference between Blood-Fed and Starved Tropical Bed Bug, *Cimex hemipterus* (F.) (Hemiptera: Cimicidae). Insects, 13(4).

Czy? KB, et al. (2022) Gain or Loss? Evidence for Legume Predisposition to Symbiotic Interactions with Rhizobia via Loss of Pathogen-Resistance-Related Gene Families. International journal of molecular sciences, 23(24).

Salinas-Restrepo C, et al. (2022) Improving the Annotation of the Venom Gland Transcriptome of *Pamphobeteus verdolaga*, Prospecting Novel Bioactive Peptides. Toxins, 14(6).

Schultz DL, et al. (2022) Sex-based de novo transcriptome assemblies of the parasitoid wasp *Encarsia suzannae*, a host of the manipulative heritable symbiont *Cardinium hertigii*. GigaByte (Hong Kong, China), 2022, gigabyte68.

Voshall A, et al. (2021) A consensus-based ensemble approach to improve transcriptome assembly. BMC bioinformatics, 22(1), 513.

Poursalavati A, et al. (2021) Toward understanding of the methoxylated flavonoid biosynthesis pathway in *Dracocephalum kotschy* Boiss. Scientific reports, 11(1), 19549.