

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 18, 2026

[RNAplex](#)

RRID:SCR_002763

Type: Tool

Proper Citation

RNAplex (RRID:SCR_002763)

Resource Information

URL: <http://www.bioinf.uni-leipzig.de/Software/RNAplex/>

Proper Citation: RNAplex (RRID:SCR_002763)

Description: Software tool to rapidly search for short interactions between two long RNAs.

Abbreviations: RNAplex

Resource Type: software resource, source code

Defining Citation: [PMID:21593134](#), [PMID:18434344](#)

Keywords: interaction, rna, bio.tools

Availability: Free, Freely available, Available for download

Resource Name: RNAplex

Resource ID: SCR_002763

Alternate IDs: rid_000107, biotools:rnalex

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

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260912T200313+0000

Ratings and Alerts

No rating or validation information has been found for RNAplex.

No alerts have been found for RNAplex.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 37 mentions in open access literature.

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

Wang Y, et al. (2024) LncRNA NONHSAT227443.1 Confers Esophageal Squamous Cell Carcinoma Chemotherapy Resistance by Activating PI3K/AKT Signaling via Targeting MRTFB. *Technology in cancer research & treatment*, 23, 15330338241274369.

Salabi F, et al. (2024) First transcriptome analysis of the venom glands of the scorpion *Hottentotta zagrosensis* (Scorpions: Buthidae) with focus on venom lipolysis activating peptides. *Frontiers in pharmacology*, 15, 1464648.

Guo F, et al. (2023) Comprehensive analysis of aberrantly expressed circRNAs, mRNAs and lncRNAs in patients with nasopharyngeal carcinoma. *Journal of clinical laboratory analysis*, 37(2), e24836.

Chen C, et al. (2023) Comprehensive analysis of miRNAs, lncRNAs and mRNAs profiles in backfat tissue between Daweizi and Yorkshire pigs. *Animal bioscience*, 36(3), 404.

Chen Y, et al. (2023) Genome-Wide Analysis of microRNAs and Their Target Genes in Dongxiang Wild Rice (*Oryza rufipogon* Griff.) Responding to Salt Stress. *International journal of molecular sciences*, 24(4).

Fu Y, et al. (2023) Integrated microRNA and whole-transcriptome sequencing reveals the involvement of small and long non-coding RNAs in the fiber growth of ramie plant. *BMC genomics*, 24(1), 599.

Yang B, et al. (2022) Evaluation of Early Biomarkers of Atherosclerosis Associated with Polychlorinated Biphenyl Exposure: An in Vitro and in Vivo Study. *Environmental health perspectives*, 130(3), 37011.

Ma L, et al. (2022) Identification and functional prediction of long non-coding RNAs related to skeletal muscle development in Duroc pigs. *Animal bioscience*, 35(10), 1512.

Zhan S, et al. (2022) Transcriptome analysis reveals long non-coding natural antisense transcripts involved in muscle development in fetal goat (*Capra hircus*). *Genomics*, 114(2), 110284.

Lin W, et al. (2022) C/EBP β promotes porcine pre-adipocyte proliferation and differentiation via mediating MSTRG.12568.2/FOXO3 trans-activation for STYX. *Biochimica et biophysica acta. Molecular and cell biology of lipids*, 1867(10), 159206.

Qi L, et al. (2022) Identification of a hippocampal lncRNA-regulating network in a natural aging rat model. *BMC neuroscience*, 23(1), 56.

Du X, et al. (2021) LncRNA landscape analysis identified LncRNA LEF-AS1 as an oncogene that upregulates LEF1 and promotes survival in chronic lymphocytic leukemia. *Leukemia research*, 110, 106706.

Hao Z, et al. (2021) Identification and Functional Analysis of lncRNAs Responsive to Hypoxia in *Eospalax fontanieri*. *Current issues in molecular biology*, 43(3), 1889.

Zhao B, et al. (2021) Comprehensive transcriptome and methylome analysis delineates the biological basis of hair follicle development and wool-related traits in Merino sheep. *BMC biology*, 19(1), 197.

Lv B, et al. (2021) Effects of Salvianolic acid B on RNA expression and co-expression network of lncRNAs in brown adipose tissue of obese mice. *Journal of ethnopharmacology*, 278, 114289.

Bao W, et al. (2021) Comprehensive analysis of the long non-coding RNA expression profile and functional roles in a contrast-induced acute kidney injury rat model. *Experimental and therapeutic medicine*, 22(1), 739.

Wen B, et al. (2021) Transcriptome Analysis Reveals the Potential Role of Long Noncoding RNAs in Regulating Fowl Adenovirus Serotype 4-Induced Apoptosis in Leghorn Male Hepatocellular Cells. *Viruses*, 13(8).

Song L, et al. (2021) Exosomal lncRNA TCONS_00064356 derived from injured alveolar epithelial type II cells affects the biological characteristics of mesenchymal stem cells. *Life sciences*, 278, 119568.

Han CL, et al. (2020) Integrated transcriptome expression profiling reveals a novel lncRNA associated with L-DOPA-induced dyskinesia in a rat model of Parkinson's disease. *Aging*, 12(1), 718.

Huang X, et al. (2020) Genome-wide analysis of differentially expressed mRNAs, lncRNAs, and circRNAs in chicken bursae of Fabricius during infection with very virulent infectious bursal disease virus. *BMC genomics*, 21(1), 724.