

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 2026

## RNAdb

RRID:SCR\_003578

Type: Tool

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### Proper Citation

RNAdb (RRID:SCR\_003578)

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### Resource Information

**URL:** <http://research.imb.uq.edu.au/rnadb>

**Proper Citation:** RNAdb (RRID:SCR\_003578)

**Description:** A comprehensive mammalian noncoding RNA database containing sequences and annotations for tens of thousands of noncoding RNAs. These include a wide range of microRNAs, small nucleolar RNAs and larger mRNA-like ncRNAs. All raw data from the original RNAdb 2.0 database can be downloaded in XML or FASTA format. This website serves to archive the final snapshot of the RNAdb 2.0 datasets for legacy purposes. It will remain active indefinitely.

**Abbreviations:** RNAdb

**Synonyms:** RNAdb 2.0 - A database of mammalian noncoding RNAs

**Resource Type:** data or information resource, database

**Defining Citation:** [PMID:17145715](#)

**Keywords:** non-protein-coding rna, rna

**Resource Name:** RNAdb

**Resource ID:** SCR\_003578

**Alternate IDs:** nif-0000-03417

**Record Creation Time:** 20220129T080219+0000

**Record Last Update:** 20260729T044045+0000

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### Ratings and Alerts

No rating or validation information has been found for RNAdb.

No alerts have been found for RNAdb.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Loganathan T, et al. (2023) Non-coding RNAs in human health and disease: potential function as biomarkers and therapeutic targets. *Functional & integrative genomics*, 23(1), 33.

Zhong G, et al. (2021) Long non-coding RNA AK001903 regulates tumor progression in cervical cancer. *Oncology letters*, 21(2), 77.

Chen S, et al. (2021) The biogenesis and biological function of PIWI-interacting RNA in cancer. *Journal of hematology & oncology*, 14(1), 93.

Tosar JP, et al. (2018) Non-coding RNA fragments account for the majority of annotated piRNAs expressed in somatic non-gonadal tissues. *Communications biology*, 1, 2.

Li Y, et al. (2017) Microarray expression profile analysis of long non-coding RNAs in optineurin E50K mutant transgenic mice. *Molecular medicine reports*, 16(2), 1255.

Yi Z, et al. (2014) Identification of differentially expressed long non-coding RNAs in CD4+ T cells response to latent tuberculosis infection. *The Journal of infection*, 69(6), 558.

Michelhaugh SK, et al. (2011) Mining Affymetrix microarray data for long non-coding RNAs: altered expression in the nucleus accumbens of heroin abusers. *Journal of neurochemistry*, 116(3), 459.

Nordström KJ, et al. (2006) Comprehensive comparisons of the current human, mouse, and rat RefSeq, Ensembl, EST, and FANTOM3 datasets: identification of new human genes with specific tissue expression profile. *Biochemical and biophysical research communications*, 348(3), 1063.

Willingham AT, et al. (2006) TUF love for "junk" DNA. *Cell*, 125(7), 1215.