

Resource Summary Report

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Noncoding RNA database

RRID:SCR_007815

Type: Tool

Proper Citation

Noncoding RNA database (RRID:SCR_007815)

Resource Information

URL: <http://biobases.ibch.poznan.pl/ncRNA/>

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Description: It is intended to provide information on the sequences and functions of transcripts which do not code for proteins, but perform regulatory roles in the cell. Currently, the database includes over 30,000 individual sequences from 99 species of Bacteria, Archaea and Eukaryota. The primary source of sequences included in the database was the GenBank. Additional annotation information for mouse and human ncRNAs was derived from FANTOM3 database and H-inviational Integrated Database of Annotated Human Genes version 3.4, respectively. Genome mapping information was derived from the data available at the UCSC Genome Browser site. The sequences and annotations of small cytoplasmic RNAs from bacteria, for which annotation is lacking in the genome sequences, were derived from the Rfam database. The microRNAs or snoRNAs which were available in previous editions, as well as other housekeeping (infrastructural) RNAs (e.g. rRNA, tRNA, snRNA, SRP RNA) are not included in our database to avoid redundancy with more specialized databases which emerged in recent years.

Abbreviations: ncRNA

Synonyms: Noncoding RNA database

Resource Type: data or information resource, database

Keywords: bio.tools

Resource Name: Noncoding RNA database

Resource ID: SCR_007815

Alternate IDs: nif-0000-03183, biotools:ncrna

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

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260729T044156+0000

Ratings and Alerts

No rating or validation information has been found for Noncoding RNA database.

No alerts have been found for Noncoding RNA database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Zhou L, et al. (2019) Revealing Drug-Target Interactions with Computational Models and Algorithms. *Molecules* (Basel, Switzerland), 24(9).

Han W, et al. (2015) High-Throughput Sequencing Reveals Hypothalamic MicroRNAs as Novel Partners Involved in Timing the Rapid Development of Chicken (*Gallus gallus*) Gonads. *PloS one*, 10(6), e0129738.

Wang H, et al. (2013) Sequence recombination and conservation of *Varroa destructor* virus-1 and deformed wing virus in field collected honey bees (*Apis mellifera*). *PloS one*, 8(9), e74508.

Hou ZC, et al. (2012) Elephant transcriptome provides insights into the evolution of eutherian placentation. *Genome biology and evolution*, 4(5), 713.

Liang H, et al. (2011) Identification and functional characterization of small non-coding RNAs in *Xanthomonas oryzae* pathovar *oryzae*. *BMC genomics*, 12, 87.

Zanca AS, et al. (2010) Identification and expression analysis of microRNAs and targets in the biofuel crop sugarcane. *BMC plant biology*, 10, 260.

Ge X, et al. (2008) Transcriptomic profiling of mature embryo from an elite super-hybrid rice LYP9 and its parental lines. *BMC plant biology*, 8, 114.

Calin GA, et al. (2007) Investigation of microRNA alterations in leukemias and lymphomas. *Methods in enzymology*, 427, 193.

Sevignani C, et al. (2006) Mammalian microRNAs: a small world for fine-tuning gene expression. *Mammalian genome : official journal of the International Mammalian Genome Society*, 17(3), 189.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.

Young TL, et al. (2005) The noncoding RNA taurine upregulated gene 1 is required for differentiation of the murine retina. Current biology : CB, 15(6), 501.

Szymański M, et al. (2002) Beyond the proteome: non-coding regulatory RNAs. Genome biology, 3(5), reviews0005.

French PJ, et al. (2001) Ntab, a novel non-coding RNA abundantly expressed in rat brain. Neuroscience, 108(2), 207.