

Resource Summary Report

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functional RNAdb

RRID:SCR_007664

Type: Tool

Proper Citation

functional RNAdb (RRID:SCR_007664)

Resource Information

URL: <http://www.ncrna.org/frnadb>

Proper Citation: functional RNAdb (RRID:SCR_007664)

Description: fRNAdb is a database of comprehensive non-coding RNA (ncRNA) sequences including known (or previously reported) ncRNAs, which are acquired from other sequence databases, and ncRNA sequences reported by the joint research groups of the Functional RNA Project. It is funded by the New Energy and Industrial Technology Development Organization.

Synonyms: fRNAdb

Resource Type: database, data or information resource

Keywords: functional rna, ncrna, non-coding rna

Funding:

Resource Name: functional RNAdb

Resource ID: SCR_007664

Alternate IDs: nif-0000-02853

Record Creation Time: 20220129T080243+0000

Record Last Update: 20250412T055206+0000

Ratings and Alerts

No rating or validation information has been found for functional RNAdb.

No alerts have been found for functional RNAdb.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 25 mentions in open access literature.

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

Xie S, et al. (2017) An integrated analysis revealed different microRNA-mRNA profiles during skeletal muscle development between Landrace and Lantang pigs. Scientific reports, 7(1), 2516.

Zhang H, et al. (2017) Identification and characterization of L1-specific endo-siRNAs essential for early embryonic development in pig. Oncotarget, 8(14), 23167.

Terasaka N, et al. (2016) A human microRNA precursor binding to folic acid discovered by small RNA transcriptomic SELEX. RNA (New York, N.Y.), 22(12), 1918.

Guo X, et al. (2016) Advances in long noncoding RNAs: identification, structure prediction and function annotation. Briefings in functional genomics, 15(1), 38.

Wang J, et al. (2015) Genetic basis of sRNA quantitative variation analyzed using an experimental population derived from an elite rice hybrid. eLife, 4, e04250.

Luk AC, et al. (2015) GermlncRNA: a unique catalogue of long non-coding RNAs and associated regulations in male germ cell development. Database : the journal of biological databases and curation, 2015, bav044.

Chatterjee A, et al. (2015) A cross comparison of technologies for the detection of microRNAs in clinical FFPE samples of hepatoblastoma patients. Scientific reports, 5, 10438.

Yang L, et al. (2015) Bichir microRNA repertoire suggests a ray-finned fish affinity of Polypteriforme. Gene, 566(2), 242.

Wagner A, et al. (2014) Mutational robustness accelerates the origin of novel RNA phenotypes through phenotypic plasticity. Biophysical journal, 106(4), 955.

Kim JY, et al. (2014) Genome-wide profiling of the microRNA-mRNA regulatory network in skeletal muscle with aging. Aging, 6(7), 524.

- Akkuratov EE, et al. (2014) Bioinformatics analysis of plant orthologous introns: identification of an intronic tRNA-like sequence. *Gene*, 548(1), 81.
- Wang Y, et al. (2014) A survey of overlooked viral infections in biological experiment systems. *PloS one*, 9(8), e105348.
- Shakoor N, et al. (2014) A Sorghum bicolor expression atlas reveals dynamic genotype-specific expression profiles for vegetative tissues of grain, sweet and bioenergy sorghums. *BMC plant biology*, 14, 35.
- Khudayberdiev SA, et al. (2013) A comprehensive characterization of the nuclear microRNA repertoire of post-mitotic neurons. *Frontiers in molecular neuroscience*, 6, 43.
- Tatsumoto S, et al. (2013) Development and characterization of cDNA resources for the common marmoset: one of the experimental primate models. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 20(3), 255.
- Li J, et al. (2013) Long non-coding RNAs and complex human diseases. *International journal of molecular sciences*, 14(9), 18790.
- Wu P, et al. (2013) Roles of long noncoding RNAs in brain development, functional diversification and neurodegenerative diseases. *Brain research bulletin*, 97, 69.
- de Boer FK, et al. (2012) Less can be more: RNA-adapters may enhance coding capacity of replicators. *PloS one*, 7(1), e29952.
- Andersen KL, et al. (2012) Experimental identification and analysis of macronuclear non-coding RNAs from the ciliate *Tetrahymena thermophila*. *Nucleic acids research*, 40(3), 1267.
- Gu W, et al. (2012) CapSeq and CIP-TAP identify Pol II start sites and reveal capped small RNAs as *C. elegans* piRNA precursors. *Cell*, 151(7), 1488.