Resource Summary Report

Generated by NIF on May 16, 2025

NONCODE

RRID:SCR_007822
Type: Tool

Proper Citation

NONCODE (RRID:SCR_007822)

Resource Information

URL: http://www.noncode.org/

Proper Citation: NONCODE (RRID:SCR_007822)

Description: Collection of non-coding RNAs (excluding tRNAs and rRNAs) as an integrated knowledge database. Used to get text information such as class,name,location,related publication,mechanism through which it exerts its function, view figures which show their location in the genome or in a specific DNA fragment, and the regulation elements flanking the ncRNA gene sequences.

Synonyms: NONCODE 2016

Resource Type: data or information resource, database

Defining Citation: PMID:26586799

Keywords: collection, long, non, coding, RNA, integrated, database, FASEB list

Funding: National High Technology Research and Development Program of China ;
Training Program of the Major Research Plan of the National Natural Science Foundation of China ;
National Natural Science Foundation of China ;
Chinese Academy of Science Strategic Project of Leading Science and Technology

Availability: Free, Freely available

Resource Name: NONCODE

Resource ID: SCR_007822

Alternate IDs: nif-0000-03195

Alternate URLs: http://www.bioinfo.org/noncode/

Old URLs: http://bioinfo.ibp.ac.cn/NONCODE/index.htm,
http://www.noncode.org/NONCODERv3/

Record Creation Time: 20220129T080243+0000

Record Last Update: 20250507T060526+0000

Ratings and Alerts

No rating or validation information has been found for NONCODE.

No alerts have been found for NONCODE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 450 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Xu M, et al. (2025) BASAL: a universal mapping algorithm for nucleotide base-conversion sequencing. Nucleic acids research, 53(2).

Liu L, et al. (2025) ncPlantDB: a plant ncRNA database with potential ncPEP information and cell type-specific interaction. Nucleic acids research, 53(D1), D1587.

Rishik S, et al. (2025) miRNATissueAtlas 2025: an update to the uniformly processed and annotated human and mouse non-coding RNA tissue atlas. Nucleic acids research, 53(D1), D129.

Khan W, et al. (2025) Identification of differentially expressed non-coding RNAs in the plasma of women with preterm birth. RNA biology, 22(1), 1.

Vanamamalai VK, et al. (2024) Breed and timepoint-based analysis of chicken harderian gland transcriptome during Newcastle disease virus challenge. Frontiers in molecular biosciences, 11, 1365888.

Xiong W, et al. (2024) Long non-coding RNAs with essential roles in neurodegenerative disorders. Neural regeneration research, 19(6), 1212.

Tan Z, et al. (2024) Mechanism study of lncRNA RMRP regulating esophageal squamous cell carcinoma through miR-580-3p/ATP13A3 axis. Discover oncology, 15(1), 150.

Zhang M, et al. (2024) CBIL-VHPLI: a model for predicting viral-host protein-lncRNA interactions based on machine learning and transfer learning. Scientific reports, 14(1), 17549.

Vanamamalai VK, et al. (2024) Integrative study of chicken lung transcriptome to understand the host immune response during Newcastle disease virus challenge. Frontiers in cellular and infection microbiology, 14, 1368887.

Sahraei S, et al. (2024) Transcriptomic analysis reveals role of lncRNA LOC100257036 to regulate AGAMOUS during cluster compactness of Vitis vinifera cv. sistan yaghooti. Scientific reports, 14(1), 28331.

Pang D, et al. (2024) The Long Non-Coding RNA NR3C2-8:1 Promotes p53-Mediated Apoptosis through the miR-129-5p/USP10 Axis in Amyotrophic Lateral Sclerosis. Molecular neurobiology, 61(10), 7466.

Gou N, et al. (2024) 15-cis-Phytoene Desaturase and 15-cis-Phytoene Synthase Can Catalyze the Synthesis of ?-Carotene and Influence the Color of Apricot Pulp. Foods (Basel, Switzerland), 13(2).

Khoa LTP, et al. (2024) Quiescence enables unrestricted cell fate in naive embryonic stem cells. Nature communications, 15(1), 1721.

Oboh MA, et al. (2024) Transcriptomic analyses of differentially expressed human genes, micro RNAs and long-non-coding RNAs in severe, symptomatic and asymptomatic malaria infection. Scientific reports, 14(1), 16901.

Papazoglou A, et al. (2024) Sex- and region-specific cortical and hippocampal whole genome transcriptome profiles from control and APP/PS1 Alzheimer's disease mice. PloS one, 19(2), e0296959.

Ranjan G, et al. (2024) SCAR-6 elncRNA locus epigenetically regulates PROZ and modulates coagulation and vascular function. EMBO reports, 25(11), 4950.

Chen C, et al. (2024) Investigation of Polymorphisms Induced by the Solo Long Terminal Repeats (Solo-LTRs) in Porcine Endogenous Retroviruses (ERVs). Viruses, 16(11).

Ma M, et al. (2024) Identification and functional analysis of circulating small extracellular vesicle lncRNA signatures in children with fulminant myocarditis. Journal of cellular and molecular medicine, 28(2), e18034.

Xie J, et al. (2024) LncRNA-miRNA interactions prediction based on meta-path similarity and

Gaussian kernel similarity. Journal of cellular and molecular medicine, 28(19), e18590.

Poloni JF, et al. (2024) Localization is the key to action: regulatory peculiarities of lncRNAs. Frontiers in genetics, 15, 1478352.