

Resource Summary Report

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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: database, data or information resource

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 ;
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Resource Name: NONCODE

Resource ID: SCR_007822

Alternate IDs: nif-0000-03195, r3d100012169

Alternate URLs: <http://www.bioinfo.org/noncode/>, <https://doi.org/10.17616/R3194Q>,
<https://doi.org/10.17616/R3194Q>

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

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260803T040513+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 475 mentions in open access literature.

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

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

Jin M, et al. (2025) LncRNA Gm35585 transcriptionally activates the peroxidase EHHADH against diet-induced fatty liver. *Experimental & molecular medicine*, 57(3), 652.

Khilwani B, et al. (2025) Characterization of lncRNA-protein interactions associated with Prostate cancer and Androgen receptors by molecular docking simulations. *Biochemistry and biophysics reports*, 42, 101959.

Kore H, et al. (2025) Identification of Small Open Reading Frame-encoded Proteins in the Human Genome. *Genomics, proteomics & bioinformatics*, 23(1).

Duan R, et al. (2025) Analysis of Non-Coding RNAs and N6-Methyladenosine-Modified Genes in Response to flg22 in Grape Immunity. *Plant biotechnology journal*, 23(12), 5435.

Rasheed MA, et al. (2025) An ensemble strategy for piRNA identification through hybrid moment-based feature modeling. *Scientific reports*, 15(1), 30157.

Huang Y, et al. (2025) RegRNA 3.0: expanding regulatory RNA analysis with new features for motif, interaction, and annotation. *Nucleic acids research*, 53(W1), W485.

Brisot E, et al. (2025) The Non-Coding RNome Landscape in Erythropoiesis: Pathophysiological Implications. *Cells*, 14(24).

Liu H, et al. (2025) RNA-protein interaction prediction using network-guided deep learning. *Communications biology*, 8(1), 247.

Telkar N, et al. (2025) Profiling the cell-specific small non-coding RNA transcriptome of the human placenta. *Scientific reports*, 15(1), 14666.

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.

Sharma E, et al. (2025) RNA sequencing of the lncRNA regulome modulated by *Withania somnifera* in human neuroblastoma SK-N-SH cells. *Molecular biology reports*, 52(1), 890.

Lamberti J, et al. (2025) Non-coding RNA profiling in BRAFV600E-mutant cutaneous melanoma before and after Spry1 depletion. *Scientific data*, 12(1), 1538.

Liu J, et al. (2025) lncRNA-ZFAS1, an Emerging Gate-Keeper in DNA Damage-Dependent Transcriptional Regulation. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(31), e12385.

Riquier S, et al. (2025) RNA-Seq analysis reveals the long noncoding RNAs associated with immunity in wild *Myotis myotis* bats. *BMC genomics*, 26(1), 345.

Yang X, et al. (2025) FEZF1-AS1 drives autophagy-mediated progression of colon cancer and reduces chemosensitivity through inhabiting the PI3K/AKT/mTOR signaling pathway. *Frontiers in genetics*, 16, 1514205.

Xie J, et al. (2025) Comprehensive identification of proteins interacting with long non-coding RNA TUG1 in R-loop regulation. *Journal of biochemistry*, 178(4), 251.

Ajorlou P, et al. (2025) FGD5-AS1 and Th1/Th2 imbalance in the progression of diabetic nephropathy: evidence from bioinformatic and experimental validation. *Clinical and experimental medicine*, 26(1), 38.

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.

Guan J, et al. (2025) Graph-RPI: predicting RNA-protein interactions via graph autoencoder and self-supervised learning strategies. *Briefings in bioinformatics*, 26(3).