

Resource Summary Report

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snoRNABase- a comprehensive database of human H/ACA and C/D box snoRNAs.

RRID:SCR_007939

Type: Tool

Proper Citation

snoRNABase- a comprehensive database of human H/ACA and C/D box snoRNAs.
(RRID:SCR_007939)

Resource Information

URL: <http://www-snorna.biotoul.fr/>

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Description: This is a database of human C/D box and H/ACA modification guide RNAs. Information on a particular snoRNA can be accessed by three ways: 1- On the Search page, just type the name of the snoRNA (for example ACA17) in the Id window. 2- The Find guide RNA contains the sequences of the human ribosomal rRNAs 28S, 18S and 5.8S, and of the snRNAs U1, U2, U4, U5 and U6, with the positions of modified (2'O-ribose methylated or pseudo-uridinylated) nucleotides, and the identity of the corresponding modification guide RNAs. You can click on the name of the relevant snoRNA. 3- By utilizing the link to the UCSC Human Genome Browser.

Synonyms: snoRNABase

Resource Type: database, data or information resource

Keywords: human c/d box, human h/aca, human rna, human snorna

Resource Name: snoRNABase- a comprehensive database of human H/ACA and C/D box snoRNAs.

Resource ID: SCR_007939

Alternate IDs: nif-0000-03476

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260803T040518+0000

Ratings and Alerts

No rating or validation information has been found for snoRNABase- a comprehensive database of human H/ACA and C/D box snoRNAs..

No alerts have been found for snoRNABase- a comprehensive database of human H/ACA and C/D box snoRNAs..

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 59 mentions in open access literature.

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

Ramirez C, et al. (2025) Computational limitations and future needs to unravel the full potential of 2'-O-methylation and C/D box snoRNAs. *RNA biology*, 22(1), 1.

Liu S, et al. (2024) NAP-seq reveals multiple classes of structured noncoding RNAs with regulatory functions. *Nature communications*, 15(1), 2425.

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Zhao D, et al. (2023) The landscape of small nucleolar RNA expression in multiple myeloma is determined by cytogenetic alterations. *Leukemia*, 37(12), 2526.

Zhou F, et al. (2023) A Dynamic rRNA Ribomethylome Drives Stemness in Acute Myeloid Leukemia. *Cancer discovery*, 13(2), 332.

Deschamps-Francoeur G, et al. (2022) The snoGloBe interaction predictor reveals a broad spectrum of C/D snoRNA RNA targets. *Nucleic acids research*, 50(11), 6067.

Estevez M, et al. (2022) Identification and mapping of post-transcriptional modifications on the HIV-1 antisense transcript Ast in human cells. *RNA (New York, N.Y.)*, 28(5), 697.

Wang J, et al. (2022) Plasma tRNA-derived small RNAs signature as a predictive and prognostic biomarker in lung adenocarcinoma. *Cancer cell international*, 22(1), 59.

Nir R, et al. (2022) A systematic dissection of determinants and consequences of snoRNA-guided pseudouridylation of human mRNA. *Nucleic acids research*, 50(9), 4900.

Shome S, et al. (2021) Non-coding RNA in raw and commercially processed milk and putative targets related to growth and immune-response. *BMC genomics*, 22(1), 749.

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Seal RL, et al. (2020) A guide to naming human non-coding RNA genes. The EMBO journal, 39(6), e103777.

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Kaur G, et al. (2020) RNA-Seq profiling of deregulated miRs in CLL and their impact on clinical outcome. Blood cancer journal, 10(1), 6.

Marcel V, et al. (2020) Ribosomal RNA 2'O-methylation as a novel layer of inter-tumour heterogeneity in breast cancer. NAR cancer, 2(4), zcaa036.

Deryusheva S, et al. (2020) "Lost and Found": snoRNA Annotation in the Xenopus Genome and Implications for Evolutionary Studies. Molecular biology and evolution, 37(1), 149.

Tsybulskiy V, et al. (2020) R-chie: a web server and R package for visualizing cis and trans RNA-RNA, RNA-DNA and DNA-DNA interactions. Nucleic acids research, 48(18), e105.

Lu D, et al. (2019) Limited differential expression of miRNAs and other small RNAs in LPS-stimulated human monocytes. PloS one, 14(3), e0214296.

Lee MY, et al. (2019) Distinct Profiles of Cell-Free MicroRNAs in Plasma of Veterans with Post-Traumatic Stress Disorder. Journal of clinical medicine, 8(7).

Wright C, et al. (2019) Comprehensive assessment of multiple biases in small RNA sequencing reveals significant differences in the performance of widely used methods. BMC genomics, 20(1), 513.