

Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 2026

CoRAL - Classification of RNAs by Analysis of Length

RRID:SCR_010828

Type: Tool

Proper Citation

CoRAL - Classification of RNAs by Analysis of Length (RRID:SCR_010828)

Resource Information

URL: <http://wanglab.pcbi.upenn.edu/coral/>

Proper Citation: CoRAL - Classification of RNAs by Analysis of Length (RRID:SCR_010828)

Description: A machine learning software package that can predict the precursor class of small RNAs present in a high-throughput RNA-sequencing dataset. In addition to classification, it also produces information about the features that are most important for discriminating different populations of small non-coding RNAs.

Abbreviations: CoRAL

Synonyms: Classification of RNAs by Analysis of Length

Resource Type: software resource

Defining Citation: [PMID:23700308](#)

Availability: Acknowledgement requested

Resource Name: CoRAL - Classification of RNAs by Analysis of Length

Resource ID: SCR_010828

Alternate IDs: OMICS_00372

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260725T190707+0000

Ratings and Alerts

No rating or validation information has been found for CoRAL - Classification of RNAs by Analysis of Length.

No alerts have been found for CoRAL - Classification of RNAs by Analysis of Length.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Kraft K, et al. (2025) Enhancer activation from transposable elements in extrachromosomal DNA. Nature cell biology, 27(11), 1914.

Zhu K, et al. (2024) CoRAL accurately resolves extrachromosomal DNA genome structures with long-read sequencing. bioRxiv : the preprint server for biology.

Zhu K, et al. (2024) CoRAL accurately resolves extrachromosomal DNA genome structures with long-read sequencing. Genome research, 34(9), 1344.

Jessa S, et al. (2024) FOXR2 targets LHX6+/DLX+ neural lineages to drive CNS neuroblastoma. Cancer research.

Loganathan T, et al. (2023) Non-coding RNAs in human health and disease: potential function as biomarkers and therapeutic targets. Functional & integrative genomics, 23(1), 33.

Han Y, et al. (2016) Integrating Epigenomics into the Understanding of Biomedical Insight. Bioinformatics and biology insights, 10, 267.

Ryvkin P, et al. (2014) Using machine learning and high-throughput RNA sequencing to classify the precursors of small non-coding RNAs. Methods (San Diego, Calif.), 67(1), 28.

Leung YY, et al. (2013) CoRAL: predicting non-coding RNAs from small RNA-sequencing data. Nucleic acids research, 41(14), e137.