

Resource Summary Report

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Modomics

RRID:SCR_007804

Type: Tool

Proper Citation

Modomics (RRID:SCR_007804)

Resource Information

URL: <http://genesilico.pl/modomics/>

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Description: A database of RNA modification pathways. The MODOMICS database contains the following types of items: * Modified Bases : Each modified base consists of a unique chemical structure. They are sorted by the regular RNA bases they originate from. The modified base queuosine is special, since it is synthesized first, and then attached to the ribose by a transglycosylation reaction. The letters in the small modification icons indicate what kingdoms of life the modifications occur in (Eukaryota, Archaea, EuBacteria, Mitochondria). In the download section, the .mol structure files for alare available. * Modification Pathways : Here, we present four pathway graphs showing what modifications emerge from the different bases. The letters in the small modification icons indicate what kingdoms of life the modifications occur in (Eukaryota, Archaea, EuBacteria, Mitochondria). All lines connecting two modifications are clickable, and show details on a particular reaction. * Enzymes : Lists enzymes that catalyse known reactions between modified bases. In the table, several alternatively used names for the enzymes are given, as well as a list of participating proteins. * Sequences : Shows sequences of RNAs with modifications highlighted. Currently, tRNAs and small and large subunit rRNAs are included in MODOMICS. * Publications : exactly that.

Synonyms: Modomics

Resource Type: data or information resource, database

Resource Name: Modomics

Resource ID: SCR_007804

Alternate IDs: nif-0000-03154

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260801T190945+0000

Ratings and Alerts

No rating or validation information has been found for Modomics.

No alerts have been found for Modomics.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 34 mentions in open access literature.

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

Mohl DA, et al. (2025) On the Quest for Biomarkers: A Comprehensive Analysis of Modified Nucleosides in Ovarian Cancer Cell Lines. *Cells*, 14(9).

Tsai YL, et al. (2025) Comprehensive nucleoside analysis of archaeal RNA modification profiles reveals an m7G in the conserved P loop of 23S rRNA. *Cell reports*, 44(4), 115471.

Tsui HT, et al. (2025) tRNA Modification Landscapes in Streptococci: Shared Losses and Clade-Specific Adaptations. *bioRxiv : the preprint server for biology*.

Lucas MC, et al. (2024) Quantitative analysis of tRNA abundance and modifications by nanopore RNA sequencing. *Nature biotechnology*, 42(1), 72.

Love O, et al. (2024) modXNA: A Modular Approach to Parametrization of Modified Nucleic Acids for Use with Amber Force Fields. *Journal of chemical theory and computation*, 20(21), 9354.

Han H, et al. (2024) RNA modification-related genes illuminate prognostic signature and mechanism in esophageal squamous cell carcinoma. *iScience*, 27(3), 109327.

Lang X, et al. (2024) PRMD: an integrated database for plant RNA modifications. *Nucleic acids research*, 52(D1), D1597.

Lei HT, et al. (2023) tModBase: deciphering the landscape of tRNA modifications and their dynamic changes from epitranscriptome data. *Nucleic acids research*, 51(D1), D315.

Tavares RCA, et al. (2023) MRT-ModSeq - Rapid detection of RNA modifications with MarathonRT. *bioRxiv : the preprint server for biology*.

Lampi M, et al. (2023) Bacteriophage Infection of the Marine Bacterium *Shewanella glacialis* Induces Dynamic Changes in tRNA Modifications. *Microorganisms*, 11(2).

Bian P, et al. (2023) Research Advances on Deafness Genes Associated with Mitochondrial tRNA-37 Modifications. *The journal of international advanced otology*, 19(5), 414.

- Fostier CR, et al. (2023) Regulation of the macrolide resistance ABC-F translation factor MsrD. *Nature communications*, 14(1), 3891.
- Wolff P, et al. (2023) Identification of Up47 in three thermophilic archaea, one mesophilic archaeon, and one hyperthermophilic bacterium. *RNA (New York, N.Y.)*, 29(5), 551.
- Abebe JS, et al. (2022) Nanopore-Based Detection of Viral RNA Modifications. *mBio*, 13(3), e0370221.
- Ramakrishnan M, et al. (2022) The plant epitranscriptome: revisiting pseudouridine and 2'-O-methyl RNA modifications. *Plant biotechnology journal*, 20(7), 1241.
- D'Ascenzo L, et al. (2022) Pytheas: a software package for the automated analysis of RNA sequences and modifications via tandem mass spectrometry. *Nature communications*, 13(1), 2424.
- Mailhot O, et al. (2022) Sequence-sensitive elastic network captures dynamical features necessary for miR-125a maturation. *PLoS computational biology*, 18(12), e1010777.
- Albers S, et al. (2021) Repurposing tRNAs for nonsense suppression. *Nature communications*, 12(1), 3850.
- Monticolo F, et al. (2021) Translation machinery reprogramming in programmed cell death in *Saccharomyces cerevisiae*. *Cell death discovery*, 7(1), 17.
- Luo QJ, et al. (2021) RNA structure probing reveals the structural basis of Dicer binding and cleavage. *Nature communications*, 12(1), 3397.