SSU rRNA Modification Database

RRID:SCR_005046
Type: Tool

Proper Citation

SSU rRNA Modification Database (RRID:SCR_005046)

Resource Information

URL: http://library.med.utah.edu/SSUmods/

Proper Citation: SSU rRNA Modification Database (RRID:SCR_005046)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on August 23,2022. In this database data can be searched and browsed. Very few SSU rRNA modification maps are believed to be complete, i.e., with all sites and structures of modified nucleosides unambiguously established. The exception is perhaps E. coli, the subject of investigation for many years; Lingering discrepancies were mostly resolved upon completion of the gene sequence, with the final modified residue (Y-516) placed in 1994. When using the present compilation, the reader should be aware of several major sources of incomplete listings for some organisms. The first is that only portions of the rRNA molecule may have been sequenced, thus giving the (possibly incorrect) appearance in comparative alignments that portions of the rRNA are unmodified. For example in the case of B. stearothermophilus only the 52 3'-terminal nucleotides were sequenced, but which produces an incomplete picture when B. stearothermophilus is aligned with the E. coli map, which is complete. An additional source of incomplete listings lies in data derived from RNase T1 catalogs in the earlier literature. Most such studies were made for the purpose of establishing patterns of phylogenetic relatedness. For this reason most reported catalog sequences purposely omitted short sequences, some of which were undoubtedly modified, because they were of less use in establishing unique "signature" sequences. The extent of this problem in judging modification map completeness is difficult to judge unless a total modification assay (as from HPLC or LC/MS analysis of a complete nucleoside digest) has been carried out in order to determine the identities and approximate numbers of modifications. A third source of incompleteness may result from the method used for detection of modification. For instance pseudouridine residues (which are abundant in eukarya) would not be reported if the 14C-methionine method, resulting in labeled methyl groups, were used. Similarly, maps reporting locations of pseudouridine have in recent years often been based on the modification-reverse transcriptase method of Ofengand, and was thus not intended to detect ribose methylation. Reference to the original citations will usually be required to establish whether the methodology used would have influenced the reported modification distribution. Supported by: National Institute of General Medical Sciences, grant GM29812.

Synonyms: The SSU rRNA Modification Database

Resource Type: data or information resource, database

Defining Citation: PMID:15608163, PMID:11752288

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SSU rRNA Modification Database

Resource ID: SCR_005046

Alternate IDs: nif-0000-03552

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250521T061025+0000

Ratings and Alerts

No rating or validation information has been found for SSU rRNA Modification Database.

No alerts have been found for SSU rRNA Modification Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.