

Resource Summary Report

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RsiteDB- RNA binding sites database

RRID:SCR_007906

Type: Tool

Proper Citation

RsiteDB- RNA binding sites database (RRID:SCR_007906)

Resource Information

URL: <http://bioinfo3d.cs.tau.ac.il/RsiteDB/>

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Description: It is a database that details the interactions of extruded, unpaired RNA nucleotide bases. It presents and classifies the protein binding pockets that accommodate them, and also allows the recognition of similar protein binding patterns involved in interactions with different RNA molecules. Given an unbound structure of a target protein, it allows the prediction of its RNA nucleotide binding sites. The goal of this database is to describe, classify, and predict the interactions between protein binding sites and single-stranded RNA bases. Specifically, RsiteDB describes the protein binding pockets that accommodate extruded nucleotides not involved in RNA base pairing. RsiteDB has two modes of operation. Analysis and classification of protein-RNA interactions: Given a protein-RNA complex RsiteDB analyzes its nucleotide and dinucleotide binding sites. It details the properties of the protein binding pockets that accommodate these extruded nucleotides and presents a list of proteins with similar binding pockets. These proteins may have a totally different overall sequences and structural folds. RsiteDB details and visualizes the features shared by all the binding sites classified to the same cluster. Prediction of RNA dinucleotide binding sites: Given a target, potentially unbound, protein structure we search its surface for regions similar to the created 3-D consensus binding patterns of RNA dinucleotides. The recognized regions are predicted to serve as binding sites. Using leave-one-out tests, the success rate of these predictions was estimated to be about 80%. It must be noted that currently we do not aim to predict whether a protein can bind RNA; rather, given an unbound RNA binding protein, our goal is to predict its binding sites and their modes of interaction. In addition, due to a low number of single nucleotide clusters, currently, we do not use them for the prediction.

Synonyms: RsiteDB, RNA binding sites database

Resource Type: data or information resource, database

Resource Name: RsiteDB- RNA binding sites database

Resource ID: SCR_007906

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260905T133147+0000

Ratings and Alerts

No rating or validation information has been found for RsiteDB- RNA binding sites database.

No alerts have been found for RsiteDB- RNA binding sites database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Miao Z, et al. (2015) A Large-Scale Assessment of Nucleic Acids Binding Site Prediction Programs. PLoS computational biology, 11(12), e1004639.

Kubrycht J, et al. (2012) Virtual interactomics of proteins from biochemical standpoint. Molecular biology international, 2012, 976385.