

Resource Summary Report

Generated by [NIF](#) on Sep 3, 2026

MeRNA

RRID:SCR_007776

Type: Tool

Proper Citation

MeRNA (RRID:SCR_007776)

Resource Information

URL: <http://merna.lbl.gov>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on July 15, 2013. A database of metal ion binding sites in RNA. It provides information that allows the classification of and search for specific metal binding motifs (e.g., tandem G-U pairs, loop E motif, A-platform motif). The RNA binding sites of 23 different metal ions are described, the most common of these being Mg²⁺, Na⁺, Ca²⁺, Cd²⁺ and K⁺. The user can browse the database or search by PDB or NDB identifier, metal ion, binding motif, type of binding, distance cutoff criteria, experimental conditions (NMR, X-ray, etc.), resolution and R-values, and any combination of the aforementioned criteria or author(s) name. The design and development of the database of metal ion binding sites in RNA is part of a research program which focuses on classification and understanding of RNA motif structure, function, tertiary interactions and their relationships. Using the information contained in our database, we will explore approaches to predicting metal ion binding sites in RNA sequence and structure and to identifying new RNA metal ion binding motifs, which will eventually lead to the design of RNA structures with specific metal binding characteristics.

Synonyms: MeRNA

Resource Type: data or information resource, database

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MeRNA

Resource ID: SCR_007776

Alternate IDs: nif-0000-03111

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260829T183004+0000

Ratings and Alerts

No rating or validation information has been found for MeRNA.

No alerts have been found for MeRNA.

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 [NIF](#) .

Zhang S, et al. (2025) Frontoparietal and temporal brain alterations post-cardiopulmonary bypass. iScience, 28(4), 112187.

Zhou Q, et al. (2024) Altered histone acetylation patterns in pancreatic cancer cell lines induce subtype-specific transcriptomic and phenotypical changes. International journal of oncology, 64(3).