

Resource Summary Report

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Nucleic Acid Database

RRID:SCR_003255

Type: Tool

Proper Citation

Nucleic Acid Database (RRID:SCR_003255)

Resource Information

URL: <http://ndbserver.rutgers.edu/>

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Description: A database of three-dimensional structural information about nucleic acids and their complexes. In addition to primary data, it contains derived geometric data, classifications of structures and motifs, standards for describing nucleic acid features, as well as tools and software for the analysis of nucleic acids. A variety of search capabilities are available, as are many different types of reports. NDB maintains the macromolecular Crystallographic Information File (mmCIF).

Abbreviations: NDB

Resource Type: data or information resource, database

Defining Citation: [PMID:24185695](#), [PMID:1384741](#)

Keywords: nucleic acid, dna, nucleopeptide, nucleoprotein, nucleotide, rna, transfection, sequence, structure, function, bio.tools, FASEB list

Funding: NSF ;
DOE ;
NIH

Availability: Free, Available for download, Freely available

Resource Name: Nucleic Acid Database

Resource ID: SCR_003255

Alternate IDs: nif-0000-03184, biotools:ndb, r3d100010415

Alternate URLs: <https://bio.tools/ndb>, <https://doi.org/10.17616/R3531R>

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260729T044045+0000

Ratings and Alerts

No rating or validation information has been found for Nucleic Acid Database.

No alerts have been found for Nucleic Acid Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 36 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Chen L, et al. (2024) AptaDB: a comprehensive database integrating aptamer-target interactions. RNA (New York, N.Y.), 30(3), 189.

Zeng C, et al. (2023) Evaluating native-like structures of RNA-protein complexes through the deep learning method. Nature communications, 14(1), 1060.

Dayie TK, et al. (2022) Isotope Labels Combined with Solution NMR Spectroscopy Make Visible the Invisible Conformations of Small-to-Large RNAs. Chemical reviews, 122(10), 9357.

Paithankar H, et al. (2022) Inherent conformational plasticity in dsRBDs enables interaction with topologically distinct RNAs. Biophysical journal, 121(6), 1038.

Vihinen M, et al. (2021) Systematics for types and effects of RNA variations. RNA biology, 18(4), 481.

Liu G, et al. (2021) A deformation energy model reveals sequence-dependent property of nucleosome positioning. Chromosoma, 130(1), 27.

Gao W, et al. (2020) Deep Learning in Protein Structural Modeling and Design. Patterns (New York, N.Y.), 1(9), 100142.

Zheng J, et al. (2019) RMAalign: an RNA structural alignment tool based on a novel scoring function RMscore. BMC genomics, 20(1), 276.

Burley SK, et al. (2019) RCSB Protein Data Bank: biological macromolecular structures enabling research and education in fundamental biology, biomedicine, biotechnology and energy. Nucleic acids research, 47(D1), D464.

Kleywegt GJ, et al. (2018) Structural biology data archiving - where we are and what lies ahead. FEBS letters, 592(12), 2153.

Zagrovic B, et al. (2018) RNA-protein interactions in an unstructured context. FEBS letters, 592(17), 2901.

Mak CH, et al. (2018) Topological Constraints and Their Conformational Entropic Penalties on RNA Folds. Biophysical journal, 114(9), 2059.

Zhang K, et al. (2018) Structure of the 30??kDa HIV-1 RNA Dimerization Signal by a Hybrid Cryo-EM, NMR, and Molecular Dynamics Approach. Structure (London, England : 1993), 26(3), 490.

Li J, et al. (2018) RNA3DCNN: Local and global quality assessments of RNA 3D structures using 3D deep convolutional neural networks. PLoS computational biology, 14(11), e1006514.

Schlick T, et al. (2017) Opportunities and Challenges in RNA Structural Modeling and Design. Biophysical journal, 113(2), 225.

Huang J, et al. (2016) The Non-Coding RNA Ontology (NCRO): a comprehensive resource for the unification of non-coding RNA biology. Journal of biomedical semantics, 7, 24.

Zeng P, et al. (2016) Rsite2: an efficient computational method to predict the functional sites of noncoding RNAs. Scientific reports, 6, 19016.

Liu G, et al. (2016) A deformation energy-based model for predicting nucleosome dyads and occupancy. Scientific reports, 6, 24133.

Parlea LG, et al. (2016) The RNA 3D Motif Atlas: Computational methods for extraction, organization and evaluation of RNA motifs. Methods (San Diego, Calif.), 103, 99.

Arrigo P, et al. (2015) Effect of Environmental Chemical Stress on Nuclear Noncoding RNA Involved in Epigenetic Control. BioMed research international, 2015, 761703.