

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Amino Acid-Nucleotide Interaction Database

RRID:SCR_004617

Type: Tool

Proper Citation

Amino Acid-Nucleotide Interaction Database (RRID:SCR_004617)

Resource Information

URL: <http://aant.icmb.utexas.edu/>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented September 6, 2016. AANT, the Amino Acid-Nucleotide Interaction Database, contains information derived from all of the protein/nucleic acid complexes with experimentally determined structures in the Protein Data Bank. You can visualize the AANT models using the simple web interface, which relies on the Chime plug-in. You can also download these models for further analysis using publicly available tools for manipulating PDB structures. The software that generates AANT uses HBPLUS to predict hydrogen bond interactions between single bases and single amino acid residues within these complexes. The AANT software uses this information to break down a single PDB structure into scores of individual interactions between either the base, sugar, or phosphate of a nucleotide and the side chain or peptide backbone of an amino acid. The software then superimposes all the interactions between a particular moiety of a nucleotide and a particular moiety of an amino acid residue into a single 3D model, centering on a particular point in the base, sugar, or phosphate. The AANT software then groups geometrically similar interactions into clusters.

Abbreviations: AANT

Resource Type: data or information resource, database, service resource

Defining Citation: [PMID:14681388](#)

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Amino Acid-Nucleotide Interaction Database

Resource ID: SCR_004617

Alternate IDs: nlx_61417

Record Creation Time: 20220129T080225+0000

Record Last Update: 20260905T133125+0000

Ratings and Alerts

No rating or validation information has been found for Amino Acid-Nucleotide Interaction Database.

No alerts have been found for Amino Acid-Nucleotide Interaction 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](#) .

Bazzi A, et al. (2011) Structural insights into the cTAR DNA recognition by the HIV-1 nucleocapsid protein: role of sugar deoxyribose in the binding polarity of NC. Nucleic acids research, 39(9), 3903.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.