

# Resource Summary Report

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## CADB - Conformational Angles DataBase of Proteins

RRID:SCR\_007573

Type: Tool

### Proper Citation

CADB - Conformational Angles DataBase of Proteins (RRID:SCR\_007573)

### Resource Information

**URL:** <http://cluster.physics.iisc.ernet.in/cadb/>

**Proper Citation:** CADB - Conformational Angles DataBase of Proteins (RRID:SCR\_007573)

**Description:** Conformation Angles DataBase is a comprehensive, authoritative and timely knowledge base developed to facilitate retrieval of information related to the conformational angles (main-chain and side-chain) of the amino acid residues present in the non-redundant (both 25% and 90%) data set. The database includes the options of determining the dependency of the conformation angles of a particular residue upon the flanking residues in main-chain, doublet analysis, triplet analysis and analysis of a particular protein structure. It is worth mentioning that for all the options, a user-friendly and convenient Java Graphical User Interface (GUI) has been provided to display the output on the client machine.

**Synonyms:** CADB

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

**Keywords:** amino acid residue, conformation, conformation angle

**Resource Name:** CADB - Conformational Angles DataBase of Proteins

**Resource ID:** SCR\_007573

**Alternate IDs:** nif-0000-02629

**Record Creation Time:** 20220129T080242+0000

**Record Last Update:** 20260821T193824+0000

### Ratings and Alerts

No rating or validation information has been found for CADB - Conformational Angles DataBase of Proteins.

No alerts have been found for CADB - Conformational Angles DataBase of Proteins.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

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