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/

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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: 20260804T043325+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.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at ASWG .

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