Resource Summary Report

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The Protein Coil Library

RRID:SCR_008233
Type: Tool

Proper Citation

The Protein Coil Library (RRID:SCR_008233)

Resource Information

URL: http://www.roselab.jhu.edu/coil/

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Description: The Protein Coil Library is a library of protein structure fragments derived from the Protein Data Bank (PDB). The fragments in this library are those fragments in the PDB that cannot be classified as either alpha-helix or beta-strand. Three-dimensional structures as well as side-chain and backbone torsion angles are stored in the database. The Protein Coil Library allows rapid and comprehensive access to non-alpha-helix and non-beta-strand fragments contained in the Protein Data Bank (PDB). The library contains both sequence and structure information together with calculated torsion angles for both the backbone and side chains. Several search options are implemented, including a query function that uses output from popular PDB-culling servers directly. Additionally, several popular searches are stored and updated for immediate access. The library is a useful tool for exploring conformational propensities, turn motifs, and a recent model of the unfolded state. The library stores the complete torsion angle descriptions for the fragments as well as the three dimensional structures of the fragments themselves. The goal of extracting and pre-calculating this data is to allow for more straightforward investigation of peptide structure without the background of secondary structure elements. In addition to searching by PDB ID, it is possible to download a particular size class, perform a batch search of PDB/chain ID''s, or download precompiled lists of PDB ID''s of interest (PDB Select, etc.). For users interested in browsing the entire database at once or maintaining their own locally-updated copy of the library, FTP access instructions are also provided. The files stored in the coil library FTP site or returned after a batch search are organized heirarchically by PDB ID. This is done to reduce filesystem access times and fascilitate searches using the UNIX find utility. At the lowest directory level in the heirarchy, files are further sorted by fragment length. As a result, the number of files in a particular directory is generally less then 50, yielding relatively fast access on UNIX/Linux filesystems. The heirarchical organization is based on the middle two letters of the PDB ID. For example, hen egg lysozyme, which has a PDB ID of 1HEL, will be located in the directory h/he/. At the final level, fragments of varying sizes are stored in directories that correspond to their fragment length. Again, using lysozyme as an example, any seven-residue fragments, if they exist, will reside in the directory h/he/7/. Similarly, seven-residue fragments from 2HEX and 1HE0 will also be in this location. Sponsors: The Protein Coil Library is funded by Johns Hopkins University.

Synonyms: The Coil Library

Resource Type: data or information resource, database

Keywords: element, fragment, alpha helix, angle, backbone, beta, coil, lysozyme, peptide, protein, protein structure databases, secondary, sequence, side chain, strand, structure, torsion

Funding:

Resource Name: The Protein Coil Library

Resource ID: SCR_008233

Alternate IDs: nif-0000-21338

Record Creation Time: 20220129T080246+0000

Record Last Update: 20250422T055442+0000

Ratings and Alerts

No rating or validation information has been found for The Protein Coil Library.

No alerts have been found for The Protein Coil Library.

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 NIF.

Unal EB, et al. (2010) VitAL: Viterbi algorithm for de novo peptide design. PloS one, 5(6), e10926.