

# Resource Summary Report

Generated by [NIF](#) on Apr 8, 2025

## ccPDB - Compilation and Creation of datasets from PDB

RRID:SCR\_005870

Type: Tool

### Proper Citation

ccPDB - Compilation and Creation of datasets from PDB (RRID:SCR\_005870)

### Resource Information

**URL:** <http://crdd.osdd.net/raghava/ccpdb/>

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**Description:** ccPDB (Compilation and Creation of datasets from PDB) is designed to provide service to scientific community working in the field of function or structure annotation of proteins. This database of datasets is based on Protein Data Bank (PDB), where all datasets were derived from PDB. ccPDB have four modules; i) compilation of datasets, ii) creation of datasets, iii) web services and iv) Important links. \* **Compilation of Datasets:** Datasets at ccPDB can be classified in two categories, i) datasets collected from literature and ii) datasets compiled from PDB. We are in process of collecting PDB datasets from literature and maintaining at ccPDB. We are also requesting community to suggest datasets. In addition, we generate datasets from PDB, these datasets were generated using commonly used standard protocols like non-redundant chains, structures solved at high resolution. \* **Creation of datasets:** This module developed for creating customized datasets where user can create a dataset using his/her conditions from PDB. This module will be useful for those users who wish to create a new dataset as per ones requirement. This module have six steps, which are described in help page. \* **Web Services:** We integrated following web services in ccPDB; i) Analyze of PDB ID service allows user to submit their PDB on around 40 servers from single point, ii) BLAST search allows user to perform BLAST search of their protein against PDB, iii) Structural information service is designed for annotating a protein structure from PDB ID, iv) Search in PDB facilitate user in searching structures in PDB, v) Generate patterns service facility to generate different types of patterns required for machine learning techniques and vi) Download useful information allows user to download various types of information for a given set of proteins (PDB IDs). \* **Important Links:** One of major objectives of this web site is to provide links to web servers related to functional

annotation of proteins. In first phase we have collected and compiled these links in different categories. In future attempt will be made to collect as many links as possible.

**Abbreviations:** ccPDB

**Synonyms:** Compilation and Creation of datasets from PDB, ccPDB - Compilation Creation of datasets from PDB

**Resource Type:** database, data access protocol, web service, data or information resource, software resource

**Defining Citation:** [PMID:22139939](#)

**Keywords:** secondary structure, nucleic acid interaction, ligand interaction, structure, nucleic acid, interaction, ligand, data set, function, protein, annotate, tight-turn, nucleotide interacting residue, metals interacting residue, dna/rna binding residue, bio.tools

**Funding:** OSDD ;  
DBT ;  
Council of Scientific and Industrial Research; New Delhi; India

**Resource Name:** ccPDB - Compilation and Creation of datasets from PDB

**Resource ID:** SCR\_005870

**Alternate IDs:** biotools:ccpdb, nlx\_149416

**Alternate URLs:** <https://bio.tools/ccpdb>

**Record Creation Time:** 20220129T080232+0000

**Record Last Update:** 20250407T215548+0000

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## Ratings and Alerts

No rating or validation information has been found for ccPDB - Compilation and Creation of datasets from PDB.

No alerts have been found for ccPDB - Compilation and Creation of datasets from PDB.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Agrawal P, et al. (2019) ccPDB 2.0: an updated version of datasets created and compiled from Protein Data Bank. Database : the journal of biological databases and curation, 2019.

Singh H, et al. (2014) Evaluation of protein dihedral angle prediction methods. PloS one, 9(8), e105667.