Resource Summary Report

Generated by RRID on Aug 4, 2026

Relibase

RRID:SCR_014888
Type: Tool

Proper Citation

Relibase (RRID:SCR_014888)

Resource Information

URL: http://www.ccdc.cam.ac.uk/free_services/relibase_free

Proper Citation: Relibase (RRID:SCR_014888)

Description: Web-based system for searching and analysing protein-ligand structures in the Protein Data Bank (PDB). The database provides an easily accessible web-browser interface and clear 3D structure visualisation that allows for 3D protein-ligand interaction searches, automatic superimposition and detailed analysis of related binding sites to identify protein flexibility, ligand overlap, and conserved water positions.

Resource Type: data or information resource, software resource, database, web application

Keywords: structural biology, protein, ligand, protein data bank, pdb, visualization, analysis, molecular recognition

Availability: Available to the academic community

Resource Name: Relibase

Resource ID: SCR_014888

Record Creation Time: 20220129T080322+0000

Record Last Update: 20260804T043555+0000

Ratings and Alerts

No rating or validation information has been found for Relibase.

No alerts have been found for Relibase.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Mooibroek TJ, et al. (2019) Intermolecular Non-Covalent Carbon-Bonding Interactions with Methyl Groups: A CSD, PDB and DFT Study. Molecules (Basel, Switzerland), 24(18).

Bauz?? A, et al. (2017) NO3- anions can act as Lewis acid in the solid state. Nature communications, 8, 14522.

Steinkellner G, et al. (2014) Identification of promiscuous ene-reductase activity by mining structural databases using active site constellations. Nature communications, 5, 4150.

Diago LA, et al. (2007) Setting up a large set of protein-ligand PDB complexes for the development and validation of knowledge-based docking algorithms. BMC bioinformatics, 8, 310.

Hillisch A, et al. (2004) Utility of homology models in the drug discovery process. Drug discovery today, 9(15), 659.