

Resource Summary Report

Generated by [Kravitz](#) on Sep 17, 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, database, software resource, 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: 20260912T195822+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

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

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.