

Resource Summary Report

Generated by [dkNET](#) on Sep 2, 2026

PSCDB - Protein Structural Change DataBase

RRID:SCR_006116

Type: Tool

Proper Citation

PSCDB - Protein Structural Change DataBase (RRID:SCR_006116)

Resource Information

URL: <http://idp1.force.cs.is.nagoya-u.ac.jp/pscdb/>

Proper Citation: PSCDB - Protein Structural Change DataBase (RRID:SCR_006116)

Description: Database for protein structural change upon ligand binding that are classified into 7 classes in terms of the ligand binding sites and the location where the dominant motion occurs. # Coupled Domain motions are the domain motions induced upon ligand binding. # Independent Domain motions are the observable domain motions regardless of ligand binding. # Coupled Local motions are the local motions induced upon ligand binding. # Independent Local motions are the observable local motions regardless of ligand binding. # Burying ligand motions are imaginable motions required to hold ligand protein-inside. # No significant motions mean just nothing happen. # Other motions are motions unclassified into domain and local motions. Proteins are flexible molecules that undergo structural changes to function. The Protein Data Bank contains multiple entries for identical proteins determined under different conditions, e.g. with and without a ligand molecule, which provides important information for understanding the structural changes related to protein functions. We gathered 839 protein structural pairs of ligand-free and ligand-bound states from monomeric or homo-dimeric proteins, and constructed the Protein Structural Change DataBase (PSCDB). In the database, we focused on whether the motions were coupled with ligand binding. As a result, the protein structural changes were classified into seven classes, i.e. coupled domain motion (59 structural changes), independent domain motion (70), coupled local motion (125), independent local motion (135), burying ligand motion (104), no significant motion (311) and other type motion (35). PSCDB provides lists of each class. On each entry page, users can view detailed information about the motion, accompanied by a morphing animation of the structural changes.

Abbreviations: PSCDB

Synonyms: Protein Structural Change DataBase (PSCDB), Protein Structural Change DataBase

Resource Type: data or information resource, database, image collection

Defining Citation: [PMID:22080505](#), [PMID:21376729](#)

Keywords: protein, structure, ligand binding, ligand-free, ligand-bound, monomeric protein, homo-dimeric protein, animation, ligand, structural change

Funding: Japanese Ministry of Education Culture Sports Science and Technology MEXT 20370063;

Japanese Ministry of Education Culture Sports Science and Technology MEXT 21107523

Resource Name: PSCDB - Protein Structural Change DataBase

Resource ID: SCR_006116

Alternate IDs: nlx_151591

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260829T182231+0000

Ratings and Alerts

No rating or validation information has been found for PSCDB - Protein Structural Change DataBase.

No alerts have been found for PSCDB - Protein Structural Change DataBase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.