Resource Summary Report

Generated by NIF on Sep 2, 2026

LPDB: Ligand-Protein DataBase

RRID:SCR_008172
Type: Tool

Proper Citation

LPDB: Ligand-Protein DataBase (RRID:SCR_008172)

Resource Information

URL: http://lpdb.chem.lsa.umich.edu/

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Description: The Ligand Protein Database is designed to allow the selection of complexes based on various properties of receptors and ligands for the design and parametrization of new scoring functions or to assess and improve existing ones. Moreover, for each complex, a continuum of ligand positions ranging from the crystallographic position to points on the surface of the protein receptor allows an assessment of the energetic behavior of particular scoring functions. Access to the database is password protected. To obtain access to the LPDB, complete a form, available online, have it signed by your research advisor, and fax the completed form back to the attention of Professor Charles L. Brooks III, (858) 784-8688. There is no fee for academic use of the LPDB. We are currently working out details for licensing to our colleagues in industry. Please contact Professor Brooks to obtain current information on access to the LPDB.

Synonyms: LPDB

Resource Type: data or information resource, database

Keywords: complexes, ligand, protein, receptors

Resource Name: LPDB: Ligand-Protein DataBase

Resource ID: SCR_008172

Alternate IDs: nif-0000-21245

Record Creation Time: 20220129T080245+0000

Record Last Update: 20260829T183017+0000

Ratings and Alerts

No rating or validation information has been found for LPDB: Ligand-Protein DataBase.

No alerts have been found for LPDB: Ligand-Protein DataBase.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Asquith CRM, et al. (2024) Discovery and optimization of narrow spectrum inhibitors of Tousled like kinase 2 (TLK2) using quantitative structure activity relationships. European journal of medicinal chemistry, 271, 116357.

Kaufmann KW, et al. (2010) Practically useful: what the Rosetta protein modeling suite can do for you. Biochemistry, 49(14), 2987.