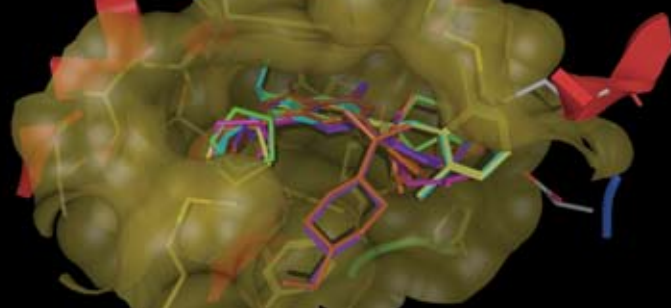


# PSILO



PSILO™ is a database system that provides an easily accessible, consolidated repository for macromolecular and protein-ligand structural information. It offers research organizations a means to systematically track, register and search both experimental and computational macromolecular structural data. A web-based interface facilitates the searching and accessing of public and private structural data.

## Web-based Search

- Flexible and intuitive user interface
- Fast and powerful Google™-like search
- BLAST searches, small molecule similarity and protein family searching
- Track favorite searches, hit lists, email notifications
- PSILO integration into browser search bar
- Download structures as PDB, mmCIF or XML
- Superimpose related protein sites to compare binding modes

## Version Control

- Easy to import data
- Deposit new structures/edit existing structures to create new versions
- Track and maintain structure versions
- Graphical comparisons of structure files
- Increase quality of structures with commenting

## Central Data Repository

- Automatic annotation with PFAM, GO and geometric checks
- Straightforward deposit (bulk deposit via command language)
- Easily linked to proprietary sequence and/or ligand databases
- Automatic updates of the Protein Data Bank (PDB)
- Download search results (MOL, image format, XML, PDB)

## Standard Web Infrastructure

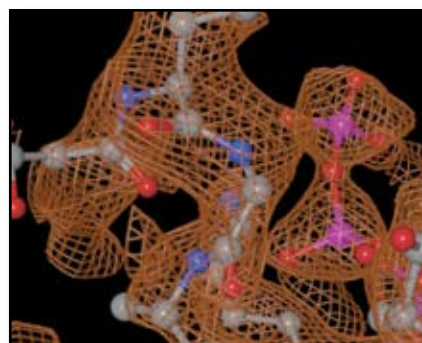
- Works with Oracle® and MySQL®
- HTTP-based Application Programming Interface (API)
- Source code provided
- Simple to maintain and deploy
- Customizable — to work with non-standard PDB files

## Benefits

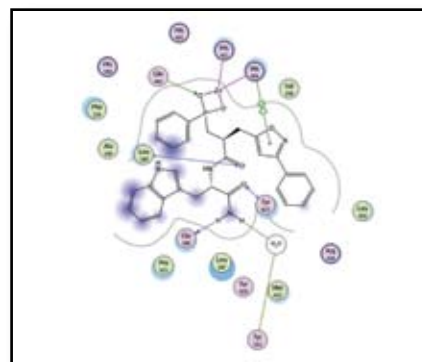
- Collaborative improvements to in-house structures
- Facilitates the dissemination of information to user community
- Flexible integration with external databases
- Safeguards data

PDB	Project	Ligand	Title	Res (Å)	Status
1A68	PDB		Human alpha-thrombin inhibition by Ect-D-Phe-Pro-arg-lys-Orn	2	public
1B2V	PDB		Beta-trypsin complexed with APPU	1.8	public
1G00	PDB		Crystal structure of human alpha-thrombin in complex with benzochinone inhibitor 4	2.04	public
2F4Z	PDB		Toxoplasma gondii atropurin conjugating enzyme (pIsmecan_272)-E2 domain	2.11	public
1GJ8	PDB		Engineering inhibitors highly selective for the S1 sites of Ser190 trypsin-like serine protease drug targets	1.9	public
1SHY	PDB		HIV integrase core domain complexed with tetrahydropyridazinone	1.7	public
1KLU	PDB		Bovine trypsin-inhibitor complex	2.2	public
1LE4	PDB		Structural basis for altered function in the common mutants of human Apolipoprotein-II	2.5	public

Search and Download Structures



View Electron Densities



Visualize Active Site Interactions