

Need help?

Tutorials: pdbe.org/motif/help

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Protein Data Bank in Europe
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The Worldwide Protein Data Bank

The Worldwide Protein Data Bank (wwPDB) consists of four organisations that act as deposition, data-processing and distribution centres for the PDB. The founding members are the Research Collaboratory for Structural Bioinformatics (RCSB, USA), the PDBe team at EMBL-EBI (Europe) and PDBj (Japan). In 2006, the BioMagResBank (BMRB) in the USA joined wwPDB. The mission of the wwPDB is to maintain a single Protein Data Bank archive of macromolecular structural data that is freely and publicly available to the global community.

wwpdb.org

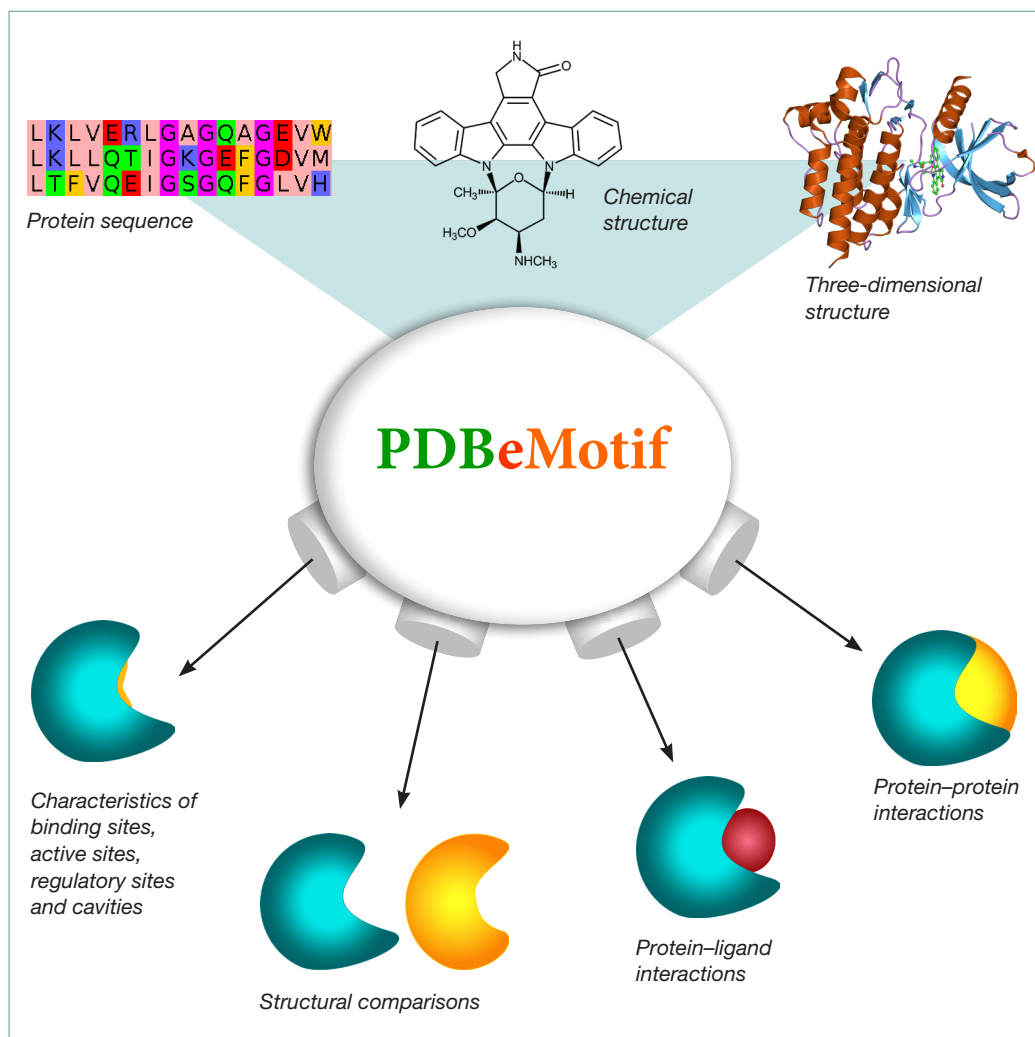
PDBeMotif

pdbe.org/motif

An understanding of the three-dimensional structure of proteins and how they interact with each other and with smaller molecules is important in the fields of biomedical research and drug discovery. Whilst there are well-developed tools and algorithms available to examine and perform comparative analyses on the amino acid sequences of proteins, there are few tools for the study of more complex 3D interactions. Currently, PDBeMotif is the only tool that can execute integrated searches of primary, secondary, tertiary and quaternary structures. This allows users to analyse proteins from the level of single amino acids to the level of interactions between components of protein complexes.

What is PDBeMotif?

PDBeMotif is a fast, integrated and powerful protein structure and interaction search tool that can be used to combine protein sequence, chemical structure and 3D data in a single search. It provides flexible searching, visualisation and statistics on structural data derived from the Protein Data Bank (PDB; see side bar). PDBeMotif covers the entire PDB, including thousands of structures of potential drug targets.



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Types of data in PDBeMotif (protein sequence, chemical structure and three-dimensional structure) and an illustration of how this data can be used to explore protein characteristics.

What can I do with PDBeMotif?

PDBeMotif can be used to examine the characteristics of the binding sites of either single proteins or classes of proteins, such as protein kinases and GPCRs, which are important drug targets. PDBeMotif can also be used to compare the conserved structural features of proteins, either within the same species or across different species. For example, it can highlight a conserved activation loop common to protein kinases, which is important in regulating kinase activity and is marked by conserved DFG (Asp-Phe-Gly) and APE (Ala-Pro-Glu) motifs at the start and end of the loop, respectively.

Analyses carried out in PDBeMotif can be used to predict how modifications to small molecules that bind to the active and/or regulatory sites of proteins can affect their efficacy as drug targets.

PDBeMotif can also be used to investigate:

- the 3D binding of ligands to proteins, in order to determine which ligands bind in a given environment and the frequency of such binding modes;
- protein–protein interactions, for example in determining which bonds occur between a pair of molecules, where they are located and what statistics are associated with them;
- the 3D geometry of protein active sites, regulatory sites and cavities;
- the primary and secondary structure of motifs, including the presence of motifs within other motifs or domains;
- local structural similarities across different protein families;
- the frequency that a particular ligand, amino acid or nucleotide interacts with other residues (i.e. ligands, amino acids, nucleotides), or with PROSITE motifs, Pfam domains and small 3D structural motifs.

Retrieving data from PDBeMotif

- Using PDBeMotif's sophisticated web interface, you can search PDB entries by combining one or more criteria such as: single molecules or their chemical substructures, sequences of amino acids, sequence motifs, 3D structural motifs, sequences of dihedral angles (ϕ/ψ), sequences of secondary structure elements (helices, strands and loops) and text searches.
- Selected search results can be aligned in 3D for closer examination using various interactive 3D viewers. Full structural representation and binding statistics of ligands and motifs are provided in tabular and graph formats.
- From PDB entry pages, you can construct a search to identify other proteins with similar highlighted features, such as those in 3D cavities. Further searches can be executed on the new result set, a process that can be repeated many times. ●

Further reading

Golovin, A. & Henrick, K. Chemical Substructure Search in SQL. *J. Chem. Inf. Model*, 49, 22-27 (2009)

Golovin, A. & Henrick, K. MSDmotif: exploring protein sites and motifs. *BMC Bioinformatics*, 312 (2008)

Golovin, A. *et al.* MSDsite: A Database Search and Retrieval System for the Analysis and Viewing of Bound Ligands and Active Sites. *Proteins: Structure, Function, and Bioinformatics*, 58, 190-199 (2005)

About PDBeMotif

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