[P42] sc-PDB: a 3D-database of druggable binding sites

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The Protein Data Bank (PDB) is the international public archive of experimental three-dimensional structures of biopolymers, mainly proteins. Since 2002, we have extracted from the PDB all druggable binding sites in complex with a small ligand (PM < 1 000). Standardized processes have been developed to correct the structures of the protein, its ligand, and their binding site (e.g., definition of atomic formal charges, covalent bonding between the multiple residues forming a single molecular entity, or addition of hydrogen). Annotation made for each entry characterized the protein function, the ligand physico-chemical properties and non-bonded intermolecular interactions in the complex.

Structure files and annotations constitute the sc-PDB database, which is freely available at http://cheminfo.u-strasbg.fr/scPDB.[1]

The sc-PDB is annually updated and its content is regularly improved. In 2011, we have provided comparison of protein binding site, thereby allowing the clustering of the different sites observed for a given protein, as well as the retrieval of all sites similar to a query site.[2] In 2012, all the water molecules with at least two hydrogenn bonds to the binding site were included in the protein. In addition, binding sites druggability was assessed based on structural and physico-chemical descriptors.[3] The next release (July 2014) will contain the following new features:

−query for complexes with similar pattern of ligand-protein interactions[4]

−identification of mutated residues in binding sites

−consistent numbering between protein residues in cluster-aligned files and corresponding residues in UNIPROT protein entry

The 2014 release describes 9 427 non-redundant complexes, which involve 5 624 different ligands and 2 822 different proteins.

[1] Kellenberger, E.; Muller, P.; Schalon, C.; Bret, G.; Foata, N.; Rognan, D. J. Chem. Inf. Model., 46 (2006), (2), 717-727.

[2] Meslamani, J.; Rognan, D.; Kellenberger, E., Bioinformatics, 27 (2011), (9), 1324-1326.

[3] Desaphy, J.; Azdimousa, K.; Kellenberger, E.; Rognan, D., J. Chem. Inf. Model. 52 (2012), (8), 2287-99.

[4] Desaphy, J.; Raimbaud, E.; Ducrot, P.; Rognan, D., J. Chem. Inf. Model. 53 (2013), (3), 623-637