Structure evaluation and selection criteria for software development and SBDD

A simple set of guidelines for analyzing protein-ligand structures and selecting the best structure to use for structure-based drug design (SBDD). This table is derived from a review in Drug Discovery Today, G. L. Warren, et al., Essential considerations for using protein-ligand structures in drug discovery. Drug Discovery Today, 17, 1270 (2012)

Global

– Use coordinate error to select the best structure (< 0.7)

– Experimental data is available

– The reported Rfree < 0.45 when resolution ≤ 3.5 Å

– The reported difference between R and Rfree ≤ 0.05

Active site

– Identify ligand atoms where there are crystal packing atoms within 6 Å

– The ligand must have at least partial density (check visually or RSCC > 0.80)

– All ligand and active site atoms with occupancy <1.0 are identified

– Active site atoms with partial density are identified

– Alternate conformations for ligand and active site atoms are identified

– Identify covalent ligands

*Goto, J. et al. (2004) Ph4Dock: pharmacophore-based protein–ligand docking. J. Med. Chem. 47, 6804–6811

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