A SIFt-guided approach to docking restrains assignment. An application to Virtual Screening.

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Docking experiments play a crucial role in a Virtual Screening (VS) cascade we designed [1]. However, unrestrained docking may result in highly scored ligand conformations within active site which are significantly different from the biochemically confirmed binding mode.

Docking restrains allow enforcing the correct ligand conformation by indulging the ligand positions which meet predefined requirements. In research presented here we focus on positional restrains, where specific functional groups of ligand must neighbour selected residues' sidechains. To achieve this, the previously developed a tool, based on **S**tructural **I**nteraction **F**igerprin**t**s (SIFt) profiles [2]. The tool can be used to quantify amino acids participating in binding the ligand and to select the most frequent interactions. The list of the important residues is the basis for assigning complementary SMARTS patterns used for prescreening the ligands and then creating positional restrains the automatic way.

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