MED-SuMo: from target based drug design to innovative cheminformatics tools

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The discovery of new chemical entities follows a number of critical steps especially in the pre-clinical phase which decides eventually the destiny of a given molecule in the industrial pipeline. Nowadays, "*in silico*" drug design fully participates in making these decisive choices and is basically an interdisciplinary field: (1) bioinformatics which are all DNA/protein sequences software based, (2) chemoinformatics more devoted to register/characterize natural and synthetic molecules for medicinal chemists, and (3) molecular modeling to build powerful predictive 3D models.

MED-SuMo, a target based drug design tool, offers a procedure to adequately characterize the protein binding site. This tool is based on the identification of local shape and chemical similarities in the target binding site with other proteins (with their co-crystallized ligands). MED-SuMo uses the binding site of the target as a query to search either the whole Protein Data Bank (or any corporate protein structure databank) for all the binding sites that display a local match with the query. This precious information can then be used to identify which residues of the binding site are potentially important for ligand binding affinity and selectivity. The presence of multiple matches for a given residue (or type of residues, e.g acidic or basic) whose interaction with a ligand fragment is confirmed can be intimately associated to a potential affinity. Similarly, it is possible to identify the residues that are specific to the target or that fold in a specific way, thus indicating potential spots to target for selectivity. Such information can be used in several key steps of drug design: (1) fragment based drug design, (2) docking (3) and design of structure-based 3D pharmacophores. I will present MED-SuMo and the recent interface development concerning the co-crystallized ligands. I will include a demo at the end of the talk.