Hybridization of ligands as a way of generating combinatorial libraries of drug candidates

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Computational methods and its application in the process of drug design is a central theme in chemoinformatics. Virtual screening techniques are widely used in the process of searching drug candidates and thanks to them we can evaluate large libraries of chemical compounds. VS methods are divided into two main groups – those that rely on knowledge about the protein target (structure-based VS) and those ones that are based on the information of known actives (ligand-based VS). [1,2]

Structure databases that undergo the process of virtual screening may come from commercially available resources or they may be generated in combinatorial way. We generated a combinatorial library of 5-HT6 ligands by hybridization of known actives using BREED technique. [3] Then the multistep virtual screening protocol (Lipinski's Rule of Five, Veber's Filter, Physicochemical property filter, ADMET filter, Pharmacophore filter, Docking) was applied and the best compounds were selected and ordered to determine their affinity towards 5-HT6 receptor.[4]

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