activity (presented by pargyline in 10μM conc.) were chosen for further investigation. For 13 compounds IC_{50} and K_i values were experimentally calculated. IC_{50} values ranged between 45nM and 8300nM.
Conclusions: From the large group of investigated compounds we managed to find xanthine derivatives that exhibit inhibition activity towards MAO-B. The structure-activity relationship can be helpful in drug development in this group of compounds.
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Pharmacophore modeling of UDP-N-acetylmuramoylalanine glutamate ligase inhibitors – methodology and application for virtual screening procedure

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Background: UDP-N-acetylmuramoylalanine glutamate ligase (MurD) is one of the most promising biological targets in development of next-generation of anti-bacterial compounds. Along with other members of the amide ligases (MurC-F), MurD inhibits the synthesis of peptidoglycan (PG) – key bacterial metabolite, crucial for bacterial growth. Anti-bacterial action of MurC-F is indeed very promiscuous, given that this metabolic pathway is common for bacteria and inhibitors of a single enzyme may be multipotent antibacterial agents.
Material and methods: Due to the increasing numbers of published MurD inhibitors (87 structures in February 2016) some standard *in silico* approaches may be utilized for the discovery of new ligands. Here we have used pharmacophore modeling pipeline, as described before. All known MurD inhibitors were hierarchically clustered using Canvas with manual refinements to ensure proper chemotypes classification. Multiple hypotheses were developed for each cluster, employing the previously utilized approach. After application of DUD-like test set, one model per cluster was selected (according to Yourden's statistics value) to form the linear combination of pharmacophore models, i.e. the first, general pharmacophore hypothesis of MurD inhibitors.
Results and conclusions: This combination was applied as one of the steps in the virtual screening protocol for reducing space of ca. 8M of compounds from seven commercial databases and 100K compounds from virtual library of easily synthetically accessible compounds.
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