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Machine Learning Method as a Tool for Searching New 5-HT$_6$ Ligands in Fingerprint-Based Consensus Experiment.

Sabina Smusz [1,2], *Rafał Kurczab* [1], *Andrzej J. Bojarski* [1]

[1] *Department of Medicinal Chemistry, Institute of Pharmacology, Polish Academy of Sciences, Smętna 12, Kraków, Poland*
[2] *Faculty of Chemistry, Jagiellonian University, Ingardena 3, Kraków, Poland*
e-mail: smusz@if-pan.krakow.pl

The 5-HT$_6$ receptor is a seven transmembrane domain protein, positively coupled to adenylyl cyclase via G$_s$ protein, located almost exclusively in the central nervous system. It seems to be involved in regulation of glutamatergic and cholinergic neuronal activity and is considered to play role in learning and memory, mood control and feeding behaviour [1]. Therefore, it has become a widely explored target for treating cognitive dysfunctions associated with many neuropsychiatric disorders, such as Alzheimer's disease and schizophrenia, depression and anxiety [2].
A number of computational techniques are used in the challenging problem of finding new drug candidates. Among various approaches applied in drug discovery campaigns, virtual screening tools (both ligand- and structure based) can be distinguished [3]. They cover an automatic evaluation of chemical compound libraries in order to identify structures with potential activity towards desired target protein.
Machine learning belong to the group of widely explored methodologies in the field of virtual screening. Major tasks of this artificial intelligence tools are connected with the assignment of objects (in our case: molecules) into classes (here: active or inactive) [4].
In our research, we applied Sequential Minimal Optimization algorithm in the search of new 5-HT$_6$ ligands from the Enamine database [5]. Three different fingerprints were used for molecules representation and consensus prediction was taken as the final answer. Compounds selected according to this procedure are going to be ordered and they will undergo biological evaluation.

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