

## **The Development and Validation of a Novel Virtual Screening Cascade Protocol to Identify Potential Serotonin 5-HT<sub>7</sub>R Antagonists.**

Rafał Kurczab<sup>a</sup>, Mateusz Nowak<sup>a</sup>, Małgorzata Jarończyk<sup>b</sup>, Zdzisław Chilmonczyk<sup>b</sup>

<sup>a</sup> *Department of Medicinal Chemistry, Institute of Pharmacology,  
Polish Academy of Sciences, Smętna 12, 31-343 Kraków*

<sup>b</sup> *National Institute of Medicines, Chelmska 30/34, 00-725 Warsaw*  
e-mail: [rkurczab@gmail.com](mailto:rkurczab@gmail.com)

The 5-HT<sub>7</sub> receptor is a well known target for the treatment of CNS disorders. In attempt to identify new potential ligands for this receptor, we performed a multistep virtual screening (VS) based on two-dimensional (2D) pharmacophore similarity, physico-chemical scalar descriptors, ADME/Tox filter, three-dimensional (3D) pharmacophore searches and docking protocol. The six chemical classes of 5-HT<sub>7</sub>R antagonists [1] were used as a query structures in double-path virtual screening scheme. The Enamine screening database [2] consisting of approximately 730 000 commercially available compounds was adopted and used in this study. The binding mode of selected virtual hits are shown in comparison to that of known antagonists [1].

This study was partly supported by the Network "Synthesis, structure and therapeutic properties of compounds and organic substances" coordinated by the Institute of Organic Chemistry Polish Academy of Sciences.

[1] Kołaczkowski M., Nowak M., Pawłowski M., Bojarski A. J.: *J. Med. Chem.* 49 (2006), 6732.

[2] <http://www.enamine.net/>