# Abstract

Melatonin (N-Acetyl-5-methoxytryptamine) is the main hormone synthesized by the vertebrate pineal gland. In mammals, the melatonin is known to play an important role in the regulation of physiological and neuroendocrine functions, such as synchronization of seasonal reproductive rhythms, and entrainment of circadian cycles.

MT2 receptor is a G-protein coupled receptor (GPCR) and its activation modulates a wide range of intracellular messengers, e.g. cAMP, cGMP, or $Ca^{2+}$. All GPCRs are thought to share the basic structural organization characterized by bundle of seven putative transmembrane domains that form a ligand-binding site. Despite growing collection of experimental data, in most cases the actual arrangement of transmembrane domains and their conformational changes induced by the ligand-binding are not completely understood. Recently published high-resolution crystal structure of bovine rhodopsin (Palczewski *et al.* (2000) [1]) enabled homology modelling of other GPCR structures, such as human melatonin MT2 receptor.

Main goals of this diploma thesis are: (1) to create a homology model of human melatonin MT2 receptor; (2) to select residues possibly involved in the ligand binding for site-directed mutagenesis; (3) to perform flexible docking of melatonin molecule into the predicted ligand-binding site; (4) to compare obtained results with experimental data based on site-directed mutagenesis.