

## **Abstract**

In the first part of the thesis we investigated the origin of selected surface CD markers of human, namely CD19, CD20, CD21, CD24, CD27 and CD38 molecules. In addition, nucleotide and amino acid sequences of these molecules were compared using *in silico* approach. Bioinformatic databases of sequences of selected molecules at DNA, mRNA and protein level, such as GeneBank, NCBI BLAST, Homologene and OrthoDB, have been used. The intent was to identify at the domain level the first organism in which it is possible to find the searched molecule. At the N-terminal domain of the CD38 of birds, a sequence showing significant similarity to the archaebacterial flagellin domain was found. This flagellin sequence in the CD38 avian molecule is located in the region of transmembrane domain, indicating that the occurrence of this sequence might be related to the formation of the transmembrane domain. The approach used here could be implemented in comparative hybridization studies as a tool in the preparatory non-laboratory phase of the research of the presence of paralogs and orthologs in phylogenetically old species.

**Keywords:** CD marker, immunocyte, B lymphocyte, innate and adaptive immunity, sequence database, amino acid, nucleotide