Influenza is a contagious disease and is a serious threat for human life. Moreover, it has significant economic consequence. World Health Organization (WHO) estimates that each year, seasonal influenza affects 5-10% of the world's population resulting 250 000 – 500 000 deaths. WHO indicates that during 2003 in United States, there were 24.7 million cases of influenza, 31.4 million patients visits, over 334 000 hospitalizations and approximately 41 000 deaths. The economic cost of it was estimated at approximately 87.1 $ billion.

The disease is caused by influenza virus, which was isolated for the first time in 1933 by researchers from National Institute for Medical Research in London. Since then, intensive studies on influenza virus have been started. It is related to expand the specific knowledge about mechanisms of the virus life cycle to design new, more effective vaccines and to search for new effective treatment. It leads to decrease the morbidity and mortality and limit the epidemic and pandemic caused by influenza virus. Epidemic is the rapid spread of infectious disease to a large number of people in a given population within a short period of time. Whereas, pandemic is an epidemic of infectious disease that has spread through human populations across a large region; for instance multiple continents, or even worldwide and indicates high mortality.

Influenza virus belong to *Orhotmyxoviridae* family. There can be distinguished 3 types – A, B and C. Moreover, influenza A virus can be divided into subtypes, based on the surface proteins (hemagglutinin – H, and neuraminidase – N). To date, 18 variants of H and 9 variants of N were described. The combination of these proteins form a subtype's name, e.g. H1N1, H5N1 or H7N2. The genetic material of influenza virus represents a ribonucleic acid (RNA), which is divided into 8 fragments called segments. Each RNA segment (vRNA – viral RNA) contain the genetic information for at least one protein crucial during viral life cycle. Moreover, each vRNA most of the time is bound with nucleoprotein and form ribonucleoprotein complex (vRNP – viral ribonucleoprotein complex). vRNP serves as a template to obtain other viral RNAs, as well as it is packaged into progeny virion. Infectious influenza virus need to contain all 8 vRNP inside the virion.

RNA molecules play many essential roles inside the cells. They serve as genetic material (e.g. influenza virus), they serve as a template for protein translation – mRNA (messenger RNA), they transport amino acids during translation – tRNA (transfer RNA), they play role during biological processes – miRNA (micro RNA) and many other. An important part of RNAs is not only nucleotides sequence (primary structure), but its secondary and tertiary structure. For example, when the RNA interact with protein, either the RNA sequence is important to bound the protein, and the tertiary structure must fit to protein structure. Therefore, the knowledge about RNA structure is essential to understand RNA function, which can be easily disrupted by mutation.

The main aim of this study is to determine the secondary structure of segment 8 vRNA of influenza A virus (vRNA8) in the native vRNP8 complex. Moreover, we postulate that there will be indicated structural motifs, which can form locally in vRNA and can have functional role during virus life cycle. The vRNP8 will be isolated and purified from the HEK 293 cells infected with modified influenza A/California/04/2009 (H1N1) virus. Next, the vRNP8 will be mapped using chemicals and enzymes, which allow to determine the secondary structure. The experimental results will serve to model the secondary structure in the RNAsturcture software. In the next part of this project, the structural motifs and their function during the viral life cycle will be study. For that purpose, some point mutations, which disrupt the secondary structure, will be introduced in particular structural motifs. We assume that the introduced changes in the regions important for virus replication will result in a reduction of virus titer and will change virus morphology.

The proposed research allows to expand specific knowledge about influenza A virus biology. The distinguished structural motifs can be especially interesting for other researchers, and particularly they can be new therapeutics target.