

Viruses are microscopic infectious agents that reproduce in the living hosts' cells. They "hijack" the host's molecular machinery and force it to produce thousands of copies of the original virus to infect neighboring cells. Usually, the viruses are built of two main parts: protein capsid - a "car" used to carry genetic material between cells and hosts, and the genetic material itself - a "driver" with all the crucial information on how to hijack hosts.

Viruses typically are classified by the type of genetic material they possess - either ribonucleic acid (RNA) or deoxyribonucleic acid (DNA). They can infect all kinds of living organisms - bacteria, plants, animals and humans. DNA viruses are responsible for such human diseases as - herpes simplex, smallpox, skin diseases, sexually transmitted diseases or cancer. RNA viruses may cause - common cold, hepatitis A, polio or severe acute respiratory syndrome (the condition caused by the SARS-CoV-2 virus, responsible for the ongoing pandemic).

Viral diseases have been with us for centuries, and for many of them, we still do not have an effective cure. One way of defending from viruses is vaccines, which usually consist of some small parts of the viral capsid, which forces our immune system to create defensive systems for specific viral species. Another way of defeating viruses are drugs; however, in this case, the procedure of obtaining a cure is much more complicated than creating a vaccine. Medications are usually developed in such a way to target specific viral elements or structures, and prevent the virus from reproducing. In order to pinpoint a feature crucial for viral replication, there is a need to discover and understand the structure of those elements.

In this project, we aim to discover structurally stable elements of all of the single-stranded positive-sense RNA viruses (+ssRNA). Based on the results of our recent studies on the structural elements of the SARS-CoV-2 virus, we plan to further develop the methodology of finding the stable modules in the viral genome, and use this methodology on all of the +ssRNA viruses. By combining experimental and computational biology, we will derive a universal method for the discovery of highly-structured modules in viral RNA, group them, and classify them based on their potential function.

We plan to answer the questions, "Are the structures that we found in coronaviruses also present in other related viruses? Is there a set of universal structures that are present in most of the viral RNA genomes? Are there any structural elements in viruses that are also present in hosts' genomes?". By describing the structural modules of +ssRNA viruses, we will provide an important resource for understanding viral RNA structures' importance. Modules present in many viral families are likely essential for viral replication; hence, they may be potential targets for the cure.