The purpose of this project is to fully characterize the interaction of the SARS coronaviruses with the human cell receptor by the mean of the thermodynamic (ITC) and spectroscopic techniques.

Among the seven known coronaviruses infecting humans, there are three that cause severe disease — SARS-CoV, Middle East respiratory syndrome (MERS-CoV) and SARS-CoV-2 (causing ongoing COVID-19 disease). Bats are the main reservoir of these viruses. The outbreak of SARS in 2003 showed the world how easily these kind of coronaviruses could kill people. As of 13 may 2020, there are around 4,400,000 SARS-CoV-2 cases and more than 295,000 deaths.
Now, as the numbers of the COVID-19 cases and deaths are strongly rising, researchers are struggling to uncover as much as possible about the biology of the novel coronavirus, named SARS-CoV-2. It has been discovered that SARS-CoV-2 shares 96% of its genetic material with a virus found in a horsehoe bat, however it is also genetically very similar to a coronavirus from pangolin-a wild animal being sold in Chinese markets.

However, there are still many pivotal questions regarding this virus, e.g. how exactly it attacks human cells, whether it will evolve into something more, and what it can teach us about the next possible outbreak of other similar coronavirus? There is a possibility that SARS-CoV-2 will enter the group of the "seasonal infections" in the future. Most antiviral drugs weaken viruses by inducing mutations. However, coronaviruses have a genomic proofreading mechanism that keeps the virus from accumulating mutations which could weaken it. SARS-CoV-2 is much better at infecting people than SARS or the seasonal flu. One of the reason is that, contrary to previous SARS virus, it can shed viral particles from the throat into saliva even before symptoms start.

This virus, responsible for COVID-19 disease, uses its spike (S) proteins to bind to the receptor of the human cells (namely ACE2 protein). Scientists working on a vaccine against COVID19 must determine which antibodies bind to the spike structure but also ensure that they don't trigger in this same time a negative immune response.
Our project is focusing on the spike protein. We want to reveal how exactly it works. Very recently the structures of this spike protein and human cell receptor were resolved by using Cryo electron microscopy and X-ray crystallography. The structure of the receptor binding domain of spike protein is also known. Many coronavirus branches in bats and pangolins carry very similar receptor binding domain at S protein as SARS-CoV-2, so they can in the future cause a analogous deadly pandemic.

Using a set of unique techniques (isothermal titration calorimetry, CD-spectroscopy, and some of the biochemical and molecular biology tools) we will find which of the S protein aminoacid residues are crucial for ACE2 binding, what is the strength of that binding, which are the thermodynamic forces driving these reactions and what is the difference between SARS-CoV-2 and other similar viruses binding to the human cells.

The results of our project will bring understanding of the interaction of SARS and SARS-CoV-2 with human cell receptor, what can help to discover potent and safe for people vaccines/treatment against virus causing current pandemic and also prevent from other epidemic diseases which can arise when similar virus will possess the ability to leap into humans from animal reservoirs.