AIMPID is focused on predicting mutations in SARS-CoV-2 genome and developing small inhibitor molecules which target the virulent protein products of predicted mutations to block their activities. This helps in controlling the spread of pandemic as frequent mutations in SARS-CoV-2 genome (especially in case of targeted RNA vaccines) are taking place rendering the developed drugs useless. Being an RNA virus, SARS-CoV-2 is prone to mutations therefore, it necessitates the tracing of mutation patterns in the viral genome to find the least mutable regions in order to design enduring and more stable inhibitor molecules. The main tasks constituting the conduction of the whole project are mutation rate prediction, mutation prediction and development of small inhibitor molecules against proteins translated from mutated RNA sequences. The primary objective is to produce small molecule inhibitors of a critical SARS-CoV-2 protein that will have an extended lifetime compared to classically developed small molecules.

**Goals**

- Development of deep learning based models for the prediction of mutations and mutation rates in the genome of SARS-CoV-2.
- Testing, optimization and benchmarking of the designed algorithms on the genomic datasets of SARS-CoV-2 from Gisaid.
- Significance analyses of predicted mutations and mutation rates to explore effects of the mutation on the virulence of virus.
- Protein stability analyses and computational development of inhibitor molecules.
- Experimentation on the basis of quantitative wet lab based assays to explore the behavior of the potential inhibitor molecules.
- Experimentation in *Escherichia coli* to analyze the behavior of the molecules against the virus.
- Testing the effect of the designed drugs on SARS-CoV-2 via human cell lines.