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STUDY OF SARS-CoV2-S WILD-TYPE SPIKE PROTEIN INTERACTION WITH RANDOMLY AND ORIENTED ANTIBODIES BY QUARTZ CRYSTAL MICROBALANCE

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In 2020, new SARS-CoV-2 virus emerged and spread around the world. Even though global pandemic was declared over, the SARS-CoV-2 virus was not eradicated. COVID-19 disease, which is caused by this virus, still causes health problems for people. There is high demand for diagnostic measures that can sensitively and rapidly detect virus molecules. Faster diagnosis leads to an earlier prescription of right medicine and more effective treatment of the patients.

In our study, we investigated how not mutated SARS-CoV-2 wild-type spike (SCoV2-S wild-type) protein interacts with monoclonal antibodies (mAbs-RBD) against SARS-CoV-2 spike proteins' receptor binding domain (RBD) when mAbs-RBD are immobilized in two different ways on the sensing gold surface. For random mAbs-RBD immobilization we used 11-mercaptoundecanoic acid (11-MUA) which forms self-assembling monolayer on the gold surface. Protein G was applied to form ordered mAbs-RBD layer on the sensing surface. After different immobilization procedures we investigated SCoV2-S wild-type interactions with mAbs-RBD.

Antigen-antibody interactions were investigated by quartz crystal microbalance with dissipation (QCM-D) method which allows to obtain the information about formed proteins layer viscoelastic properties. Further we used mathematical modelling for evaluation of rate and affinity constants for SCoV2-S wild-type and mAbs-RBD interactions. Moreover, we calculated mAbs-RBD and SCoV2-S wild-type proteins' layers thickness and surface mass densities.