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Research activities at the HZB-MX beamlines directed towards fighting SARS-CoV-2

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Since the worldwide outbreak of the Covid-19 pandemic in early 2020, researchers in many different parts of the world have started activities directed towards a better understanding of the SARS-CoV-2 virus life cycle or even towards medical treatment of Covid-19. Large-scale research facilities such as for instance synchrotron radiation facilities are playing a particularly important role in this respect by providing state-of-the-art Macromolecular crystallography (MX) facilities. MX has been instrumental in deciphering the first atomic resolution structure of the SARS-CoV-2 main protease (Figure 1) [1]. Several other viral protein structures have been determined following that [2]. Furthermore, owing to the manifold developments of MX towards automation and the concomitant increase in throughput, MX has also been employed as a primary screening technique for finding new substances, which might be active against SARS-CoV-2. In the presentation several user and in-house projects will be highlighted, which are directed towards this goal.

References:

- [1] L. Zhang, et al., 'Crystal structure of SARS-CoV-2 main protease provides a basis for design of improved α -ketoamide inhibitors', *Science* 368, 409-412 (2020)
- [2] M. Scudellari, 'The sprint to solve coronavirus protein structures - and disarm them with drugs', *Nature* 581, 252-255 (2020)

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