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## The Corona-year 2020 at Biodiffraction Beamline P11

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Beamline P11 at PETRA III in Hamburg is a versatile instrument for macromolecular crystallography (1). During 'the Corona-year'2020 we operated in very exceptional conditions. Here we describe DESY responses to the pandemic situation, such as the fast-track access to the beamline, exceptional user regulations and remote access.

To date, 35 PDB depositions have arisen from P11 related to Covid-19 by our fast-track, proposal and priority access users (2-5). Additionally, P11 participates to three DESY Strategic Fund projects relating to Covid-19 research: 1) Inhibitor screening and structural characterization of virulence factors from SARS-CoV-2, 2) Multidimensional serial crystallography of Sars-CoV-2 proteins to unravel structure and dynamics of function and inhibition and 3) Automated X-ray crystallography compound screening pipeline at DESY.

In spite of the restricted user operations, the beamline had a very busy user run and the scarce commissioning time was used to employ our new Eiger2 X 16M. We successfully employed the detector for serial data collections. Dedicated nodes in our central computational cluster Maxwell will be at the disposal of our users for processing (and autoprocessing) their Eiger data next year. Inspired by the properties of our new detector, we started to streamline the serial crystallography methods available at the beamline and to integrate both the data collection and the data processing more tightly into the beamline environment.

- 1) Burkhardt et al. (2016) Eur. Phys. J. Plus 131 56.
- 2) Zhang et al. (2020) Science 368 409-412
- 3) Günter et al. (2020) BioRxiv (doi.org/10.1101/2020.05.02.043554)
- 4) Rut et al. (2020) Nat Chem Biol (doi.org/10.1038/s41589-020-00689-z)
- 5) Oerlemans et al. (2021) RSC Med Chem (DOI: 10.1039/D0MD00367K)

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