## Drug Design for inhibition of the main protease and papain-like protease of the SARS-CoV-2 causing COVID19

Lara Scharbert, Birgit Strodel

Institute of Biological Information Processing: Structural Biochemistry (IBI-7), Forschungszentrum Juelich GmbH, Wilhelm-Johnen-Straße, 52428 Juelich, Germany I.scharbert@fz-juelich.de

Since the outbreak of the global pandemic of the coronavirus disease 2019 (COVID19) caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) over 754 million cases and over 6.8 million deaths have been reported globally.<sup>1</sup> With seven different vaccines and eight medicines authorized for the use in the European Union (EU), as well as a vaccination rate of 82.4% (primary course) in the EU adult population, the pandemic seems to be largely under control.<sup>2,3</sup> However, with constantly mutating SARS-CoV-2 variants contributing to increased transmission and higher antibody resistance towards current vaccines, there remains the need for medicines that effectively target also new variants with minimal side effects.<sup>4</sup> The main protease (3CL<sup>pro</sup>) and the papain-like protease (PL<sup>pro</sup>) are both critical for the replication of the SARS-CoV-2 virus, since they process together sixteen non-structural proteins.<sup>5</sup> In previous *in silico* studies, we have already screened over 1 Mio compounds including approved and under investigation drugs, as well as natural products against the active site of 3CL<sup>pro.6</sup> We then investigated the inhibition activity of the most promising candidates from the *in silico* studies and additionally several African plant extracts against the 3CL<sup>pro</sup> in the wet lab with promising results.<sup>7</sup> In order to increase the selection and diversity of potential lead compounds in the fight against COVID19, our next step includes the computational design of D-peptides against the active sites of 3CL<sup>pro</sup> and PL<sup>pro</sup> considering the cleavage site consensus sequence of the substrate polypeptides. D-peptides are considerably more resistant to proteolytic degradation than L-peptides, which is why they are promising for oral drug treatment.<sup>8</sup> The aim of this project is to identify potential inhibitors of 3CL<sup>pro</sup> and PL<sup>pro</sup> using molecular docking and dynamics (MD) simulations followed by in vitro and in cell testing.

- Weekly epidemiological update on COVID-19 8 February 2023, <u>https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports</u>, June 2022
- [2] European Medicines Agency COVID-19 vaccines and treatments, https://www.ema.europa.eu/en, February 2023
- [3] Country overview report: week 5 2023, https://covid19-country-overviews.ecdc.europa.eu, February 2023
- [4] Lippi, G., Mattiuzzi, C., & Henry, B. M. (2022). Updated picture of SARS-CoV-2 variants and mutations. Diagnosis, 9(1), 11-17.
- [5] V'kovski, P., Kratzel, A., Steiner, S., Stalder, H., & Thiel, V. (2021). Coronavirus biology and replication: implications for SARS-CoV-2. Nature Reviews Microbiology, 19(3), 155-170.
- [6] Olubiyi, O. O., Olagunju, M., Keutmann, M., Loschwitz, J., & Strodel, B. (2020). High throughput virtual screening to discover inhibitors of the main protease of the coronavirus SARS-CoV-2. Molecules, 25(14), 3193.

- [7] Loschwitz, J., Jäckering, A., Keutmann, M., Olagunju, M., Eberle, R. J., Coronado, M. A., ... & Strodel, B. (2021). Novel inhibitors of the main protease enzyme of SARS-CoV-2 identified via molecular dynamics simulation-guided in vitro assay. Bioorganic Chemistry, 111, 104862.
- [8] Liu, M., Li, X., Xie, Z., Xie, C., Zhan, C., Hu, X., ... & Lu, W. (2016). D-peptides as recognition molecules and therapeutic agents. The Chemical Record, 16(4), 1772-1786.