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The SARS-CoV-2 main protease as a target for antivirals: Crystal structures, new inhibitors, and mutants

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Structure-based design of new inhibitors of the SARS-CoV-2 main protease (Mpro) is discussed and corresponding crystal structures are described. Pharmacokinetics of frontrunner inhibitors are presented. The evolution of the Mpro from the original Wuhan strain via the Alpha, Beta, Delta, and Omicron variants of concern is followed in terms of three-dimensional (crystal) structures, enzymatic activities, and inhibitor potencies.

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