Therapeutic options such as SARS-CoV-2 main-protease (M\textsuperscript{pro}) inhibitors are essential due to the ongoing evolution toward escape from natural or induced immunity. Although mutation rates are considered moderate to high in coronaviruses, as observed in recent years with the spike protein, the mutational dynamics of M\textsuperscript{pro} have generally been considered negligible. Analyses of recent SARS-CoV-2 genomic data suggested accelerated mutational dynamics near the active site of M\textsuperscript{pro} since early December 2021. Our findings emphasise the importance of monitoring the mutational dynamics of M\textsuperscript{pro} and the potential consequences of arising amino-acid exchanges in regions critical for the susceptibility of the virus to antivirals targeting the protease.