The global COVID-19 pandemic caused by the novel coronavirus SARS-CoV-2 has resulted in over 40 million confirmed cases and more than 1 million deaths worldwide since the first reported case in late 2019. To date, no novel therapeutics have been made available for the treatment of COVID-19 and therefore the development of new anti-viral drug leads is of utmost importance. Recently, a new mRNA display technology known as Random nonstandard Peptide Integrated Discovery (RaPID) has been developed for the discovery of novel cyclic peptide drug leads directed at a therapeutic target of interest. The technology allows genetic-code reprogramming facilitated by aminoacylation of tRNA with non-natural amino acids using small ribozymes called "flexizymes". We have successfully applied this technology for discovery of high-affinity sulfated chemokine binding peptides that mimic natural anti-inflammatory chemokine binding proteins produced by pathogens. Following this, we have since applied this method for discovery of modulators of a range of therapeutic targets to inhibit SARS-CoV-2 replication to discover novel drug leads for COVID-19. In particular, we have focused on both human and viral proteases critical to the SARS-CoV-2 replication cycle. Using genetic code reprogramming we incorporated cysteine-reactive warheads into the peptide libraries with a view to discovering covalent inhibitors of these enzymes. To date we have discovered micromolar inhibitors of protease function, with a follow up protein cross-linking strategy underway predicted to afford peptides with higher affinity and better efficacy.