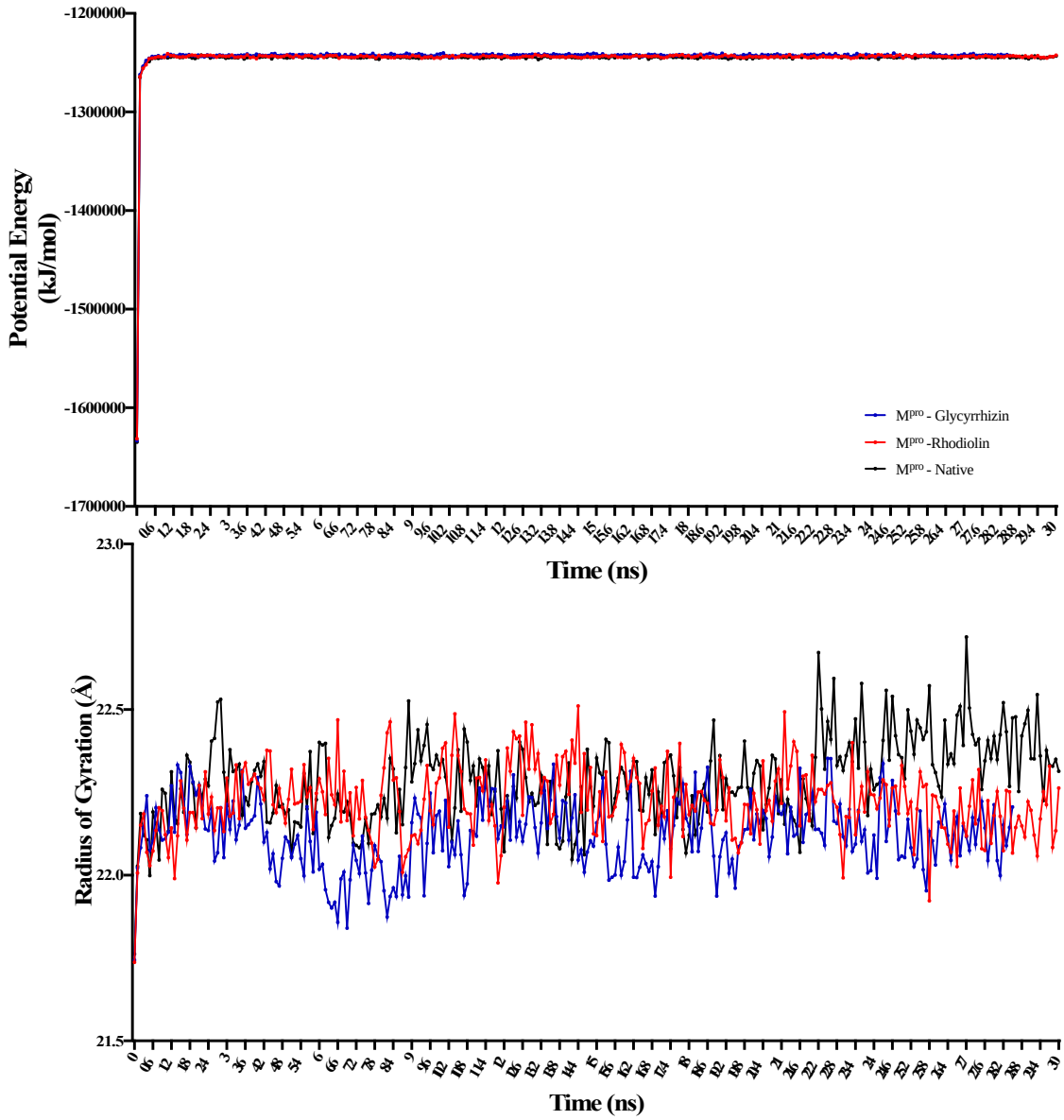

Figure S1: 30 ns Molecular dynamics simulation of Glycyrrhizin (blue) and Rhodiolin (red) docked with SARS-CoV-2 main protease (MPro)

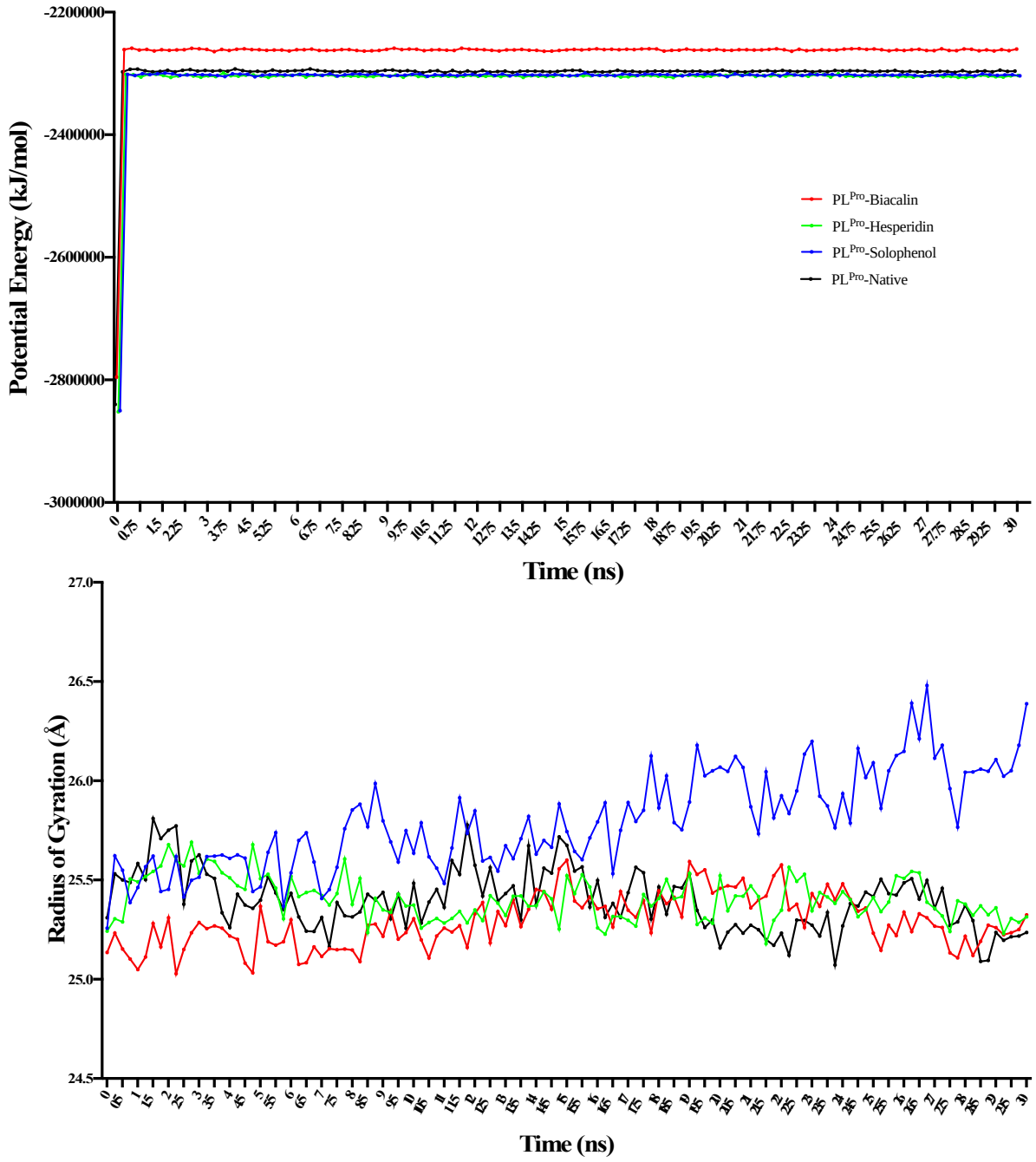

Figure S2: 30 ns Molecular dynamics simulation of Baicalin (red), Hesperidin (green), and Solophenol (blue) docked with SARS-CoV-2 PLpro

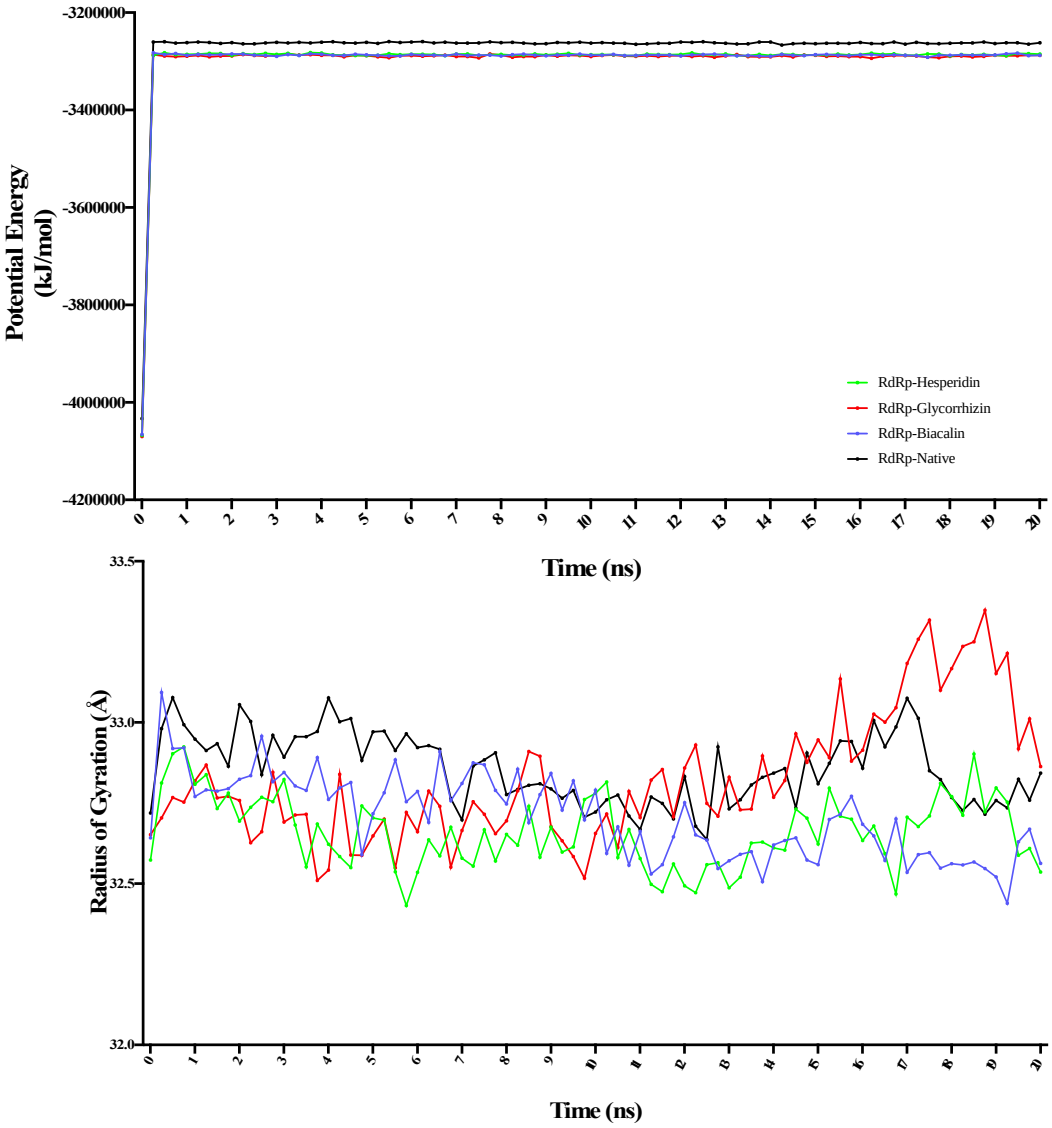

Figure S3: 30 ns Molecular dynamics simulation of Glycyrrhizin (red), Hesperidin (green), Baicalin (blue) in complex with SARS-CoV-2 RdRp.

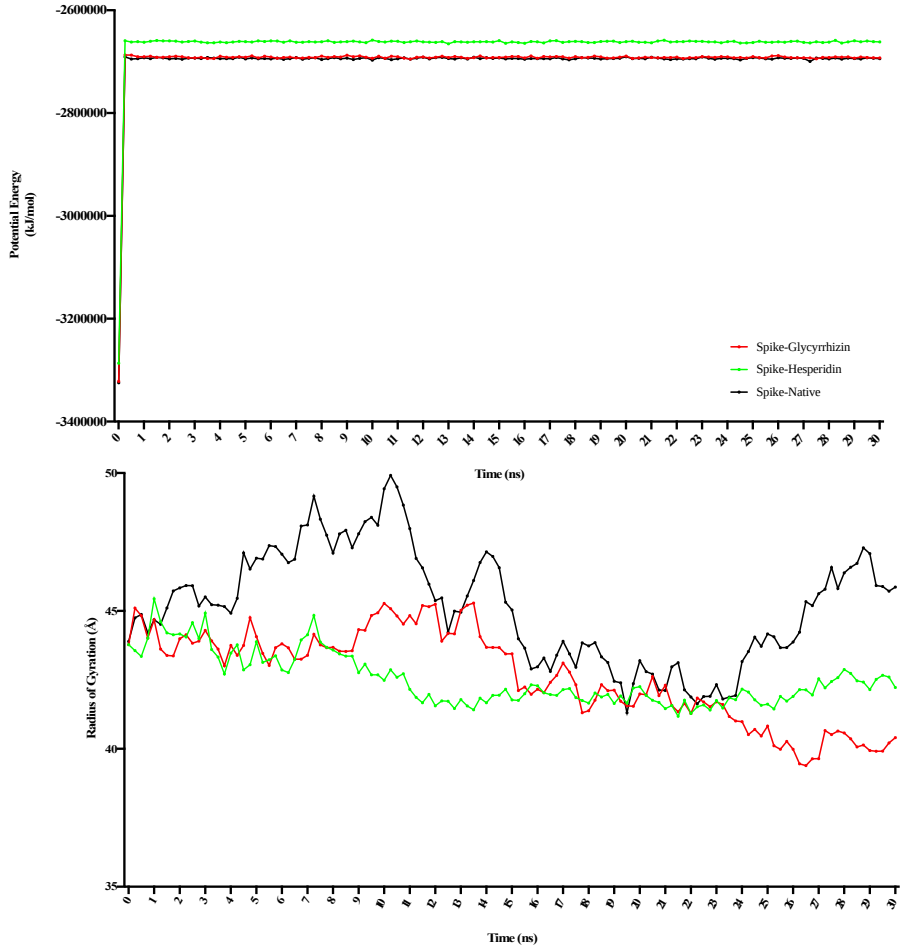

Figure S4: 30 ns Molecular dynamics simulation of Glycyrrhizin (red) and Hesperidin (green) in complex with SARS-CoV-2 spike protein (closed state)

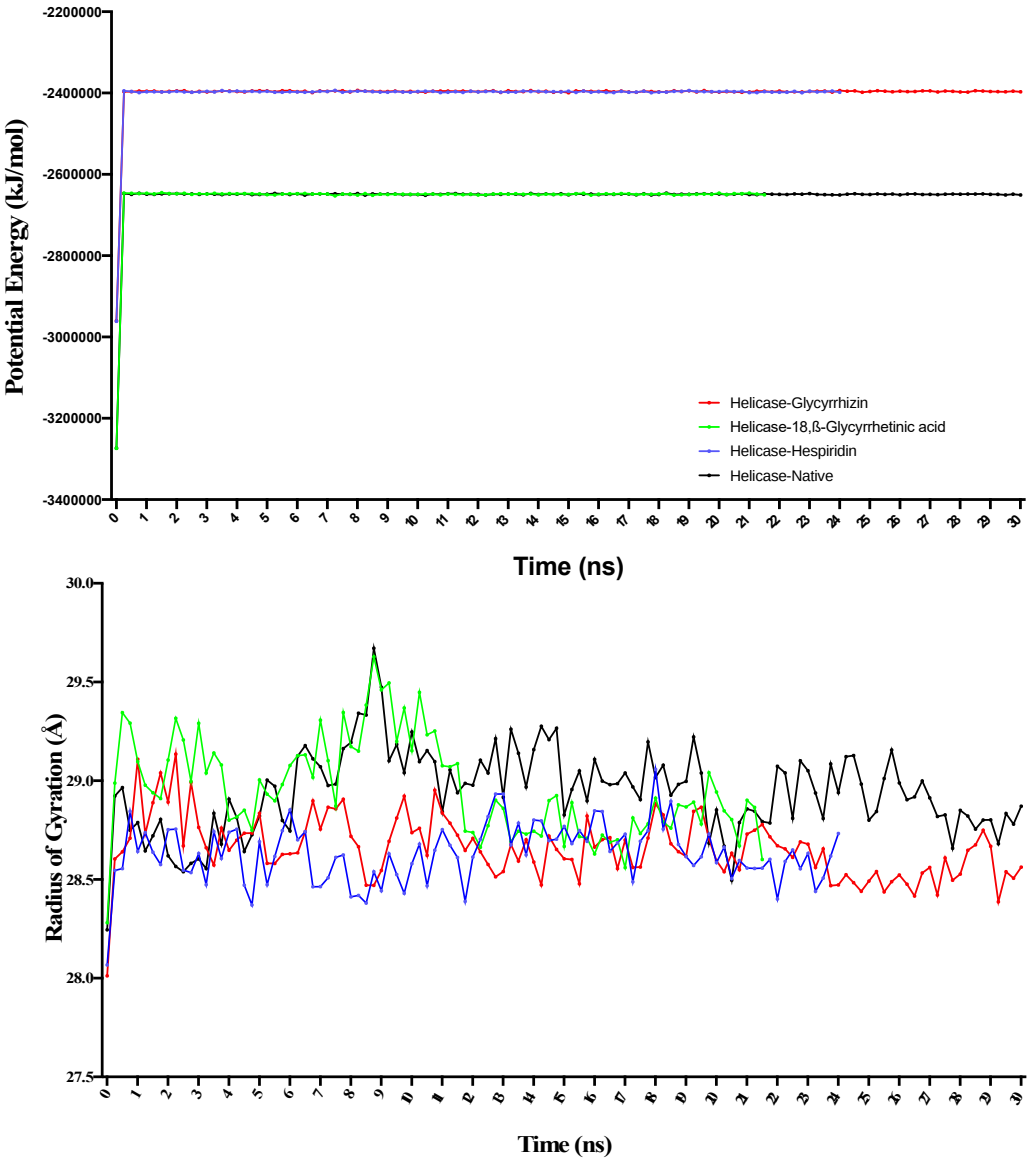

Figure S5: 30 ns Molecular dynamics simulation of Glycyrrhizin (red), Hesperidin (green), Baicalin (blue) in complex with SARS-CoV-2 helicase

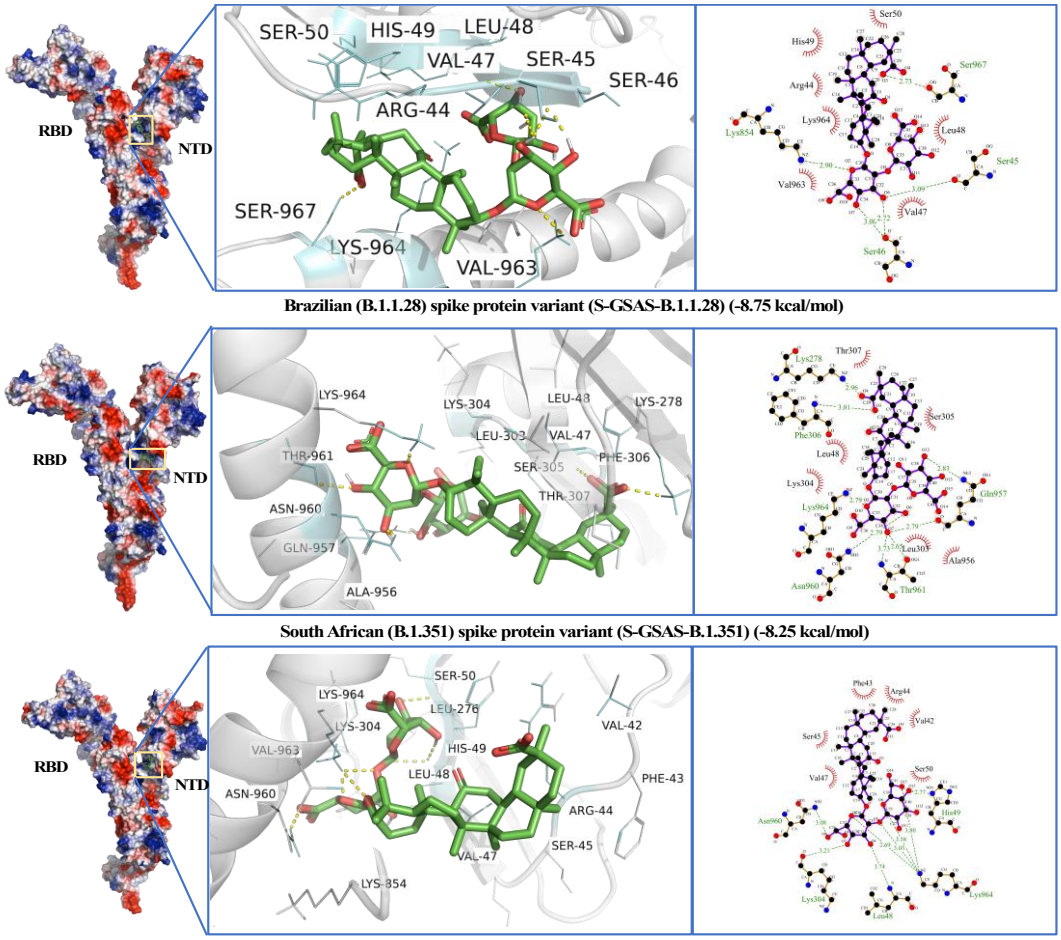

Figure S6: Glycyrrhizin interactions with variants of Spike protein of SARS-CoV-2