Computational analysis by molecular docking of 30 alkaloid compounds from medicinal plants as potent inhibitors of SARS-CoV-2 main protease

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SUPPLEMENTARY MATERIAL

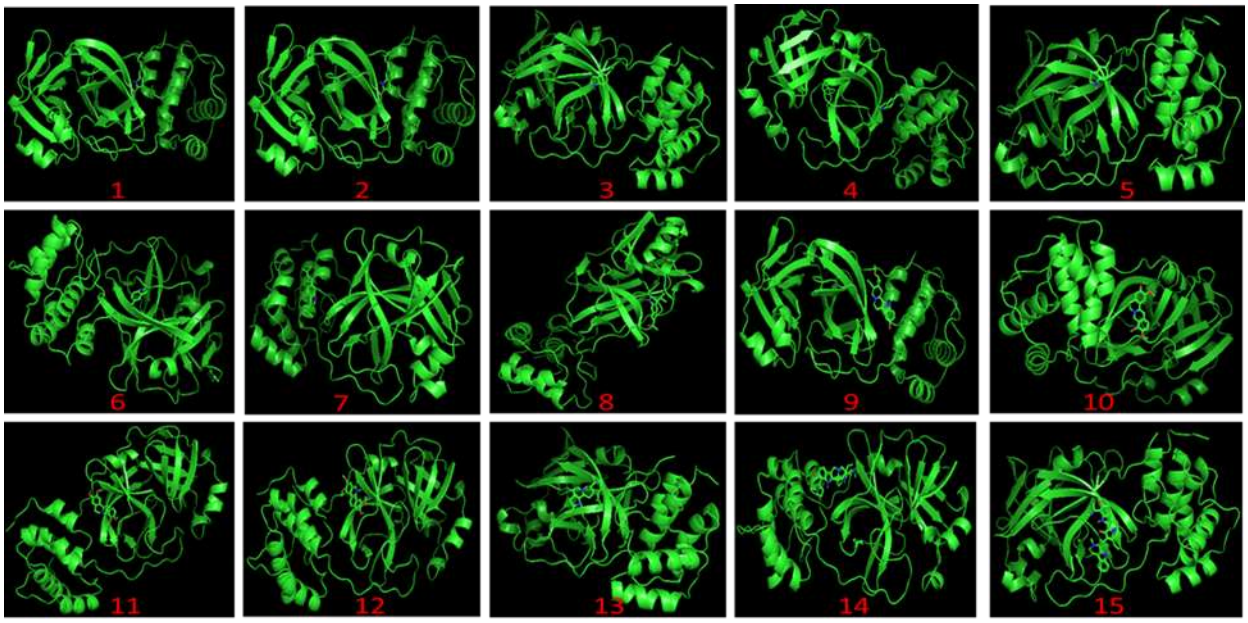

Figure S1. Docked indole alkaloids Ligands in the binding pocket of the protein (complexes)

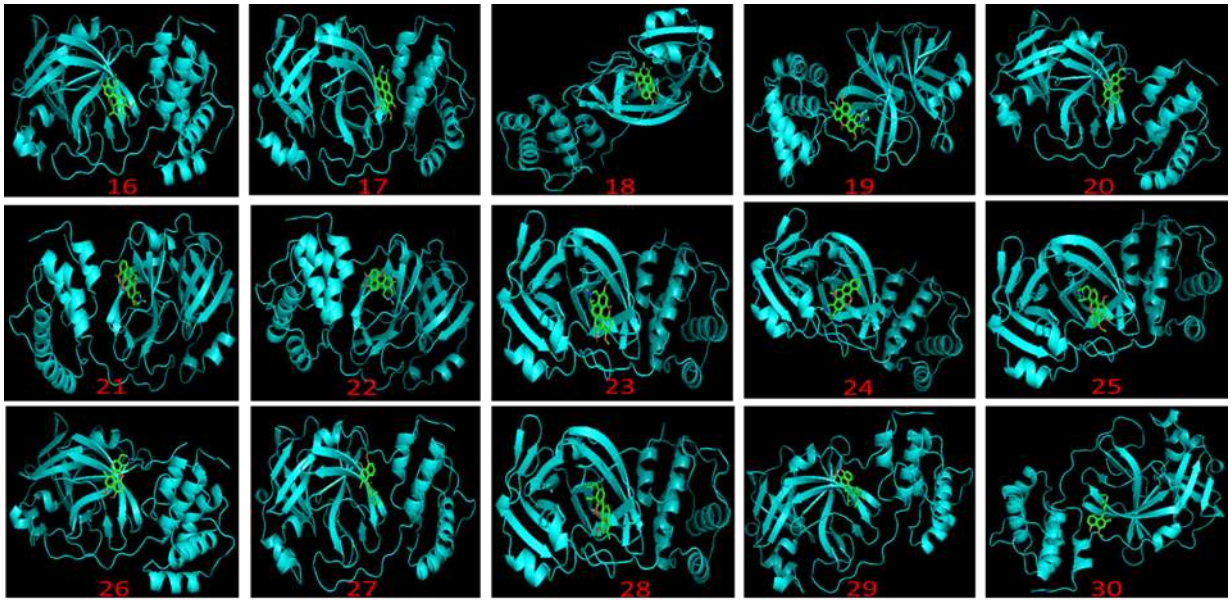

Figure S2. Docked naphthoisoquinolines ligands in the binding pocket of the protein (complexes)