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Fighting against COVID-19: A computational biophysics approach

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Previously it was reported that cell-surface Glucose Regulated Protein 78 (CS-GRP78), also termed heat shock protein A5 (HSPA5), could be a possible route for SARS-CoV-2 internalization. The binding site on the spike protein of SARS-CoV-2, which can recognize CS-GRP78, was predicted in a previous study. The spike glycoprotein of the SARS-CoV-2 bear many conserved motifs to the previously determined human coronavirus strains such as HKU1, 229E, NL63, OC43, MERS-CoV, and SARS-CoV. 2 However, we would like to emphasize that using a simple bioinformatics approach can suggest a possible role of the GRP78 in cross immunization against COVID-19. Additionally, different antiviral drugs have the potential to be SARS-CoV-2 inhibitors, thus can be used against COVID-19. These drugs are tested in silico at the beginning of the pandemic, and currently, some are approved against COVID-19.

Biography

I'm working in the Biophysics Department, Faculty of Sciences, Cairo University, Giza, Egypt as a Lecturer then Associate Professor starting from the year 2013. My interest in Molecular Biophysics pushes me to work in Structural Bioinformatics and Drug Design to find potent inhibitors against viral and pathogenic fungal proteins utilizing in silico techniques. During the past 6 years, I focused my research on polymerase protein due to its vital role in the life cycle of the pathogenic organisms. I studied also other proteins like protease, estrogen receptors and kinases. Currently, I'm working on fungal CotH kinase family proteins crucial for Mucormycosis virulence and the unfolded protein response master chaperone protein, GRP78.