

## عنوان مقاله:

In-silico comparison of post-translational modifications of SARS-CoV and SARS-CoV- $\gamma$  structural proteins

## محل انتشار:

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## خلاصه مقاله:

Background and aims: Severe acute respiratory syndrome coronavirus  $\gamma$  (SARS-CoV- $\gamma$ ) is a newly discovered coronavirus which causes an infectious disease. The severe acute respiratory syndrome (SARS-CoV) and the Middle East respiratory syndrome (MERS) broke out in 2003 and 2012, respectively. These viruses have some structural proteins, including spike (S), membrane (M), envelope (E), and nucleocapsid (N) proteins. These proteins assist the virus in infecting cells through interaction with cell receptors, penetration into the cell, and proliferation. These coronavirus proteins are modified by post-translational modifications (PTMs) which activate various functional and interactional activities of proteins. This study aimed to investigate the PTMs in SARS-CoV/CoV- $\gamma$ , as well as to examine the effect of these PTMs on the pathogenicity of these two viruses. Methods: In this study, PTMs sites were detected by different bioinformatics tools. Evaluation and comparison of PTMs were performed and their roles in structural proteins activities of SARS-CoV/CoV- $\gamma$  coronaviruses were examined in order to gain a richer understanding of these modifications' relationships with the protein activities. Results: The PTMs sum and percentages of four structural proteins of SARS-CoV/CoV- $\gamma$  were evaluated, with a focus on their effects on viral replication and pathogenesis in order to develop a method for treating these diseases. According to our study results, some of the PTMs in SARS-CoV/CoV- $\gamma$  were different from each other. Conclusion: It was concluded that SARS-CoV- $\gamma$  had more pathogenicity than SARS-CoV.

## کلمات کلیدی:

PTMs, Structural proteins, Coronaviruses, Bioinformatics tools

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