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Research Article

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Analysis of Viral Genome which encodes Non-structural proteins of COVID- SARS-coV

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Abstract

Proteins are inimitable as principal functional agent of living system. Therefore, comprehension of protein sequence and structure and its correlation with its function is equivalent to deciphering almost all of fundamental features of any biological/living system. A treasure of in- silico tools is accessible for analysis of protein. Understanding and regeneration of protein function requires comprehension of reliance between protein sequence and its structure, its localization in cell and its interaction with other functional partners. This review provides an insight for various tools for insilico analysis of protein.

Keywords: Protein analysis, RNA dependent RNA polymerase, Main protease(Mpro), papain-like protease (PLpro)

Introduction

Coronavirus disease (COVID-19) is an infectious disease caused by the SARS-CoV-2 virus. Most people who fall sick with COVID-19 will experience mild to moderate symptoms and recover without special treatment. However, some will become seriously ill and require medical attention.

The virus can spread from an infected person's mouth or nose in small liquid particles when they cough, sneeze, speak, sing or breathe. These particles range from larger respiratory droplets to smaller aerosols.

You can be infected by breathing in the virus if you are near someone who has COVID-19, or by touching a contaminated surface and then your eyes, nose or mouth. The virus spreads more easily indoors and in crowded settings.



Materials and Methods

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2. Primary structure prediction



3. Secondary structure prediction



4. Tertiary structure prediction



5. Validation of predicted models

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7. Prediction of Active Site of protein

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8. Predicting phosphorylation sites

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9. Predicting protein ubiquitination sites

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10. Prediction of methylation and acetylation

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| MultiLoc2 👌 🔹 | | |
| MultiLoc2 predicts animal, plant and fungal protein s | ubcellulariocalizations by integrating phylogeny and Gene Ontology terms to the | new version of the software. |
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Conclusion

The computational or in silico approach that has been highlighted in this review for predicting the structure and function of unknown protein apprehends the efficacy of various tools of bioinformatics. These tools are pre-requisite in predicting structural and functional features thereby facilitating experimental analysis of proteins. The study of proteins made here can be explored and utilized further so that it can be beneficial for therapeutic purposes.

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