

Chapter 4

Physiochemical Characterization and Domain Annotation of ORF1ab Polyprotein of Novel Corona Virus 19



The detailed structural analysis of the ORF1ab polyprotein was carried out to study its Physiochemical characterization as well as its domain annotations. Various *in silico* tools have been used for the said purpose.

4.1 Physiochemical Characterization of ORF1ab Polyprotein Using Protparam

Protparam is a tool from ExPASy proteomic server, for the annotation of complete physiological and chemical characteristics of the protein. The analysis is completely based on the input sequence and depends on the amino acid characteristics. A detailed annotation of the protein can be performed by the tool (Fig. 4.1).

Inference: The ORF1ab polyprotein is comprised of 7096 amino acids. The Molecular weight and the Isoelectric point are 794,057.79 and 6.32 respectively. This indicates that at the pH 6.32 the protein exists in its zwitter ionic state. Total number of negatively charged residues is the sum of Aspartic acid residues and Glutamic acid residues which is calculated to be 729 amino acids. Similarly the total number of positively charged residues is the total of Arginine and Lysine residues which is calculated to be 678. The presence of more number of acidic amino acids makes the protein acidic in nature. The instability index of the protein is 33.31 which imparts stability to the protein. The protein is hydrophilic i.e. water soluble which is indicated by its hydropathicity index being -0.070 .