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abundant S protein varies from 1,160 amino acids (IBV, infectious bronchitis virus, in poultry) to 1,400 amino acids (FCoV, feline coronavirus) (43). It lies in a trimer on the virion surface, giving the virion a corona or crown-like appearance. Functionally it is required for the entry of the infectious virion particles into the cell through interaction with various host cellular receptors (44). Furthermore, it acts as a critical factor for tissue tropism and the determination of host range (45). Notably, S protein is one of the vital immunodominant proteins of CoVs capable of inducing host immune responses (45). The ectodomains in all CoVs S proteins have similar domain organizations, divided into two subunits, S1 and S2 (43). The first one, $1, helps in host receptor binding, while the second one, S2, accounts for fusion. The former (S1) is further divided into two subdomains, namely, the N-terminal domain (NTD) and C-terminal domain (CTD). Both of these subdomains act as\_ receptor-binding domains, interacting efficiently with various host receptors (45). The Sl CTD contains the receptor-binding motif (RBM). In each coronavirus spike protein, the trimeric S1 locates itself on top of the trimeric S2