class I viral transmembrane protein. The size of this

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 $2 (43). The first one, $1, helps in host receptor

binding, while the second one, $2, 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