mutations that occur during subsequent human-to-

human transmission is warranted.

M Protein

The M protein is the most abundant viral protein

present in the virion particle, giving a definite shape

to the viral envelope (48). It binds to the

nucleocapsid and acts as a central organizer of

coronavirus assembly (49). Coronavirus M proteins

are highly diverse in amino acid contents but

maintain overall structural similarity within different

genera (50). The M protein has three transmembrane

domains, flanked by a short amino terminus outside

the virion and a long carboxy terminus inside the

virion (50). Overall, the viral scaffold is maintained

by M-M interaction. Of note, the M protein of

SARS-CoV-2 does not have an amino acid

substitution compared to that of SARS-CoV (16).

E Protein

The coronavirus E protein is the most enigmatic

and smallest of the major structural proteins (51). It

plays a multifunctional role in the pathogenesis,

assembly, and release of the virus (52). It is a small

integral membrane polypeptide that acts as a

viroporin (ion channel) (53). The inactivation or