CREATIVE BIOMART®
Diagnostic Proteins

Recombinant Human Coronavirus 229E Spike Glycoprotein (S1), His-tagged

Product Information

Cat#	
HUM-298	
Product Name	
Recombinant Human Coronavirus 229E Spike Glycoprotein (S1), His-tagged	
Description	
Human coronavirus 229E spike glycoprotein is a recombinant HCoV-229E spike subunit 1 protein (S1), with C-terminus His-tag.	
Type	
Recombinant	
Gene	
Spike Glycoprotein (S1)	
Species	
Human Coronavirus 229E	
Source	
HEK293	
Molecular Weight	
90 kDa	
Synonyms	
Human Coronavirus 229E Spike Glycoprotein (S1)	
Formulation	
Dulbecco's phosphate buffered saline pH7.4, sterile filtered.	
Notes	
This product is intended for research and manufacturing uses only. It is not a diagnostic	

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device. The user assumes all responsibility for care, custody and control of the material, including its disposal, in accordance with all regulations.

Tags

C-terminal His

Background

Coronaviruses are enveloped, positive-stranded RNA viruses with a genome of approximately 30 kb (Lai, 1990). In animals they are significant veterinary pathogens, often causing severe disease (Holmes, 2001). Prior to early 2000, only two human coronaviruses were recognized, Human coronavirus 229E (HCoV-229E) and Human coronavirus OC43 (HCoV-OC43) which are a common cause of upper respiratory tract infections (Chibo and Birch, 2006). In late 2002, a third human coronavirus (SARS-CoV) was implicated as the aetiological agent of severe acute respiratory syndrome (SARS) (Drosten et al., 2003). Since then, several more human coronaviruses have been identified, including HCoV-NL63 associated with upper and lower respiratory tract infections (van der Hoek et al., 2004) and HCoV-HKU1 in patients with pneumonia (Woo et al., 2005) and Middle East respiratory syndrome (MERS). HCoV-229E was first described in 1966 when it was isolated from cell cultures inoculated with samples from diseased student volunteers (Hamre & Procknow, 1966).
Sequences related to HCoV-229E have been detected in captive alpacas and dromedary camels which may form an intermediate host for the virus. However, the viruses natural host is likely to be hipposiderid bats in Africa and these populations show much greater viral diversity than those from camelids. The spike genes of all HCoV-229E and camelid-associated 229E viruses contain deletions as compared to bat-associated viruses, which may have played a role in host switching. All 229E viruses from camels and all strains from bats also contain an additional gene (ORF 8) downstream of the nucleocapsid gene. Nucleocapsid proteins (nucleoproteins) are phosphoproteins that are capable of binding to helix and have flexible structure of viral genomic RNA. Nucleoprotein plays an important role in virion structure, replication and transcription of coronaviruses, as it localizes in both the replication/ transcriptional region of the coronaviruses and the ERGIC region where the virus is collected. It packages the positive strand viral genome RNA into a helical ribonucleocapsid (RNP) and

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plays a fundamental role during virion assembly through its interactions with the viral genome and membrane protein M. It also plays an important role in enhancing the efficiency of subgenomic viral RNA transcription as well as viral replication (Corman et al, 2018).

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