CREATIVE BIOMART®
Diagnostic Proteins

Recombinant SARS Coronavirus Spike Glycoprotein (S1) Mosaic

Product Information

Cat#

HUM-321

Product Name

Recombinant SARS Coronavirus Spike Glycoprotein (S1) Mosaic

Description

SARS Coronavirus Spike Glycoprotein Mosaic (N-term) is a recombinant antigen which contains the N-terminal section of the Spike protein 1-53, 90-115, 171-205 amino acids immunodominant regions. It is manufactured in E. coli and is immunoreactive with sera from SARS-infected individuals.

Type

Recombinant

Gene

Spike Glycoprotein (S1) Mosaic (N-Term)

Species

SARS Coronavirus

Source

E. coli

Synonyms

SARS Coronavirus Spike Glycoprotein (S1) Mosaic

Purity

Purity ~90% as determined by SDS-PAGE.

Notes

This product is intended for research and manufacturing uses only. It is not a diagnostic device. The user assumes all responsibility for care, custody and control of the material,

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including its disposal, in accordance with all regulations.

Applications

For use in ELISA and other immunoassays.

Background

Coronaviruses are a family of large, enveloped, positive-stranded RNA viruses that cause upper respiratory, gastrointestinal and central nervous system diseases in humans and other animals (Gallagher and Buchmeier, 2001). Human coronaviruses (HCoV-OC43, HCoV-229E, HCoV-NL63 and HCoV-HKU1) circulate in humans and cause mild respiratory diseases (Su et al., 2016). However, the outbreak of SARS-CoV in 2002 and MERS-CoV in 2012 showed that coronaviruses can cross the species barrier and emerge as highly pathogenic viruses (Lu et al., 2015). The high fatality rate and wide spread of SARS-CoV and MERS-CoV confirmed that they are a severe threat to global health.

The coronavirus spike (S) glycoprotein is a class I viral fusion protein on the outer envelope of the virion that plays a critical role in viral infection by recognizing host cell receptors and mediating fusion of the viral and cellular membranes (Li, 2016). The coronavirus S glycoprotein is synthesized as a precursor protein consisting of ~1,300 amino acids that is then cleaved into an amino (N)-terminal S1 subunit (~700 amino acids) and a carboxyl (C)-terminal S2 subunit (~600 amino acids). Three S1/S2 heterodimers assemble to form a trimer spike protruding from the viral envelope. The S1 subunit contains a receptor-binding domain (RBD), while the S2 subunit contains a hydrophobic fusion peptide and two heptad repeat regions. Triggered by receptor binding, proteolytic processing and/or acidic pH in the cellular compartments, the class I viral fusion protein undergoes a transition from a metastable prefusion state to a stable postfusion state during infection, in which the receptor-binding subunit is cleaved, and the fusion subunit undergoes large-scale conformational rearrangements to expose the hydrophobic fusion peptide, induce the formation of a six-helix bundle, and bring the viral and cellular membranes close for fusion (Belouzard et al., 2012). The trimeric SARS coronavirus (SARS-CoV) S glycoprotein consisting of three S1-S2 heterodimers binds the cellular receptor angiotensin-converting enzyme 2 (ACE2) and mediates fusion of the viral and cellular membranes through a pre- to postfusion conformation transition (Song et al., 2018).

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