CREATIVE BIOMART®
Diagnostic Proteins

Recombinant SARS-CoV-2 (S477N, D614G Mutant) Spike Glycoprotein (S1), sFc-tagged

Product Information

Cat#	
HUM-348	
Product Name	
Recombinant SARS-CoV-2 (S477N, D614G Mutant) Spike Glycoprotein (S1), sFc-tagged	
Description	
SARS-CoV-2 (S477N, D614G mutant) spike glycoprotein (S1) is a recombinant antigen which contains the Spike protein amino acids 1-674 of subunit 1. This protein is manufactured in HEK293 mammalian cells to obtain more authentic post-translational modifications, compared to other expression systems. SARS-CoV-2, previously known as the 2019 Novel Coronavirus (2019-nCoV), causes the pandemic COVID-19 disease.	
Type	
Recombinant	
Gene	
Spike Glycoprotein (S1)	
Species	
SARS-CoV-2	
Source	
HEK293	
Synonyms	
SARS-CoV-2 (S477N, D614G Mutant) Spike Glycoprotein (S1)	
Formulation	
Dulbecco's phosphate buffered saline (DPBS) pH 7.4.	
Notes	

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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, including its disposal, in accordance with all regulations.

Tags

C-terminal sheep Fc

Background

The D614G amino acid mutation in the SARS-CoV-2 Spike protein emerged early during the COVID-19 pandemic, quickly becoming the dominant circulating strain of the coronavirus. The transition from D614 to G614 occurred asynchronously in different regions throughout the world, beginning in Europe, followed by North America and Oceania and then Asia (Korber et al., 2020). Virus mutations may increase in frequency due to natural selection, random genetic drift, or features of recent epidemiology and as such it can be difficult to differentiate when a virus mutation becomes common through fitness or by chance (Korber et al., 2020). The mutation is located on the Spike protein, in the interface between the individual spike protomers, that stabilize its mature trimeric form on the virion surface through hydrogen bonding (not in the receptor-binding; RBD) (Grubaugh et al., 2020). The Spike D614G amino acid change is caused by an A-to-G nucleotide mutation at position 23,403 in the Wuhan reference strain. It is almost always accompanied by three other mutations: a C-to-T mutation in the 50 UTR (position 241 relative to the Wuhan reference sequence), a silent C-to-T mutation at position 3,037, and a C-to-T mutation at position 14,408 that results in an amino acid change in RNA dependent RNA polymerase (RdRp P323L). The haplotype comprising these 4 genetically linked mutations is now the globally dominant form (Korber et al., 2020).
The G614 variant grows to a higher titer as pseudotyped virions and in infected individuals may be associated with higher upper respiratory tract viral loads, but not with increased disease severity. Despite finding that clinical samples from G614 infections have higher levels of viral RNA, it's still not clear if G614 is more infectious or transmissible than viruses containing D614. However, if it is the case that the mutation aids transmissibility, then the virus will be harder to control (Korber et al., 2020). The mutation has also been associated with increased sensitivity to neutralization of SARS-CoV-2 pseudoviruses in vitro and may stabilize a particular

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conformational state of the RBD (Weissman et al., 2020). Spike-pseudotyped lentivirus and intact SARS-CoV-2 virus in which the D614G mutation was introduced have been found to be up to 8-fold more effective at transducing cells than wild-type virus, in multiple cell lines, including human lung epithelial cells. Minimal differences in ACE2 receptor binding was observed between the Spike variants, but the G614 variant was more resistant to proteolytic cleavage in vitro and in human cells, suggesting a possible mechanism for the increased transduction (Daniloski et al., 2020; Huang et al., 2020).

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