CREATIVE BIOMART®
Diagnostic Proteins

Recombinant SARS-CoV-2 (A222V Mutant) Spike Glycoprotein (S1), sFc-tagged

Product Information

Cat#
HUM-326
Product Name
Recombinant SARS-CoV-2 (A222V Mutant) Spike Glycoprotein (S1), sFc-tagged
Description
SARS-CoV-2 Spike protein S1 containing A222V amino acid change. Increased transmissibility of the B.1.177 lineage may be associated with the presence of this mutation. 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 (A222V Mutant) Spike Glycoprotein (S1)
Formulation
DPBS
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.

Tags

C-terminal sheep Fc

Background

Coronaviruses have a large genome and encode a 3′-to-5′-exoribonuclease that permits high-fidelity replication and a range of tolerated variation by the viral RNA-dependent RNA polymerase (Denison et al., 2011). This coronavirus exonuclease extends the coronavirus genome size through preventing lethal mutagenesis imposed by error rates of viral RNA polymerase (Smith et al., 2014). Therefore, SARS-CoV-2 could acquire rare but favorable mutations with fitness advantages and immunological resistance due to natural selection (Grubaugh et al., 2020) and a number of mutations to the SARS-CoV-2 genome have been observed throughout the COVID-19 pandemic (Erol, 2021).
2.58 million SARS-CoV-2 mutations in 200865 samples from 155 different countries (sequences downloaded from GISAID, 28 Dec 2020) were compared to the ancestral reference SARS-CoV-2 Wuhan strain showing that the most frequent nonsynonymous mutations were D614G and A222V, which occurred 176436 and 47971 times in the spike glycoprotein S gene (Ward et al., 2021). A222V is present in the 20A.EU1 SARS-CoV-2 'cluster' (also designated as lineage B.1.177), which has been spreading in Europe and seems to have originated in Spain. Multiple introductions have occurred into the UK followed by transmission across the country, suggesting that this spread was likely associated with travel to/from Spain over the summer (COG-UK, 2020) and it has been speculated that the increased transmissibility of the B.1.177 lineage may be associated with the presence of this mutation. A222V is one of five amino acid replacements (D614G, A222V, N439K, Y453F and N501Y) investigated by The COVID-19 Genomics UK (COG-UK) Consortium. It is localized relatively far from the receptor-binding site in comparison with amino acid residues 453, 439 and 501, which are in the RBD region (COG-UK, 2020). The mutation is far from the main D614G mutation being located in the N-terminal domain of the S1 subunit. Both mutations D614G and A222V are located within areas defined as possible B-cell
epitopes which could provide to the virus an evasive immunological advantage to avoid B-

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cell response (Vilar & Isom, 2021).

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