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

Cat. No. S-304S **Lot. No.** (See product label)

SPECIFICATION

Product Overview	SARS-CoV-2 A222V mutant Spike S1 protein (A222V, AA17-674) with a Sheep Fc-tag at C-terminus was expressed in HEK293 with sheep Fc-tag and purified by affinity chromatography.
Species	SARS-COV-2
Source	HEK293
ProteinLength	17-674
Description	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. This coronavirus exonuclease extends the coronavirus genome size through preventing lethal mutagenesis imposed by error rates of viral RNA polymerase. Therefore, SARS-CoV-2 could acquire rare but favorable mutations with fitness advantages and immunological resistance due to natural selection and a number of mutations to the SARS-CoV-2 genome have been observed throughout the COVID-19 pandemic. 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. 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 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 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. 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-cell response.
Form	Liquid
Molecular Mass	Expected Molecular Weight: 101 kDa Observed Molecular Weight: 140 kDa
Purity	Greater than 95% purity.
Storage	Short Term Storage: -80 centigrade Long Term Storage: -80 centigrade Can be frozen.
Concentration	1 mg/mL
Storage Buffer	DPBS
Shipping	Dry Ice

GENE INFORMATION

Gene Name	S surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]
Official Symbol	S
Synonyms	S; surface glycoprotein; spike glycoprotein; surface glycoprotein; structural protein; spike protein
Gene ID	43740568
mRNA Refseq	MN908947
Protein Refseq	YP_009724390
SDS-PAGE	Coomassie-stained SDS-PAGE showing purified SARS-CoV-2 A222V mutant spike protein.