Recombinant SARS-CoV-2 (D614G, L84I, N439K Mutant) Spike Glycoprotein (S1), Sheep Fc-tagged

Cat. No. S-311S **Lot. No.** (See product label)

SPECIFICATION

Product Overview	SARS-CoV-2 D614G, L84I, N439K mutant spike subunit 1 contains Spike protein 1-674, C-terminally tagged with sheep Fc was manufactured in HEK293 cells and purified from culture supernatant by Protein G chromatography.
Species	SARS-COV-2
Source	HEK293
ProteinLength	1-674
Description	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. 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. 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). 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

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	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. 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. The mutation has also been associated with increased sensitivity to neutralization of SARS-CoV-2 pseudoviruses in vitro and may stabilize a particular conformational state of the RBD. 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.
Form	Liquid
Molecular Mass	Expected Molecular Weight: 73 kDa Observed Molecular Weight: 130 kDa
Purity	Greater than 95% purity.
Storage	Short Term Storage: -80 centigrade Long Term Storage: -80 centigrade

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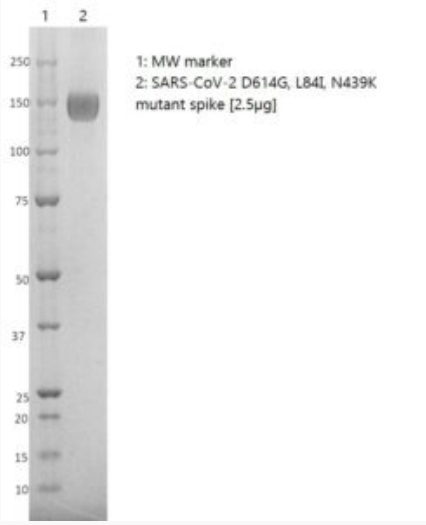
Storage Buffer	Dulbecco's phosphate buffered saline (DPBS) pH 7.4.
Shipping	Dry Ice

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	

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Coomassie-stained SDS-PAGE showing purified D614G, L84I, N439K mutant Spike protein.

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