

## 32-6253: COVID-19 Spike Glycoprotein-S1

**Alternative Name :** nCoV-S1

### Description

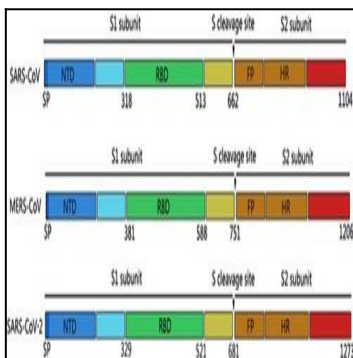
Source : HEK293

The HEK293 derived recombinant protein contains the Novel Coronavirus 2019-nCoV Spike Glycoprotein S1, Wuhan-Hu-1 strain, amino acids 1-674 fused to Sheep Fc tag at C-terminal.

A human infecting coronavirus (viral pneumonia) called 2019 novel coronavirus, 2019-nCoV was found in the fish market at the city of Wuhan, Hubei province of China on December 2019. The 2019-nCoV shares an 87% identity to the 2 bat-derived severe acute respiratory syndrome 2018 SARS-CoV-2 located in Zhoushan of eastern China. 2019-nCoV has an analogous receptor-BD-structure to that of 2018 SARS-CoV, even though there is a.a. diversity so thus the 2019-nCoV might bind to ACE2 receptor protein (angiotensin-converting enzyme 2) in humans. While bats are possibly the host of 2019-nCoV, researchers suspect that animal from the ocean sold at the seafood market was an intermediate host. RSCU analysis proposes that the 2019-nCoV is a recombinant within the viral spike glycoprotein between the bat coronavirus and an unknown coronavirus.

### Product Info

- Amount :** 50 µg / 150 µg
- Purification :** Protein is >85% pure as determined SDS-PAGE.
- Content :** nCoV-S1 protein solution is supplied in DPBS.
- Storage condition :** Protein is shipped on ice packs. Upon arrival, Store at -20°C.
- Amino Acid :** The HEK293 derived recombinant protein contains the Novel Coronavirus 2019-nCoV Spike Glycoprotein S1, Wuhan-Hu-1 strain, amino acids 1-674 fused to Fc tag at C-terminal.



Structural diagrams of spike glycoproteins of SARS-CoV, MERS-CoV, and SARS-CoV-2. All spike proteins of coronaviruses contain S1 subunit and S2 subunit, which were divided by the S cleavage sites. FP, fusion peptide; HR, heptad repeat 1 and heptad repeat 2; RBD, receptor-binding domain, contains core binding motif in the external subdomain; SP, signal peptide. Adapted from Composition and divergence of coronavirus spike proteins and host ACE2 receptors predict potential intermediate hosts of SARS-CoV-2. Liu Z, et al. J Med Virol. 2020 Feb 26. doi: 10.1002/jmv.25726.