

SARS-CoV-2 S glycoprotein (HEK293, His-mFc)

Cat. No.:	HY-P72038
Synonyms:	Spike glycoproteinRBD; ,Spike Protein RBD;
Species:	Virus
Source:	HEK293
Accession:	P0DTC2 (R319-F541)
Gene ID:	43740568
Molecular Weight:	Approximately 66.0 kDa. The reducing (R) protein migrates as 66 kDa in SDS-PAGE may be due to glycosylation.

PROPERTIES

AA Sequence	<pre> RVQPTESIVR FPNITNLCPF GEVFNATRFA SVYAWNKRKI SNCVADYSVL YNSASFSTFK CYGVSPTKLN DLCFTNVYAD SFVIRGDEV R QIAPGQTGKI ADYNYKLPDD FTGCVIAWNS NNLDSKVGGN YNYLYRFRK SNLKPFERDI STEIYQAGST PCNGVEGFNC YFPLQSYGFQ PTNGVGYQPY RVVVLSELL HAPATVCGPK KSTNLVKKNC VNF </pre>
Biological Activity	Measured by its binding ability in a functional ELISA. Immobilized human ACE2 at 0.38147-50000 µg/mL can bind SARS-CoV-2-S1-RBD at 0.2 µg/well, the EC ₅₀ of SARS-CoV-2-S1-RBD protein is 26.45-45.47 ng/mL.
Appearance	Lyophilized powder.
Formulation	Lyophilized from a 0.2 µm sterile filtered PBS, 6% Trehalose, pH 7.4.
Endotoxin Level	<1 EU/µg, determined by LAL method.
Reconstitution	It is not recommended to reconstitute to a concentration less than 100 µg/mL in ddH ₂ O.
Storage & Stability	Stored at -20°C for 2 years. After reconstitution, it is stable at 4°C for 1 week or -20°C for longer (with carrier protein). It is recommended to freeze aliquots at -20°C or -80°C for extended storage.
Shipping	Room temperature in continental US; may vary elsewhere.

DESCRIPTION

Background	The SARS-CoV-2 S glycoprotein plays a crucial role in infection by attaching the virion to the host cell membrane through
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interaction with the primary receptor, host ACE2. Upon cleavage of S2/S2', binding to the ACE2 receptor initiates either direct fusion at the cell membrane or internalization of the virus via endocytosis, leading to fusion of the virion membrane with the host endosomal membrane. Additionally, the glycoprotein may utilize NRP1/NRP2 and integrin as alternative entry receptors, possibly explaining the virus's tropism in human olfactory epithelial cells. The stalk domain of S exhibits three hinges, providing unexpected orientational freedom to the head. Acting as a class I viral fusion protein, the glycoprotein undergoes an extensive and irreversible conformational change during virus entry, triggered by host TMPRSS2 or CSTL, leading to fusion of the viral envelope with the cellular cytoplasmic membrane and release of viral genomic RNA into the host cell cytoplasm. The glycoprotein exhibits at least three conformational states: pre-fusion native, pre-hairpin intermediate, and post-fusion hairpin, with the coiled coil regions adopting a trimer-of-hairpins structure during fusion, facilitating the apposition and subsequent fusion of viral and target cell membranes.

Caution: Product has not been fully validated for medical applications. For research use only.

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