

SARS-CoV-2 Spike S1 NTD Protein (L18F & D80A & D215G & LAL242-244 deletion & R246I, His)

General Information

Protein Construction:	A DNA sequence encoding the SARS-CoV-2 (2019-nCoV) Spike S1 NTD (YP_009724390.1, with mutations L18F, D80A, D215G, LAL242-244 deletion, R246I) (Met1-Ser305) was expressed with a polyhistidine tag at the C-terminus. The mutations were identified in the SARS-CoV-2 variant (known as 20C/501Y.V2 or B.1.351 lineage) which emerged in South Africa. Predicted N terminal: Val 16
Species:	SARS-CoV-2
Expression Host:	HEK293 Cells
Accession:	A0A6G7K2L4
Molecular Weight:	33.9 kDa (predicted); 56 kDa (reducing condition, due to glycosylation)

QC Testing

Biological Activity:	Activity testing is in progress. It is theoretically active, but we cannot guarantee it. If you require protein activity, we recommend choosing the eukaryotic expression version first.
Purity:	> 95 % as determined by SDS-PAGE.
Endotoxin:	< 1.0 EU/μg of the protein as determined by the LAL method.
Formulation:	Lyophilized from a solution filtered through a 0.22 μm filter, containing PBS, pH 7.4. Typically, a mixture containing 5% to 8% trehalose, mannitol, and 0.01% Tween 80 is incorporated as a protective agent before lyophilization.

Preparation and Storage

Reconstitution:
A Certificate of Analysis (CoA) containing reconstitution instructions is included with the products. Please refer to the CoA for detailed information.

Stability & Storage:

It is recommended to store recombinant proteins at -20°C to -80°C for future use. Lyophilized powders can be stably stored for over 12 months, while liquid products can be stored for 6-12 months at -80°C. For reconstituted protein solutions, the solution can be stored at -20°C to -80°C for at least 3 months. Please avoid multiple freeze-thaw cycles and store products in aliquots.

Actual storage temperature shall be subject to the COA.

Shipping:

In general, lyophilized powders are shipped with blue ice, while solutions are shipped with dry ice.

Protein Background

The spike (S) glycoprotein of coronaviruses contains protrusions that will only bind to certain receptors on the host cell. Known receptors bind S1 are ACE2, angiotensin-converting enzyme 2; DPP4, dipeptidyl peptidase-4; APN, aminopeptidase N; CEACAM, carcinoembryonic antigen-related cell adhesion molecule 1; Sia, sialic acid; O-ac Sia,

O-acetylated sialic acid. The spike is essential for both host specificity and viral infectivity. The term 'peplomer' is typically used to refer to a grouping of heterologous proteins on the virus surface that function together. The spike (S) glycoprotein of coronaviruses is known to be essential in the binding of the virus to the host cell at the advent of the infection process. It's been reported that SARS-CoV-2 (COVID-19 coronavirus, 2019-nCoV) can infect the human respiratory epithelial cells through interaction with the human ACE2 receptor. The spike protein is a large type I transmembrane protein containing two subunits, S1 and S2. S1 mainly contains a receptor binding domain (RBD), which is responsible for recognizing the cell surface receptor. S2 contains basic elements needed for the membrane fusion. The S protein plays key parts in the induction of neutralizing-antibody and T-cell responses, as well as protective immunity. The main functions for the Spike protein are summarized as: Mediate receptor binding and membrane fusion; Defines the range of the hosts and specificity of the virus; Main component to bind with the neutralizing antibody; Key target for vaccine design; Can be transmitted between different hosts through gene recombination or mutation of the receptor binding domain (RBD), leading to a higher mortality rate.

Reference

Xiao X, et al. (2004) The SARS-CoV S glycoprotein. *Cell Mol Life Sci.* 61 (19-20): 2428-30.

Shen S, et al. (2007) Expression, glycosylation, and modification of the spike (S) glycoprotein of SARS CoV. *Methods Mol Biol.* 379: 127-35.

Du L, et al. (2009) The spike protein of SARS-CoV--a target for vaccine and therapeutic development. *Nat Rev Microbiol.* 7 (3): 226-36.

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