Recombinant SARS-CoV-2 XD Spike S1 Subunit NTD His-tag

Catalog Number: 11208-CV

DESCRIPTION

Source	Human embryonic kidney cell, HEK293-derived sars-cov-2 Spike S1 Subunit protein Val16-Leu303 (Thr19Arg, Ala27Ser, Thr95Ile, Gly142Asp, Glu156Gly, Phe157del, Arg158del, Asn211del, Leu212Ile, Glu-Pro-Glu214ins), with a C-terminal 6-His tag Accession # YP_009724390.1
N-terminal Sequence Analysis	Val16
Predicted Molecular Mass	34 kDa

SPECIFICATIONS

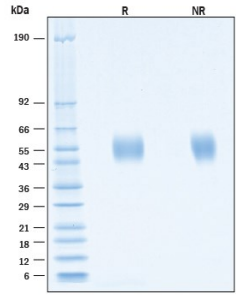
SDS-PAGE	53-59 kDa, under reducing conditions.
Activity	Bioassay data are not available.
Endotoxin Level	<0.10 EU per 1 µg of the protein by the LAL method.
Purity	>95%, by SDS-PAGE visualized with Silver Staining and quantitative densitometry by Coomassie® Blue Staining.
Formulation	Lyophilized from a 0.2 µm filtered solution in PBS with Trehalose. See Certificate of Analysis for details.

PREPARATION AND STORAGE

Reconstitution	Reconstitute at 500 µg/mL in PBS.
Shipping	The product is shipped at ambient temperature. Upon receipt, store it immediately at the temperature recommended below.
Stability & Storage	**Use a manual defrost freezer and avoid repeated freeze-thaw cycles.** • 12 months from date of receipt, -20 to -70 °C as supplied. • 1 month, 2 to 8 °C under sterile conditions after reconstitution. • 3 months, -20 to -70 °C under sterile conditions after reconstitution.

DATA

SDS-PAGE



Recombinant SARS-CoV-2 XD Spike S1 Subunit NTD His-tag Protein SDS-PAGE. 2 µg/lane of Recombinant SARS-CoV-2 XD Spike S1 Subunit NTD His-tag Protein (Catalog # 11208-CV) was resolved with SDS-PAGE under reducing (R) and non-reducing (NR) conditions and visualized by Coomassie® Blue staining, showing bands at 53-59 kDa.

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BACKGROUND

SARS-CoV-2, which causes the global pandemic coronavirus disease 2019 (Covid-19), belongs to a family of viruses known as coronaviruses that also include MERS-CoV and SARS-CoV-1. Coronaviruses are commonly comprised of four structural proteins: Spike protein (S), Envelope protein (E), Membrane protein (M) and Nucleocapsid protein (N) (1). The SARS-CoV-2 S protein is a glycoprotein that mediates membrane fusion and viral entry. The S protein is homotrimeric, with each ~180-kDa monomer consisting of two subunits, S1 and S2 (2). In SARS-CoV-2, as with most coronaviruses, proteolytic cleavage of the S protein into S1 and S2 subunits is required for activation. The S1 subunit is focused on attachment of the protein to the host receptor, while the S2 subunit is involved with cell fusion (3-5). The S1 subunit can be further divided into an N-terminal domain (NTD) and a receptor binding domain (RBD). The SARS-CoV-2 NTD shares 50% and 20% amino acid (aa) sequence identity with the NTD of SARS-CoV-1 and MERS-CoV, respectively. The NTD is reported to bind L-SIGN and DC-SIGN in cells that don't express the ACE2 receptor (6). Despite being heavily glycosylated, the NTD is capable of eliciting an immune response to produce potent neutralization antibodies, although at a reduced level than the ones targeting the RBD. Three immunogenic regions have been identified in the NTD: aa 14-20, aa 140-158, and aa 245-264 (7). Antibody cocktails targeting both NTD and RBD could provide better protection against SARS-CoV-2 infection.The XD variant is a hybrid of the delta and omicron genome (8).

References:

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