

DESCRIPTION

Source	<i>Trichoplusia ni</i> , <i>T. ni</i> (baculovirus)-derived sars-cov-2 Spike S2 Subunit protein Ser686-Lys1211, with a C-terminal 6-His tag Accession # YP_009724390.1
N-terminal Sequence Analysis	Ser686
Predicted Molecular Mass	60 kDa

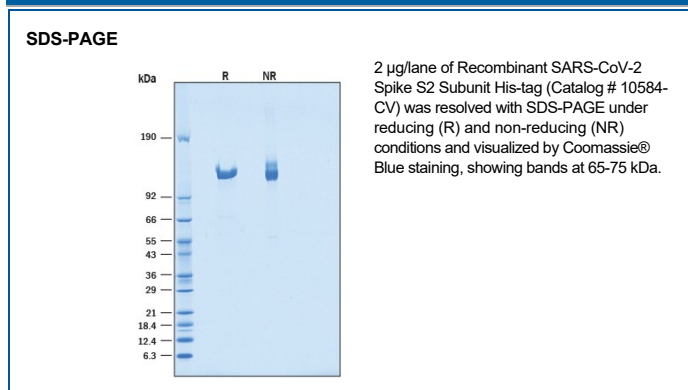
SPECIFICATIONS

SDS-PAGE	65-75 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. <ul style="list-style-type: none"> • 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



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 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). SARS-CoV-2 Spike Protein (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). As with most coronaviruses, proteolytic cleavage of the S protein into two distinct peptides, 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 (2-4). A metalloproteinase, angiotensin-converting enzyme 2 (ACE-2), has been identified as a functional receptor for SARS-CoV2, similar to SARS-CoV-1, through interaction with a receptor binding domain (RBD) located at the C-terminus of S1 subunit (5, 6). The S2 subunit of SARS-CoV-2 shares 90% and 41% amino acid sequence identity with the S2 subunit of SARS-CoV-1 and MERS, respectively. It has been demonstrated the S Protein can invade host cells through the CD147/EMMPRIN receptor and mediate membrane fusion (7, 8).

References:

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5. Li, W. *et al.* (2003) *Nature* **426**:450.
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7. Wang, X. *et al.* (2020) <https://doi.org/10.1038/s41423-020-0424-9>.
8. Wang, K. *et al.* (2020) *bioRxiv* <https://www.biorxiv.org/content/10.1101/2020.03.14.988345v1>.