

Store at
-80°C

#88587

SARS-CoV-2 Spike S1-NTD (16-316) Recombinant Protein (8xHis-Tag)

100 µg

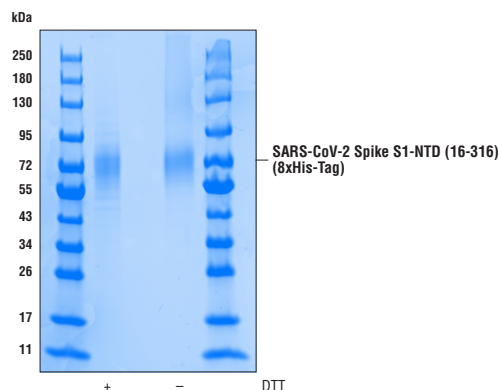
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UniProt ID #P0DTC2

New 06/20

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Description: SARS-CoV-2 Spike S1-NTD (16-316) Recombinant Protein (8xHis-Tag) is derived from a recombinant expression construct corresponding to the amino terminal domain (NTD) of the S1 fragment of SARS-CoV-2 spike protein. The expressed protein contains an 8xHis-Tag at its carboxy terminus.

Background: The cause of the COVID-19 pandemic is a novel and highly pathogenic coronavirus, termed SARS-CoV-2 (severe acute respiratory syndrome coronavirus-2). The origin of the virus has been traced to an outbreak of infections in the city of Wuhan, China, in December 2019. SARS-CoV-2 is a member of the Coronaviridae family of viruses (1). The genome of SARS-CoV-2 is similar to other coronaviruses, and is comprised of four key structural proteins: S, the spike protein, E, the envelope protein, M, the membrane protein, and N, the nucleocapsid protein (2). Coronavirus spike proteins are class I fusion proteins and harbor an ectodomain, a transmembrane domain, and an intracellular tail (3,4). The highly glycosylated ectodomain projects from the viral envelope surface and facilitates attachment and fusion with the host cell plasma membrane. The ectodomain can be further subdivided into host receptor-binding domain (RBD) (S1) and membrane-fusion (S2) subunits, which are produced upon proteolysis by host proteases at S1/S2 and S2' sites. S1 and S2 subunits remain associated after cleavage and assemble into crown-like homotrimers (2,4). In humans, both SARS-CoV and SARS-CoV-2 spike proteins utilize the angiotensin-converting enzyme 2 (ACE2) protein as a receptor for cellular entry (5-7). Spike protein subunits represent a key antigenic feature of coronavirus virions, and therefore represent an important target of vaccines, novel therapeutic antibodies, and small-molecule inhibitors (8,9).



The purity of SARS-CoV-2 Spike S1-NTD (16-316) Recombinant Protein (8xHis-Tag) was determined by densitometry after SDS-PAGE of 2 µg of protein, followed by staining with Coomassie Blue. Purity values were determined from the DTT-reduced samples (+).

Molecular Weight: 35 kDa (reduced and non-reduced)**Formulation:**

Expression Host: Human (HEK293 cells)

Supplied in a PBS solution (pH 7.2).

Purity: 97%, determined by SDS-PAGE.**Storage:** Stable at -80°C for 1 year after receipt. Avoid repeated freeze-thaw cycles.**Background References:**

- (1) Zhou, P. et al. (2020) *Nature* 579, 270-3.
- (2) Tortorici, M.A. and Veerle, D. (2019) *Adv Virus Res* 105, 93-116.
- (3) Li, F. et al. (2006) *J Virol* 80, 6794-800.
- (4) Li, F. (2016) *Annu Rev Virol* 3, 237-61.
- (5) Shang, J. et al. (2020) *Nature* 581, 221-4.
- (6) Wrapp, D. et al. (2020) *Science* 367, 1260-3.
- (7) Yan, R. et al. (2020) *Science* 367, 1444-8.
- (8) Yuan, Y. et al. (2017) *Nat Commun* 8, 15092.
- (9) Amanat, F. and Krammer, F. (2020) *Immunity* 52, 583-9.

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Applications: W—Western IP—Immunoprecipitation IHC—Immunohistochemistry ChIP—Chromatin Immunoprecipitation IF—Immunofluorescence F—Flow cytometry E-P—ELISA-Peptide **Species Cross-Reactivity:** H—human M—mouse R—rat Hm—hamster Mk—monkey Mi—mink C—chicken Dm—D. melanogaster X—Xenopus Z—zebrafish B—bovine Dg—dog Pg—pig Sc—S. cerevisiae Ce—C. elegans Hr—Horse All—all species expected Species enclosed in parentheses are predicted to react based on 100% homology.