Biotinylated Recombinant SARS-CoV-2 B.1.1.7 N501Y Spike RBD His-tag

Catalog Number: BT10730

DESCRIPTION

Source	Human embryonic kidney cell, HEK293-derived sars-cov-2 Spike RBD protein Arg319-Phe541 (Asn501Tyr), with a C-terminal 6-His tag Accession # YP_009724390.1
N-terminal Sequence Analysis	Arg319
Structure / Form	Biotinylated via amines
Predicted Molecular Mass	26 kDa

SPECIFICATIONS

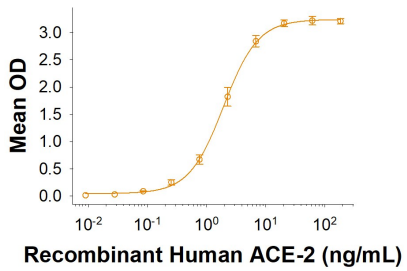
SDS-PAGE	30-40 kDa, under reducing conditions
Activity	Measured by its binding ability in a functional ELISA with Recombinant Human ACE-2 Fc Chimera (Catalog # 10544-ZN).
Endotoxin Level	<1.0 EU per 1 µg of the protein by the LAL method.
Purity	>95%, by SDS-PAGE visualized with Silver Staining and quantitative 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.

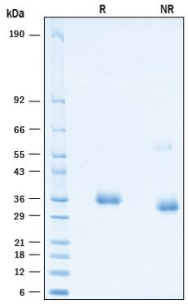
DATA

Binding Activity



Recombinant SARS-CoV-2 B.1.1.7 N501Y S RBD Biotin Protein Binding Activity Biotinylated Recombinant SARS-CoV-2 B.1.1.7 N501Y Spike RBD His-tag (Catalog # BT10730) binds Recombinant Human ACE-2 Fc Chimera (Catalog # 10544-ZN) in a functional ELISA.

SDS-PAGE



Recombinant SARS-CoV-2 B.1.1.7 N501Y S RBD His-tag Biotinylated Protein SDS-PAGE 2 µg/lane of Biotinylated Recombinant SARS-CoV-2 B.1.1.7 N501Y S RBD His-tag Protein CF (Catalog # BT10730) was resolved with SDS-PAGE under reducing (R) and non-reducing (NR) conditions and visualized by Coomassie® Blue staining, showing bands at 30-40 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 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). A metallopeptidase, angiotensin-converting enzyme 2 (ACE2), has been identified as a functional receptor for SARS-CoV-2 through interaction with a receptor binding domain (RBD) located at the C-terminus of S1 subunit (6,7). The RBD of SARS-CoV-2 shares 73% aa identity with the RBD of the SARS-CoV-1, but only 22% amino acid (aa) identity with the RBD of MERS. A SARS-CoV-2 variant carrying the aa substitution N501Y in the RBD is one of the most prevalent mutations found Covid-19 cases (8-10). This mutation was first identified in the virus variant (B.1.1.7 lineage) originally found in London and the southeast UK but rapidly spread globally (8,9). This new virus variant was reported 56% more transmissible than other preexisting variants (11). The N501Y mutation was also later identified in variants found in South Arica (B.1.351 lineage) and Brazil (P.1 lineage). Although there is no evidence to date that B.1.1.7 causes more severe illness, whether the N501Y mutation in RBD would decrease the efficacy of vaccine-induced immunity is still under investigation.

References:

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