

DESCRIPTION

Source	Human embryonic kidney cell, HEK293-derived sars-cov-2 Spike RBD protein		
	SARS-CoV-2 Spike RBD protein Arg319-Phe541 (Lys417Asn, Glu484Lys, Asn501Tyr), Accession # YP_009724390.1	6-His tag	Avi-tag
	N-terminus		C-terminus
N-terminal Sequence Analysis	Arg319		
Structure / Form	Biotinylated via Avi-tag		
Predicted Molecular Mass	26 kDa		

SPECIFICATIONS

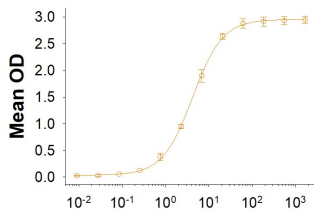
SDS-PAGE	35-40 kDa, under reducing conditions.
Activity	Measured by its binding ability in a functional ELISA with Recombinant Human ACE-2 Fc Chimera (Catalog # 10544-ZN).
Endotoxin Level	<0.10 EU per 1 µg of the protein by the LAL method.
Purity	>95%, by SDS-PAGE visualized with Silver Staining and 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	<p>Use a manual defrost freezer and avoid repeated freeze-thaw cycles.</p> <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

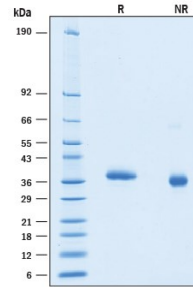
Binding Activity



Biotinylated Recombinant SARS-CoV-2 B.1.351 Spike RBD His-tag Avi-tag (ng/mL)

Biotinylated Recombinant SARS-CoV-2 B.1.351 S RBD His-tag Avi-tag Protein Binding Activity. Biotinylated Recombinant SARS-CoV-2 B.1.351 Spike RBD His-tag Avi-tag (Catalog # AV110735) binds Recombinant Human ACE-2 Fc Chimera (Catalog # 10544-ZN) in a functional ELISA.

SDS-PAGE



Biotinylated Recombinant SARS-CoV-2 B.1.351 S RBD His-tag Avi-tag Protein SDS-PAGE. 2 µg/lane of Biotinylated Recombinant SARS-CoV-2 B.1.351 Spike RBD His-tag Avi-tag (Catalog # AV110735) was resolved with SDS-PAGE under reducing (R) and non-reducing (NR) conditions and visualized by Coomassie® Blue staining, showing bands at 32-38 kDa.

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 metalloproteinase, 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% amino acid (aa) identity with the RBD of the SARS-CoV-1, but only 22% aa identity with the RBD of MERS. A SARS-CoV-2 variant carrying amino acid substitutions N501Y, K417N, and E484K in the RBD raised the most concerns. This B.1.351 lineage, also known as 501Y.V2 variant, was first identified in the Eastern Cape province of South Africa in December 2020 and spread quickly to become the most dominant strain in the second COVID wave in South Africa (8). Two of these mutations K417N and E484K locate at the receptor binding motif (RBM) and are not found in other variants (8). The N501Y mutation is also found in London (B.1.1.7 lineage) and Brazil (P.1 lineage). The B.1.351 lineage is reported to enter cells more easily due to its enhanced affinity to ACE-2 receptor (9). It is reported to reduce the efficacy of neutralizing antibody (9, 10). Our Avi-tag Biotinylated Recombinant SARS-CoV-2 B.1.351 Spike RBD features biotinylation at a single site contained within the Avi-tag, a unique 15 amino acid peptide. Protein orientation will be uniform when bound to streptavidin-coated surface due to the precise control of bionylation and the rest of the protein is unchanged so there is no interference in the protein bioactivity.

References:

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4. Belouzard, S. *et al.* (2009) *Proc. Natl. Acad. Sci.* **106**:5871.
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6. Li, W. *et al.* (2003) *Nature* **426**:450.
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8. Tegally, H. *et al.* (2020) *BioRxiv*. doi: <https://doi.org/10.1101/2020.12.21.20248640>.
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