

DESCRIPTION

Source	Human embryonic kidney cell, HEK293-derived sars-cov-2 Spike protein		
	Recombinant SARS-CoV-2 Spike (Val16-Lys1211)(Gly142Asp, Glu154Lys, Leu452Arg, Glu484Gln, Asp614Gly, Pro681Arg, Gln1071His)(Arg682Ser, Arg685Ser, Lys986Pro, Val987Pro) Accession # YP_009724390.1	GCN4-IZ	6-His tag
	N-terminus		C-terminus
N-terminal Sequence Analysis	Val16		
Structure / Form	Labeled with Alexa Fluor® 488 via amines		
	Excitation Wavelength: 488 nm Emission Wavelength: 515-545 nm		
Predicted Molecular Mass	138 kDa		

SPECIFICATIONS

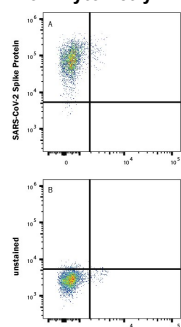
SDS-PAGE	139-167 kDa, under reducing conditions.
Activity	Measured by flow cytometry for its ability to bind HEK293 human embryonic kidney cells transfected with human ACE-2 at 0.25-1.00 µg/mL (100 µL/well). Please Note: Optimal dilutions should be determined by each laboratory for each application.
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	Supplied as a 0.2 µm filtered solution in PBS with BSA as a carrier protein. See Certificate of Analysis for details.

PREPARATION AND STORAGE

Shipping	The product is shipped with dry ice or equivalent. Upon receipt, store it immediately at the temperature recommended below.
Stability & Storage	Protect from light. Use a manual defrost freezer and avoid repeated freeze-thaw cycles. <ul style="list-style-type: none"> • 6 months from date of receipt, -20 to -70 °C as supplied. • 1 month, 2 to 8 °C under sterile conditions after opening. • 3 months, -20 to -70 °C under sterile conditions after opening.

DATA

Flow Cytometry



Detection of ACE-2 on HEK293 Transfectants with Recombinant SARS-CoV-2 B.1.617.1 Spike (GCN4-IZ) His-tag Alexa Fluor® 488 by Flow Cytometry. HEK293 human embryonic kidney cells transfected with human ACE-2 were stained with (A) 1 µg/mL (100 µL/well) Recombinant SARS-CoV-2 B.1.617.1 Spike (GCN4-IZ) His-tag Alexa Fluor® 488 Protein (Catalog # AFG10861) or (B) unstained.

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 metalloprotease, angiotensin-converting enzyme 2 (ACE-2), 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 S protein of SARS-CoV-2 shares 75% and 29% amino acid sequence identity with S protein of SARS-CoV-1 and MERS, respectively. A SARS-CoV-2 variant (B.1.617.1) carrying the amino acid substitution L452R and E484Q in the RBD was identified as a prevalent strain in India (8, 9). Whether these mutations in RBD would cause more severe symptom or decrease the efficacy of vaccine-induced immunity is still under investigation.

References:

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9. Cherian, S. *et al.* (2021) *bioRxiv* <https://doi.org/10.1101/2021.04.22.440932>.

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