Recombinant SARS-CoV-2 B.1.1.7 Spike (GCN4-IZ) His-tag Alexa Fluor® 488

Catalog Number: AFG10796

DESCRIPTION

Source

Human embryonic kidney cell, HEK293-derived sars-cov-2 Spike protein

SARS-CoV-2 B.1.1.7 Spike (Val16-Lys1211)(His69del, Val70del, Tyr145del, Asn501Tyr, Ala570Asp, Asp614Gly, Pro681His, Thr716Ile, Ser982Ala, Asp1118His)(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

140-170 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.

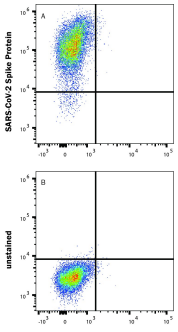
Stability & Storage

Protect from light. Use a manual defrost freezer and avoid repeated freeze-thaw cycles.

- 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.

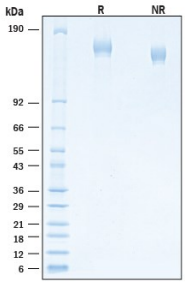
DATA

Flow Cytometry



Detection of ACE-2 on HEK293 Transfectants with Recombinant SARS-CoV-2 B.1.1.7 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.1.1.7 Spike (GCN4-IZ) His-tag Alexa Fluor® 488 Protein (Catalog # AFG10796) or (B) unstained.

SDS-PAGE



Recombinant SARS-CoV-2 S GCN4-IZ Alexa Fluor® 488 Protein SDS-PAGE. 2 µg/lane of Recombinant SARS-CoV-2 S GCN4-IZ Alexa Fluor® 488 Protein (Catalog # AFG10796) was resolved with SDS-PAGE under reducing (R) and non-reducing (NR) conditions and visualized by Coomassie® Blue staining, showing bands at 140-170 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-CoV 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). 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. The S Protein of the SARS-CoV-2 virus, like the SARS-CoV-1 counterpart, binds a metallopeptidase, Angiotensin-Converting Enzyme 2 (ACE-2), but with much higher affinity and faster binding kinetics through the receptor binding domain (RBD) located in the C-terminal region of S1 subunit (6). It has been demonstrated that the S Protein can invade host cells through the CD147/EMMPRIN receptor and mediate membrane fusion (7, 8). Polyclonal antibodies to the RBD of the SARS-CoV-2 protein have been shown to inhibit interaction with the ACE-2 receptor, confirming RBD as an attractive target for vaccinations or antiviral therapy (9). There is also promising work showing that the RBD may be used to detect presence of neutralizing antibodies present in a patient's bloodstream, consistent with developed immunity after exposure to the SARS-CoV-2 (10). Several emerging SARS-CoV-2 genomes have been identified including the B 1.1.7 (United Kingdom) variant (11). The B 1.1.7 variant contains 1 significant mutation of interest in the RBD domain, N501Y, which has been shown to result in enhanced binding affinity for hACE-2 (12). Further, the B 1.1.7 variant appears to more easily transmissible, exhibit increased viral loads and, potentially, be associated with higher mortality rates compared to preexisting variants (11, 13).

References:

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