Recombinant SARS-CoV-2 B.1.351 Spike (GCN4-IZ) His-tag Alexa Fluor® 488

Catalog Number: AFG10786

DESCRIPTION

Source

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

SARS-CoV-2 B.1.351 Spike (Val16-Lys1211) (Asp80Ala, Asp215Gly, Leu242 del, Ala243 del, Leu244 del, Lys417Asn, Glu484Lys, Asn501Tyr, Asp614Gly, Ala701Val) (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

145-168 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.

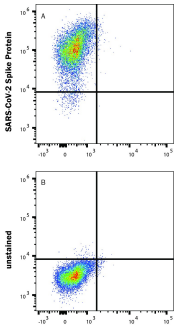
Stability & Storage

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.

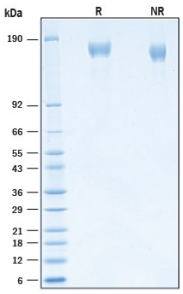
DATA

Flow Cytometry



Detection of ACE-2 on HEK293 Transfectants with Recombinant SARS-CoV-2 B.1.351 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.1.351 Spike (GCN4-IZ) His-tag Alexa Fluor® 488 (Catalog # AFG10786) or (B) unstained.

SDS-PAGE



Recombinant SARS-CoV-2 B.1.351 Spike (GCN4-IZ) His-tag Alexa Fluor® 488 Protein SDS-PAGE. 2 µg/lane of Recombinant SARS-CoV-2 B.1.351 Spike (GCN4-IZ) His-tag Alexa Fluor® 488 Protein (Catalog # AFG10786) was resolved with SDS-PAGE under reducing (R) and non-reducing (NR) conditions and visualized by Coomassie® Blue staining, showing bands at 145-168 kDa.

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Global bio-techne.com info@bio-techne.com techsupport@bio-techne.com TEL +1 612 379 2956
USA TEL 800 343 7475 Canada TEL 855 668 8722 China TEL +86 (21) 52380373
Europe | Middle East | Africa TEL +44 (0)1235 529449

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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 are commonly comprised of four structural proteins: Spike protein (S), Envelope protein (E), Membrane protein (M), and Nucleocapsid protein (N) (1). SARS-CoV-2 Spike Protein (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 the 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 (aa) sequence identity with the 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 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 (6). Based on structural biology studies, the RBD can be oriented either in the up/standing or down/lying state with the up/standing state associated with higher pathogenicity (7). 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 (8). It has been demonstrated that the S Protein can invade host cells through the CD147/EMMPRIN receptor and mediate membrane fusion (9, 10). 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 and 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 (11). Two of these mutations K417N and E484K locate at the receptor binding motif (RBM) and are not found in other variants (11). 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 (12). It is reported to reduce the efficacy of neutralizing antibody (12, 13).

References:

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