Recombinant SARS-CoV-2 B.1.620 Spike (GCN4-IZ) His-tag

Catalog Number: 10917-CV

DESCRIPTION

Source

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

Recombinant SARS-CoV-2 B.1.620 Spike (Val16-Lys1211) (Pro26Ser, His69del, Val70del, Val126Ala, Tyr144del, Lys242del, Ala243del, Lys244del, His245Tyr, Ser477Asn, Glu484Lys, Asp614Gly, Pro681His, Thr1027Ile, Asp1118His) (Arg682Ser, Arg685Ser, Lys986Pro, Val987Pro) Accession # YP_009724390.1	GCN4-IZ	6-His tag
N-terminus		C-terminus

N-terminal Sequence Analysis	Val 16
Predicted Molecular Mass	137 kDa

SPECIFICATIONS

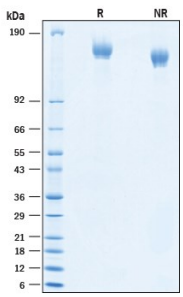
SDS-PAGE	150-170 kDa, under reducing conditions.
Activity	Measured by its binding ability in a functional ELISA with Recombinant Human ACE-2 His-tag (Catalog # 933-ZN).
Endotoxin Level	<0.10 EU per 1 µg of the protein by the LAL method.
Purity	>95%, by SDS-PAGE visualized with Silver Staining and quantitative 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	**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

SDS-PAGE



Recombinant SARS-CoV-2 B.1.620 Spike (GCN4-IZ) His-tag Protein SDS-PAGE. 2 µg/lane of Recombinant SARS-CoV-2 B.1.620 Spike (GCN4-IZ) His-tag Protein (Catalog # 10917-CV) was resolved with SDS-PAGE under reducing (R) and non-reducing (NR) conditions and visualized by Coomassie® Blue staining, showing bands at 150-170 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% aa 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 with mutations compared to the Wuhan-Hu-1 SARS-CoV-2 reference sequence. The B.1.620 variant was identified in Lithuania but most likely orginiated in central Africa and it contains several mutations of interest that effect viral fitness and transmissibility including S477N, E484K, D614G, and P681H (11). Both S477N and E484K mutations are found in the same loop of the RBD domain at the edge of the ACE-2 binding interface (12). The S477N mutation has been identified enhancing the affinity for hACE-2 and resistance to multiple neutralizing mAbs (13, 14). Structural analysis points to E484K as a potentially crucial mutation as it creates a new site for hACE-2 binding and may enhance binding affinity (13). The D614G mutation is located nearby to the RBD domain and has been shown to increase viral infectivity (15). The P618H mutation is found adjacent to the furin cleavage site and is proposed to enhance S protein cleavage and increase viral infectivity (16). Additionally, the E484K substitution alone has been shown to confer resistance to several monoclonal antibodies and is responsible for the first confirmed SARS-CoV-2 reinfection (17).

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