

Recombinant SARS-CoV-2 (B.1.1.28) Spike Glycoprotein (S1) RBD, His-tagged

Cat. No. HUM-327 **Lot. No.** (See product label)

SPECIFICATION

Product Overview

SARS-CoV-2 (B.1.1.28) RBD mutant from Brazilian variant. Contains amino acid changes K417T, E484K, N501Y relative to Wuhan Hu-1. The protein was produced in HEK293 cells and purified from culture supernatant. SARS-CoV-2, previously known as the 2019 Novel Coronavirus (2019-nCoV), causes the pandemic COVID-19 disease.

Tag His

Background

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is the virus that causes coronavirus disease 2019 (COVID-19). The sequence WIV04/2019, belonging to the GISAID S clade / PANGOLIN A lineage / Nextstrain 19B clade, is believed to be the original sequence infecting humans (Zhukova et al., 2020). However, there are many thousands of variants of SARS-CoV-2 (Koyama et al., 2020) and subtypes of the virus can be placed into much larger groupings such as lineages or clades. In Brazil, a variant of SARS-CoV-2 known as P.1 (20J/501Y.V3, Variant of Concern 202101/02) emerged that was first identified in four travelers from Brazil, who were tested during routine screening at Haneda airport outside Tokyo, Japan. The P.1 variant contains 17 non-synonymous mutations [L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, D614G, H655Y, T1027I, and V1176F] in S protein, [S1188L, K1795Q, and E5665D] in ORF1ab, [E92K] in ORF8, and [P80K] in N protein; 1 deletion: [SGF 3675-3677del] in ORF1ab; and 4 synonymous mutations. P.1 is the SARS-CoV-2 variant that accumulates the highest number of mutations in the spike protein (12 mutations) (Gómez et al., 2021). The P.1 variant is found mainly

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in outbreaks in and around Manaus, the capital of the Brazilian state of Amazonas. A second Brazilian P.2 lineage (B.1.1.28.2 or VUI-202101/01) originated in Rio de Janeiro. This variant only carries the E484K mutation and does not have N501Y or K417T. The P.2 variant occurs throughout Brazil.

One of the most worrying mutations in terms of immune evasion is the E484K, which is shared by the P.1 and the B.1.351 variants. The effect of this mutation has been shown to reduce neutralization ability of sera from convalescent or vaccinated patients. However, sera with high anti-S IgG titers were still able to neutralize the virus with the mutation, suggesting that it is important to induce the highest possible levels of specific antibodies through vaccination to improve protection against emerging variants of SARS-CoV-2 (Jangra et al., 2021). There is evidence to suggest that some of the mutations in the P.1 variant may affect its transmissibility and antigenic profile, which may affect the ability of antibodies generated through a previous natural infection or through vaccination to recognize and neutralize the virus. This has important implications for transmission, reinfection rates, and evasion of antibody-mediated immunity.

Formulation

DPBS

Notes

This product is intended for research and manufacturing uses only. It is not a diagnostic device. The user assumes all responsibility for care, custody and control of the material, including its disposal, in accordance with all regulations.

Type

Recombinant

ClassID 1

Infectious Disease

GENE INFORMATION
Synonyms

SARS-CoV-2 (B.1.1.28) Spike Glycoprotein (S1) RBD

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