Recombinant SARS-CoV-2 (B.1.1.7) Spike Glycoprotein, His-tagged

Cat. No. HUM-334 **Lot. No.** (See product label)

SPECIFICATION

Product Overview	SARS-CoV-2 Spike protein that contains all amino acid changes of the "UK variant" B.1.1.7 of SARS-CoV-2: 69-70del, Y144del, N501Y, A570D, P681H, T716I, S982A, D1118H relative to Wuhan-Hu-1. This construct has a functional furin cleavage site. 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. Lineage B.1.1.7 (Variant of Concern 202012/01) is correlated with a significant increase in the rate of COVID-19 infection in the UK. The two earliest sampled genomes were collected on 20-Sept-2020 in Kent and another on 21-Sept-2020 from Greater London. It was previously known as the first Variant Under Investigation in December 2020 (VUI – 202012/01)[20] and also as lineage B.1.1.7 or 20I/501Y.V1 (formerly 20B/501Y.V1). Genomes belonging to lineage B.1.1.7 form a monophyletic clade that is characterized by a large number of lineage-defining mutations. The B.1.1.7 lineage carries a larger than usual number of virus genetic changes with 17 mutations (14 replacements and 3 deletions) (COG-UK, 2020; Rambout et al., 2020).

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	It is thought that the unusual genetic divergence of lineage B.1.1.7 may have resulted, at least in part, from virus evolution within a chronically infected individual. B.1.1.7 mutations include spike position 501, one of the key contact residues in the receptor binding domain (RBD), and experimental data suggests mutation N501Y can increase ACE2 receptor affinity (Starr et al. 2020). N501Y has been associated with increased infectivity and virulence in a mouse model (Gu et al. 2020). P681H is a replacement of one of 4 residues comprising the insertion that creates a furin cleavage site between S1 and S2 in spike. The S1/S2 furin cleavage site of SARS-CoV-2 is not found in closely related coronaviruses and has been shown to promote entry into respiratory epithelial cells and transmission in animal models (Hoffmann et al., 2020; Peacock et al. 2020; Zhu et al. 2020). The spike deletion 69-70del has also occurred a number of times in association with other RBD changes (COG-UK, 2020).
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.1.1.7) Spike Glycoprotein

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