

# SARS-CoV-2 S1 (RBD Mutant (K417N, E484K, N501Y)), His-tag

Cat. no. P2020-036

## Product Information

Protein:	SARS-CoV-2 S1 (RBD) (K417N, E484K, N501Y), His-tag (~ 27.5 kDa)
Sequence:	MRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNADVADYSLVLYNSASFSTFKCYGVSPSTKLNDLCFTNYYADSFVIRGDEVQRQIAPGQTGNIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYYLYRFLFRKSNLKPFRDISTEIQAGSTPCNGVKGFNCFYPLQSYGFQPTYGVGYPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
	Methionine at pos. 1 present due to cloning constraints, C-terminal His-tag not shown in sequence. <b>X</b> indicates the mutation site.
Source:	Recombinantly expressed in HEK293 cells.
Tag(s):	His-tag, C-terminal
Purification:	Purified by affinity chromatography and subsequent buffer exchange.
Formulation:	PBS; pH 7.4 Liquid, stored and shipped at -80 °C.
Purity:	> 85 % (will be determined by densitometry of Coomassie stained gel, example next page)
Concentration:	Will be determined by BCA-Assay.
Long-term storage:	No recommendations.
Comment:	Protein migrates at higher molecular weight during SDS-PAGE due to posttranslational modifications.

## **Background Information:**

The spike (S) glycoprotein of coronaviruses is essential for binding of the virus to the host cell at the beginning of the infection process. The target protein is also a major immunogen and a possible target for entry inhibitors.

The SARS-CoV-2 spike (S) protein is a large type I transmembrane protein composed of two subunits, S1 and S2. The S1 subunit contains a receptor-binding domain (RBD) responsible for binding to the host cell receptor angiotensin-converting enzyme 2 (ACE2). Several mutants of the spike protein are known. A new SARS-CoV-2 lineage called 20H/501Y.V2, also known as lineage B.1.351, exhibits several mutations. Compared to the previously circulating variants, the mutation E484K of SARS-CoV-2 Spike S1 (RBD) may affect neutralization by some polyclonal and monoclonal antibodies. Furthermore, the mutation N501Y leads to a higher binding affinity of the spike protein to hACE2, which results in a higher transmissibility and makes this virus modification very dangerous.



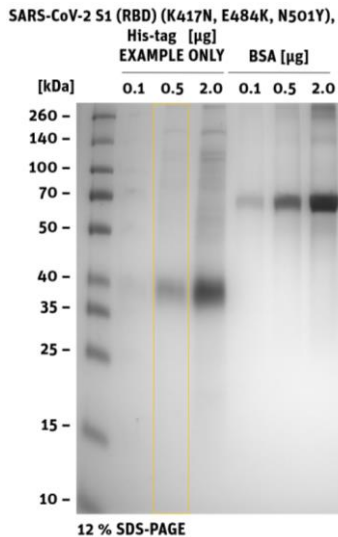
*Structural model of the receptor binding domain (RBD) of the spike protein. The location of the mutated parts are highlighted in green.*

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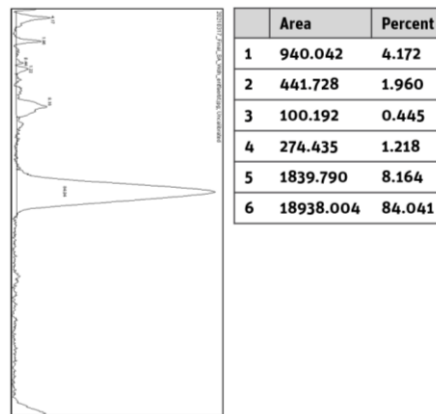
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## Product Information

Quality Information (provided for each lot):



SDS-PAGE/Coll.Coomassie



Histogram (of marked lane in gel picture)