

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

Cat. no. P2020-042

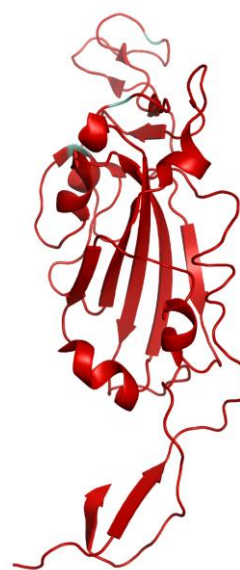
Product Information

Protein:	SARS-CoV-2 S1 (RBD) (K417N, E484K, N501Y), GFP/His-tag (~ 52.9 kDa)
Sequence:	MRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNADVSVLYNSASFSTFKCYGVSPTKLNLDLCTFNYYADSFVIRGDEVQRQIAPGQTGM ^X ADIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYYLYRFLFRKSNLKPFRDISTEIQAGSTPCNGV ^X KGFNCYFPLQSYGFPQTY ^X GVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
	Methionine at pos. 1 present due to cloning constraints, N-terminal His-tag as well as C-terminal GFP-fusion not shown in sequence. ^X indicates mutation sites.
Source:	Recombinantly expressed in HEK293 cells.
Tag(s):	GFP/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.



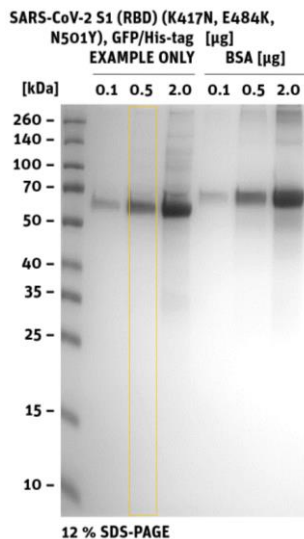
Structural model of the receptor binding domain (RBD) of the spike protein. The location of the mutated parts are highlighted in green.

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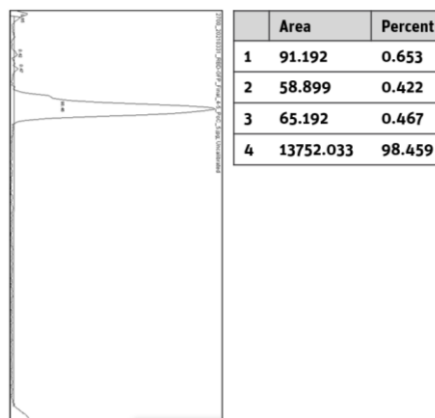
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Product Information

Quality Information (provided for each lot):



SDS-PAGE/Coll.Coomassie



Histogram (of marked lane in gel picture)