

SARS-CoV-2 S1 (RBD) (R346K, E484K, N510Y), GFP/His-tag, TEV cleavable

Cat. no. P2020-057



Product Information

Protein:	SARS-CoV-2 S1 (RBD) (R346K, E484K, N510Y), GFP/His-tag, TEV cleavable (~ 53.7 kDa)
Uniprot#:	PODTC2
Sequence:	MRVQPTESIVRFPNITNLCPFGEVFNATK FASVYAWNRRKISNVCVADYSVLYNSASFSTF KCYGVSPTKLNLDLCFTNYYADSFVIRGDEV RQIAPGQTGKIADYNYKLPDDFTGCVIAWN SNNLDSKVGGNYYLYRFLFRKSNLKPFERDISTEIQAGSTPCNGVKG FNCYFPLQSYGF QPTYG VGYQP YRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
	Methionine at pos. 1 present due to cloning constraints, C-terminal TEV-cleavage site, His-tag and 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:	> 95 % (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 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. There is strong evidence that this particular mutation increases the infectivity of SARS-CoV-2 and the ability of the host to evade the immune system. Of all the amino acid changes in the Colombian Mu variant, the E484K mutation was previously discovered in the Alpha (UK), Beta (South Africa), and Gamma (Brazil) lineages, and is thought to further enhance the ability to evade the immune system. The N501Y mutation site in this variant leads to an enhancement of viral transmission. Early studies showed that this new variant has lower susceptibility to convalescent plasma. In addition, the Mu variant contains the R346K mutation, which has been detected in dominant circulating variants of the virus responsible for COVID-19 disease.



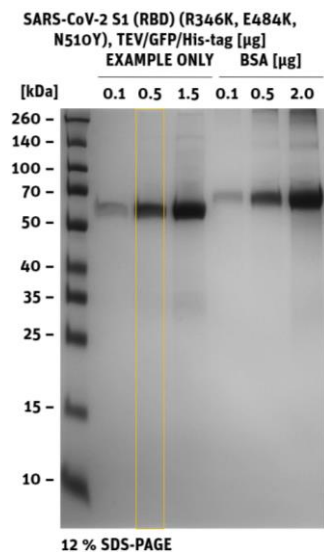
Structural model of the receptor binding domain (RBD) of the spike protein. The location of the mutated parts are highlighted in green.

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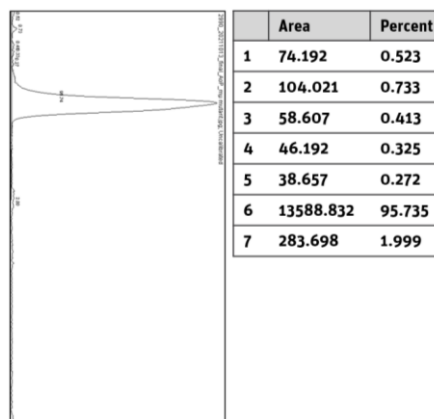
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Quality Information (provided for each lot):



SDS-PAGE/Coll.Coomassie



Histogram (of marked lane in gel picture)