

Product Information

Protein:	SARS-CoV-2 S1 (RBD) (N439K), His-tag (~ 27.5 kDa)
Sequence:	MRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNLDLCFTNYYADSFVIRGDEVRQIAPGQTGKIADYNYKLPDDFTGCVIAWN <u>S</u> KNLDSKVGGNYYLYRLFRKSNLKPFRDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVLSEFELLHAPATVCGPKKSTNLVKNKCVNF
	Methionine at pos. 1 present due to cloning constraints, C-terminal His-tag not shown in sequence. <u>X</u> 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:	> 70 % (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.

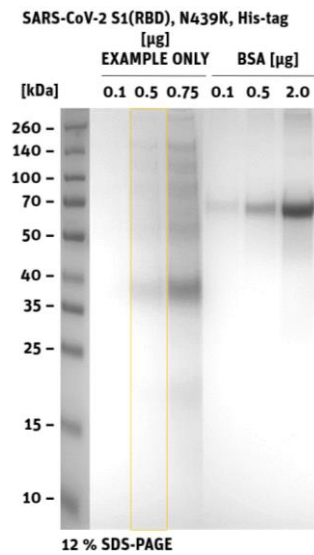
The SARS-CoV-2 spike (S) protein is a large type I transmembrane protein composed of two subunits, S1 and S2. The S1 subunit contains a receptor-binding domain (RBD) responsible for binding to the host cell receptor angiotensin-converting enzyme 2 (ACE2). Several mutants of the spike protein are known. The N439K mutation is known as the second most common mutation in the receptor binding domain and results in increased ACE2 affinity. This mutation seems to have no impact on the clinical spectrum of disease with slightly higher viral loads in vivo. However, the N439K mutants bind to the human ACE2 receptor with two-fold greater affinity and are may be resistant to some neutralising monoclonal antibodies that are used in treatments against COVID-19.



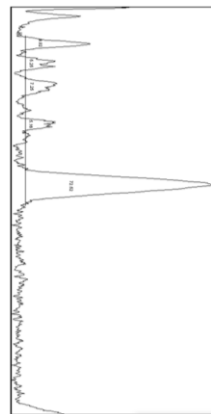
Structural model of the receptor binding domain (RBD) of the spike protein. The location of the mutated part is highlighted in green.

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Quality Information (provided for each lot):



SDS-PAGE/Coll.Coomassie



	Area	Percent
1	2035.506	9.825
2	1087.213	5.248
3	1502.163	7.250
4	1069.092	5.160
5	15024.619	75.518

Histogram (of marked lane in gel picture)