

Product Information

Protein:	SARS-CoV-2 S1(RBD Mutant (N501Y)), His-tag (~ 27.5 kDa)
Sequence:	MRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPSTKLNLDLCTFNYYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYYLYRFRKSNLKPFRDISTEIQAGSTPCNGVEGFNCYFPLQSYGFPQPTYGVGYQPYRVVVLSEFELLHAPATVCGPKKSTNLVKNKCVNF
	Methionin at pos. 1 present due to cloning constraints, C-terminal His-tag not shown in sequence. <u>Y</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:	> 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.

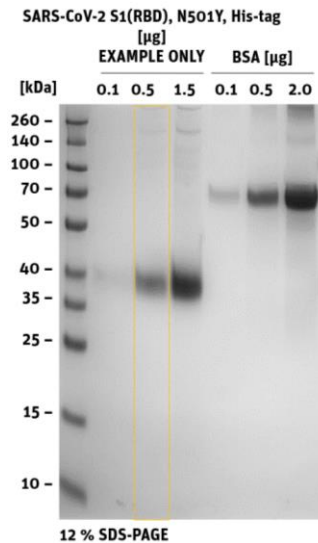
The SARS-CoV-2 spike (S) protein is a large type I transmembrane protein composed of two subunits, S1 and S2. The S1 subunit contains a receptor-binding domain (RBD) responsible for binding to the host cell receptor angiotensin-converting enzyme 2 (ACE2). Several mutants of the spike protein are known. A new SARS-CoV-2 lineage called 501Y.V2, also known as lineage B.1.1.7, exhibits several mutations. Compared to the previously circulating variants, the mutation N501Y of SARS-CoV-2 Spike S1 (RBD) results in a significant higher transmissibility. This increase is most likely due to a higher binding affinity of the spike protein to hACE2. Therefore, the N501Y mutation is considered the most dangerous modification of the virus.



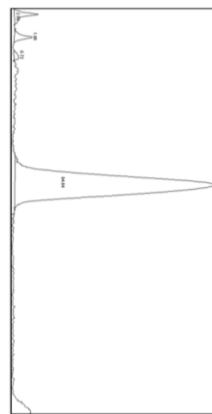
Structure model of the receptor binding domain (RBD) of the spike protein. The location of the mutated part is indicated by the green circle. Due to partially missing structure information in the X-ray data, the mutated part is not resolved in the structure model.

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Quality Information (provided for each lot):



SDS-PAGE/Coll.Coomassie



	Area	Percent
1	545.627	2.683
2	399.385	1.960
3	146.435	0.719
4	19280.368	94.638

Histogram (of marked lane in gel picture)