

# SARS-CoV-2 S1 (RBD Mutant (Y453F)), GFP/His-tag

Cat. no. P2020-039

## Product Information

Protein:	SARS-CoV-2 S1 (RBD) (Y453F), GFP/His-tag (~ 52.8 kDa)
Sequence:	MRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNLDLCFTNYYADSFVIRGDEVQRQIAPGQTKGIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYYL <u>E</u> RLFRKSNLKPFRDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVLSEFELLHAPATVCGPKKSTNLVKNKCVNF
	Methionine at pos. 1 present due to cloning constraints, N-terminal His-tag as well as C-terminal GFP-fusion not shown in sequence. <u>X</u> 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 mutation first discovered in Denmark, called "Cluster 5", also known as the  $\Delta$ FVI-spike, is related to four genetic changes. This mutation (Y453F) is located in a conservative region of the RBD directly involved in ACE2 binding and thereby could have implications for viral fitness, transmissibility, and antigenicity.



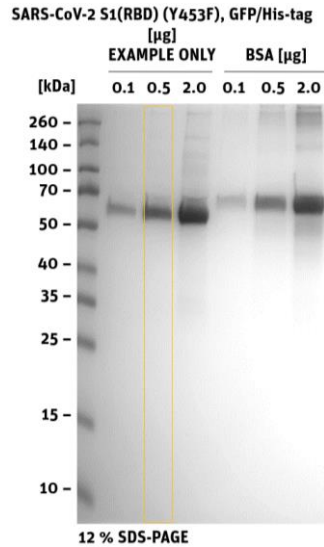
*Structural model of the receptor binding domain (RBD) of the spike protein. The location of the mutated part is highlighted in green.*

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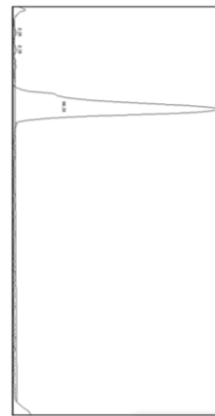
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## Product Information

Quality Information (provided for each lot):



SDS-PAGE/Coll.Coomassie



	Area	Percent
1	38.485	0.262
2	53.192	0.362
3	14617.518	99.377

Histogram (of marked lane in gel picture)