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

Cat. no. P2020-033



Product Information

Protein: SARS-CoV-2 S1 (RBD) (Y453F), His-tag (~ 27.5 kDa)

Sequence: MRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTF

KCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKLPDDFTGCVIAWN SNNLDSKVGGNYNYLFRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGF

QPTNGVGYQPYRVVVLSFELLHAPATVCGPKKSTNLVKNKCVNF

Methionine at pos. 1 present due to cloning constraints, C-terminal His-tag not shown in

sequence.

 \underline{X} 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: > 80 % (will be determined by densitometry of Coomassie stained gel, example next page)

Concentration: Will be determined by BCA-Assay.

Long-term storage: No recommendations.

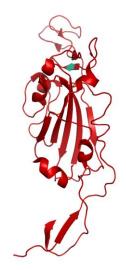
Comment: Protein migrates at higher molecular weight during SDS-PAGE due to posttranslational

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 Δ 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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Percent

4.812

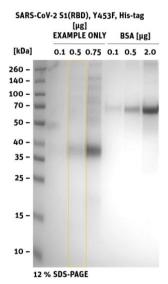
5.010

6.924

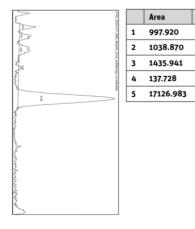
82.590

Product Information

Quality Information (provided for each lot):



SDS-PAGE/Coll.Coomassie



Histogram (of marked lane in gel picture)