

SARS-CoV-2 S1 (RBD Mutant (L452Q, F490S)), GFP/His-tag, TEV cleavable

Cat. no. P2020-054



Product Information

Protein:	SARS-CoV-2 S1 (RBD) (L452Q, F490S), GFP/His-tag, TEV cleavable (~ 53.7 kDa)
Uniprot#:	PODTC2
Sequence:	MRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNLDLCFTNYYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWN SNNLDSKVGGNYYQYRLFRKSNLKPFRDISTEIQAGSTPCNGVEGFNCYSPLQSYGF QPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF Methionine at pos. 1 present due to cloning constraints, C-terminal TEV-cleavage site, His tag and 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:	> 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 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 C.37 or Lambda variant, exhibits 7 mutations in the spike protein. Compared to the other circulating variants, the mutations L452Q and F490S of the SARS-CoV-2 Spike S1 (RBD) are known to make the virus more resistant to neutralizing antibodies and therefore may also have an influence on the effectiveness of existing vaccines. The Lambda variant is classified by the World Health Organization (WHO) as Variant of Interest (VOI).



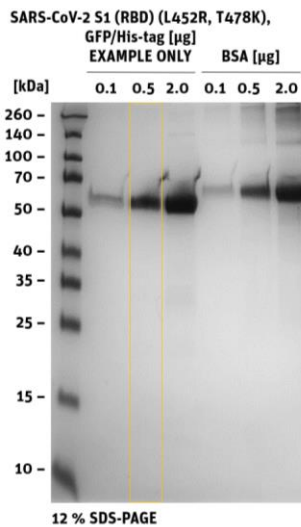
Structural model of the receptor binding domain (RBD) of the spike protein. The location of the mutated parts are highlighted in green.

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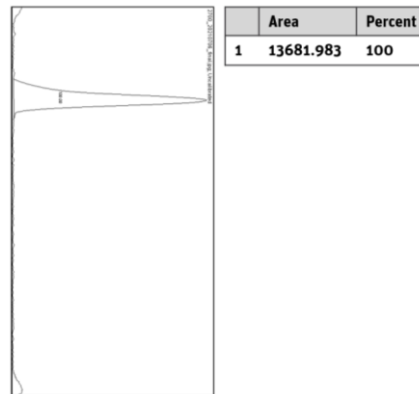
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Quality Information (provided for each lot):



SDS-PAGE/Coll.Coomassie



Histogram (of marked lane in gel picture)