

# SARS-CoV-2 S1 (RBD Mutant (L452R, E484Q)), GFP/His-tag, TEV cleavable

Cat. no. P2020-051



## Product Information

Protein:	SARS-CoV-2 S1 (RBD) (L452R, E484Q), GFP/His-tag, TEV cleavable (~ 53.7 kDa)
Uniprot#:	PODTC2
Sequence:	MRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNLDLCTFNYYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWN SNNLDSKVGGNYYR <del>Y</del> R <del>L</del> RFRKSNLKPFERDISTEIQAGSTPCNGV <del>Q</del> GFNCYFPLQSYGF QPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF
	Methionine at pos. 1 present due to cloning constraints, C-terminal TEV-cleavage site, GFP-fusion and His-tag 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 B.1.617, exhibits 13 mutations. Compared to the previously circulating variants, the mutations L452R and E484Q of the SARS-CoV-2 Spike S1 (RBD) may cause a stronger affinity of the spike protein to hACE2 and also conferring an increasing ability to evade the hosts' immune system.



*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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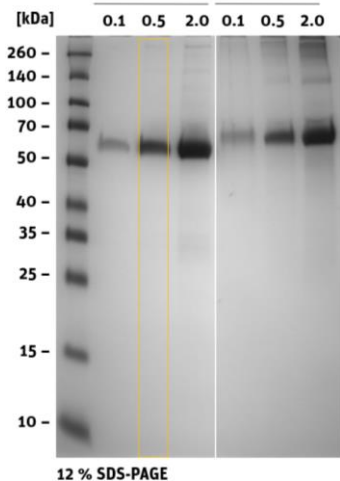
## Product Information

Quality Information (provided for each lot):

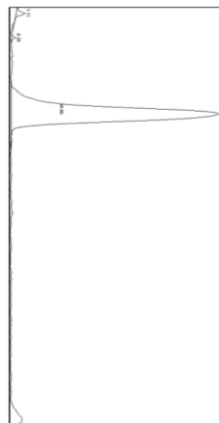
SARS-CoV-2 S1 (RBD) (L452R, E484Q),

TEV/GFP/His-tag [ $\mu$ g]

EXAMPLE ONLY      BSA [ $\mu$ g]



SDS-PAGE/Coll.Coomassie



	Area	Percent
1	174.263	1.111
2	45.778	0.292
3	15461.175	98.597

Histogram (of marked lane in gel picture)