SARS-CoV-2 S1 (RBD Mutant (K417N, L452R, T478K)), Fc/His-tag, TEV cleavable

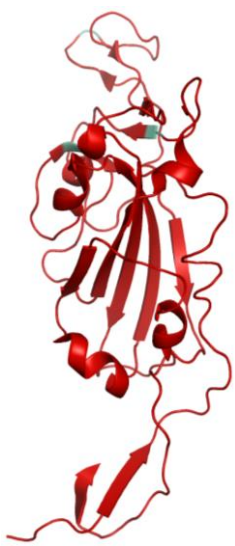
Cat. no. P2020-056

Product Information

Protein:	SARS-CoV-2 S1 (RBD) (K417N, L452R, T478K), Fc/His-tag, TEV cleavable (~ 54.3 kDa)
Uniprot#:	P0DTC2
Sequence:	MRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTF KCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQIAPGQTG**N**IADYNYKLPDDFTGCVIAWN SNNLDSKVGGNYNY**R**YRLFRKSNLKPFERDISTEIYQAGS**K**PCNGVEGFNCYFPLQSYGF QPTNGVGYQPYRVVVLSFELLHAPATVCGPKKSTNLVKNKCVNF Methionine at pos. 1 present due to cloning constraints, C-terminal TEV-cleavage site, His-tag and Fc-fusion not shown in sequence. **X** indicates mutation sites.
Source:	Recombinantly expressed in HEK293 cells.
Tag(s):	Fc/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:

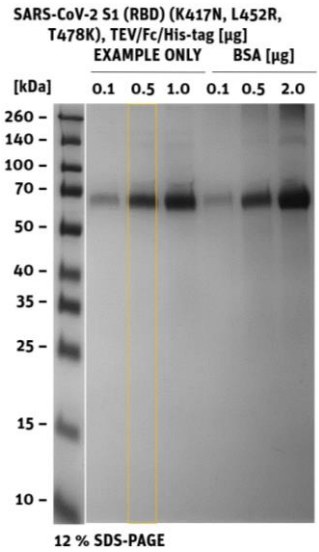
The spike (S) glycoprotein of coronaviruses is essential for binding of the virus to the host cell at the beginning of the infection process. The target protein is also a major immunogen and a possible target for entry inhibitors.
The SARS-CoV-2 spike (S) protein is a large type I transmembrane protein 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, including a novel SARS-CoV-2 lineage AY.1/AY.2/AY.3. Compared to the previously circulating variants, the mutations L452R and T478K 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. Furthermore, the Delta Plus variant has an additional K417N amino acid mutation. This mutation seems to have no significant impact on the clinical spectrum of disease and not more transmissible than Delta.



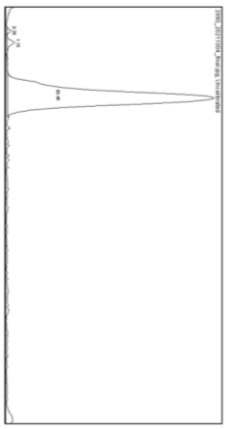
Structural model of the receptor binding domain (RBD) of the spike protein. The location of the mutated parts are highlighted in green.

Product Information

Quality Information (provided for each lot):



SDS-PAGE/Coll.Coomassie



	Area	Percent
1	57.485	0.387
2	170.849	1.150
3	14626.518	98.463

Histogram (of marked lane in gel picture)