

SARS-CoV-2 S1 (RBD Mutant (L452R, E484Q)), Fc/His-tag

Cat. no. P2020-047

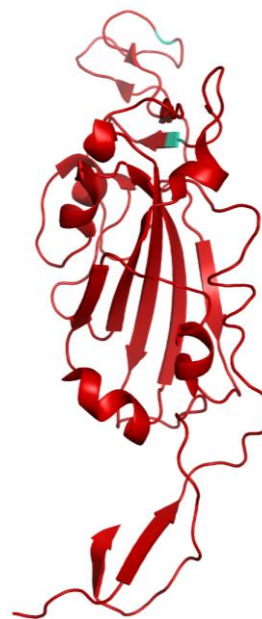
Product Information

| | |
|--------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Protein: | SARS-CoV-2 S1 (RBD) (L452R, E484Q), Fc/His-tag (~ 54.3 kDa) |
| Sequence: | MRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNADVSVLYNSASFSTFKCYGVSPSTKLNLDLCTFNYYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWN SNNLDSKVGGNYYR ^X YRLFRKSNLKPFRDISTEIQAGSTPCNGV ^X QGFNCYFPLQSYGF QPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNF |
| | Methionine at pos. 1 present due to cloning constraints, C-terminal 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: | > 90 % (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). A new SARS-CoV-2 lineage called B.1.617, exhibits several mutations. The mutations L452R-E484Q are characteristic for the fast spreading SARS-CoV-2 virus variants B.1.617 emerged in India. These mutations are affecting the receptor binding domain (RBD) of the spike protein, which the virus uses to bind to human cells receptors and enter them. Due to the mutations, the virus is allowed to bind with higher affinity to human ACE2 receptor which results in increased transmissibility of the SARS-CoV-2 virus.



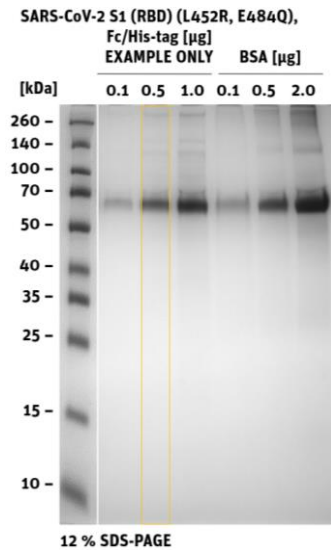
Structural model of the receptor binding domain (RBD) of the spike protein. The location of the mutated parts are highlighted in green.

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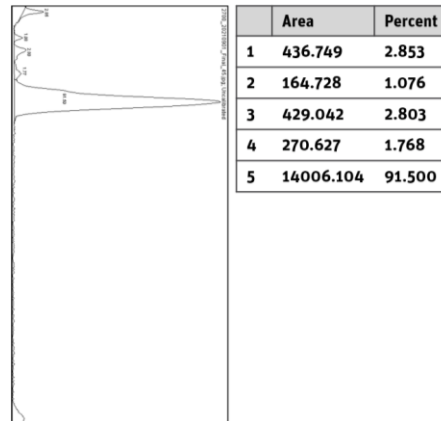
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Product Information

Quality Information (provided for each lot):



SDS-PAGE/Coll.Coomassie



Histogram (of marked lane in gel picture)