

SARS-CoV-2 S protein, His-tag, trimer

Full-length protein (N501Y, E484K, K417N)

Cat. no. P2020-044

Product Information

Protein: SARS-CoV-2 S protein (N501Y, E484K, K417N), His-tag, trimer (~ 141 kDa per monomer)

Sequence: MVNFTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTFHAIHVSQTN
GTRFRANPVLFPNDGVYFASTEKSNIRGWIFGTTLDLSTQSLIVNNATNVVIKVECFQ
FCNDPFLGVYHYHKNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVF
KNIDGYFKIYSKHTPINLVRGLPQGFSALEPLVDLPIGINITRFQTLALHISYLTGDS
SSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSEKTKLKSFTVEKGIYQ
TSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASF
STFKCYGVSPTKLNLCFTNVYADSFVIRGDEVQRQIAPGQTGNIADYNYKLPDDFTGCVI
AWNSNLLDSKVGNYLYRFRKSNLKPFRDISTEIQAGSTPCNGVKGFNCYFPLQS
YGFQPTYGVGYQPYRVVLSFELLHAPATVCGPKSTNLVKNKCVNFNGLTGTGVLTE
SNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCFSGGVSVITPGTNTSNQVAVLYQG
VNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNSYECDIPIGAGICASY
QTQTNSPGASVASQSIAYTMSLGVENSVAYSNSIAIPTNFTISVTTEILPVSMTKTSV
DCTMYICGDSSTECNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKD
FGGFNFSQILPDPSPKSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIARDLCAQKFN
GLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVL
YENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSV
LNDILSRDPPEAEVQIDRLITGRLQSLQTYVTQLLIRAAEIRASANLAATKMSECVLGQ
SKRVDFCGKGYHLSFQPSAPHGVVFLHVTVPAQEKNFTTAPAICHGDKAHFPREGVVF
SNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGVNNNTVYDPLQPELDSFKEELDKYF
KNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEYIK

Methionine at pos. 1 present due to cloning constraints, C-terminal Strep- and His-tag as well as trimerization domain not shown in sequence. **X** indicates mutation sites.

Source: Recombinantly expressed in HEK293 cells.

Tag(s): Strep- and His-tag, C-terminal

Purification: Purified by affinity chromatography and subsequent buffer exchange.

Formulation: PBS, 5 % (w/v) Trehalose; pH 7.4

Liquid, stored and shipped at -80 °C.

Purity: > 85 % (will be determined by densitometry of Coomassie stained gel, example next page)

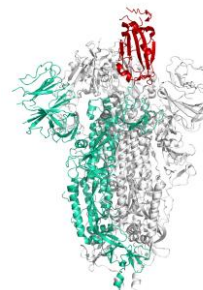
Concentration: Will be determined by BCA-Assay.

Long-term storage: No recommendations.

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

Background Information:

The SARS-CoV-2 spike consists of three identical transmembrane proteins, called spike proteins, each containing two subunits: the S1 and the S2 subunit. The engineered recombinant Spike protein contains specific amino acid substitutions to stabilize the prefusion conformation (2P). Furthermore, the furin cleavage site at the boundary between the S1/S2 subunits was deleted and an artificial trimerization domain was added to the C-terminal end of the monomer.



Structural model of the spike protein of SARS-CoV-2 as trimer, one monomer colored. The receptor binding domain (RBD) is in the 'up position' and highlighted in red.

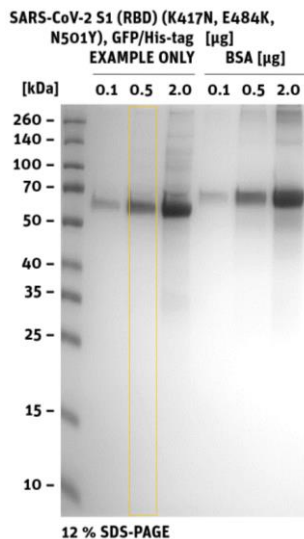
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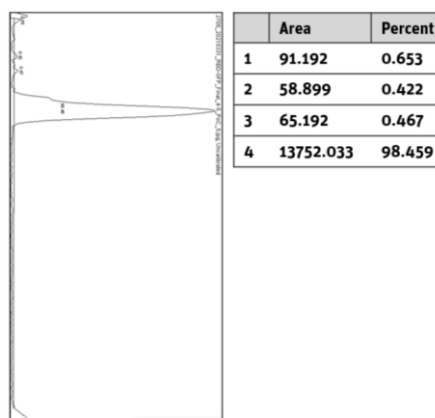
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Product Information

Quality Information (provided for each lot):



SDS-PAGE/Coll.Coomassie



Histogram (of marked lane in gel picture)