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

Full length protein

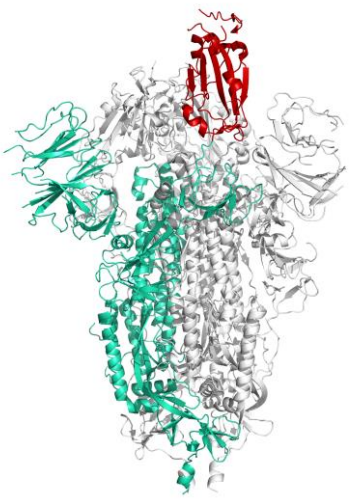
Cat. no. P2020-025

Product Information

Protein:	SARS-CoV-2 S protein, His-tag, trimer (~ 141 kDa per monomer)
Sequence:	MVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVY FASTEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTF EYVSQPFLMDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLLALHR SYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTVEKGIYQTSNFRVQPT ESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSF VIRGDEVRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAG STPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVL TESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQL TPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPGASVASQSIIAYTMSLGAENSVAYS NNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVK QIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLL TDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSST ASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIR ASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTTAPAICHDGKAHFPREGVF VSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGIN ASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIK Methionine at pos. 1 present due to cloning constraints, C-terminal Strep- and His-tag as well as trimerization domain not shown in sequence.
Source:	Recombinantly expressed in HEK293 cells.
Tag(s):	Strep- and His-tag, C-terminal
Purification:	Purified by affinity chromatography followed by size exclusion chromatography.
Formulation:	PBS; pH 7.4; contains trehalose as protectant / 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:

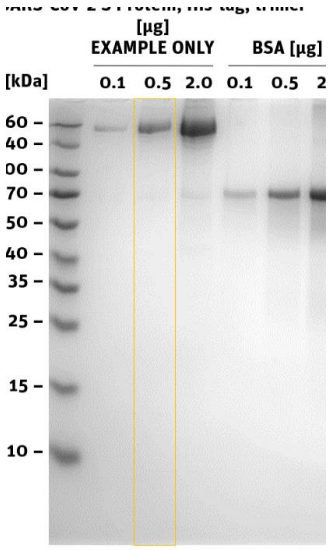
The SARS-CoV-2 spike is presented as a trimeric structure on the surface of the virus. It consists of three identical transmembrane proteins, called spike proteins, each containing two subunits: the S1 containing the receptor binding domain (RBD) and the S2 subunit. Upon binding of the host receptor hACE2 via RBD, the distal S1 domain is cleaved. This reveals the fusion machinery of the S2 subunit, which mediates the entry into the cell. Moreover, the Spike protein is heavily glycosylated by N-linked glycans that are important for the proper folding of the protein and the recognition by neutralizing antibodies. 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. Above all, the spike is a major immunogen and an interesting target for vaccine development as well as for serological assays.



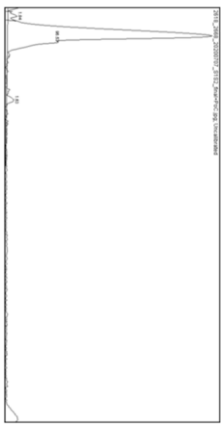
Structural model of the spike protein of SARS-CoV-2 as trimer, one monomer colored. The receptor binding domain (RBD) is in the 'up position' and highlighted in red.

Product Information

Quality Information (provided for each lot):



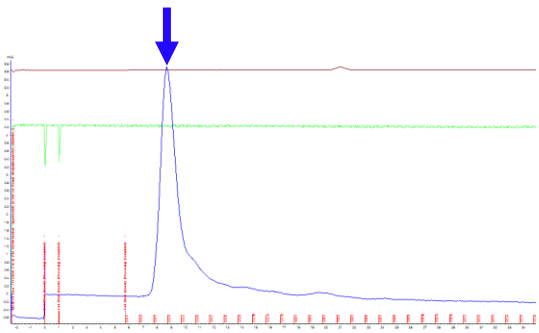
SDS-PAGE/Coll.Coomassie



	Area	Percent
1	220.849	1.835
2	11616.619	96.532
3	196.435	1.632

Histogram (of marked lane in gel picture)

Activity Information (general information, not lot specific):



Analytic size exclusion chromatography (SEC) of the purified protein confirms a trimeric running behavior (arrow).

Functionality of spike protein determined by binding of hACE2 (ELISA), results are similar to Spike S1 (RBD).