

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

Full length protein – GFP fusion

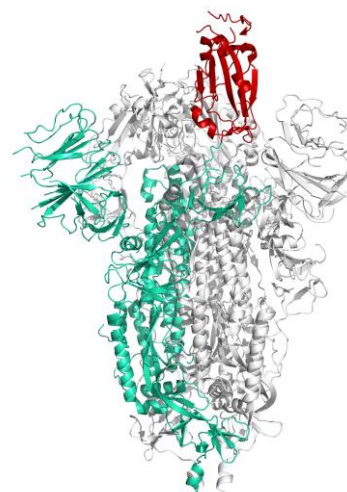
Cat. no. P2020-030

Product Information

Protein:	SARS-CoV-2 S protein, GFP/His-tag, trimer (~ 168.1 kDa per monomer)
Sequence:	<p>MVNLTRTRQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFN GVYFASTKSNIRGWIFGTTLDSTQSLIVNNATNVVVKVCEFCNDPFLGVYVYHKNNKSWMESEFRVYSS ANNCTFEYVSQPFLMDLEGKQGNFKNLREFVFNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRF QTLALHRSYLTGPDSSSGWTAGAAAYVGYLQPRTEFLKYNENGTITDAVDCALDPLSETKCTLSFTVEKGIY QTSNFRVQPTESIVRFPNITNLCFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLN DLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNLLDSKVGNGNYLYRFRKSNLK PFERDISTEIQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKN KCVNFNFNGLTGTGVLTESNKKFLPFQFGRDIADTTDAVRDPQTEILDITPCSFGGVSIVTPGNTSNQVAVL YQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSECDIPIGAGICASYQTQTNSPGASV ASQSIAYTMSLGAENSVAYSNNSIAIPTNFTISVTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQL NRALTGIAVEQDKNTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSPKSKRSFIEDLLFNKVTLADAGFIKQYGD CLGDIAARDLICAQKFNGLTVLPPLLTDEMIQAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNGIGVTV NVLYENQKLIANQFNSAIGKIQDLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDPP EAEVQIDRLITGRLQSLQTYVTQLIRAAEIRASANLAATKMSECVLQSKRVDFCGKGYHLSFPQSAPHGVV FLHVTYVPAQEKNFITAPAICHGKAHFPREGVFSNGTHWFVTQRNFYEPQIITDNTFVSGNCDVVIGIVNN TVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLESIDLQELGKYEQYIK</p> <p>Methionine at pos. 1 might be present due to cloning constraints, C-terminal Strep/His-tag and GFP not shown in sequence.</p>
Source:	Recombinantly expressed in HEK293 cells.
Tag(s):	Strep/His-tag and GFP, C-terminal
Purification:	Purified by affinity chromatography and subsequent buffer exchange.
Formulation:	PBS; pH 7.4 / Liquid, stored and shipped at -80 °C.
Purity:	> 55 % (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. Protein is fused at C-terminus with GFP.

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. As a fusion partner, the protein contains GFP at the C-terminal end. 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.

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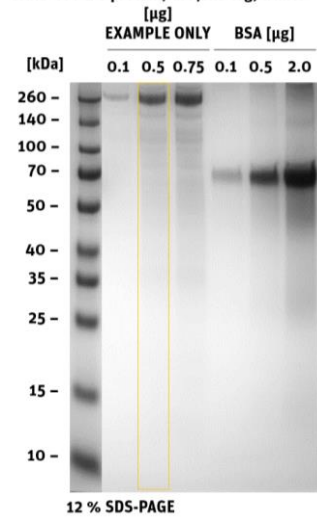
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Product Information

Quality Information (provided for each lot):

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



SDS-PAGE/Coll.Coomassie



	Area	Percent
1	11292.598	61.083
2	1326.799	7.177
3	3281.891	17.752
4	1660.891	8.984
5	407.456	2.204
6	517.527	2.799

Histogram (of marked lane in gel picture)