

SARS-CoV-2 3CL-Mpro protein

Full length protein, unmodified (authentic N-terminus)

Cat. no. P2020-027

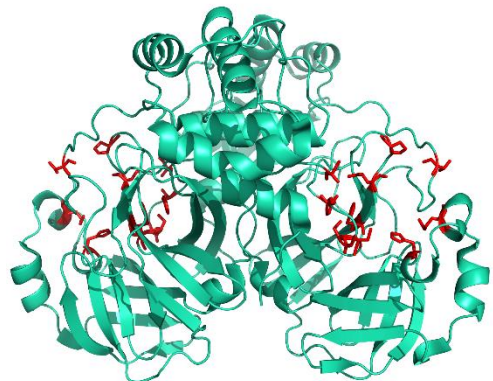
Product Information

Protein:	SARS-CoV-2 3CL-Mpro, unmodified (~ 36 kDa)
Sequence:	SGFRKMAFPSGKVEGCMVQVTCGTTTLNGLWLDDVVYCPRHVICTSEDMLNPNYEDLLIR KSNHNFVLQAGNVQLRVIGHSMQNCVLKLVDTANPKTPKYKFVRIQPGQTFSVLACYNG SPSGVYQCAMRPNFTIKGSFLNGSCGSGVGFNIDYDCVSFCYMHHMELPTGVHAGTDLEGN FYGPFVDRQTAQAAGTDTTITVNVLAWLYAAVINGDRWFLNRFITTLNDFNLVAMKYNYE PLTQDHVDILGPLSAQTGIAVLDMCASLKELLQNGMNGRTILGSALLEDEFTPFDDVVRQC SGVTFQ
	N-terminal His-tag removed by proteolytic digest to produce authentic N-terminus.
Source:	Recombinantly expressed in E.coli Rosetta2 (DE3).
Tag(s):	tag-free
Purification:	Purified by affinity chromatography and subsequent buffer exchange. Tag removal by protease digest followed by reaction cleanup (IMAC).
Formulation:	PBS, pH 7.4; contains Glycerol as protectant 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:	N-terminal His-Tag was removed by a proteolytic digest producing an authentic N-terminus to ensure highest proteolytic activity.

Background Information:

The new coronavirus SARS-CoV-2 expresses two proteases, the papain-like protease (PLpro) and 3C-like protease (3CLpro). Both belong to the group of cysteine proteases, as they have a cysteine residue at their catalytic site. Their main function is the processing of the viral polyprotein, that contains two cleavage sites to build up the viral replicase complex. Additionally, PLpro has the ability of removing ISG15 and ubiquitin from viral proteins expressed in the cell, this enables evasion from the innate immune response by the host. This presents an interesting target for drug development, as it would not only inhibit the viral replication but would also prevent the massive immunological response resulting of the over-activation of the host's immune system, that can lead to damaging of uninfected cells and therefore worsening of the patient's condition.

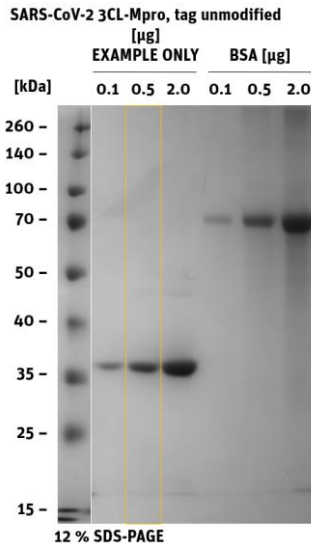
Our protein contains no additional amino acids at the N-terminus like proteins from competitors. Therefore, the protease has the authentic N-terminus which is part of the active site of the protein.



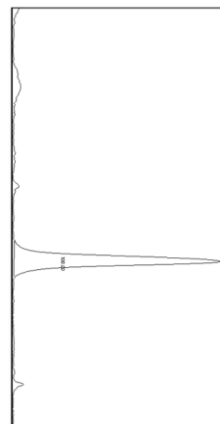
Structural model of the 3C-like protease (3CL-Mpro) of SARS-CoV-2 shown as active dimer. The amino acids relevant for binding of the substrate are highlighted (red).

Product Information

Quality Information (provided for each lot):



SDS-PAGE/Coll.Coomassie



	Area	Percent
1	8971.225	100

Histogram (of marked lane in gel picture)