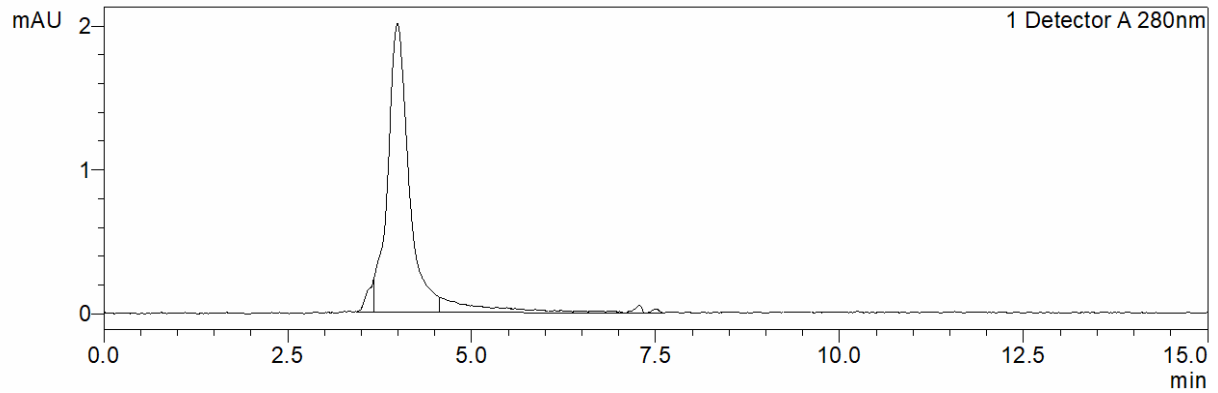


# Stabilized Trimeric SARS-CoV-2 Spike Protein

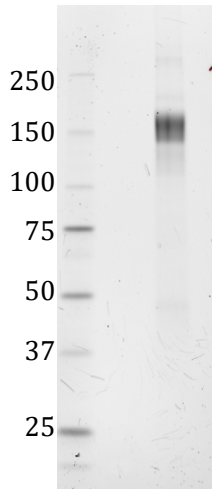
This product is for research use only.

## PRODUCT INFORMATION

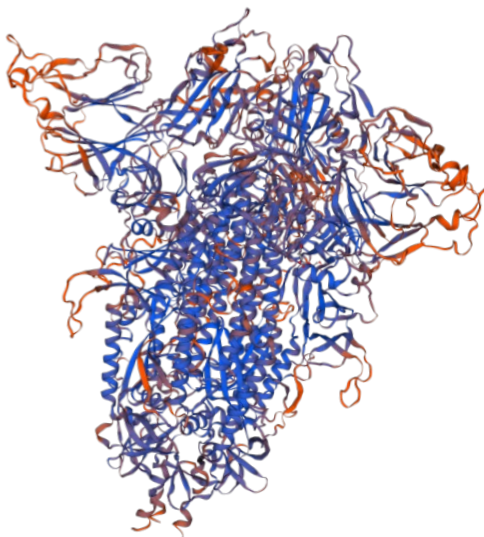
<b>Product Overview</b>	Trimeric SARS-CoV-2 spike protein in prefusion conformation.
<b>Modifications</b>	C-terminal Transmembrane region replaced with a trimerization domain and a polyhistidine tag. Two stabilizing proline mutations and scrambled S1/S2 furin cleavage site ( <i>see reference</i> ).
<b>Strain</b>	SARS-CoV-2 Betacoronavirus
<b>Isolate (Seq ID)</b>	Wuhan-Hu-1 (GenBank: MN908947)
<b>Expression System</b>	CHOExpress™ cells
<b>Purity</b>	> 90 % as determined by SDS-PAGE.
<b>Molecular Weight</b>	The recombinant SARS-CoV-2 trimeric spike protein consists of 3576 amino acids and predicts a molecular mass of ~400 kDa.
<b>Endotoxin</b>	<1.0 EU per µg protein as determined by the LAL method.
<b>Format</b>	Liquid
<b>Reference</b>	Wrapp D. et al. Cryo-EM structure of the 2019-nCoV spike in the prefusion conformation. Science 367, 1260–1263 (2020)



**Figure 1.** Verification of purity and size of the recombinant trimeric SARS-CoV-2 Spike Protein under non-denaturing conditions. Size-exclusion chromatography (SEC) plot with peak at 4.0 minutes, corresponding to a size of ~460kD.



**Figure 2.** Verification of size and purity of the trimeric SARS-CoV-2 spike protein under denaturing conditions. SDS-PAGE gel showing a band corresponding to the size of the spike monomer; ~ 150 kD.



**Figure 3.** A 3-D model of the recombinant trimeric SARS-CoV-2 spike protein using Swiss-Model – University of Basel online tools (<https://swissmodel.expasy.org/>)