

Stabilized trimeric D614G SARS-CoV-2 Spike Protein

This product is for research use only.

PRODUCT INFORMATION

Product Overview	Trimeric SARS-CoV-2 D614G spike protein in prefusion conformation.
Modifications	C-terminal Transmembrane region replaced with a trimerization domain and a polyhistidine tag. Two stabilizing proline mutations. Scrambled S1/S2 furin cleavage site. D614G amino acid change.
Strain	SARS-CoV-2 Betacoronavirus
Isolate (Seq ID)	Wuhan-Hu-1 (GenBank: MN908947) with D614G mutation.
Expression System	CHOExpress™ cells
Purity	> 95 % as determined by SDS-PAGE.
Molecular Weight	The recombinant SARS-CoV-2 trimeric spike protein consists of 3576 amino acids and predicts a molecular mass of ~400 kDa.
Endotoxin	<1.0 EU per µg protein as determined by the LAL method.
Format	Liquid
Reference	Wrapp D. et al. Cryo-EM structure of the 2019-nCoV spike in the prefusion conformation. Science 367, 1260–1263 (2020)

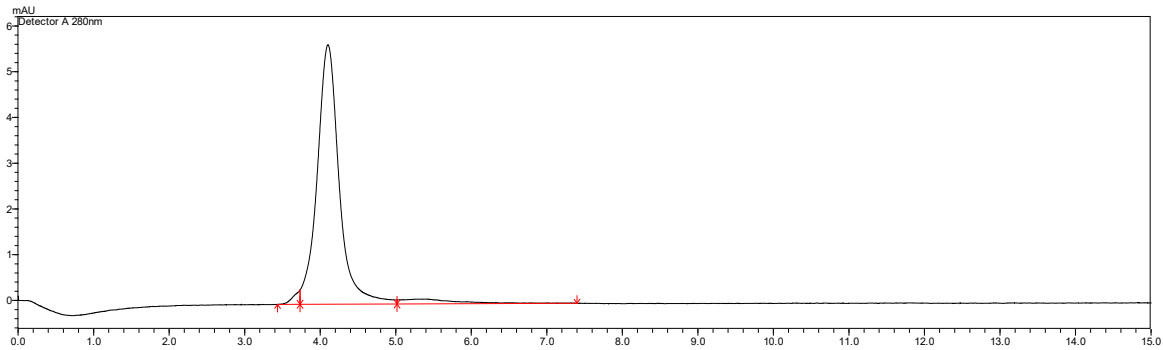
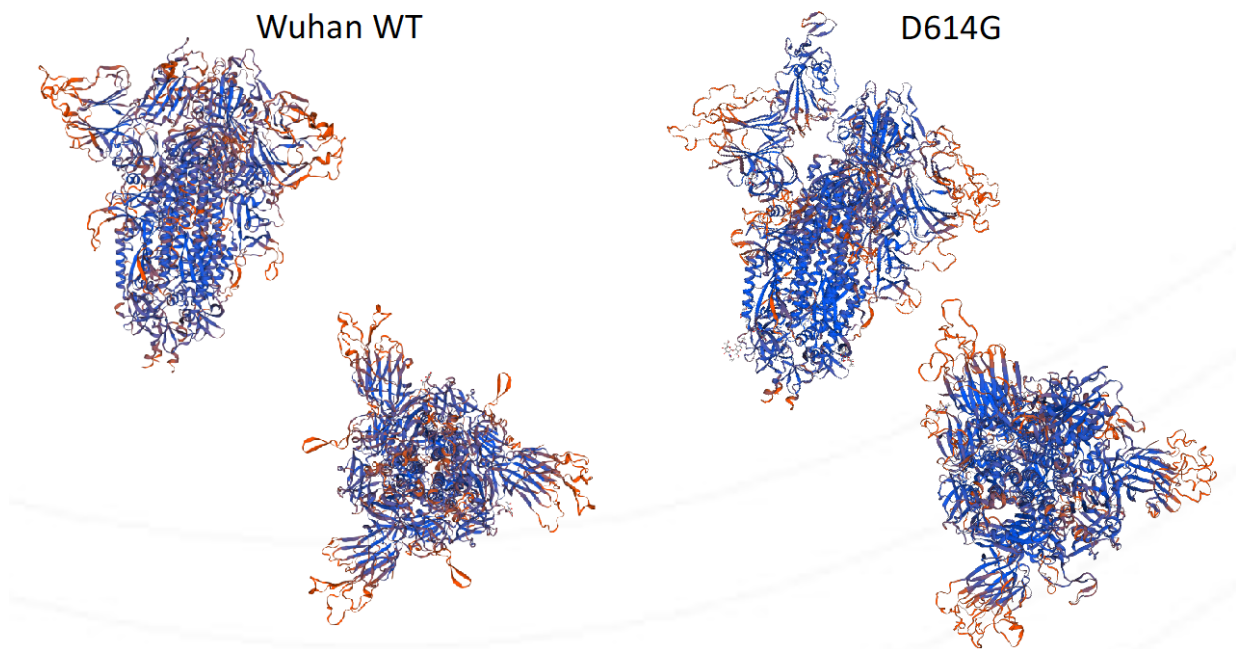


Figure 1. Verification of purity and size of the recombinant trimeric SARS-CoV-2 D614G Spike Protein under non-denaturing conditions. Size-exclusion chromatography (SEC) plot with peak at 4.0 minutes, corresponding to a size of ~400kD.

Figure 2. 3-D model of the recombinant trimeric SARS-CoV-2 spike protein and D614G mutant using Swiss-Model – University of Basel online tools (<https://swissmodel.expasy.org/>)



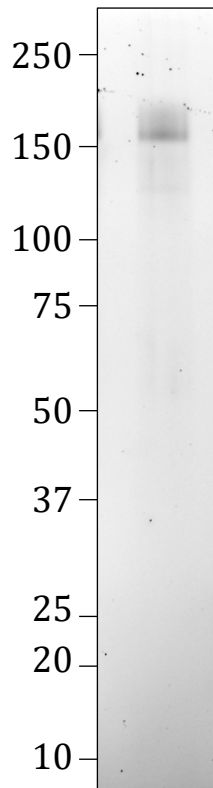


Figure 3. Verification of size and purity and size of trimeric SARS-CoV-2 D614G spike protein under denaturing conditions. 7.5% SDS-PAGE gel with a band corresponding to the size of the spike monomer; ~ 150 kD.