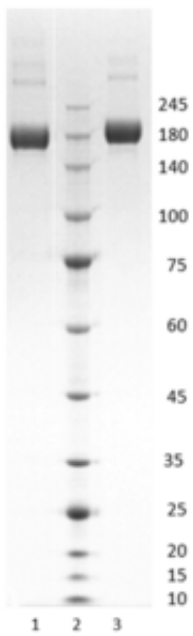




## SARS-CoV-2 Trimeric Spike Indian B.1.617.2 (delta)

Catalogue #	P-353-100
Description:	Protein contains amino acids 14-1211 and following mutations: T19R, G142D, E156G, del_F157-R158 L452R, T478K, D614G, P681R. Plus two extra amino acids (AS) in N-terminus, trimerization domain and His-6 tag at C-terminus, GS linker between protein and trimerization domain and GSG linker between trimerization domain and His-tag. Furin cleavage (RRAR) site between Spike S1 and S2 is mutated (GSAS).
Uniprot ID:	P0DTC2
Source:	Human
MW:	410.37 kDa
Host:	CHO-based cell line (expressed by QMCF Technology)
Purification:	Purified by Ni-affinity chromatography and gel-filtration from serum-free CHO growth media, sterile filtrated
Purity:	>95%
Concentration:	1 mg/ml
Buffer:	PBS pH 7.4
Endotoxine:	NA
QC:	SDS-PAGE, analytical SEC, Octet binding
Shipping:	Shipped on dry ice.
Storage:	Store at -70 °C long term. Avoid multiple freeze-thaw cycles.

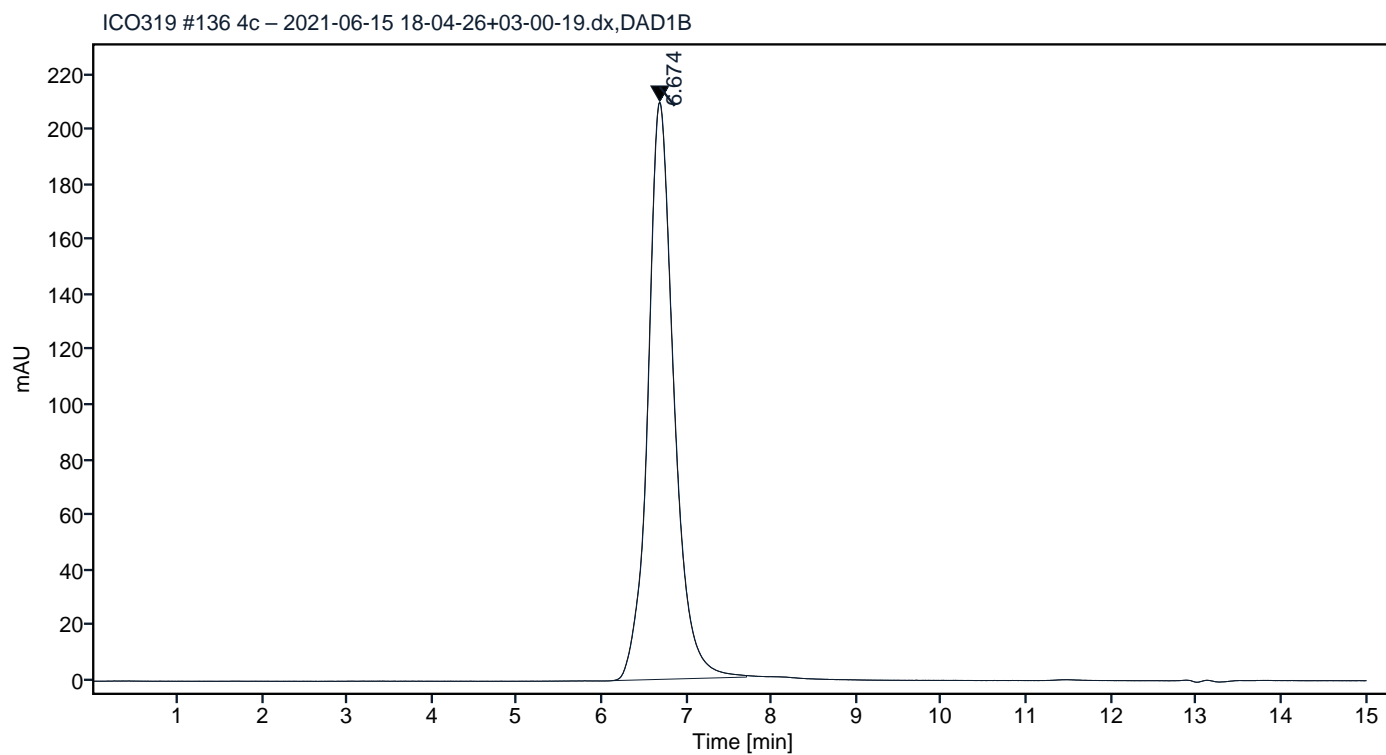


**Figure 1.** Simply Blue stained SDS-PAGE analysis of SARS-CoV-2 Trimeric Spike Indian B.1.617.2 . 4-12% gradient gel is used for analysis. Lane 1. 0.8 µg SARS-CoV-2 Trimeric Spike Indian B.1.617.2 (-DTT) Lane 2. Protein marker (Smobio) Lane 3. 0.8 µg SARS-CoV-2 Trimeric Spike Indian B.1.617.2 (+DTT).

## Peak Table

Peak #	RT (min)	Area	Area %
1	6.674	4464.49	100.00

## Chromatogram



**Figure 2.** HPLC analytical SEC for final product.

## Peak Table

Peak #	RT (min)	Area	Area %
1	6.367	99.04	2.52
2	6.680	3835.36	97.48

## Chromatogram

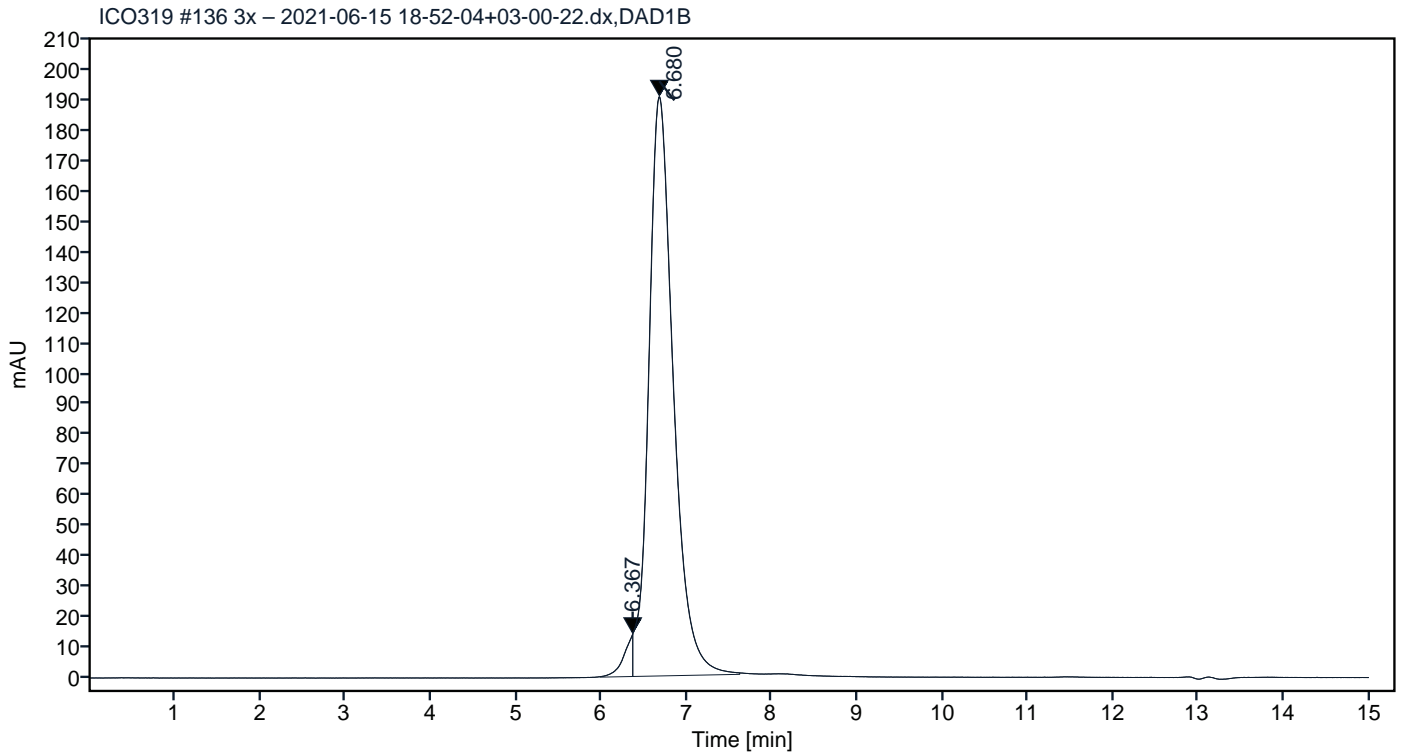


Figure 3. HPLC analytical SEC after 3 freeze-thaw cycles.

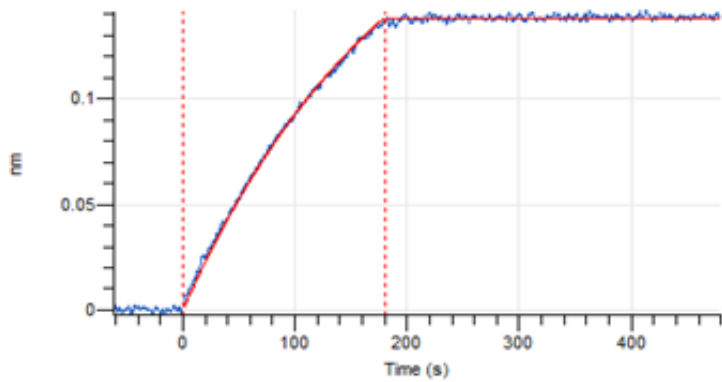


Figure 4. Octet Red96e analysis of SARS-CoV-2 Trimeric Spike Indian B.1.617.2 binding to human ACE2

receptor.