Datasheet

SARS-CoV-2 full-length Trimeric Spike Recombinant Antigen B.1.1.7 Mutation (UK Variant)

Catalogue No:	BSV-COV-PR-65	BSV-COV-PR-67	BSV-COV-PR-89
Pack Size:	100 µg	1 mg	10 mg
Product Name:	SARS-CoV-2 full-length Trimeric Spike Recombinant Antigen B.1.1.7 Mutation (UK Variant)		
WHO Reference:	SARS-CoV-2 VUI 202012/01		
Description:	Spike protein of the mutant strain B.1.1.7, also commonly known as the “UK Variant”. It is a full-length protein, which is active in its native trimeric form, that is stabilized in LMNG detergent.		
Alternative Name:	SPIKE_SARS2 Spike glycoprotein		
UniProt No:	P0DTC2		
Protein Class:	Single span transmembrane protein		
Organism:	Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)		
Sequence:	Full-length sequence (aa 1 – 1273), del 69, del 144, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H furin cleavage site “RRAR” mutated to “GSAG”; KV986PP		
Host:	Expressed in HEK293 Expi cells		
Size (Trimeric):	3 x 142 kDa = 426 kDa		
Buffer:	20 mM Hepes pH 7.5; 150 mM NaCl, 0.001% LMNG		
Form:	Liquid		
Function:	Host cell surface receptor binding; fusion of virus membrane with host endosome membrane		

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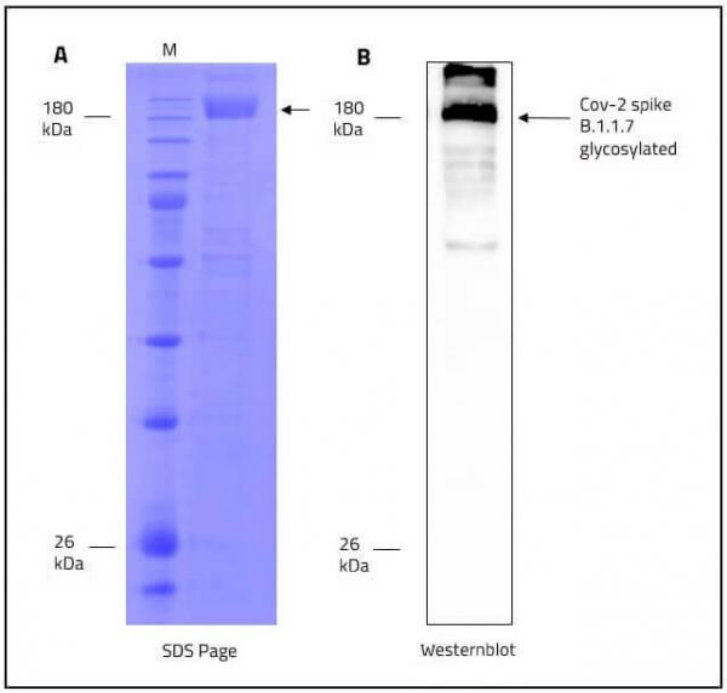
Purity:	>98% as determined by SDS-PAGE, see Fig. 1 A and B  **Fig.1: Size, purity and oligomerization state of CoV-2 spike protein assessed by SDS-PAGE and Western Blot**.
Activity:	Not Determined
Applications:	ELISA assays, Ligand Binding assays, Biochemical & Biophysical analyses
Shipping:	Dry ice
Storage:	-80°C. Avoid freeze-thaw cycles.
Background:	The B.1.1.7 variant which first emerged in the UK during September 2020 surpasses the original virus in transmissibility and risk of death. This variant has a mutation in the receptor binding domain (RBD) of the spike protein at position 501, where the amino acid asparagine (N) has been replaced with tyrosine (Y). The shorthand for this mutation is N501Y. This variant also has several other mutations, including: 69/70 deletion: occurred spontaneously many times and likely leads to a conformational change in the spike protein. P681H: near the S1/S2 furin cleavage site, a site with high variability in coronaviruses. This mutation has also emerged spontaneously multiple times.

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