

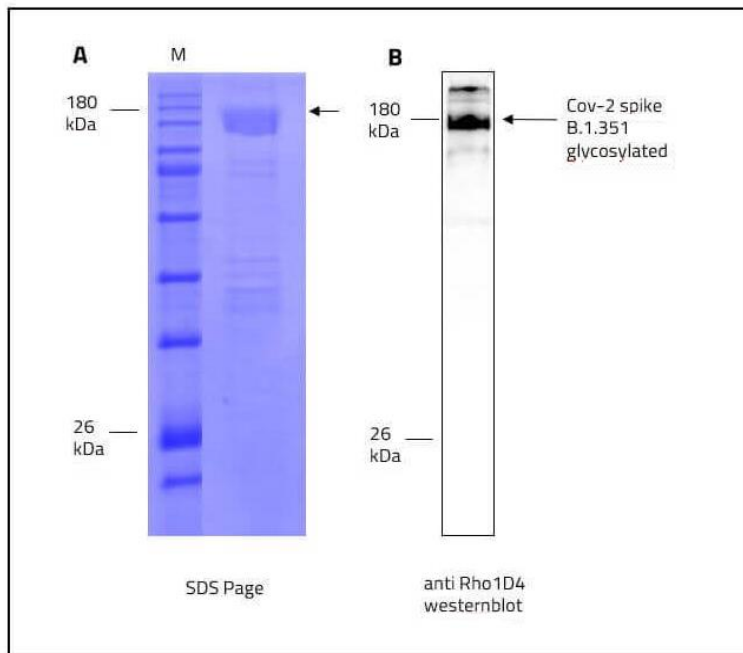
## Datasheet

### SARS-CoV-2 full-length Trimeric Spike Recombinant Antigen B.1.351 Mutation (South African Variant)

Catalogue No:	BSV-COV-PR-60	BSV-COV-PR-61	BSV-COV-PR-62	BSV-COV-PR-63
<b>Pack Size:</b>	25 µg	100 µg	500 µg	1 mg
<b>Product Name:</b>	SARS-CoV-2 full-length Spike B.1.351 Mutation (South African Variant)			
<b>WHO Reference:</b>	501Y.V2/501.V2			
<b>Description:</b>	Spike protein of the mutant strain B.1.351, also commonly known as the "South Africa Variant". It is a full-length protein, which is active in its native trimeric form, that is stabilized in LMNG detergent.			
<b>Alternative Name:</b>	SPIKE_SARS2 Spike glycoprotein			
<b>UniProt No:</b>	P0DTC2			
<b>Protein Class:</b>	Single span transmembrane protein			
<b>Organism:</b>	Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)			
<b>Sequence:</b>	del 144, K417N, E484K, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H furin cleavage site "RRAR" mutated to "GSAG"; KV986PP C-terminal Rho1D4 tag fused with spacer "GSSG" to protein sequence			
<b>Tag:</b>	C-terminal Rho1D4 tag for affinity purification			
<b>Host:</b>	Expressed in HEK293 Expi cells			
<b>Size:</b>	1286 amino acids (including Rho1D4 tag and linker) 142.11 kDa			
<b>Buffer:</b>	20 mM Hepes pH 7.5; 150 mM NaCl, 0.001% LMNG *Additional buffer can also be supplied on request			
<b>Form:</b>	Liquid			
<b>Function:</b>	Host cell surface receptor binding; fusion of virus membrane with host endosome membrane			

>98% as determined by SDS-PAGE, see Fig. 1 A and B

**Purity:**



**Fig.1: Size, purity and oligomerization state of CoV-2 spike protein assessed by SDS-PAGE, Western Blot using a Rho1D4 antibody.**

<b>Activity:</b>	Not Determined
<b>Purification:</b>	Rho1D4 Agarose
<b>Applications:</b>	<ul style="list-style-type: none"> <li>• ELISA assays</li> <li>• Ligand binding assays</li> <li>• Biochemical and Biophysical analyses</li> </ul>
<b>Shipping:</b>	Dry ice
<b>Storage:</b>	-80°C. Avoid freeze-thaw cycles.
<b>Background:</b>	<p>The B.1.351 variant first identified in South Africa has spread to numerous European countries. It is characterised by eight lineage-defining mutations in the spike protein, including three at important residues in the receptor-binding domain (K417N, E484K and N501Y) that may have functional significance. Unlike the B.1.1.7 lineage detected in the UK; this variant does not contain the deletion at 69/70. This variant was first identified in Nelson Mandela Bay, South Africa, in samples dating back to the beginning of October 2020, and cases have since been detected outside of South Africa, including the United States.</p>

**Disclaimer:** Our products are intended for molecular biology applications. These products are not intended for the diagnosis, prevention or treatment of disease.