

Datasheet

SARS-CoV-2 full-length Trimeric Spike Recombinant Antigen B.1.525 Mutation (UK/Nigerian Variant)

| | | | |
|--------------------------|---|---------------|---------------|
| Catalogue No: | BSV-COV-PR-79 | BSV-COV-PR-86 | BSV-COV-PR-87 |
| Pack Size: | 100 µg | 1 mg | 10 mg |
| Product Name: | SARS-CoV-2 full-length Trimeric Spike Recombinant Antigen B.1.525 Mutation (UK/Nigerian Variant) | | |
| PHE Reference: | VUI-21FEB-03 | | |
| Description: | Spike protein of the mutant strain B.1.525, also commonly known as the "UK/Nigerian 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 69-70, del 144, Q52R, E484K, Q677H, F888L furin cleavage site "RRAR" mutated to "GSAG"; KV986PP, V987P | | |
| 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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>98% as determined by SDS-PAGE, see Fig. 1 A and B

Purity:

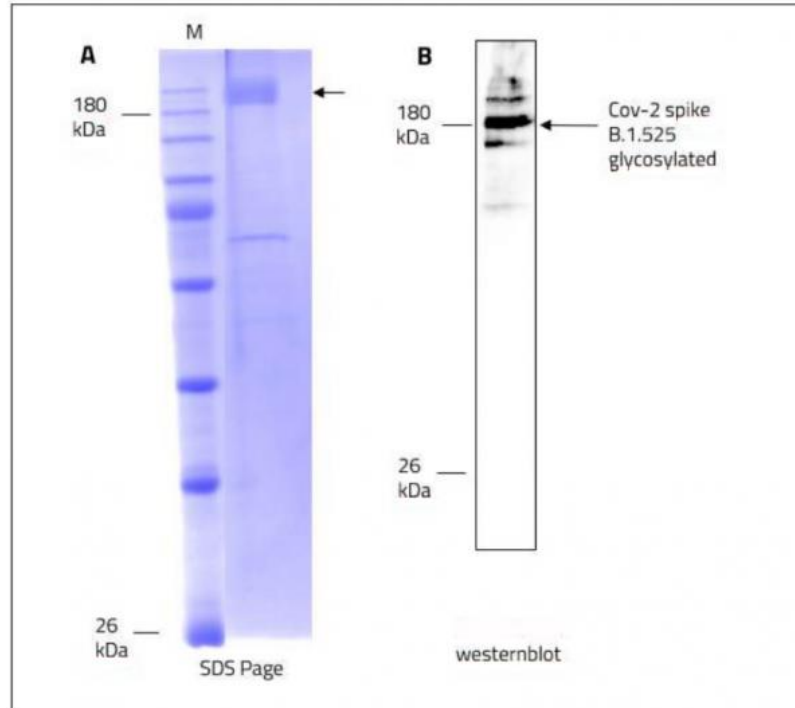


Fig.1: Size, purity and oligomerization state of CoV-2 spike protein assessed by SDS-PAGE and Western Blot.

| | |
|----------------------|---|
| 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.1.525 variant does not carry the same N501Y mutation found in B.1.1.7, 501.V2 and P.1, but carries the same E484K mutation as found in the P.1, P.2 and 501.V2 variants, and also carries the same Δ H69/ Δ V70 deletion as found in B.1.1.7, N439K variant (B.1.141 and B.1.258) and Y453F variant. B.1.525 differs from all other variants by having both the E484K-mutation and a new F888L mutation (a substitution of phenylalanine (F) with leucine (L) in the S2 domain of the spike protein). |

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