

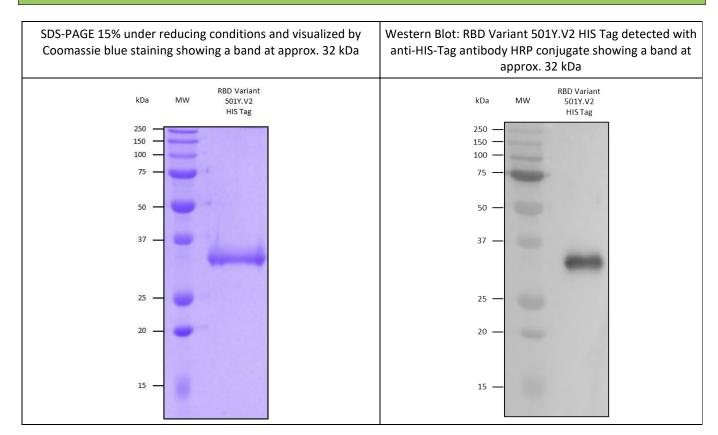
DESCRIPTION

| Description | Recombinant Human Coronavirus SARS-CoV-2 Spike Protein S1 subunit, Receptor-Binding Domain (RBD), variant 501Y.V2, Lineage B.1.351 (20C/501Y.V2, South Africa) |
|----------------------------|--|
| Sequence | Native NCBI Accession Number: MN908947 |
| | Arg319-Phe541, with mutation K417N; E484K; N501Y |
| Expression system | HEK293 cells |
| Tag | HIS Tag C-Terminus |
| Purification | Affinity chromatography |
| Extinction coefficient | 35340 M-1.cm-1 Abs 0.1% (=1 g/l) 1.35 assuming all pairs of Cys residues form cystines |
| Predicted Molecular Weight | 26.1 kDa |

SPECIFICATIONS

| SDS Page | Approx. 32 kDa |
|-----------------------|---|
| Size | 100 μg |
| Purity | >95% by SDS PAGE gel |
| Formulation | Lyophilized from PBS (Na2HPO4/NaH2PO4 50mM pH 7,2, NaCl 150mM, Trehalose) |
| Reconstitution | Centrifuge the vial prior opening It is recommended to reconstitute in sterile water at 100 µg/ml |
| Activity | Recognized by CR3022 anti RBD recombinant antibody and Covid-19 positive patients serum samples. |
| Stability and Storage | Store at minimum -20°C. Avoid repeated freeze-thaw cycles Stable 1 month -20°C to -80°C after reconstitution under sterile conditions |

DATA



Rec SARS-CoV-2 RBD variant 501Y.V2 (Lineage B.1.351) 715-H21-0BU



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Recombinant Human SARS-CoV-2 Spike RBD Variant 501Y.V2, Lineage B.1.351 (HEK) Catalog number: 715-H21-0BU

SARS-CoV-2 Spike Glycoprotein (S1) RBD variant 501Y.V2 Lineage B.1.351

Spike protein (S protein) is one of four structural proteins of Coronavirus (SARS-Cov, SARS-Cov-2, MERS amongst other), S protein plays the most important role in viral attachment, fusion and entry, and it serves as a target for development of antibodies, entry inhibitors and vaccines.

In the S protein, the Receptor Binding Domain (RBD) mediates viral entry of SARS-Cov and SARS-Cov-2 into host cells by its interaction with the membrane receptor ACE2 (Angiotensin-converting enzyme 2).

Recently, the variant 20C/501Y.V2 also named 501Y.V2 (Lineage B.1.351) has been first identified in South Africa in the middle of December 2020. It has been reported the 501Y.V2 variant causes more frequently serious illness in such cases than other

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