

DESCRIPTION

<i>Description</i>	Recombinant Human Coronavirus SARS-CoV-2 Spike Protein S1 subunit, Receptor-Binding Domain (RBD), variant Lineage B.1.617 (G/452.V3, India)
<i>Sequence</i>	Native NCBI Accession Number: MN908947 Arg319-Phe541, with mutation L452R; E484Q
<i>Expression system</i>	HEK293 cells
<i>Tag</i>	HIS Tag C-Terminus
<i>Purification</i>	Affinity chromatography
<i>Extinction coefficient</i>	33850 M <sup>-1</sup> .cm <sup>-1</sup> Abs 0.1% (=1 g/l) 1.30 assuming all pairs of Cys residues form cystines
<i>Predicted Molecular Weight</i>	26.1 kDa

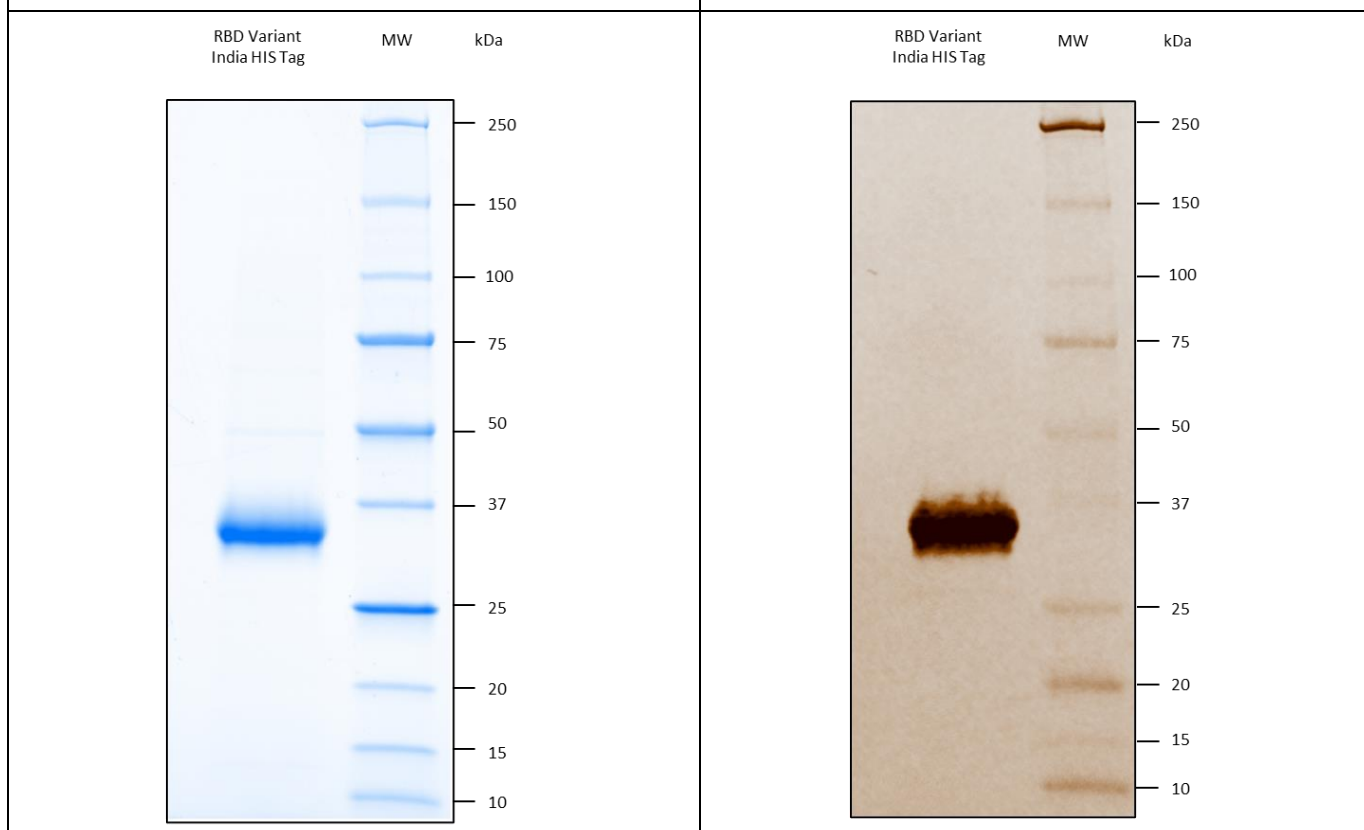
SPECIFICATIONS

<i>SDS Page</i>	Approx. 32 kDa
<i>Concentration</i>	1 mg/ml
<i>Purity</i>	>95% by SDS PAGE gel
<i>Formulation</i>	Liquid PBS
<i>Activity</i>	Not tested
<i>Stability and Storage</i>	Store at minimum -20°C. Avoid repeated freeze-thaw cycles

DATA

SDS-PAGE 4-15% under reducing conditions and visualized by Coomassie blue staining showing a band at approx. 32 kDa

Western Blot: RBD Variant India HIS Tag detected with anti-HIS-Tag antibody HRP conjugate showing a band at approx. 32 kDa



## SARS-CoV-2 Spike Glycoprotein (S1) RBD variant Indian Lineage B.1.617

Spike protein (S protein) is one of the four structural proteins of Coronavirus (SARS-Cov, SARS-Cov-2, MERS amongst others), 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).

The variant lineage B.1.617 of SARS-CoV-2 was first identified in India on October 2020 and at the end of March 2021 has shown a sustained spread across India, likely to be responsible for the third wave of COVID-19 in that region. Also detected since February 2021 in other countries (United Kingdom, United States, France, Canada...), this variant carries two important mutations – L452R and E484Q. These two mutations have been previously described in other SARS-CoV-2 variants and are known to confer immune escape and to increase infectivity. Nevertheless, this is the first time the two RBD mutations are detected on the same lineage of SARS-CoV-2 which is often referred to as a “double mutant”.

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Rec SARS-CoV-2 RBD variant Lineage B.1.617 715-H24-0BU

Version 1 12/05/2021