

**Spike Protein RBD**  
Catalog # PVGS1671**Specification**

---

**Spike Protein RBD - Product Information**Primary Accession [P0DTC2](#)**Species**  
SARS-CoV-2**Sequence**  
Arg319-Ser591 (K417N, L452R, T478K)**Purity**  
> 90% as analyzed by SDS-PAGE**Endotoxin Level**  
< 0.2 EU/ µg of protein by gel clotting method**Biological Activity**  
This protein is validated to bind with human ACE2 in functional ELISA assay.**Expression System**  
CHO**Theoretical Molecular Weight**  
33.7 kDaFormulation **Supplied as a solution in PBS, pH 7.4.****Storage & Stability**  
Upon receiving, this product remains stable for up to 6 months at -20°C or below. Please avoid repeated freeze-thaw cycles.**Spike Protein RBD - Additional Information****Gene ID** 43740568**Other Names**

Spike glycoprotein {ECO:0000255|HAMAP-Rule:MF\_04099}, S glycoprotein {ECO:0000255|HAMAP-Rule:MF\_04099}, E2 {ECO:0000255|HAMAP-Rule:MF\_04099}, Peplomer protein {ECO:0000255|HAMAP-Rule:MF\_04099}, Spike protein S1 {ECO:0000255|HAMAP-Rule:MF\_04099}, Spike protein S2 {ECO:0000255|HAMAP-Rule:MF\_04099}, Spike protein S2' {ECO:0000255|HAMAP-Rule:MF\_04099}, S {ECO:0000255|HAMAP-Rule:MF\_04099}

**Target Background**

SARS-CoV-2 (Severe Acute Respiratory Syndrome Coronavirus 2) also known as 2019-nCoV (2019 Novel Coronavirus) is a virus that causes illnesses ranging from the common cold to severe diseases. As of May 2021, three sublineages have been found. Despite its name, B.1.617.3 was the first sublineage of this variant to be detected, in October 2020 in India. This sublineage has

remained relatively uncommon compared to the two other sublineages, B.1.617.1 (also known as variant Kappa) and B.1.617.2 (also known as variant Delta), both of which were first detected in December 2020. This variant has the double mutations E484Q and L452R in the spike proteins. Emerging research suggests the variant may be more transmissible than previously evolved ones. The Delta Plus variant, also known as B.1.617.2.1 or AY.1, is considered a “subvariant” of the Delta version, which has a mutation (K417N) that allows the virus to better attack lung cells and potentially escape vaccines.

## Spike Protein RBD - Protein Information

**Name** S {ECO:0000255|HAMAP-Rule:MF\_04099}

### Function

[Spike protein S1]: Attaches the virion to the cell membrane by interacting with host receptor, initiating the infection. The major receptor is host ACE2 (PubMed:<a href="http://www.uniprot.org/citations/32142651" target="\_blank">32142651</a>, PubMed:<a href="http://www.uniprot.org/citations/32155444" target="\_blank">32155444</a>, PubMed:<a href="http://www.uniprot.org/citations/33607086" target="\_blank">33607086</a>). When S2/S2' has been cleaved, binding to the receptor triggers direct fusion at the cell membrane (PubMed:<a href="http://www.uniprot.org/citations/34561887" target="\_blank">34561887</a>). When S2/S2' has not been cleaved, binding to the receptor results in internalization of the virus by endocytosis leading to fusion of the virion membrane with the host endosomal membrane (PubMed:<a href="http://www.uniprot.org/citations/32075877" target="\_blank">32075877</a>, PubMed:<a href="http://www.uniprot.org/citations/32221306" target="\_blank">32221306</a>). Alternatively, may use NRP1/NRP2 (PubMed:<a href="http://www.uniprot.org/citations/33082294" target="\_blank">33082294</a>, PubMed:<a href="http://www.uniprot.org/citations/33082293" target="\_blank">33082293</a>) and integrin as entry receptors (PubMed:<a href="http://www.uniprot.org/citations/35150743" target="\_blank">35150743</a>). The use of NRP1/NRP2 receptors may explain the tropism of the virus in human olfactory epithelial cells, which express these molecules at high levels but ACE2 at low levels (PubMed:<a href="http://www.uniprot.org/citations/33082293" target="\_blank">33082293</a>). The stalk domain of S contains three hinges, giving the head unexpected orientational freedom (PubMed:<a href="http://www.uniprot.org/citations/32817270" target="\_blank">32817270</a>).

### Cellular Location

Virion membrane {ECO:0000255|HAMAP-Rule:MF\_04099, ECO:0000269|PubMed:32979942}; Single-pass type I membrane protein {ECO:0000255|HAMAP-Rule:MF\_04099, ECO:0000269|PubMed:34504087}. Host endoplasmic reticulum-Golgi intermediate compartment membrane {ECO:0000255|HAMAP-Rule:MF\_04099, ECO:0000269|PubMed:34504087}; Single-pass type I membrane protein {ECO:0000255|HAMAP-Rule:MF\_04099}. Host cell membrane {ECO:0000255|HAMAP-Rule:MF\_04099, ECO:0000269|PubMed:34504087}; Single-pass type I membrane protein {ECO:0000255|HAMAP-Rule:MF\_04099}. Note=Accumulates in the endoplasmic reticulum-Golgi intermediate compartment, where it participates in virus particle assembly. Some S oligomers are transported to the host plasma membrane, where they may mediate cell-cell fusion (PubMed:34504087). An average of 26 +/-15 S trimers are found randomly distributed at the surface of the virion (PubMed:32979942) {ECO:0000255|HAMAP-Rule:MF\_04099, ECO:0000269|PubMed:32979942, ECO:0000269|PubMed:34504087}

## Spike Protein RBD - Protocols

Provided below are standard protocols that you may find useful for product applications.

- [Western Blot](#)

- [Blocking Peptides](#)
- [Dot Blot](#)
- [Immunohistochemistry](#)
- [Immunofluorescence](#)
- [Immunoprecipitation](#)
- [Flow Cytometry](#)
- [Cell Culture](#)

### **Spike Protein RBD - Images**