

### Spike Protein RBD

Catalog # PVGS1669

### **Specification**

## **Spike Protein RBD - Product Information**

Primary Accession **Species** SARS-CoV-2 PODTC2

Sequence

Arg319-Ser591 (E484Q, L452R)

**Biological Activity** 

This protein is validated to bind with human ACE2 (Cat. No. Z03516) in functional ELISA assay.

**Expression System** 

CHO

Formulation Supplied as a solution in PBS, pH 7.4, 0.1%

ProClin 300.

**Storage & Stability** 

Upon receiving, this product remains stable for up to 3 months at 2-8°C. Protect from light.

# **Spike Protein RBD - Additional Information**

Gene ID 43740568

#### **Other Names**

 $\label{lem:spike-glycoprotein-glycoprotein} $$\sup_{CO:0000255|HAMAP-Rule:MF_04099}, S \ glycoprotein $$\{ECO:0000255|HAMAP-Rule:MF_04099\}, Spike-Rule:MF_04099\}, Peplomer protein $$\{ECO:0000255|HAMAP-Rule:MF_04099\}, Spike protein $$1$$\{ECO:0000255|HAMAP-Rule:MF_04099\}, Spike protein $$2$$\{ECO:0000255|HAMAP-Rule:MF_04099\}, Spike protein $$2'$$\{ECO:0000255|HAMAP-Rule:MF_04099\}, S$$\{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. Lineage B.1.617, also known as G/452.V3, was first identified in October 2020 in India. 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. Whether the effectiveness of currently-deployed vaccines is affected remains under investigation. Moreover, the sublineage B.1.617.2 has been redesignated as "variant of concern" (VOC-21APR-02) in May 2021, which spreads more quickly than the original version of the virus.

### **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 using host TFRC and GRM2 and 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>, PubMed:<a href="http://www.uniprot.org/citations/34903715" target="blank">34903715</a>, PubMed:<a href="http://www.uniprot.org/citations/36779763" target="blank">36779763</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}. 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
- <u>Immunohistochemistry</u>
- Immunofluorescence
- Immunoprecipitation
- Flow Cytomety
- Cell Culture

# Spike Protein RBD - Images