

# Spike Protein RBD

Catalog # PVGS1583

### Specification

# Spike Protein RBD - Product Information

Primary Accession Species SARS-CoV-2

### <u>P0DTC2</u>

Sequence Arg319-Ser591 (E484K, K417T, N501Y)

Purity > 90% as analyzed by SDS-PAGE

**Endotoxin Level** < 0.2 EU/ μg of protein by gel clotting method

**Biological Activity** SARS-CoV-2 Spike protein (RBD, E484K, K417T, N501Y, Avi & His Tag) can bind with human ACE2 in functional ELISA assay.

Expression System CHO

**Theoretical Molecular Weight** 33.7 kDa

FormulationSupplied as a solution in PBS, pH 7.4.Storage & StabilityUpon 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. Lineage P.1, also known as the Brazil(ian) variant is one of the variants of SARS-CoV-2.



This variant has 17 amino acid changes, ten of which are in its spike protein, including these three designated to be of particular concern: N501Y, E484K and K417T. SARS-CoV-2 Spike protein (RBD, E484K, K417T, N501Y, Avi & His Tag) carries a Avi Tag followed by a polyhistidine tag at the C-terminus. It has high binding affinity to human chimeric ACE2.

### **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}; Singlepass 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.

<u>Western Blot</u>



- Blocking Peptides
- Dot Blot
- Immunohistochemistry
- Immunofluorescence
- Immunoprecipitation
- Flow Cytomety
- <u>Cell Culture</u>

Spike Protein RBD - Images