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Spike Protein RBD

Catalog # PVGS1577

Product Information

Primary Accession	P0DTC2
Species	SARS-CoV-2
Sequence	Arg319-Ser591 (E484K, K417N, N501Y)
Biological Activity	This protein is validated to bind with human ACE2 (Cat. No. Z03516) in functional ELISA assay.
Expression System	Human Cells
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.

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. The spike protein mutation N501Y (UK variant) is one of six key contact residues within the receptor-binding domain (RBD) and has been identified as increasing binding affinity to human and murine ACE. Recently, more SARS-CoV-2 variants have been identified, such as the B.1.351 lineage, first identified in South Africa in December 2020, carrying amino acid mutations N501Y, K417N, and E484K in the RBD domain. The B.1.351 lineage is reported to enter cells more easily due to its enhanced affinity to ACE-2 receptor. It is also reported to reduce the efficacy of neutralizing antibody.

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:32142651, PubMed:32155444, PubMed:33607086). When S2/S2' has been cleaved, binding to the receptor triggers direct fusion at the cell membrane (PubMed:34561887). 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:32075877, PubMed:32221306, PubMed:34903715, PubMed:36779763). Alternatively, may use NRP1/NRP2 (PubMed:33082294, PubMed:33082293) and integrin as entry receptors (PubMed:35150743). 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:33082293). The stalk domain of S contains three hinges, giving the head unexpected orientational freedom (PubMed:32817270).
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}