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Spike Protein RBD

Catalog # PVGS1583

Product Information

Primary Accession	P0DTC2
Species	SARS-CoV-2
Sequence	Arg319-Ser591 (E484K, K417T, N501Y)
Purity	> 90% as analyzed by SDS-PAGE
Endotoxin Level	
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
Formulation	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.

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.

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). Uses also ASGR1 as an alternative receptor in an ACE2-independent manner (PubMed:34837059). 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}

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