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Spike Protein RBD

Catalog # PVGS1575

Product Information

Primary Accession	P0DTC2
Species	SARS-CoV-2
Sequence	Arg319-Ser591
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	Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is the virus that causes coronavirus disease 2019 (COVID-19), the respiratory illness responsible for the COVID-19 pandemic. SARS-CoV-2 also known as 2019-nCoV, is a positive-sense single-stranded RNA virus and is believed to have zoonotic origins and has close genetic similarity to bat coronaviruses. The receptor binding domain (RBD) of spike protein of the SARS-CoV-2 virus binds Angiotensin-Converting Enzyme 2 (ACE2) to invade the host cells. Based on structural biology studies, the RBD can be oriented either in the up/standing or down/lying state with the up/standing state associated with higher pathogenicity.

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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