

Spike Protein RBD

Catalog # PVGS1676

Product Information

Primary Accession Species	P0DTC2 SARS-CoV-2
Sequence	Arg319-Ser591 (L452Q, F490S)
Biological Activity	This protein is validated to bind with human ACE2 (Cat. No. Z03516) in functional ELISA assay.
Expression System	CHO
Formulation Storage & Stability	Supplied as a solution in PBS, pH 7.4, 0.1% ProClin 300. 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 SARS-CoV-2 lambda variant was first identified in Peru in August 2020, and has quickly spread to other parts of South America and the United States. WHO classified lambda as a global "variant of interest". This variant carries a number of mutations with suspected implications, such as potential increased transmissibility or possible increased resistance to neutralizing antibodies. However, the full extent of those mutations' impact isn't yet well understood and will need further study. The lambda variant mainly contains L452Q and F400S point mutations in RBD domain, G75V, T76I and deletion mutation of 246-252 are located in S1 domain, which may enhance the infectivity.

Protein Information

Name	S {ECO:0000255 HAMAP-Rule:MF_04099}
Function	<p>[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).</p>
Cellular Location	<p>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}</p>

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