Spike protein RBD

Catalog # PVGS1684

Product Information

Primary Accession	P0DTC2
Species	SARS-CoV-2
Sequence	Arg319-Phe541 (G339D, S371F, S373P, S375F, T376A, D405N, R408S, K417N, N440K, S477N, T478K, E484A, Q493R, Q498R, N501Y, Y505H)
Biological Activity	This protein is validated to bind with human ACE2 (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	The Omicron variant of concern is currently the dominant variant circulating globally, accounting for nearly all sequences reported to GISAID. Omicron is made up of several sublineages, each of them being monitored by WHO and partners. Of them, the most common ones are BA.1, BA.1.1 (or Nextstrain clade 21K) and BA.2 (or Nextstrain clade 21L). At a global level, the proportion of reported sequences designated BA.2 has been increasing relative to BA.1 in recent weeks, however the global circulation of all variants is reportedly declining. BA.2 differs from BA.1 in its genetic sequence, including some amino acid differences in the spike protein and other proteins. Studies have shown that BA.2 has a growth advantage over BA.1. Studies are ongoing to understand the reasons for this growth advantage, but initial data suggest that BA.2 appears inherently more transmissible than BA.1, which currently remains the most common Omicron sublineage reported. This difference in transmissibility appears to be much smaller than, for example, the difference between BA.1 and Delta. Further, although BA.2 sequences are increasing in proportion relative to other Omicron sublineages (BA.1 and BA.1.1), there is

still a reported decline in overall cases globally.

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}