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# Spike Protein S1

Catalog # PVGS1677

## Product Information

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| **Primary Accession** | P0DTC2 |
| **Species** | SARS-CoV-2 |
| **Sequence** | Gln14-Arg685 (G75V, T76I, del 247-253, L452Q, F490S) |
| **Purity** | ≥ 90% as analyzed by SDS-PAGE |
| **Endotoxin Level** | ≤ 1 EU/ μg of protein by gel clotting method |
| **Biological Activity** | This protein is validated to bind with human ACE2 in functional ELISA assay. |
| **Expression System** | CHO |
| **Theoretical Molecular Weight** | 75.7 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

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| **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

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| **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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