

Human coronavirus 229E Spike glycoprotein (His & Myc)

General Information

Synonyms:	S glycoprotein;E2;Peplomer protein;Spike glycoprotein
Protein Construction:	785-873 aa
Species:	HCoV-229E
Expression Host:	E. coli
Accession:	P15423
Molecular Weight:	17.2 kDa (predicted)
AA Sequence:	DVLQENQKILAASFNKAMTNIVDAFTGVNDAITQTSQALQTVATALNKIQDVVNQQGNSLNHLTSQLRQNF QAISSSIQAIYDRLDTIQ

QC Testing

Biological Activity:	Activity has not been tested. It is theoretically active, but we cannot guarantee it. If you require protein activity, we recommend choosing the eukaryotic expression version first.
Purity:	> 85% as determined by SDS-PAGE.
Endotoxin:	< 1.0 EU/μg of the protein as determined by the LAL method.
Formulation:	If the delivery form is liquid, the default storage buffer is Tris/PBS-based buffer, 5%-50% glycerol. If the delivery form is lyophilized powder, the buffer before lyophilization is Tris/PBS-based buffer, 6% Trehalose, pH 8.0.

Preparation and Storage

Reconstitution:

Reconstitute the lyophilized protein in sterile deionized water. The product concentration should not be less than 100 μg/mL. Before opening, centrifuge the tube to collect powder at the bottom. After adding the reconstitution buffer, avoid vortexing or pipetting for mixing.

Stability & Storage:

Lyophilized powders can be stably stored for over 12 months, while liquid products can be stored for 6-12 months at -80°C. For reconstituted protein solutions, the solution can be stored at -20°C to -80°C for at least 3 months. Please avoid multiple freeze-thaw cycles and store products in aliquots.

Actual storage temperature shall be subject to the COA.

Shipping:

In general, lyophilized powders are shipped with blue ice, while solutions are shipped with dry ice.

Protein Background

S1 region attaches the virion to the cell membrane by interacting with host ANPEP/aminopeptidase N, initiating the infection. Binding to the receptor probably induces conformational changes in the S glycoprotein unmasking the fusion peptide of S2 region and activating membranes fusion. S2 region belongs to the class I viral fusion

protein. Under the current model, the protein has at least 3 conformational states: pre-fusion native state, pre-hairpin intermediate state, and post-fusion hairpin state. During viral and target cell membrane fusion, the coiled coil regions (heptad repeats) regions assume a trimer-of-hairpins structure, positioning the fusion peptide in close proximity to the C-terminal region of the ectodomain. The formation of this structure appears to drive apposition and subsequent fusion of viral and target cell membranes.

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