Data Sheet (Cat.No.TMPH-00153)

IBV (strain UK/123/82) Spike glycoprotein (His)

General Information

Synonyms:	S glycoprotein;E2;Spike glycoprotein;Peplomer protein
Protein Construction:	300-520 aa
Species:	IBV
Expression Host:	HEK293 Cells
Accession:	P30206
Molecular Weight:	27 kDa (predicted)
AA Sequence:	ESDYMYGSYHPSCKFRLETINNGLSFNPLSVSLGYGPIQGGCKQSVFENRATCCYAYSYNGPPLCKGVYRGELTKSFECGLLVFVTKTDGSRIQTRNEPFTLTQHNYNNITLDRCVEYNIYGRVGQGFITNVTNYAINYNYLADGGMAILDTSGAIDIFVVQGEYGLNYYKVNPCEDVNQQFVVSGGKLVGILTSRNETGSQPLENQFYIKIINGTRRSRR

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:	> 90% 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 attaches the virion to the cell membrane by interacting with cell receptors, initiating the infection.; S2 is a 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) 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.