

## IBV (strain UK/123/82) Spike glycoprotein (E. coli, His)

### General Information

Synonyms:	Spike glycoprotein;Peplomer protein;E2;S glycoprotein
Protein Construction:	300-520 aa
Species:	IBV
Expression Host:	E. coli
Accession:	P30206
Molecular Weight:	25.7 kDa (predicted)
AA Sequence:	ESDYMYGSYHPSCKFRLETINNGLSFNPLSVSLGYGPIQGGCKQSVFENRATCCYAYSYNGPPLCKGVYRGEL TKSFECGLLVFVTKTDGSRIRTRNEPFTLTQHNYYNNITLDRCEVYNIYGRVGGQFITNVTNYAINYNYLADGGM AILDTSGAIDIFVVQGEYGLNYYKVNPCEDVNQFVVS GGKLVGILTSRNETGSQPLENQFYIKIINGTRRSRR

### 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. <small>Actual storage temperature shall be subject to the COA.</small>
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.

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