

## HA (B/Austria/1359417/2021) (B/Victoria lineage)-like virus

CATALOG NUMBER: IB-HA-A21WP, 50 µg, 1 mg

### Introduction

Influenza hemagglutinin (HA) is a type of hemagglutinin found on the surface of the influenza viruses. HA is an antigenic glycoprotein, like all other hemagglutinins, it causes red blood cells to agglutinate. HA is responsible for binding the virus to the cell that is being infected. HA proteins bind to cells with sialic acid on the membranes, such as cells in the upper respiratory tract or erythrocytes.

HA is a homotrimeric integral membrane glycoprotein. HA monomer is synthesized as a single polypeptide that is subsequently cleaved into two smaller polypeptides, the HA1 and HA2 subunits. Each HA monomer consists of a long, helical chain anchored in the membrane by HA2 and topped by a large HA1 globule.

### Description

Recombinant hemagglutinin protein purified from HEKs293 cells

### Viral Protein

C-terminal 8xHis tagged HA (B/Austria/1359417/2021) protein (amino acid 16-545) (GISAID Accession No. EPI1857129). A trimerization domain sequence has been introduced into the C-terminal of HA to stabilize the formation of trimer HA.

### Applications

Western blot standard, antibody ELISA, antigen, *etc.*

### Storage

Store at -20 °C; Stable for 6 months from the date of shipment when kept at 4 °C.

### Concentration

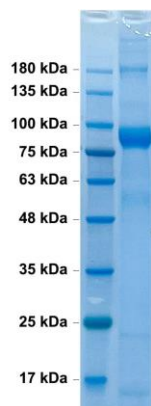
1 µg/µl in PBS

### Endotoxin Level

<0.01 EU per 1 µg of the protein by LAL test

### Purity

≥ 95% purity (SDS PAGE)



**SDS-PAGE:** purified HA (B/Austria/1359417/2021)(aa 16-545) protein

### HA (B/Austria/1359417/2021)(aa 16-545) SEQ:

```
DRICTGITSSNSPHVVKATATQGEVNVTVGVIPLTTPTKSHFANLKGTETRGKLCPKCLNCTDLVALGRPKCTGKIP SARVSI LHEVRPVTSGCFPI MH
DRTKIRQLPNLLRGYEHVRLSTHNVINTE DAPGGPYEIGTSGSCLNITNGKGFATMAWAVPKNKTATNPLTIEVPYICTEEDQITVWGFHSDDETQM
ARLYGDSKPQKFTSSANGVTTHYVSQIGGFNPQTEDGGLPQSGRIVVDYMVQKSGKTGTITYQRGILLPQKVVWCASGKSKVIKGSPLIGEADCLHEKY
GGLNKS KPYTGEHAKAIGNCPIWVKTP LKLANGTKYRPPAKLLKERGFFGAIAGFLEGGWEGMIAGWHGYTSHGAHGVAVAADLKSTQEAINKITKNL
NSLSELEVKNLQRLSGAMDELHNEILELDEKVDLDRADTISSQIELAVLLSNEGIINSEDEHLLALERKLLKMLGPSAVEIGNGCFETKHKCNQTCLDR
IAAGTFDAGEFSLPTFDSL NITAASLNDDGLDNHT
```