

## HA1 (H7N9)(A/Hong Kong/125/2017)(aa 19-339)

CATALOG NUMBER: IA-H7-HK017P, 50 µg

### 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.

H7N9 is a serotype of the species Influenza virus A (avian influenza virus or bird flu virus). Avian influenza A H7 viruses normally circulate amongst avian populations, but recently new H7N9 variants was first reported to have infected humans in 2013 in China. It is believed that certain mutations might have caused person to person H7N9 transmission.

### Description

Viral recombinant protein purified from 293 cell culture

### Viral Protein

C-terminal 6xHis tagged hemagglutinin (H7N9)(A/Hong Kong/125/2017) protein (amino acid 19-339)(GISAID Accession# EPI977395)

### Applications

Western blot standard, antibody ELISA, antigen, etc.

### Storage

Store at -20 °C; Stable for 3-months from the date of shipment when kept at 4 °C. Non-hazardous. No MSDS required.

### Endotoxin Level

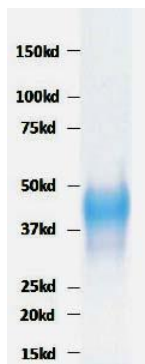
<0.01 EU per 1 µg of the protein by LAL test

### Concentration

1 µg/µl in PBS

### Specificity

≥ 95% purity (SDS PAGE)



**SDS-PAGE:** purified HA1 (H7N9)(A/Hong Kong/125/2017)(aa19-339) protein

### HA (aa19-339)(H7N9)(A/Hong Kong/125/2017) SEQ:

DKICLGHHAVSNGTKVNTLTERGVEVVNATETVERTNIPRICSKGKRTVDLGQCGLLGTTGPPQCDQFLEFSADLI IERREGSDVCYPGKFV  
NEEALRQILRESGGIDKETMGFTYNGIRTNGVTSACKRSGSSFYAEMKWLNSNTDNAAFPQMTKSYKNTRKSPAI I VWGIHHSVSTAEQTKLY  
GSGNKLVTVGSSNYQQSFVPSPGARPQVNGLSGRIDFHWLILNPNDTVTFNFNGAFIAPDRASFLRGKSMGIQSGVQVDANCEGDCYHSGGTI  
ISNLPFQNI DSRVAGKCPRYVKQRSLLLATGMKNVPEIPKGRHHHHHH