HA (A/Hong Kong/1/1968)(H3N2)(aa 17-529)

CATALOG NUMBER: IA-H3-00418t, 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.

Description

Recombinant protein purified from HEK293 cell culture

Viral Protein

C-terminal 6x His tagged hemagglutinin (A/Hongkong/1/1968)(H3N2)(aa 17-529) protein (GenBank Accession#: AAK51718). A trimerization domain sequence has been introduced into the C-terminal of HA to stabilize the formation of trimer HA.

Applications

WB standard, antibody ELISA, immunogen, etc.

Storage

Store at -20 ºC; Stable for 3 months from the date of shipment when kept at 4 ºC. Non-hazardous.

Concentration

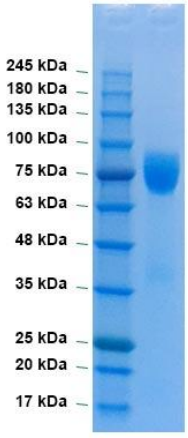
1 µg/µl in PBS

Endotoxin Level

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

Purity

> 95% purity (SDS PAGE)



SDS-PAGE: trimerized HA (A/Hong Kong/1/1968)(H3N2) protein (reducing condition).

Recombinant HA (A/Hong Kong/1/1968)(H3N2)(aa 17-529) Sequence:

QDLPGNDNSTATLCLGHHAVPNGTLVKTITDDQIEVTNATELVQSSSTGKICNNPHRILDGIDCTLIDALLGDPHCDVFQNETWDLFVERSKAFSNCYP
YDVPDYASLRSLVASSGTLEFITEGFTWTGVTQNGGSNACKRGPGSGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYIWGVHHPSTNQEQTSLYVQA
SGRVTVSTRRSQQTIIPNIGSRPWVRGLSSRISIYWTIVKPGDVLVINSNGNLIAPRGYFKMRTGKSSIMRSDAPIDTCISECITPNGSIPNDKPFQNV
NKITYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGAIAGFIENGWEGMIDGWYGFRHQNSEGTGQAADLKSTQAAIDQINGKLNRVIEKTNEKFHQIE
KEFSEVEGRIQDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTRRQLRENAEDMGNGCFKIYHKCDNACIESIRNGTYDHDVYRDEA
LNNRFQIKGVELKSGYKD

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