

HA (H3N2)(A/Texas/50/2012)(aa 17-529)

CATALOG NUMBER: IA-H3-050WP, 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

Viral protein produced from HEK 293 cells

Viral Protein

C-terminal 6xHis tagged Hemagglutinin (amino acid 17-529)(H3N2)(A/Texas/50/2012) (GenBank accession# AGL07159.1)

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. Non-hazardous. No MSDS required.

Concentration

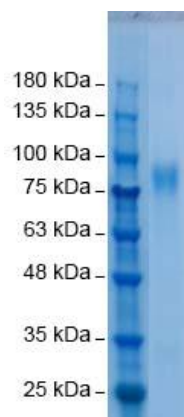
1 µg/µl in PBS with 20 % glycerol, 0.1% sodium azide

Endotoxin Level

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

Purity

>95% pure by 10% SDS PAGE gel



SDS-PAGE: purified HA (H3N2)(A/Texas/50/2012) protein

Reference:

1. Shcherbik SV, et al. Rapid strategy for screening by pyrosequencing of influenza virus reassortants--candidates for live attenuated vaccines. PLoS One. 9:e92580, 2014.

Recombinant HA (A/Texas/50/2012/H3N2) protein Sequence:

(17) QKLP GNDNSTATLC LGHHAVPNGT IVKTITNDRI EVTNATELVQ NSSIGEICDS PHQILDGENC TLIDALLGDP
QCDGFQNKKW DLFVERSKAY SNCYPYDVPD YASLRSLVAS SGTLEFNES FNWNGVTQNG TSSACIRRSN NSFFSRLNWL
THLNFKYPAL NVTMPNNEQF DKLYIWGVHH PGTDKDQIFL YAQPSGRITV STKRSQQAVI PNIGSRPRIR NIPSRISIW
TIVKPGDILL INSTGNLIAP RGYFKIRSGK SSIMRSDAPI GKCKSECITP NGSIPNDKPF QNVNRTITYGA CTRYVKQSTL
KLTATGMRNVP EKQTRGIFGA IAGFIENGWE GMVDGWYGFH HQNSEGRGQA ADLKSTQAAI DQINGKLNRL IGKTNEKFHQ
IEKEFSEVEG RIQDLEKYVE DTKIDLWSYN AELLVALENQ HTIDLTDSM NKLFKTKKQ LRENAEDMGN GCFKIYHKCD
NACIGSIRNG TYDHDVYRDE ALNNRFQIKG VELKSGYKD (529)