

HA1 (aa 17-341)(A/gyrfalcon/Washington/41088-6/2014)(H5N8)

Catalogue Number: IA-H5-058P, 50 ug

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 purified from 293 cell culture

Viral Protein

C-terminal 6xHis tagged Hemagglutinin (amino acid 17-341)(H5N8)
(A/gyrfalcon/Washington/41088-6/2014) (GenBank accession# AJE30333)

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

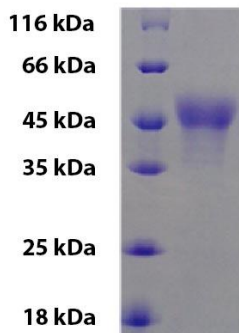
1 µg/µl in PBS with 20 % glycerol, 0.1% sodium azide

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 HA1 (H5N8)(A/ gyrfalcon/Washington/41088-6/2014) protein

Reference:

1. Ip HS etc. Novel eurasian highly pathogenic avian influenza a h5 viruses in wild birds, washington, USA, 2014. Emerg. Infect. Dis. 21: 886-890, 2015.

Recombinant HA1 (aa 17-341)(H5N8)(A/ gyrfalcon/Washington/41088-6/2014) protein Sequence:

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(17)DQIC IGYHANNSTK QVDTIMEKNV TVTHAQDILE KTHNGKLCDL NGVKPLILKD CSVAGWLLGN PMCDEFIRVP
EWSYIVERAN PANDLCYPGT LNDYEELKHL LSRINHFECT LIIPRSSWPN HETSLGVSA CPYQGASSFF RNVVWLIKKN
DAYPTIKISY NNTNREDLLI LWGIHHSNNA AEQTNLYKNP DTYVSVGTST LNQRLVPKIA TRSQVNGQSG RMDFFWTILK
PNDAIHFESN GNFIAPPEYAY KIVKKG DSTI MKSEMEYGH C NTKCQTPIGA INSSMPFHNI HPLTIGEC PK YVKS NKL VLA
TGLRNSPLRE R(341)
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