

HA (A/District of Columbia/27/2023)(H3N2)-Like Virus

CATALOG NUMBER: IA-H3-DC23Wp

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 HA protein expressed and purified from HEK293 cells

Viral Protein

C-terminal 8x His tagged hemagglutinin (A/District of Columbia/27/2023)(H3N2)(aa 17-529) protein (GISAID Accession#: EPI_ISL_18937823)(recommended FLU vaccine virus strain for 2025-2026 season). 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 °C; Stable for 6-months from the date of shipment when kept at 4 °C. Non-hazardous. No MSDS required.

Concentration

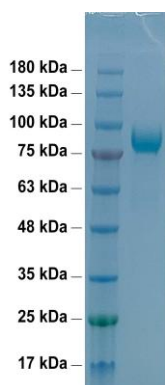
1 µg/µl in PBS

Endotoxin Level

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

Purity

> 95% purity (SDS PAGE)



SDS-PAGE: HA (A/District of Columbia/27/2023)(H3N2) protein

HA(H3N2)(A/District of Columbia/27/2023) SEQ:

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      QKIP GNDNSTATLC LGHHA V P N G T I V K T I T N D R I E V T N A T E L V Q N S S I G K I C N S P H Q I L D G G N C
TLIDALLGDP QCDGFQNK EW DLFVERSRAN SSCYPYDVPD YASLRSLVAS SGTLEFKDES FNWTGVKQNG TSSACKRGSS
NSFFSRLNWL TSLNNIYPAQ NVTMPNKEQF DKLYIWGVHH PDTDNQFSL FAQSSGRITV STKRSQQAVI PNIGSRPRVR
DIPSRISIW TIVKPGDILL INSTGNLIAP RGYFKIRSGK SSIMRSDAPI GECKSECITP NGSIPNDKPF QNVNRITYGA
CPRVYKQSTL KLATGMRNVP EKQTRGIFGA IAGFIENGWE GMVDGWYGF R H QNSEGRGQA ADLKSTQAAI DQISGKLNRL
IGKTNEKFHQ IEKEFSEVEG RVQDLEKYVE DTKIDLWSYN AELLVALENQ HTIDLTDSEM NKLFEKTKKQ LRENAEDMGN
GCFKIYHKCD NACIGSIRNE TYDHNVYRDE ALNNRFQIKG VELKSGYKD
  
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