HA (aa 16-548)(B/Massachusetts/02/2012)

CATALOG NUMBER: IA-BM7-005WP

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 HA (B/Massachusetts/02/2012) protein (amino acid 16-548) (GenBank Accession No. AGL06036), recommended FLU vaccine virus strain by WHO and FDA for the 2013-2014 and 2014-2015 seasons in North America.

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

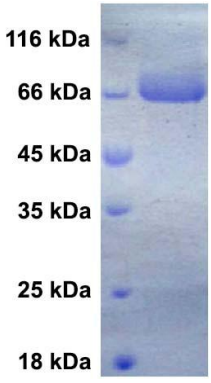
<0.01 EU per 1 μg of the protein by LAL test

Size

50 μg (1 μg/μL in PBS)

Purity

>95% pure by 10% SDS PAGE gel



SDS-PAGE: purified HA (B/Massachusetts/02/2012) protein

Tel: 1-800-919-0755 • Fax: 1-240-683-5852 • info@eEnzyme.com • www.eEnzyme.com

Reference:

1. COMMITTEE ON INFECTIOUS DISEASES. Recommendations for prevention and control of influenza in children, 2014-2015. Pediatrics. 134:e1503-1519, 2014.

HA (aa 16-548)(B/Massachusetts/02/2012) SEQ:

DRICTGITSSNSPHVVKTATQGEVNVTGVIPLTTTPTKSYFANLKGTKTRGKLCPDCLNCTDLDVALGRPMCVGTTPSAKASILHEVRP
VTSGCFPIMHDRTKIRQLANLLRGYENIRLSTQNVIDAEKAPGGPYRLGTSGSCPNATSKSGFFATMAWAVPKDNNKNATNPLTVEVPY
ICAEGEDQITVWGFHSDDKTQMKNLYGDSNPQKFTSSANGVTTHYVSQIGGFPDQTEDGGLPQSGRIVVDYMMQKPGKTGTIVYQRGVL
LPQKVWCASGRSKVIKGSLPLIGEADCLHEKYGGLNKSKPYYTGEHAKAIGNCPIWVKTPLKLANGTKYRPPAKLLKERGFFGAIAGFL
EGGWEGMIAGWHGYTSHGAHGVAVAADLKSTQEAINKITKNLNSLSELEVKNLQRLSGAMDELHNEILELDEKVDDLRADTISSQIELA
VLLSNEGIINSEDEHLLALERKLKKMLGPSAVDIGNGCFETKHKCNQTCLDRIAAGTFNAGEFSLPTFDSLNITAASLNDDGLDNHTI***H***
HHHHH