HA (A/California/06/09)(H1N1)(aa 18-530)

CATALOG NUMBER: IA-11SW-005P, 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 membrance 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 18-530) (H1N1)(A/California/06/09) protein (GenBank No. ACP41935).

Applications

Western blot standard, antibody ELISA, antigen, etc.

Storage

Store at -20 ^{o}C; Stable for 6-months from the date of shipment when kept at 4 ^{o}C. Non-hazardous. No MSDS required.

Concentration

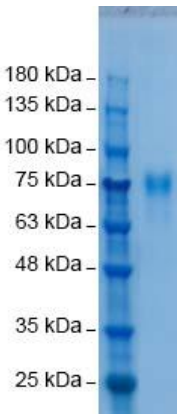
1 µg/µl in PBS

Endotoxin Level

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

Purity

≥ 95% purity (SDS PAGE)



SDS-PAGE: purified HA (A/California/06/09)(H1N1) protein

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Reference:

1. Dawood,F.S., et al. Emergence of a novel swine-origin influenza A (H1N1) virus in humans. N. Engl. J. Med. 360, 2605-2615, 2009.
2. Garten,R.J., et al. Antigenic and genetic characteristics of swine-origin 2009 A(H1N1)influenza viruses circulating in humans. Science 325, 197-201, 2009.

HA-SEQ:

DTLCIGYHAN NSTDTVDTVL EKNVTVTHSV NLLEDKHNGK LCKLRGVAPL HLGKCNIAGW ILGNPECESL STASSWSYIV
ETSSSDNGTC YPGDFIDYEE LREQLSSVSS FERFEIFPKT SSWPNHDSNK GVTAACPHAG AKSFYKNLIW LVKKGNSYPK
LSKSYINDKG KEVLVLWGIH HPSTSADQQS LYQNADAYVF VGSSRYSKKF KPEIAIRPKV RDQEGRMNYY WTLVEPGDKI
TFEATGNLVV PRYAFAMERN AGSGIIISDT PVHDCNTTCQ TPKGAINTSL PFQNIHPITI GKCPKYVKST KLRLATGLRN
VPSIQSRGLF GAIAGFIEGG WTGMVDGWYG YHHQNEQGSG YAADLKSTQN AIDEITNKVN SVIEKMNTQF TAVGKEFNHL
EKRIENLNKK VDDGFLDIWT YNAELLVLLE NERTLDYHDS NVKNLYEKVR SQLKNNAKEI GNGCFEFYHK CDNTCMESVK
NGTYDYPKYS EEAKLNREEI DGVKLESTRI YQIHHHHHH

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