

HA (A/Puerto Rico/8/1934)(H1N1), trimerization domain added

CATALOG NUMBER: IA-H1-PR8t

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 viral protein purified from 293 cell culture

Viral Protein

C-terminal 6xHis tagged hemagglutinin (amino acid 18-518) (H1N1)(A/Puerto Rico/8/1934) protein (GenBank Accession No. AB671289.1). A trimerization domain sequence has been introduced into the C-terminal of HA to enhance the formation of trimer HA.

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.

Concentration

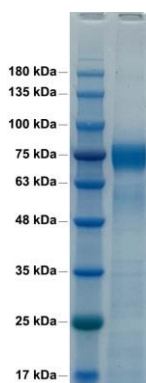
1 µg/µl (PBS pH7.5 OR 50mM HEPES, 0.3M NaCl, 1mM DTT, 0.01% Tween-80, pH 8.0)

Endotoxin Level

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

Purity

>95% pure by 4-20% SDS PAGE gel



Reduced SDS-PAGE: purified HA (aa 18-518)(A/Puerto Rico/8/1934)(H1N1) protein;

HA (AA 18-518)(A/PUERTO RICO/8/1934/H1N1) SEQ:

DTICIGYHANNSTDTVDTVLEKNVTVTHSVNLLLEDHNGKLCRLKGIAPLQLGKCNIA GWLLGNPECDPLL PVR SWSYIVETPNSENGICYPGDFIDYE
ELREQLSSVSSFERFEIFPKESSWPNHNTNGVTAAC SHEGKSSFYRNLLWLTEKEGSYPKLNKNSYVNKKGKVLVWGIHHP PNSKEQQNLYQENAYV
SVVTSNYNRRFTPEIAERPKVRDQAGRMNYYWTLKPGDTIIFEANGNLIAPMYAFALSRGFGSGIITSNASMHECNTKCCQTP LGAINSSLPYQNIHPV
TIGCEPKYVRS AKLRMVTGLRNI PSIQSRGLFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSYAADQKSTQNAINGITNKVNTVIEKMNIQFTAVGKEF
NKLEKR MENLNKKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQ LKNNAKEI GNGCFEFYHKCDNECMESVRNGTYDYPKYSEESKLN
REKVDG