

HA (A/Wisconsin/588/2019)(H1N1)pdm09-like virus

CATALOG NUMBER: IA-H1-W19WP

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 (aa 18-530)(A/Wisconsin/588/2019/H1N1)pdm09-like virus protein (GenBank Accession#:QRV63266). 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.

Size

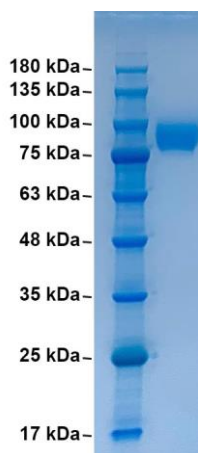
50 µg in PBS

Endotoxin Level

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

Purity

> 95% purity (SDS PAGE)



SDS-PAGE: purified HA (A/Wisconsin/588/2019)(H1N1)pdm09-like virus (reducing condition)

HA (aa 18-530)(A/Wisconsin/588/2019/H1N1) Seq:

DTLCIGYHANNSTDTVDTVLEKNVTVTHSVNLLLEDKHNKGLCKLRGVAPLHLGKCNIAAGWILGNPECESLSTARWSYIVETSNSDNGTCYPGDFINYE
ELREQLSSVSSFERFEIFPKTSSWPNHSDSNGVTAACPAGAKSFYKNLIWLVKKGKSYPKINQTYINDKGKEVLVLWGIHHPPTIADQQSLYQNADAY
VFGTSTRYSKKFKPEIATRPKVRDQEGRMNYYWTLVEPGDKITFEATGNLVAPRYAFTMERDAGSGIIISDTPVHDCNTTCQTPEGAINSTLSPFQNVHP
ITIGKCPKYVKSTKLRRLATGLRNVPSIQSRGLFGAIAAGFIEGGWTGMVDGWYGYHHQNEQSGYAADLKSTQNAIDKITNKVNSVIEKMNTQFTAVGKE
FNHLEKRIENLNKKVDDGFLDIWTYNAELLVLENERLTDYHDSNVKNLYEKVRNQLKNNAKEIGNGCFEFYHKDCNTCMESVKNGTYDYPKYSEEAKL
NREKIDGVKLDSTRIYQI