

Hemagglutinin HA(Y98F)(A/Cambodia/e0826360/2020/H3N2)

CATALOG NUMBER: IA-H3-C20WPm

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

C-terminal 8xHis-tagged glycosylated recombinant hemagglutinin (aa 17-529) (A/Cambodia/e0826360/2020)(H3N2)-like virus (GISAID Accession# EPI1837753) with the Y98F amino acid change; a trimerization domain sequence was introduced into the C-terminal of HA to stabilize the formation of trimer HA; produced in human 293 cells.

Applications

Western blot standard, antibody ELISA, antigen, *etc.*

Storage

Stable for 6 months from the date of shipment when kept at 4 °C.
Store at -20 °C or -70 °C for long term storage.

Concentration

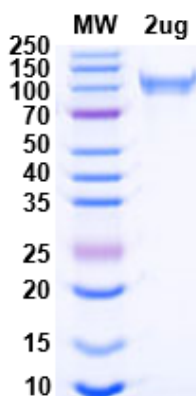
50 µg (1 µg/µl) in PBS (pH7.5)

Endotoxin Level

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

Purity

>95% pure by 10% SDS PAGE gel



SDS-PAGE: purified HA (H3N2)(A/Cambodia/e0826360/2020) protein

HA(Y98F)(A/Cambodia/e0826360/2020/H3N2)(aa 17-529) Sequence:

QKIPGNDNSTATLCLGHHAVPNGTIVKTIITNDRIEVTNATELVQNSSIGEICDSPHQILDGGNCTLIDALLGDPQCDGFQNKEDLFEVE
RSRANSNCFPYDVPDYASLRSLVASSGTLEFKNESFNWTGVKQNGTSSACIRGSSSSFFSRLNWLTHLNTYTPALNVTMPNNEQFDKLY
IWGVHHPSTDKDQISLFAQPSGRITVSTKRSQQAVIPNIGSRPRIRDIPSRSIYWTIVKPGDILLINSTGNLIAPRGYFKIRSGKSSI
MRSDAPIGKCKSECITPNSIPNDKPFQNVNRIITYGACPRYVKQSTLKLATGMRNVPEKQTRGIFGAIAGFIENGWEGMVDGWYGFRHQ
NSEGRGQAADLKSTQAAIDQINGKLNRLIGKTNEKFHQIEKEFSEVEGRVQDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDSEMN
KLFKTKKQLRENAEDMGNGCFKIYHKCDNACIGSIRNETYDHNVYRDEALNNRFQIKGVELKSGYKD

