Influenza HA (A/Kansas/14/2017)(H3N2)-Like Virus, Trimer

CATALOG NUMBER: IA-H3-K17t, 50 µg, 1mg

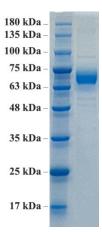|	
Introduction	Influenza hemagglutinin (HA) is a type of hemagglutinin found on the surface of the influenza viruses. HA is an antigenic glycoprotein, like all other hemagglutinins, it causes red blood cells to agglutinate. HA is responsible for binding the virus to the cell that is being infected. 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 cells
Viral Protein	C-terminal 6xHis tagged Hemagglutinin (amino acid 17-529)(A/Kansas/14/2017)(H3N2)-like virus (passage details: E7) (GenBank Accession# AXQ12067.1). A trimerization domain sequence has been introduced into the C-terminal of HA to stabilize 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 in PBS
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/Kansas/14/2017)-like virus protein*

HA(H3N2)(A/Kansas/14/2017) SEQ:

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QKIPGNDNSTATLCLGHHAVPNGTIVKTITNDRIEVTNATELVQNSSIGEICDSPHQILDGENCTLIDALLGDPQCDGFQNKKWDLFVERNKAYSNCYP
YDVPDYASLRSLVASSGTLEFNNESFNWAGVTQNGTSSSCIRGSKSSFFSRLNWLTHLNSKYPALNVTMPNNEQFDKLYIWGVHHPGTDKNQISLYAQS
SGRITVSTKRSQQAVIPNIGSRPRIRDIPSRISIYWTIVKPGDILLITSTGNLIAPRGYFKIRSGKSSIMRSDAPIGKCKSECITPNGSIPNDKPFQNV
NRITYGACPRYVKQSTLKLATGMRNVPERQTRGIFGAIAGFIENGWEGMVDGWYGFRHQNSEGRGQAADLKSTQAAIDQINGKLNRLIGKTNEKFHQIE
KEFSEVEGRIQDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTKKQLRENAEDMGNGCFKIYHKCDNACMGSIRNGTYDHNVYRDEA
LNNRFQIKGVELKSGYKD
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