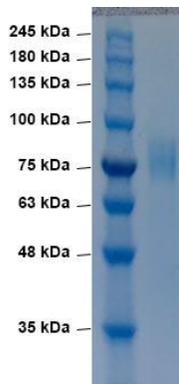


## HA Trimer (A/Vietnam/1203/2004)(H5N1)

CATALOG NUMBER: IA-H5-0051t, 50 µg

<b>Introduction</b>	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.
<b>Description</b>	Viral protein purified from HEK293 cells
<b>Viral Protein</b>	C-terminal 6xHis tagged HA (H5N1) (A/Vietnam/1203/2004) protein (amino acid 18-530) (GenBank accession# AAW80717). A trimerization domain sequence has been introduced into the C-terminal of HA to stabilize the formation of trimer HA.
<b>Applications</b>	Western blot standard, antibody ELISA, antigen, <i>etc.</i>
<b>Storage</b>	Store at -20 °C; stable for 3 months from the date of shipment when kept at 4 °C.
<b>Concentration</b>	1 µg/µl in PBS
<b>Endotoxin Level</b>	<0.01 EU per 1 µg of the protein by LAL test
<b>Purity</b>	≥ 95% purity (SDS PAGE)



**SDS-PAGE:** purified HA (H5N1)(A/Vietnam/1203/2004)(aa18-530) protein

### Recombinant HA (aa 18-530)(A/Vietnam/1203/2004)(H5N1) Sequence:

QICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKKHNGKLCDDLGVKPLILRDCSVAGWLLGNPMCDEFINVPESYIVEKANPVNDLCYPGDFNDYEE  
LKHLLSRINHFEKIQIIPKSSWSSHEASLGVSSACPYQGKSSFFRNVVWLIIKKNSTYPTIKRSYNNTNQEDLLVLWGIHHPNDAAEQTKLYQNPTYIS  
VGTSTLNQRLVPRIATRISKVNGQSGRMEFFWTILKPNDAINFESNGNFIAPEYAYKIVKKG DSTIMKSELEYGNCNTKCQTPMGAINSSMPFHNHPLT  
IGCEPKYVKS NRLVLATGLRNSPQREGLFGAIAGFIEGGWQGMVDGWYGYHHSNEQGSYAADKESTQK AIDGVTNKVNSIIDKMNTQFEAVGREFNNL  
ERRIENLNKKMEDGFLDVWWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDN AKEELGNGCFEFYHKCDNECMESVRNGTYDYPQYSEEARLKREE  
ISGVKLESIGIY