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Produktinformation



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Diagnostik & molekulare Diagnostik



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Lieferung & Zahlungsart

siehe unsere [Liefer- und Versandbedingungen](#)

Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

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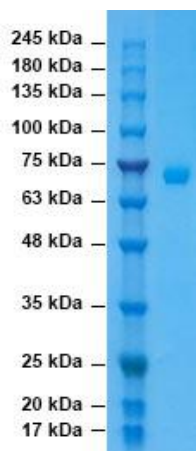
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HA (aa 17-527)(H7N7) (A/Chicken/Netherlands/1/03)

CATALOG NUMBER: IA-008W-005P, 50 µg

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 cell culture.
Viral Protein	C-terminal 6xHis tagged HA (H7N7)(A/Chicken/Netherlands/1/03) protein (amino acid 17-527) (GenBank accession # AAR02639)
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. No MSDS required.
Endotoxin Level	<0.01 EU per 1 µg of the protein by LAL test
Concentration	1 µg/µl in PBS.
Purity	>95% pure by 10% SDS PAGE gel.



SDS-PAGE: purified HA (H7N7)(A/Chicken/Netherlands/1/03) protein

HA (H7N7)(A/Chicken/Netherlands/1/03)(aa 17-517) Sequence:

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LVAIIPTNAD KICLGHHA VS NGTKVNTL TE RGVVVNATE TVERTNVPRI CSKGKRTVDL GQCGLLGTTT GPPQCDQFLE FSADLI IERR
EGSDVCYPGK FVNEEALRQI LRESGGIDKE TMGFTYSGIR TNGATSACRR SGSSFYAEMK WLLSNTDNAA FPQMTKSYKN TRKDPALI IW
GIHHSGSTTE QTKLYGSGNK LITVGSSNYQ QSFVPSPGAR PQVNGQSGRI DFHWLILNPN DTVTFSFNGA FIAPDRASFL RGKSMGIQSE
VQVDANCEGD CYHSGGTIIS NLPFQINISR AVGKCPRYVK QESLLLATGM KNPPEIPKRR RRGLFGA IAG FIENGWEGLI DGWYGFRHQ N
AQGEGTAADY KSTQSAIDQI TGKLNRLIEK TNQQFELIDN EFTEVEKQIG NVINWTRDSM TEVWSYNAEL LVAMENQHTI DLADSEM NKL
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