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Produktinformation



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Lieferung & Zahlungsart

siehe unsere [Liefer- und Versandbedingungen](#)

Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

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HA (A/Puerto Rico/8/1934)(H1N1)(aa 18-518) Trimer

CATALOG NUMBER: IA-H1-PR8t, 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 cell culture

Viral Protein

C-terminal 6xHis tagged hemagglutinin (amino acid 18-518) (H1N1)(A/Puerto Rico/8/1934) protein (GenBank Accession No. AB671289.1). Over 95% are trimeric fraction collected from column chromatography (trimeric protein size has been confirmed by filtration HPLC). 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. No MSDS required.

Trimer Level

Approximately 97% based on HPLC analysis

Concentration

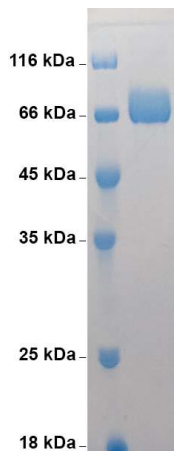
1 µg/µl in PBS

Endotoxin Level

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

Purity

>95% pure by 4-20% SDS PAGE gel



Reduced SDS-PAGE: purified HA (aa 18-518)(A/Puerto Rico/8/1934)(H1N1) protein;

HA (AA 18-518)(A/PUERTO RICO/8/1934/H1N1) SEQ:

DTICIGYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCRLKGIAPLQLGKCN IAGWLLGNPECDPLLPVRSWSYIVETPNS ENGICYPGDFIDYE
ELREQLSSVSSFERFEIFPKESSWPNHNTNGVTAAC SHEGKSSFYRNLLWLTEKEGSYPKLN SYVNKKGKEVLVLWGIHHPNSKEQQNLYQ NENAYV
SVVTSNYNRRFTPEIAERP KVRDQAGRMNYYWTL LKPGDTIIIFEANGNLIAPMYAFALS RGFSGIITSNASMHECNTK CQTPLGAINSSLPYQNIHPV
TIGECPKYVRS AKLRMVTGLRNIPSIQSRGLFGA IAGFIEGGWTGMIDGWYGYHHQNEQGSYAADQKSTQNAINGITNKVNTVIEKMNIQFTAVGKEF
NKLEKRMENLNKKVDDGFLDIWTYNAELLV LLENERTLDFHDSNVKNLYEKVKSQ LKNNAKEIGNC FEFYHKCDNECMESVRNGTYDYPKYSEESKLN
REKVDGRLVPRGSPGSGYIPEAPRDGQAYVRK DGEWVLLSTFLGHHHHHH