

Datasheet for ABIN6941945

**Influenza Hemagglutinin HA1 Chain (HA1) (AA 19-338) protein  
(His tag)**[Go to Product page](#)

## Overview

Quantity:	100 µg
Target:	Influenza Hemagglutinin HA1 Chain (HA1)
Protein Characteristics:	AA 19-338
Origin:	Influenza A Virus H9N2
Source:	HEK-293 Cells
Protein Type:	Recombinant
Purification tag / Conjugate:	His tag

## Product Details

Purpose:	Recombinant Influenza A [A/Guinea fowl/Hong Kong/WF10/99 (H9N2)] Hemagglutinin 1(HA1) protein produced in HEK293 cells. Protein contains a C-terminal 6x His-tag
Specificity:	Recombinant Influenza A [A/Guinea fowl/Hong Kong/WF10/99 (H9N2)] Hemagglutinin 1(HA1) protein comprising amino acids 19-338, incorporating a C-terminal 6xHis tag, produced in mammalian HEK293 cells. Greater than 95% purity.
Characteristics:	Influenza Virus Hemagglutinin 1 (HA1) (H9N2)
Purity:	>95 %

## Target Details

Target:	Influenza Hemagglutinin HA1 Chain (HA1)
Alternative Name:	Hemagglutinin 1 (HA1) ( <a href="#">HA1 Products</a> )
Background:	Influenza, commonly known as “the flu”, is an infectious disease of birds and mammals caused

## Target Details

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by RNA viruses of the family Orthomyxoviridae, the influenza viruses. The virus is divided into three main types (Influenza virus A, Influenza virus B, and Influenza virus C), which are distinguished by differences in two major internal proteins (hemagglutinin (HA) and neuraminidase (NA), which are the most important targets for the immune system. The type A viruses are the most virulent human pathogens among the three influenza types and cause the most severe disease.

Influenza virus hemagglutinin (HA) is a trimer of identical subunits, each of which contains two polypeptides that result from proteolytic cleavage of a single precursor. The two polypeptides are designated HA1 and HA2. The HA2 monomer is a long helical chain, anchored into the membrane, and is "topped" by a "globule" of HA1. Cleavage of the precursor is essential for activation of membrane fusion potential and hence infectivity. For HAs of most subtypes, the site of cleavage is a single arginine residue, and cleavage occurs extracellularly by an as yet unidentified enzyme. However, some members of the H5 and H7 subtypes have acquired a series of basic residues at the cleavage site, which are recognized by an intracellular subtilisin-like enzyme. In these cases, cleavage is efficient, virus infectivity is high, and the viruses are highly pathogenic. The avian H5 influenza, which continues to spread throughout the world, excluding the Americas, is caused by such viruses. The structure of HA has been reviewed by Gamblin and Skehel in 2010.

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UniProt: [Q80KD9](#)

## Application Details

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Comment: This Influenza virus hemagglutinin 1 protein is derived from the HA sequence of the A/Guinea fowl/Hong Kong/WF10/99 (H9N2) strain, (Accession # Q80KD9), expressing Asp19 – Arg338, and is fused with a polyhistidine tag at the C-terminus. The total calculated MW is 37.5kDa. The influenza virus hemagglutinin protein is expressed in HEK293 cells, and DTT-reduced protein migrates as a band of 50-66kDa.

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Restrictions: For Research Use only

## Handling

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Format: Lyophilized

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Buffer: PBS pH 7.4

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Storage: 4 °C

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Storage Comment: 4°C