

## HA2 (B/Brisbane/60/2008)(aa 361-547)

CATALOG NUMBER: IB-HA2-2608P, 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 6x His tagged HSA-HA2 (B/Brisbane/60/2008) protein (amino acid 361-547) (GenBank Accession No. ACN29380) (a fusion protein with 605 amino acid human serum albumin (HSA) at N-terminal of HA2 sequence).

### 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.

### Concentration

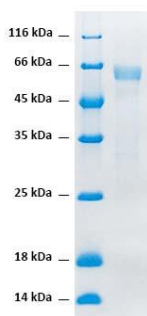
1 µg/µl in PBS

### Endotoxin Level

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

### Purity

≥ 95% purity (SDS PAGE)



**SDS-PAGE:** purified HSA-HA2 (B/Brisbane/60/2008)(aa 361-547) protein

### HA SEQ:

ERGFFGAIAGFLEGGWEGMIAGWHGYTSHGAHGVAADLKSTQEAINKITKNLNSLSELEVKNLQRLSGAMDELHNEIILELDEKVDLDRADTISSQIE  
LAVLLSNEGIINSEDEHLLALERKLLKMLGPSAVEIGNGCFETKHKCNQTCLDRIAAGTFDAGEFSLPTFDSLNI TAASLNDDGLDNHHHHHH

**HSA (human serum albumin) sequence:**

DAHKSEVAHRFKDLGEENFKALVLI AFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERN  
ECFLQHKDDNPNL PRLVLRPEVDVMCTAFHDNEETF LKKYLYE IARRHPYFYAPELLFFAKRYKAAFTECCQAADKAAACLLPKLDEL RDEGKASSAKQRL  
KCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLT KVHTECCHGDLL ECADDRADLAKY ICENQDSISSKLKECCEKPLEKSHCIAEVENDE  
MPADLPSLAADFVESKDVCNKYAEAKDVFLGMFLY EYARRHPDYSV VLLLRLAKTYETTLEKCCAAADPHECYAKVDFEFKPLVEEPQNLIKQNC ELF E  
QLGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCTESLVNRRPCFSALEVDE  
TYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKKADDKETCF AEEGKKLVAASQAALGLGGSGGGGS  
GGSGGGGSAS