Recombinant Influenza B [B/Austria/1359417/2021 (B/Victoria lineage)-like virus] Hemagglutinin (HA), His-tagged

Product Information

Cat#

INF-459

Product Name

Recombinant Influenza B [B/Austria/1359417/2021 (B/Victoria lineage)-like virus] Hemagglutinin (HA), His-tagged

Description

This Influenza virus hemagglutinin protein is derived from the HA sequence of the B/Austria/1359417/2021 (B/Victoria lineage)-like virus, expressing aa 1-529, and fused with a polyhistidine tag at the C-terminus. The influenza virus hemagglutinin protein is expressed in HEK293 cells. This virus is recommended by WHO for inclusion in the quadrivalent and trivalent vaccines for use in the 2022 southern hemisphere influenza season.

Type

Recombinant

Gene

HA

Species

Influenza B [B/Austria/1359417/2021 (B/Victoria lineage)-like virus]

Source

HEK293

Synonyms

Influenza B [B/Austria/1359417/2021 (B/Victoria lineage)-like virus] Hemagglutinin (HA)

Formulation

DPBS

Purity

greater than >90% purity by SDS-PAGE.

Notes

This product is intended for research and manufacturing uses only. It is not a diagnostic device. The user assumes all responsibility for care, custody and control of the material, including its disposal, in accordance with all regulations.

Tags

C-terminal His

Background

The influenza A viruses are negative-sense, single-stranded, segmented RNA viruses of the genus Alphainfluenzavirus, family Orthomyxoviridae. There are several subtypes, named according to the type of Haemagglutinin (H1-18) and Neuraminidase (N1-11) (Centers for Disease Control and Prevention, 2017). Humans are generally infected by influenza viruses of the subtypes H1, H2 or H3, and N1 or N2. In April 2009, a new virus, referred to as A/(H1N1) pdm09, appeared in Mexico and California (US), and was responsible for the first pandemics of the 21st century (claiming several hundred lives). It spreads rapidly from person to person, and is not related to any circulating inter-pandemic viruses. It is a quadruple reassortant virus, consisting of two swine-origin viruses, one avian-origin virus and one human-origin virus. It has a high fatality rate and shows higher incidence among younger people (Baldo et al., 2016).
WHO convenes technical consultations in February and September each year to recommend viruses for inclusion in influenza vaccines for the northern and southern hemisphere influenza seasons, respectively.
Globally, from September 2020 through January 2021, overall influenza A virus detections were in the minority during this period compared to influenza B virus detections. However, from September to November 2020, influenza A virus detections predominated in some countries. In most countries, areas and territories reporting influenza A viruses, both A(H1N1)pdm09 and A(H3N2) subtypes were detected. All influenza B viruses collected in the period February through August 2021 were of the B/Victoria/2/87 lineage.
Globally, from September 2020 through January 2021, overall influenza A virus detections were in the minority during this period compared to influenza B virus detections. However, from

Recombinant Influenza B [B/Austria/1359417/2021 (B/Victoria lineage)-like virus] Hemagglutinin (HA), His-tagged

September to November 2020, influenza A virus detections predominated in some countries. In most countries, areas and territories reporting influenza A viruses, both A(H1N1)pdm09 and A(H3N2) subtypes were detected. WHO has identified four strains as the most likely to circulate in the 2022 influenza season, including B/Austria/1359417/2021 (B/Victoria lineage)-like virus (WHO, 2021).

Since December, 2019, coronavirus disease 2019 (COVID-19) has been an international public health emergency and co-infection with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and other respiratory viruses have been reported, complicating their diagnosis (Azekawa et al., 2020; Cuadrado-Payán et al., 2020; Wu et al., 2020).