Native hMPV 18 Type B2 Lysate

Product Information

Cat#

HUM-416

Product Name

Native hMPV 18 Type B2 Lysate

Description

Human metapneumovirus 18 type B2 (Strain: IA18-2003) lysate from LLC-mk2 cell line. Purified by sucrose density gradient ultracentrifugation and heat-inactivated, followed by verification with validated tissue culture infectivity assay. Suitable for the development of immunoassays, Western blotting, dot blotting and other protein-based assays.

Type

Native

Gene

hMPV 18 Type B2 Lysate

Species

HMPV

Synonyms

hMPV 18 Type B2 Lysate

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.

Applications

Appropriate for the development of immunoassays, Western blotting, dot blotting and other protein-based assays.

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Background

Human metapnuemoviruses (hMPV) are negative-sense, single-stranded RNA viruses of the family Pneumoviridae. hMPV was first isolated in 2001 in the Netherlands using RAP-PCR for identification of unknown viruses growing in cultured cells. hMPV infection is the second most common cause of lower respiratory tract infections in young children after respiratory syncytial virus (RSV). Most infants who are hospitalised with hMPV infection are between 6–12 months of age and the clinical features and severity of HMPV are similar to those of RSV. The genomic organisation of hMPV is similar to RSV, however, hMPV lacks the non-structural genes, NS1 and NS2, and the hMPV antisense RNA genome contains eight open reading frames in slightly different gene order than RSV (viz. 3'-N-P-M-F-M2-SH-G-L-5') (van den Hoogen et al., 2002). The genome is about 13kb in size and is composed of eight genes encoding nine proteins: nucleoprotein (N), phosphoprotein (P), matrix protein (M), fusion protein (F), matrix-2 proteins (M2-1 and M2-2), small hydrophobic (SH) protein, glycoprotein (G), and large (L) polymerase protein. hMPV is genetically similar to the avian metapneumoviruses A, B and in particular type C. Phylogenetic analysis of hMPV shows there are two main genetic lineages, termed A and B, which contain within them the subgroups A1/A2 and B1/B2, respectively (Shafagati et al., 2018).