

Tytuł: Brud z paneli slonecznych

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Abstract Transcription and replication of the influenza virus RNA genome is catalyzed by the viral heterotrimeric RNA-dependent RNA polymerase in the context of viral ribonucleoprotein (vRNP)

Influenza virus contains a single-stranded negative-sense RNA genome. Replication of the genome is carried out by the viral RNA-dependent RNA polymerase in the context of the viral ribonucleoprotein

Influenza viruses (types A, B, C, and D) belong to the family orthomyxoviridae. Out of all the influenza types, influenza A virus (IAV) causes human pandemic outbreaks. Its pandemic potential is

Influenza viruses are enveloped negative-stranded RNA viruses with segmented genomes containing eight gene segments. The influenza virus belongs to the Orthomyxoviridae family and consists of four

Viruses have evolved to efficiently navigate host cells to deliver, express, and replicate their genetic material. Understanding the mechanisms underlying viral RNA localisation is paramount to designing

The influenza A virus (IAV), a respiratory pathogen for humans, poses serious medical and economic challenges to global healthcare systems. The IAV genome, consisting of eight single-stranded viral

Influenza virus is an infectious agent belonging to the virus family Orthomyxoviridae that causes a respiratory tract infection (influenza or "flu") in vertebrates.

Structures of RNA polymerase of human and avian influenza A viruses reveal that the interface of the RNA polymerase dimer is required to initiate viral RNA synthesis in viral genome replication.

Influenza virus can be classified into four different genera: influenza A-D, with the former two, influenza A and B, relevant to humans. The capacity of antigenic drift and shift in Influenza A has given rise to

Influenza virus poses a long-standing public health issue worldwide, causing both recurring seasonal flu and

