Viral mRNA Splicing (M, NS segments)

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Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

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Literature references

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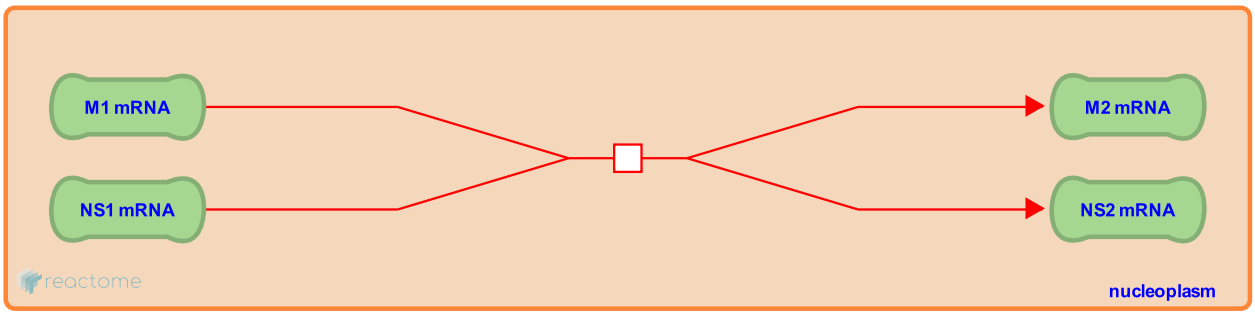
Stable identifier: R-HSA-192781

Type: transition

Compartments: nucleoplasm

Diseases: influenza



The viral polymerase complex produces positive-sense viral mRNA with host-cell derived 5' methyl caps. Alternately spliced mRNA transcribed from M and NS vRNA segments 7 and 8, producing the spliced mRNA for M2 and NEP/NS2, respectively, are thought to be coupled to the cellular splicing and export mechanisms (Lamb, 1980; Lamb, 1981; Chen, 2000; Li, 2001). As segments 7 and 8 each encode two proteins, splicing must be regulated allowing for alternative mRNAs, with the spliced products in the minority (approximately 10%). M1 splicing may be regulated by the viral polymerase and the cellular SR splicing protein SF2/ASF (Shih, 1995; Shih, 1996); while NS1 splicing appears to be regulated by the viral mRNA intrinsically (Alonso-Caplen, 1991; Valcarel, 1991).

Literature references

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Editions

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