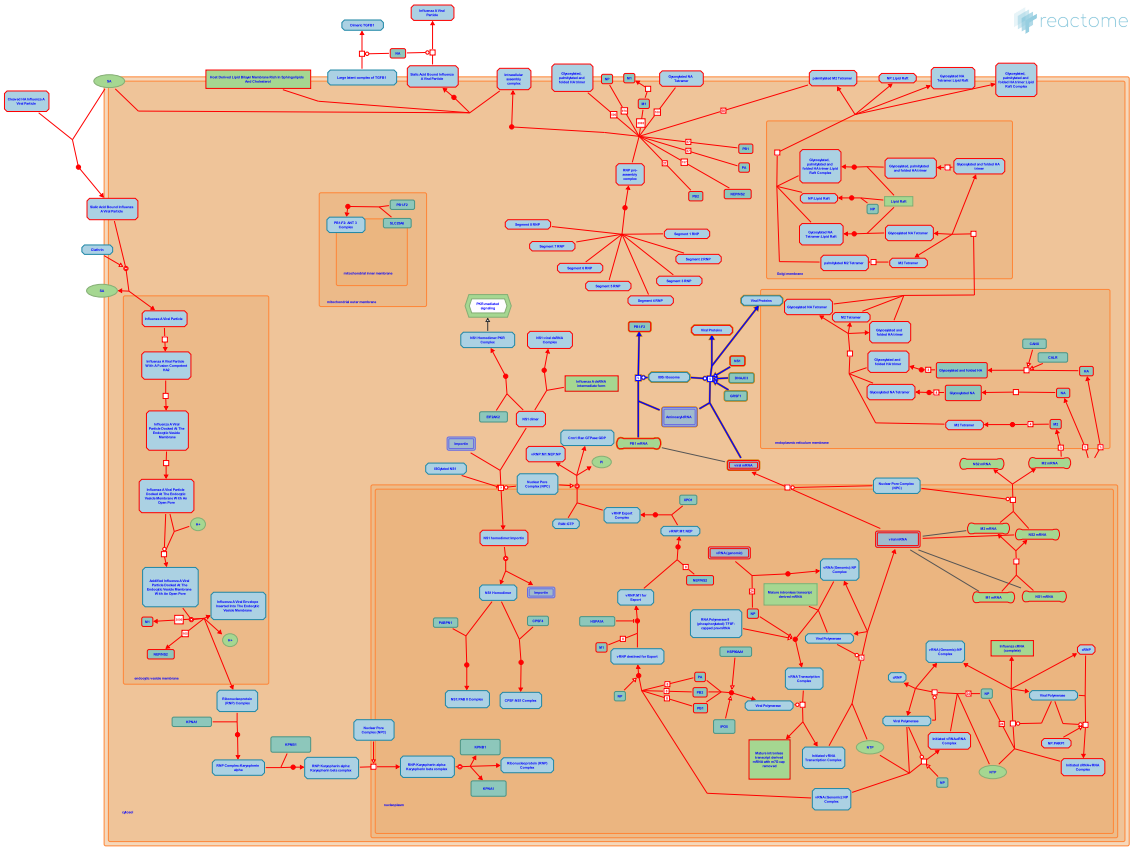
Viral mRNA Translation



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This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the Reactome Textbook.

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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.
The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

Literature references

Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics, 18*, 142. ↗

Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

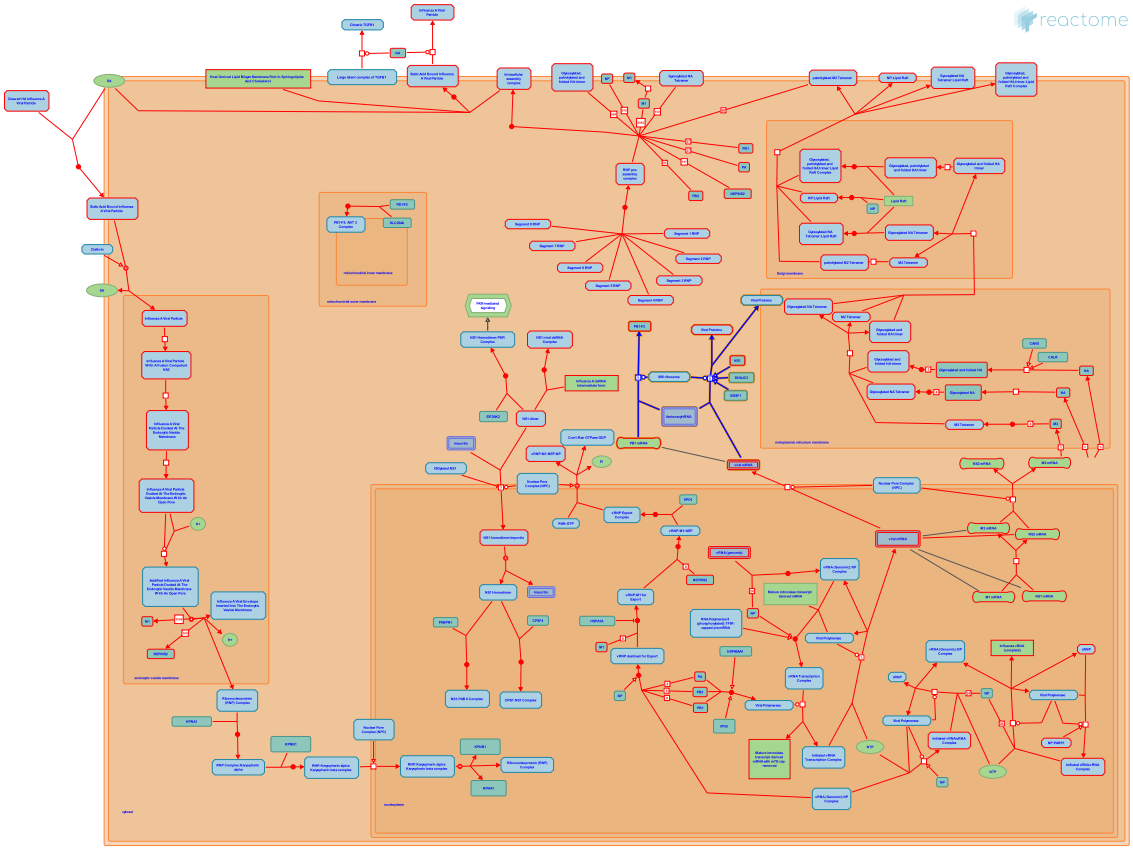
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Viral mRNA Translation ↗

Stable identifier: R-HSA-192823

Compartments: cytosol

Diseases: influenza



Spliced and unspliced viral mRNA in the cytoplasm are translated by host cell ribosomal translation machinery (reviewed in Kash, 2006). At least ten viral proteins are synthesized: HA, NA, PB1, PB2, PA, NP, NS1, NEP/NS2, M1, and M2. Viral mRNA translation is believed to be enhanced by conserved 5'UTR sequences that interact with the ribosomal machinery and at least one cellular RNA-binding protein, G-rich sequence factor 1 (GRSF-1), has been found to specifically interact with the viral 5' UTRs. (Park, 1995; Park, 1999). The viral NS1 protein and the cellular protein P58(IPK) enhance viral translation indirectly by preventing the activation of the translational inhibitor PKR (Salvatore, 2002; Goodman, 2006). The viral NS1 protein has also been proposed to specifically enhance translation through interaction with host poly(A)-binding protein 1 (PABP1) (Burgui, 2003). Simultaneously, host cell protein synthesis is downregulated in influenza virus infection through still uncharacterized mechanisms (Katze, 1986; Garfinkel, 1992; Kash, 2006). In most human influenza A strains (such as PR8), the PB1 mRNA segment is capable of producing a second protein, PB1-F2, from a short +1 open reading frame initiating downstream of the PB1 ORF initiation codon (Chen, 2001).

Literature references

Korth, MJ., Katze, MG., Kash, JC., Goodman, AG. (2006). Hijacking of the host-cell response and translational control during influenza virus infection. *Virus Res, 119*, 111-20. ↗

Editions

2007-02-13	Authored	Garcia-Sastre, A., Bortz, E.
2007-02-13	Reviewed	Squires, B.

Synthesis of PB1-F2 ↗

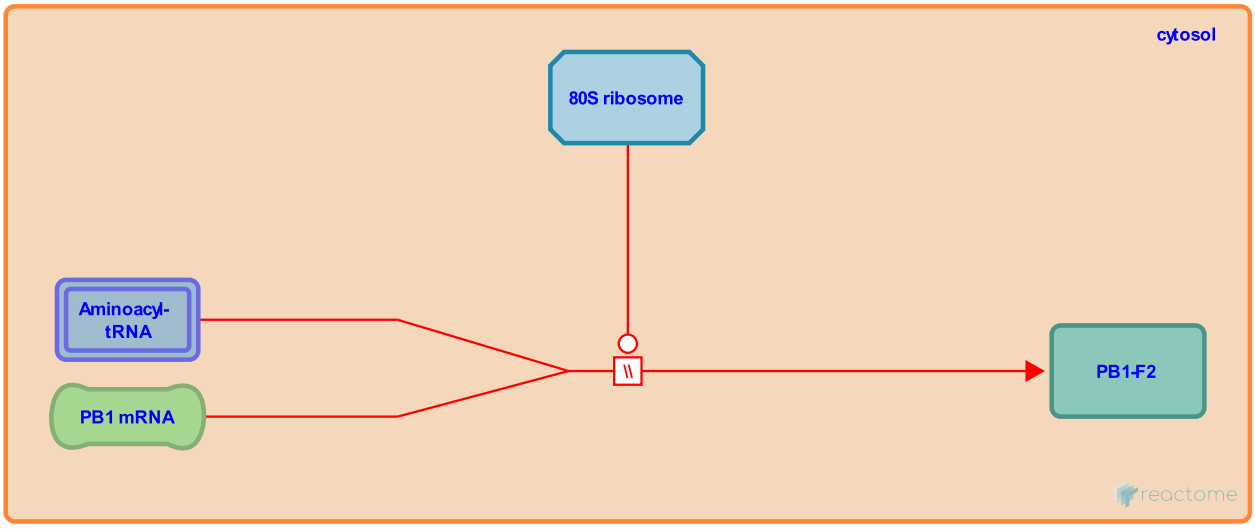
Location: Viral mRNA Translation

Stable identifier: R-HSA-192704

Type: omitted

Compartments: cytosol

Diseases: influenza



For most influenza A strains (such as PR8), the PB1 mRNA segment produces a second protein, PB1-F2, from the +1 open reading frame (Chen, 2001). PB1-F2 is a pro-apoptotic, mitochondria-localized protein (Chen, 2001; Gibbs, 2003) that oligomerizes (Bruns, 2007) and sensitizes cells to death in concert with the mitochondrial ANT3 and VDAC proteins (Zamarin, 2005).

Literature references

Chen, W., Palese, P., Malide, D., Calvo, PA., Gibbs, J., Henklein, P. et al. (2001). A novel influenza A virus mitochondrial protein that induces cell death. *Nat Med, 7*, 1306-12. ↗

Editions

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Viral Protein Synthesis ↗

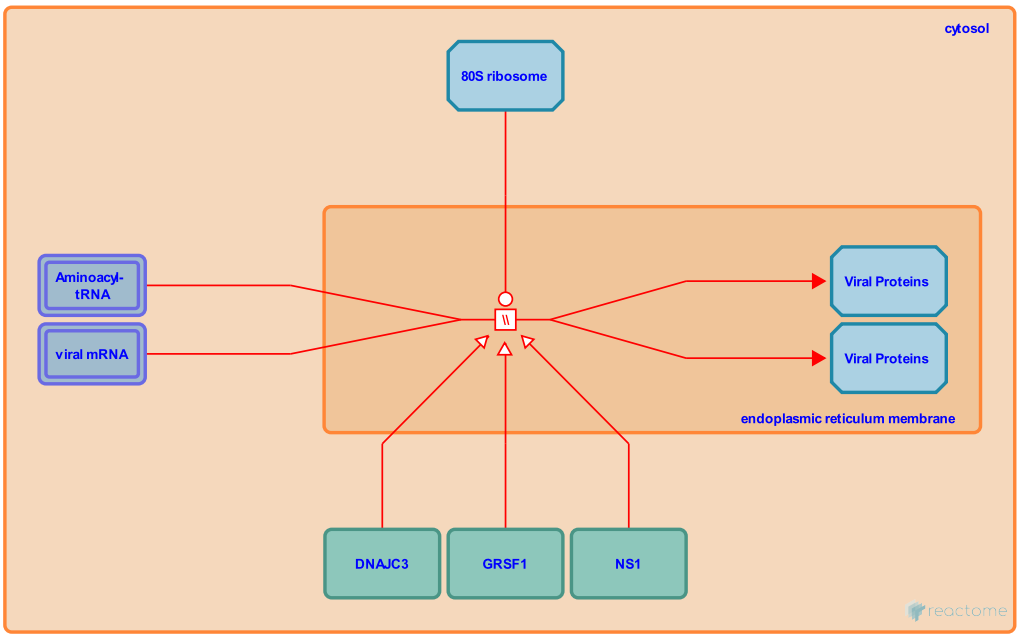
Location: Viral mRNA Translation

Stable identifier: R-HSA-192841

Type: omitted

Compartments: endoplasmic reticulum membrane, cytosol

Diseases: influenza



Spliced and unspliced viral mRNA exported into the cytoplasm are translated by the host cell ribosomal translation machinery (reviewed in Kash, 2006). At least ten viral proteins are synthesized: HA, NA, PB1, PB2, PA, NP, NS1, NEP/NS2 (from spliced NS mRNA), M1, and M2 (from spliced M mRNA). The abundance of each of these proteins is thought to be controlled by differential mRNA abundances and stability (Tekamp, 1980; Hatada, 1989). As the localization of the nascent polypeptides is different between viral proteins with transmembrane domains (HA, NA and M2, which translocate to the ER and are transported through the Golgi to the plasma membrane) and soluble viral proteins (such as NP, the polymerase subunits, and NS1), mechanisms linking the translation of particular viral mRNA with subsequent protein localization rely on signal sequences recognized by the cell.

Literature references

Korth, MJ., Katze, MG., Kash, JC., Goodman, AG. (2006). Hijacking of the host-cell response and translational control during influenza virus infection. *Virus Res, 119*, 111-20. ↗

Editions

2007-02-13	Authored	Garcia-Sastre, A., Bortz, E.
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