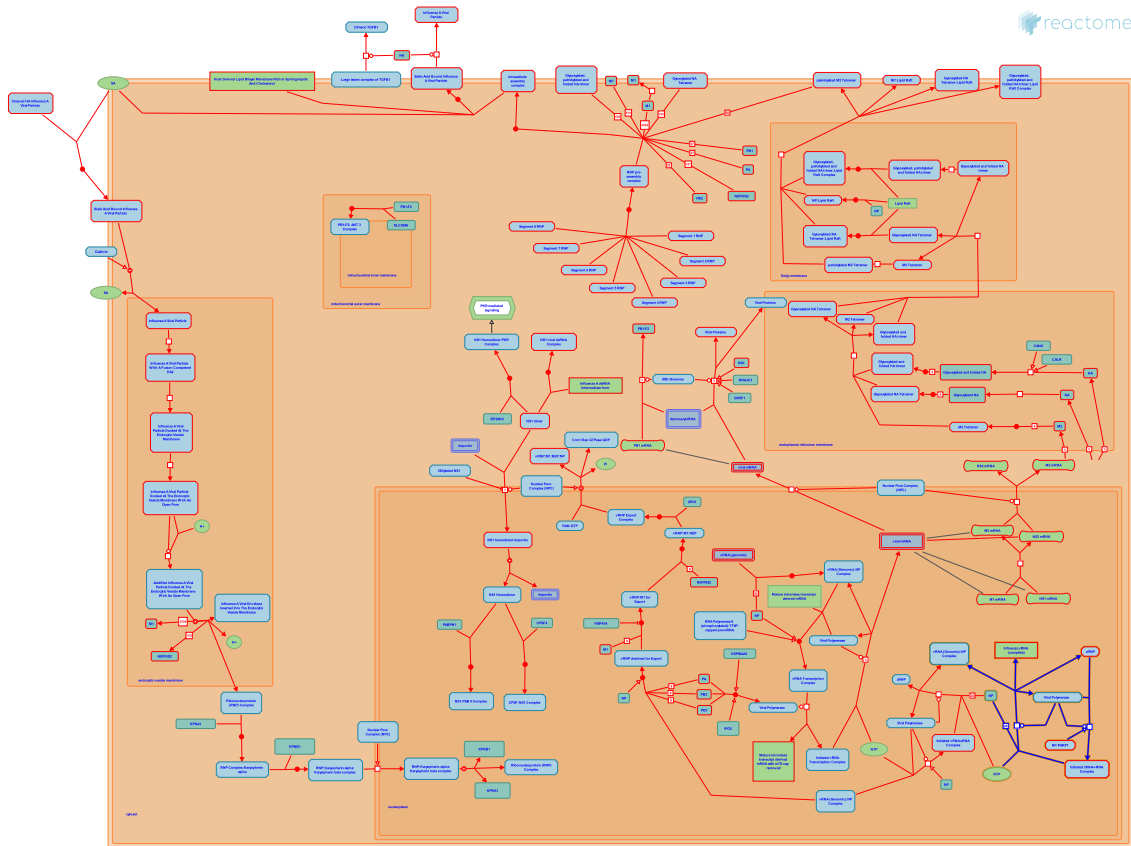


vRNA Synthesis



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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](https://reactome.org/textbook/).

03/05/2024

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

- 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. [↗](#)

Reactome database release: 88

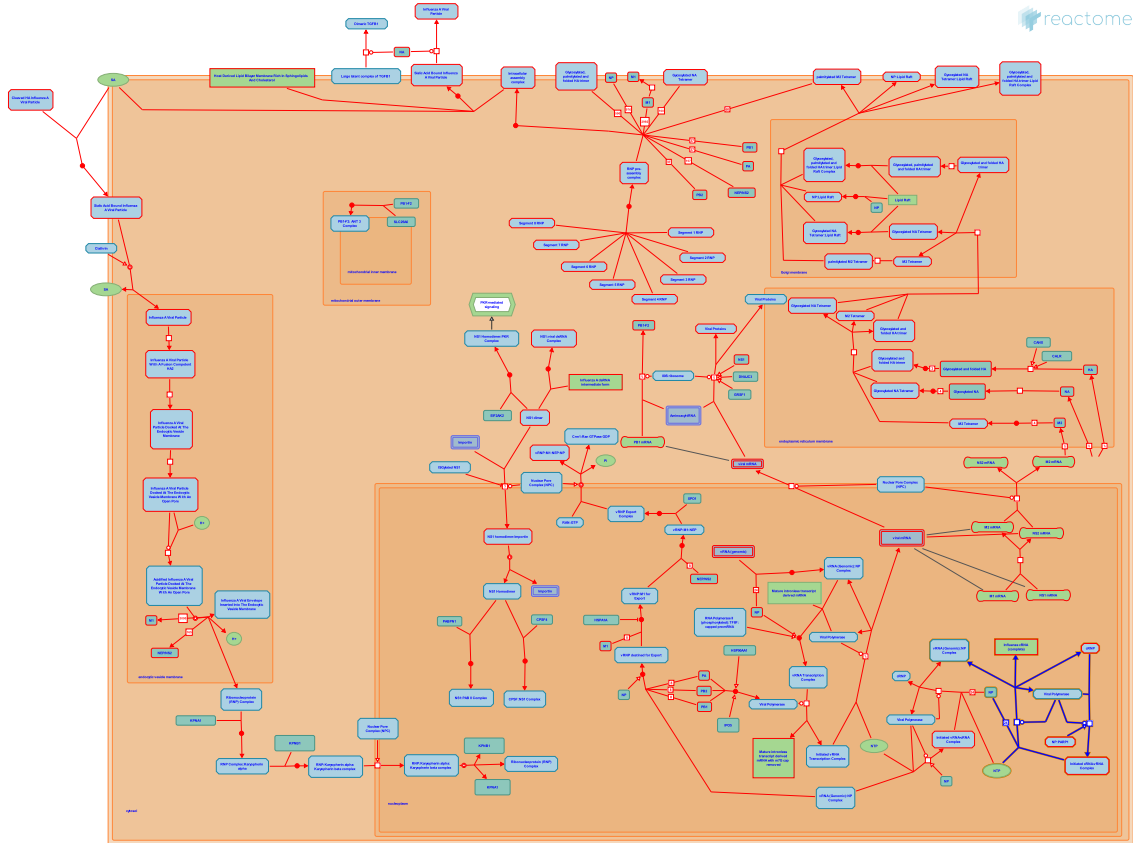
This document contains 1 pathway and 2 reactions ([see Table of Contents](#))

vRNA Synthesis ↗

Stable identifier: R-HSA-192814

Compartments: nucleoplasm

Diseases: influenza



The synthesis of full-length negative strand viral RNA from a cRNA template is believed to follow the same principles as the synthesis of cRNA from a vRNA template. The cRNA, complexed with viral nucleocapsid (NP) protein, is used as template by the trimeric viral polymerase (Pritlove, 1995; Vreede, 2004; Crow, 2004), and newly synthesized vRNA molecules are immediately packaged with NP molecules to form ribonucleoprotein complexes (Vreede, 2004). There is some evidence that the production of vRNA-containing vRNP occurs in the nuclear matrix as well as the nucleoplasm (Takizawa, 2006).

Literature references

- Jung, TE., Brownlee, GG., Vreede, FT. (2004). Model suggesting that replication of influenza virus is regulated by stabilization of replicative intermediates. *J Virol*, 78, 9568-72. ↗
- Seong, BL., Fodor, E., Pritlove, DC., Brownlee, GG. (1995). In vitro transcription and polymerase binding studies of the termini of influenza A virus cRNA: evidence for a cRNA panhandle. *J Gen Virol*, 2205-13. ↗
- Crow, M., Brownlee, GG., Deng, T., Addley, M. (2004). Mutational analysis of the influenza virus cRNA promoter and identification of nucleotides critical for replication. *J Virol*, 78, 6263-70. ↗

Editions

2007-02-13	Authored	Garcia-Sastre, A., Bortz, E.
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Initiation of vRNA Synthesis ↗

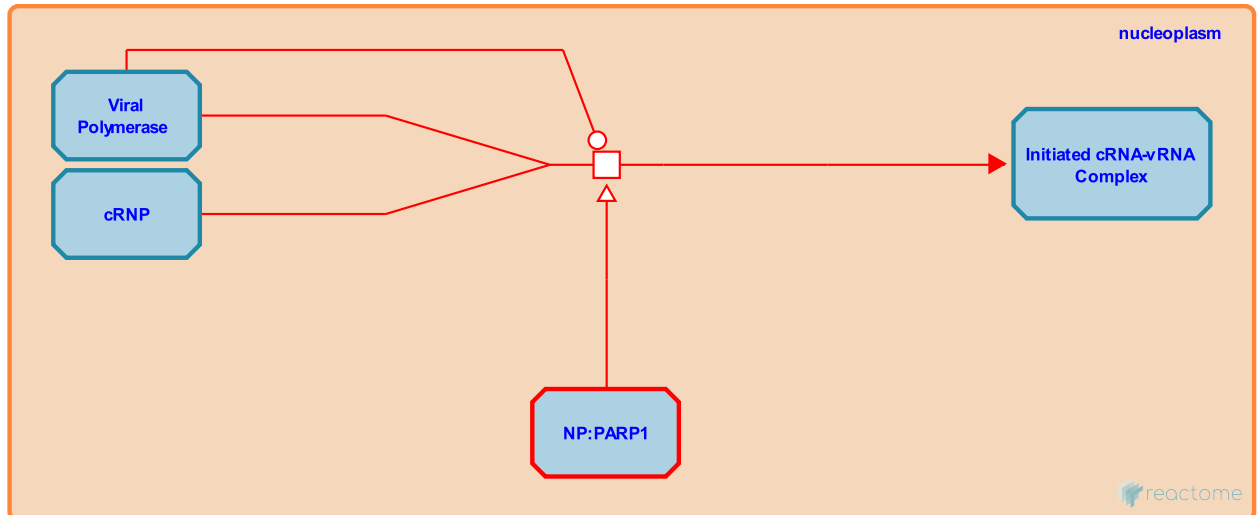
Location: [vRNA Synthesis](#)

Stable identifier: R-HSA-192916

Type: transition

Compartments: nucleoplasm

Diseases: influenza



For efficient Influenza virus (IAV) replication, several cellular barriers and host factors must be overtaken by the virus to complete its life cycle.

The host factor PARP1 has been demonstrated to participate in cellular events responding to DNA damage or cellular stress.

PARP1 is an interacting partner of IAV polymerases required for efficient IAV replication and necessary for synthesis of the viral nucleoprotein (NP).

Initiation of synthesis of the viral genomic RNA (vRNA) is thought to require hairpin (or panhandle/corkscrew) RNA loop structures formed by both the 5' and 3' ends of the cRNA (Pritlove, 1995; Crow, 2004; Park, 2003; Deng, 2006). The cRNA promoter has a similar structure to the vRNA promoter, but slight sequence differences are believed to result in a stronger cRNA promoter. As with the vRNA promoter, the polymerase is thought to first bind to the 5' end of the cRNA, then to the 3' end, and subsequently initiate RNA synthesis.

Followed by: [vRNA Extension](#)

Literature references

Brownlee, GG., Vreede, FT., Deng, T. (2006). Different de novo initiation strategies are used by influenza virus RNA polymerase on its cRNA and viral RNA promoters during viral RNA replication. *J Virol*, 80, 2337-48. ↗

Seong, BL., Fodor, E., Pritlove, DC., Brownlee, GG. (1995). In vitro transcription and polymerase binding studies of the termini of influenza A virus cRNA: evidence for a cRNA panhandle. *J Gen Virol*, 2205-13. ↗

Crow, M., Brownlee, GG., Deng, T., Addley, M. (2004). Mutational analysis of the influenza virus cRNA promoter and identification of nucleotides critical for replication. *J Virol*, 78, 6263-70. ↗

Lee, MK., Bae, SH., Varani, G., Choi, BS., Park, CJ. (2003). Solution structure of the influenza A virus cRNA promoter: implications for differential recognition of viral promoter structures by RNA-dependent RNA polymerase. *Nucleic Acids Res*, 31, 2824-32. ↗

Editions

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vRNA Extension ↗

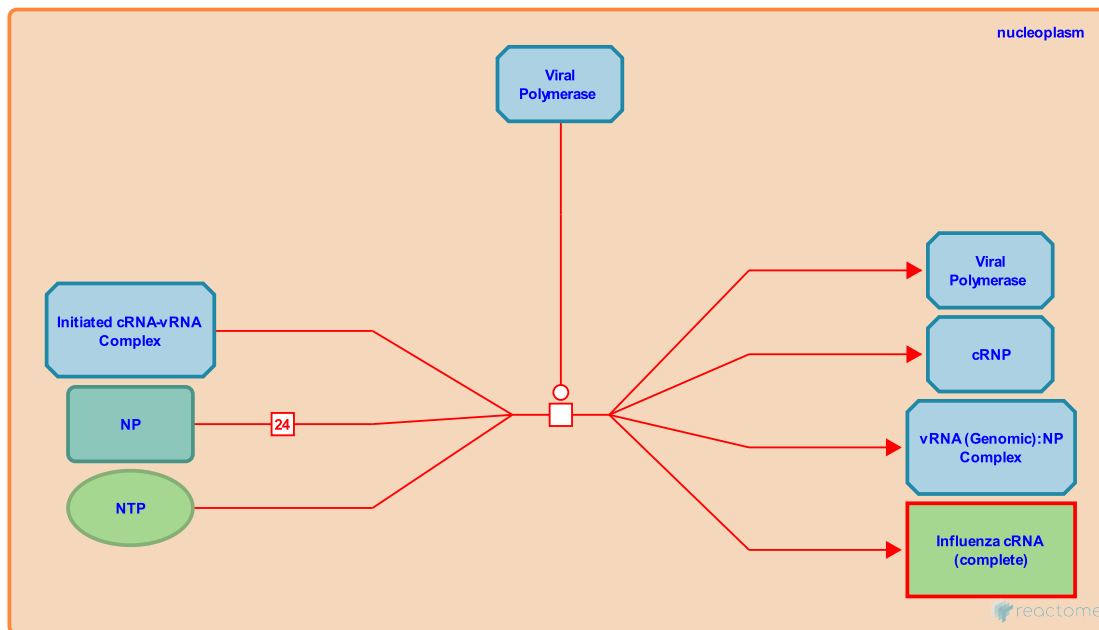
Location: [vRNA Synthesis](#)

Stable identifier: R-HSA-192851

Type: transition

Compartments: nucleoplasm

Diseases: influenza



vRNA is synthesized from the complementary cRNA strand by the trimeric polymerase complex, and bound by free NP protein (Honda, 1988; Mikulasova, 2000; Neumann, 2004). The PB1 subunit, with PA, catalyzes extension (Nakagawa, 1996). The cRNA is released.

Preceded by: [Initiation of vRNA Synthesis](#)

Literature references

- Fodor, E., Neumann, G., Brownlee, GG., Kawaoka, Y. (2004). Orthomyxovirus replication, transcription, and polyadenylation. *Curr Top Microbiol Immunol*, 283, 121-43. ↗
- Fodor, E., Mikulasova, A., Vareckova, E. (2000). Transcription and replication of the influenza a virus genome. *Acta Virol*, 44, 273-82. ↗
- Nakada, S., Oda, K., Nakagawa, Y. (1996). The PB1 subunit alone can catalyze cRNA synthesis, and the PA subunit in addition to the PB1 subunit is required for viral RNA synthesis in replication of the influenza virus genome. *J Virol*, 70, 6390-4. ↗
- Honda, A., Ishihama, A., Ueda, K., Nagata, K. (1988). RNA polymerase of influenza virus: role of NP in RNA chain elongation. *J Biochem (Tokyo)*, 104, 1021-6. ↗

Editions

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