Priming and Initiation of Transcription

Bortz, E., Garcia-Sastre, A., Squires, B.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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.

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. ↗

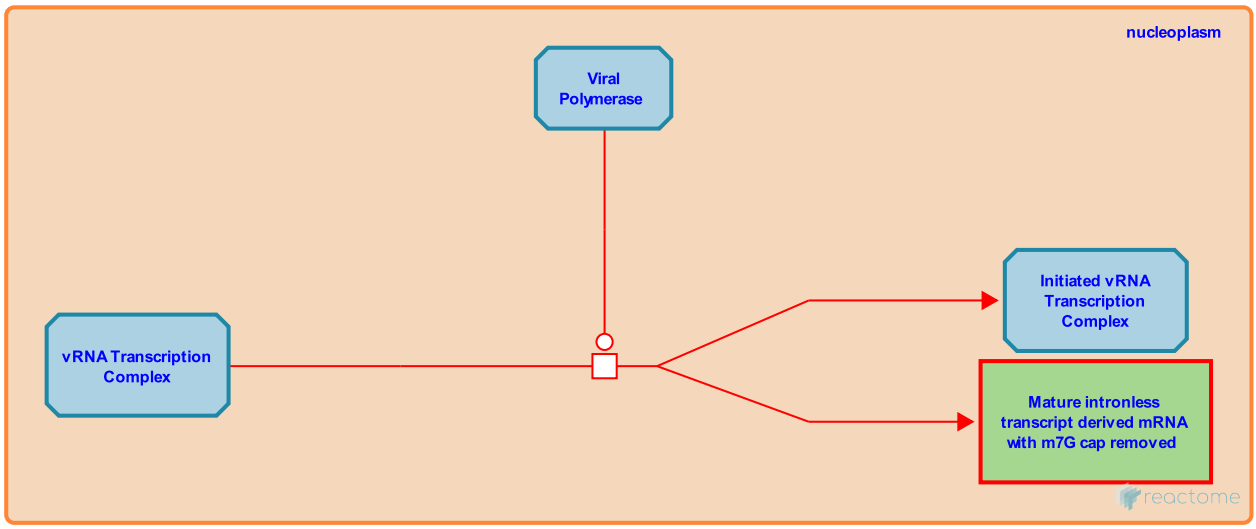
Priming and Initiation of Transcription ↗

Stable identifier: R-HSA-168280

Type: transition

Compartments: nucleoplasm

Diseases: influenza



The host cell mRNA bound to viral RNA polymerase PB2 subunit is cleaved by the viral RNA polymerase PB1 subunit's endonuclease activity, and the capped 5' end plus 10-13 nucleotides of the host mRNA remains bound to the polymerase complex (Plotch, 1981; Krug, 1981; Hagen, 1994; Cianci, 1995, Li, 1998; Li, 2001). Viral mRNA may be protected against cap-snatching by the polymerase complex itself, which tightly binds capped viral mRNA (Shih, 1996). A guanine residue, complementary to a cytosine in the vRNA, is added to the host-derived cap, catalyzed by the RNA polymerase activity of the PB1 viral RNA polymerase subunit (Beaton, 1981; Toyoda, 1986).

Literature references

Krug, RM., Rao, P., Li, ML. (2001). The active sites of the influenza cap-dependent endonuclease are on different polymerase subunits. *EMBO J, 20*, 2078-86. ↗

Chung, TD., Krystal, M., Butcher, JA., Hagen, M. (1994). Recombinant influenza virus polymerase: requirement of both 5' and 3' viral ends for endonuclease activity. *J Virol, 68*, 1509-15. ↗

Krug, RM. (1981). Priming of influenza viral RNA transcription by capped heterologous RNAs. *Curr Top Microbiol Immunol, 93*, 125-49. ↗

Plotch, SJ., Krug, RM., Bouloy, M., Ulmanen, I. (1981). A unique cap(m7GpppXm)-dependent influenza virion endonuclease cleaves capped RNAs to generate the primers that initiate viral RNA transcription. *Cell, 23*, 847-58. ↗

Editions

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