Addition of nucleotides 10 and 11 on the growing transcript: Third Transition

Joshi-Tope, G., Timmers, HTM.

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

19/10/2024

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. ↗

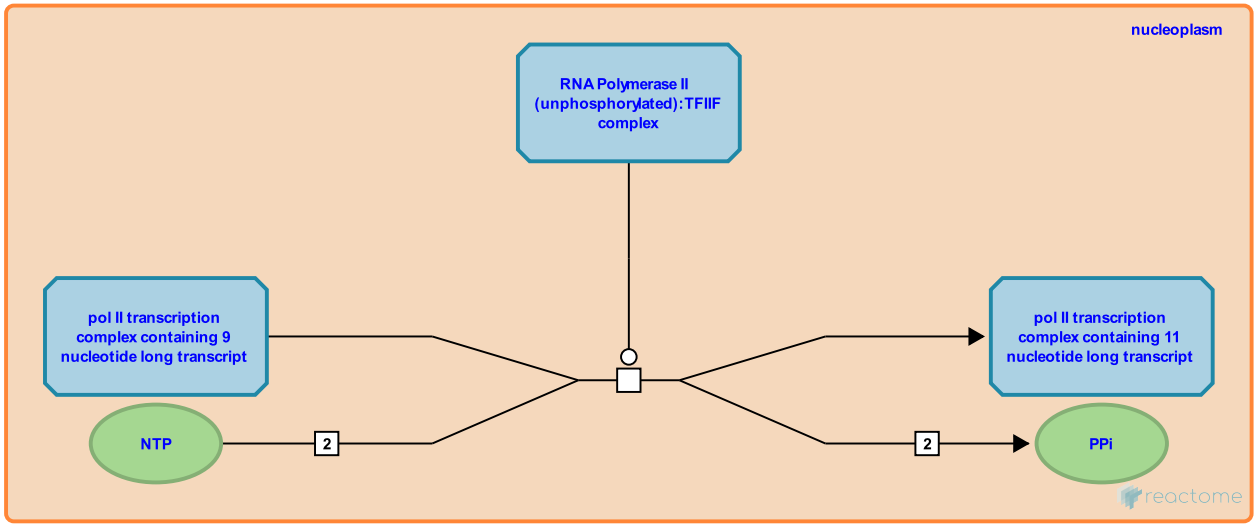
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Addition of nucleotides 10 and 11 on the growing transcript: Third Transition

Stable identifier: R-HSA-76576

Type: transition

Compartments: nucleoplasm



Formation of phosphodiester bonds nine and ten creates RNA products, which do not dissociate from the RNA pol II initiation complex. The transcription complex has enter the productive elongation phase. TFIIH and ATP-hydrolysis are required for efficient promoter escape. The open region ("transcription bubble") expands concomitant with the site of RNA-extension. The region upstream from the transcription start site (-9 to -3) collapses to the double-stranded state. TFIIH remains associated to the RNA pol II initiation complex.

Literature references

Zawel, L., Kumar, KP., Reinberg, D. (1995). Recycling of the general transcription factors during RNA polymerase II transcription. *Genes Dev, 9*, 1479-90.

Fiedler, U., Timmers, HT., Holstege, FC. (1998). Three transitions in the RNA polymerase II transcription complex during initiation. *EMBO J, 16*, 7468-80.

Editions

2003-09-11	Authored	Timmers, HTM.
2024-08-27	Edited	Joshi-Tope, G.