Unwinding of DNA for the Nascent Transcript: Second Transition

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02/05/2024

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

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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. ↗

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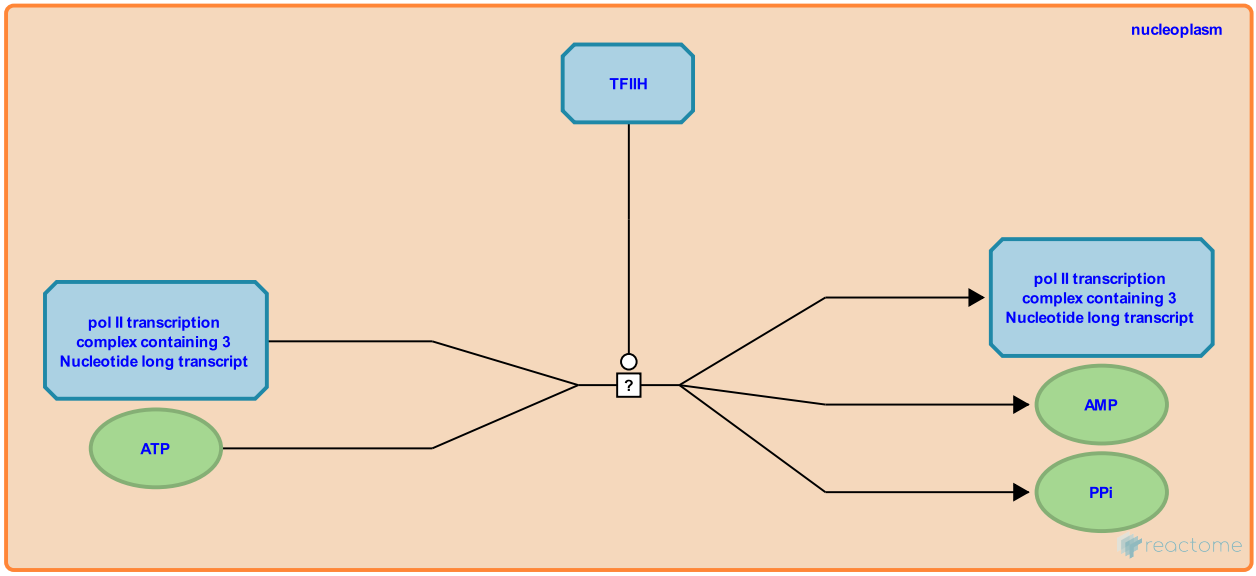
Stable identifier: R-HSA-9613494

Type: uncertain

Compartments: nucleoplasm



The human BTF2 basic transcription factor (also called TFIIH), is required for class1 gene transcription of the second round of transcripts. TFIIH has an adenosine triphosphate-dependent DNA helicase activity. The helicase activity is closely associated with the multi-subunit BTF2/TFIIH transcription factor which also has a CTD protein kinase activity.

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Editions

2003-09-11	Authored	Timmers, HTM.
2024-03-06	Edited	Joshi-Tope, G.