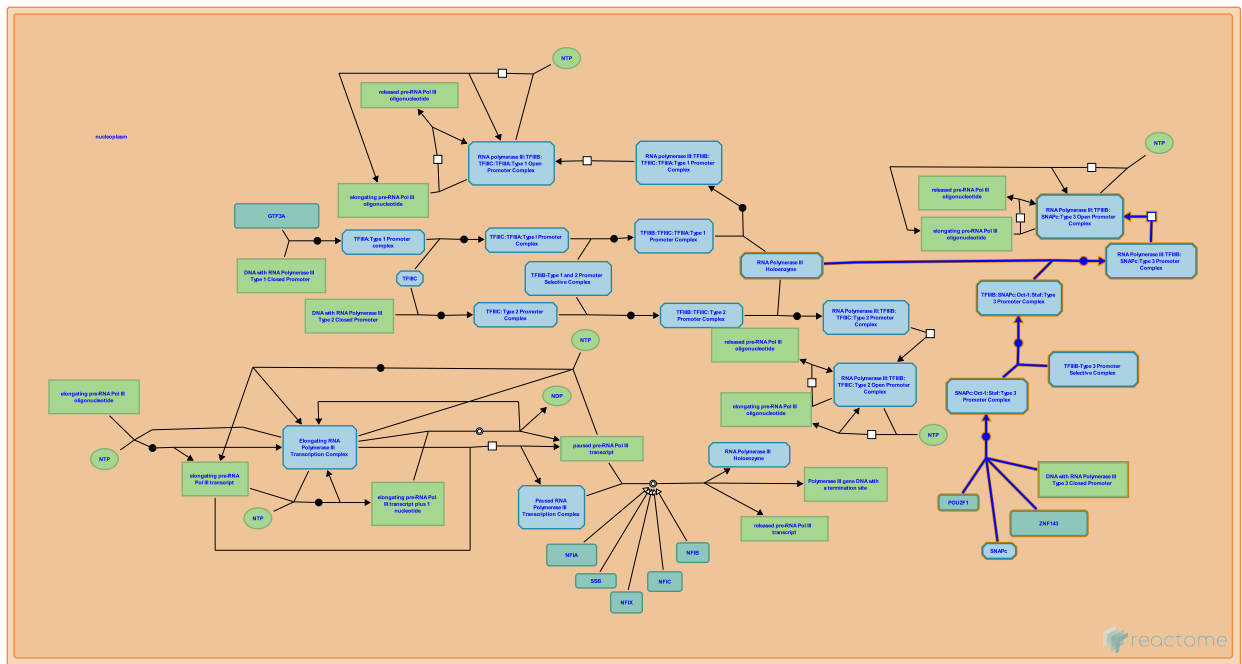


RNA Polymerase III Transcription Initiation From Type 3 Promoter



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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/about/reactome-textbook/).

06/05/2024

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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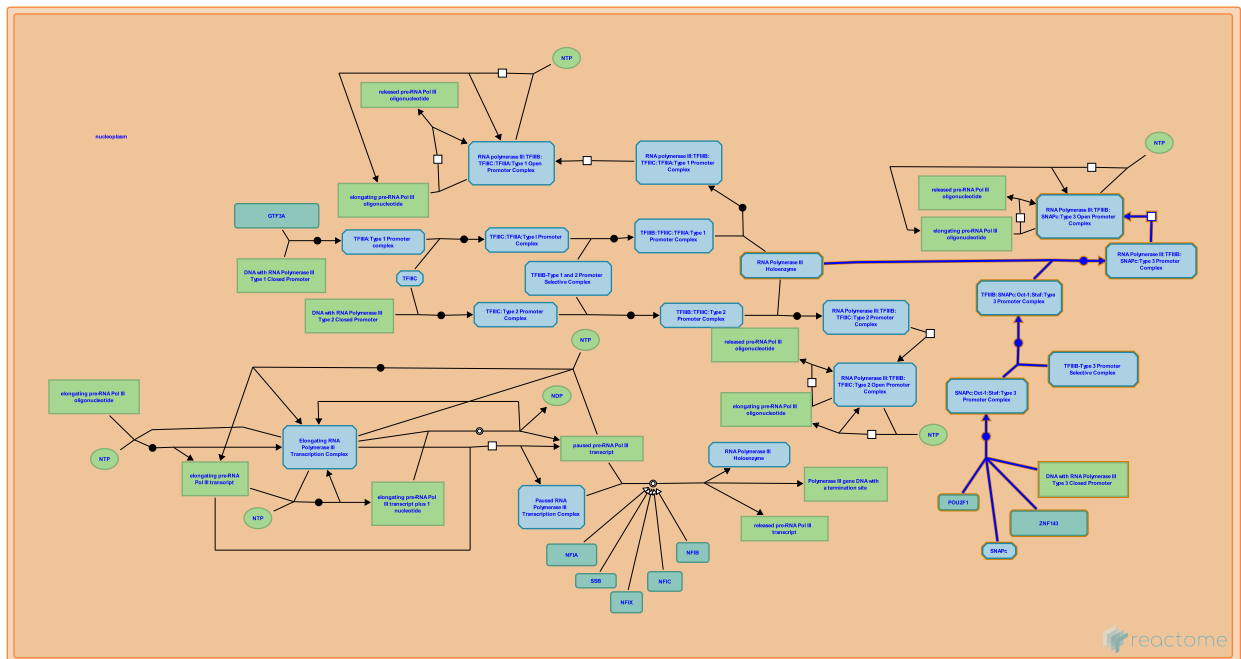
Reactome database release: 88

This document contains 1 pathway and 4 reactions ([see Table of Contents](#))

RNA Polymerase III Transcription Initiation From Type 3 Promoter ↗

Stable identifier: R-HSA-76071

Compartments: nucleoplasm



The metazoan-specific type 3 promoters, which are exemplified by the human U6 promoter, recruit a complex variously called the snRNA activating protein complex (SNAPc) (Sadowski et al., 1993), the PSE binding protein (PBP) (Waldschmidt et al., 1991), or the PSE transcription factor (PTF) (Murphy et al., 1992). The complex contains five types of subunits and binds to the PSE. Type 3 promoters also recruit Brf2-TFIIB through a combination of protein-protein contacts with SNAPc and a direct association of the TBP component of Brf2-TFIIB with the TATA box. This then allows RNA polymerase III to join the complex.

The down stream element (DSE) of type 3 promoters, which enhances transcription from the core promoter, almost invariably contains an octamer sequence and an SPH element (also called NONOCT element)(Cheung et al., 1993; Danzeiser et al., 1993; Kunkel et al., 1996; Myslinski et al., 1992). The octamer sequence recruits the POU domain protein Oct-1 (Herr et al., 1988; Sturm et al., 1988), and the SPH element recruits a zinc finger protein known as Staf or SPH binding factor (SBF), which has been cloned from humans (Myslinski et al., 1998; Rincon et al., 1998).

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Editions

2003-09-11	Authored	Hernandez, N.
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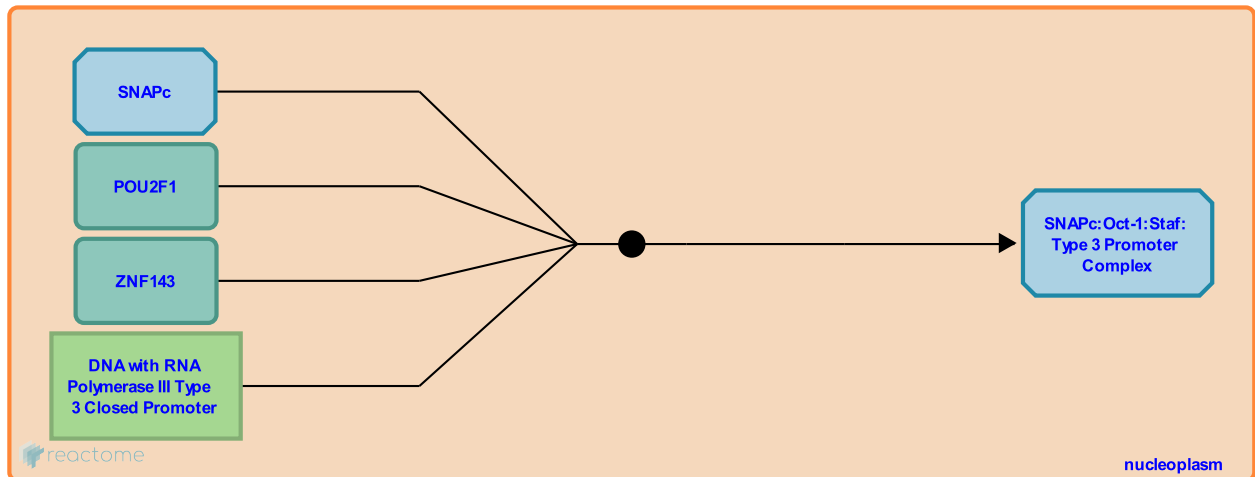
Binding of SNAPc, Oct-1, and Staf to Type 3 Promoter ↗

Location: [RNA Polymerase III Transcription Initiation From Type 3 Promoter](#)

Stable identifier: R-HSA-83791

Type: binding

Compartments: nucleoplasm



SNAPc binds specifically to the PSE. This binding is mediated in part by an unusual Myb domain within SNAP190 (Mittal et al., 1999; Wong et al., 1998). However, even though a SNAP190 segment consisting of just the Myb domain binds DNA, within the complex the Myb domain is not sufficient for binding. The smallest characterized subassembly of SNAPc subunits that binds specifically to DNA consists of SNAP190 aa 84-505, SNAP43 aa 1-268, and SNAP50 (Ma and Hernandez, 2000). Consistent with the requirement for parts of SNAP190 and SNAP50 for DNA binding, UV cross-linking experiments suggest that both SNAP190 (Yoon et al., 1995) and SNAP50 (Henry et al., 1996) are in close contact with DNA.

The binding of SNAPc to the PSE is stabilized by a number of cooperative interactions with other members of the transcription initiation complex including Oct-1, TBP, and Brf2.

The binding of SNAPc to the core promoter is stabilized by a direct protein-protein contact with the Oct-1 POU domain.

SNAPc does not bind very efficiently to the PSE on its own. It contains a damper of DNA binding that resides within the C-terminal two thirds of SNAP190 and/or SNAP45, because a subcomplex of SNAPc (mini-SNAPc) lacking these sequences binds much more efficiently to DNA than complete SNAPc (Mittal et al., 1999). The damper within SNAPc is deactivated, probably through a conformational change, by a direct protein-protein contact with the Oct-1 POU domain. The transcription initiation complex is illustrated in Figure 6. The protein-protein contact between the Oct-1 POU domain and SNAPc involves a glutamic acid at position 7 within the Oct-1 POU domain and a lysine at position 900 within SNAP190, which are symbolized in Figure 6 by small triangles (Ford et al., 1998; Hovde et al., 2002; Mittal et al., 1999). The octamer sequence within the DSE and the PSE are separated by more than 150 base pairs, but the direct protein-protein contact is rendered possible by the presence of a positioned nucleosome between the DSE and the PSE, which, as shown in the figure, probably brings into close proximity the Oct-1 POU domain and SNAPc (Stunkel et al., 1997; Zhao et al., 2001).

Followed by: [Binding of TFIIB to SNAPc:Oct-1:Staf:Type 3 Promoter Complex](#)

Literature references

Hernandez, N., Pendergrast, PS., Zhao, X. (2001). A positioned nucleosome on the human U6 promoter allows recruitment of SNAPc by the Oct-1 POU domain. *Mol. Cell*, 7, 539-49. ↗

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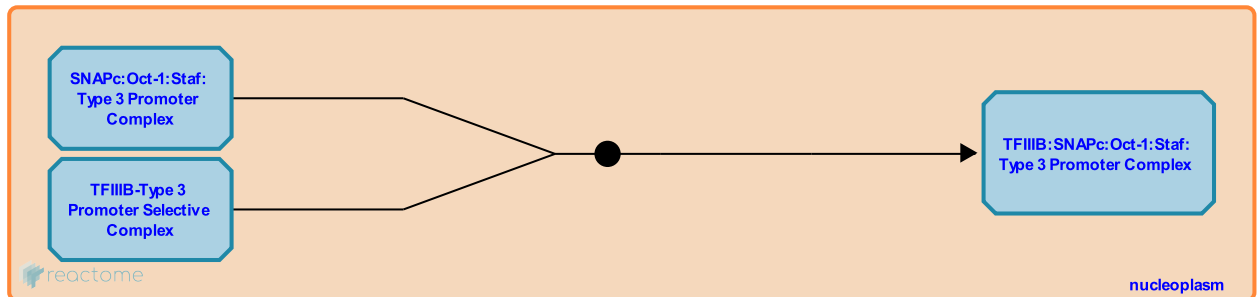
Binding of TFIIB to SNAPc:Oct-1:Staf:Type 3 Promoter Complex ↗

Location: [RNA Polymerase III Transcription Initiation From Type 3 Promoter](#)

Stable identifier: R-HSA-83793

Type: binding

Compartments: nucleoplasm



The snRNA activating protein complex (SNAPc) (Sadowski et al., 1993), the PSE binding protein (PBP) (Waldschmidt et al., 1991), or the PSE transcription factor (PTF) (Murphy et al., 1992). The complex contains five types of subunits and binds to the PSE. Type 3 promoters also recruit Brf2-TFIIB through a combination of protein-protein contacts with SNAPc and a direct association of the TBP component of Brf2-TFIIB with the TATA box. This then allows RNA polymerase III to join the complex.

Preceded by: [Binding of SNAPc, Oct-1, and Staf to Type 3 Promoter](#)

Followed by: [Recruitment of RNA Polymerase III to TFIIB:SNAPc:Type 3 Promoter Complex](#)

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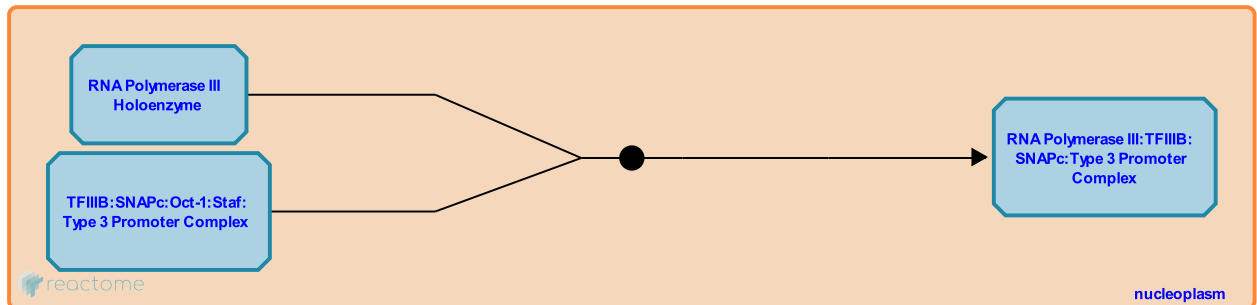
Recruitment of RNA Polymerase III to TFIIB:SNAPc:Type 3 Promoter Complex ↗

Location: [RNA Polymerase III Transcription Initiation From Type 3 Promoter](#)

Stable identifier: R-HSA-83803

Type: binding

Compartments: nucleoplasm



The binding of SNAPc to the PSE is stabilized not only by cooperative interactions with the Oct-1 POU domain, but also by cooperative interactions with TBP and Brf2 (Hinkley et al., 2003 ; Ma and Hernandez, 2002; Mittal and Hernandez, 1997). Moreover, Brf2, which cannot bind to DNA on its own, recognizes and stabilizes TBP bound to the TATA box (Cabart and Murphy, 2001; Cabart and Murphy, 2002; Ma and Hernandez, 2002). Thus, the U6 transcription initiation complex is stabilized by a complex network of protein-protein and protein-DNA interactions. Nothing is known, however, about how the complex recruits RNA polymerase III.

Preceded by: [Binding of TFIIB to SNAPc:Oct-1:Staf:Type 3 Promoter Complex](#)

Followed by: [RNA Polymerase III Promoter Opening at Type 3 Promoters](#)

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RNA Polymerase III Promoter Opening at Type 3 Promoters ↗

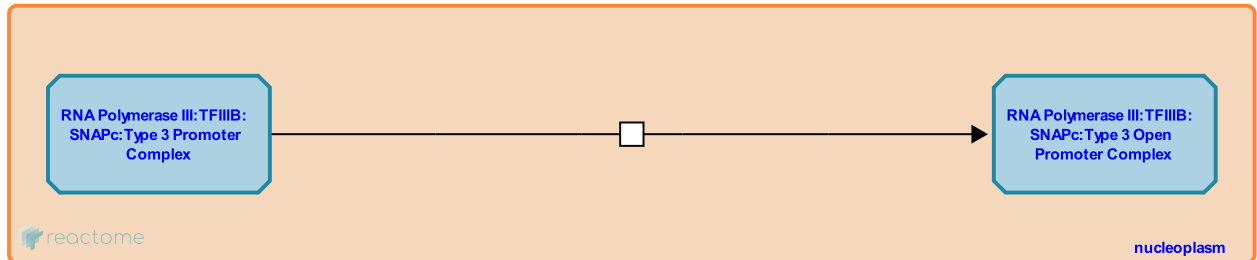
Location: [RNA Polymerase III Transcription Initiation From Type 3 Promoter](#)

Stable identifier: R-HSA-112152

Type: transition

Compartments: nucleoplasm

Inferred from: [RNA Polymerase III Promoter Opening \(Saccharomyces cerevisiae\)](#)



Pol III initiation complexes open the promoter spontaneously. Indeed, this is the general case for DNA-dependent RNA polymerases. Only pol II, with its requirement for TFIIF-directed and ATP-dependent promoter opening is exceptional. TFIIF introduces a layer of mechanism that is not in the repertoire of any other transcriptase. Thus, it is pol III-mediated transcription that is, from a mechanistic perspective, most directly comparable with archaeal and also bacterial transcription.

As promoter opening has been analyzed only in the *S. cerevisiae* this event is Inferred from the homologous pathway in yeast.

Preceded by: [Recruitment of RNA Polymerase III to TFIIB:SNAPc:Type 3 Promoter Complex](#)

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Table of Contents

Introduction	1
RNA Polymerase III Transcription Initiation From Type 3 Promoter	2
↳ Binding of SNAPc, Oct-1, and Staf to Type 3 Promoter	3
↳ Binding of TFIIB to SNAPc:Oct-1:Staf:Type 3 Promoter Complex	5
↳ Recruitment of RNA Polymerase III to TFIIB:SNAPc:Type 3 Promoter Complex	6
↳ RNA Polymerase III Promoter Opening at Type 3 Promoters	7
Table of Contents	8