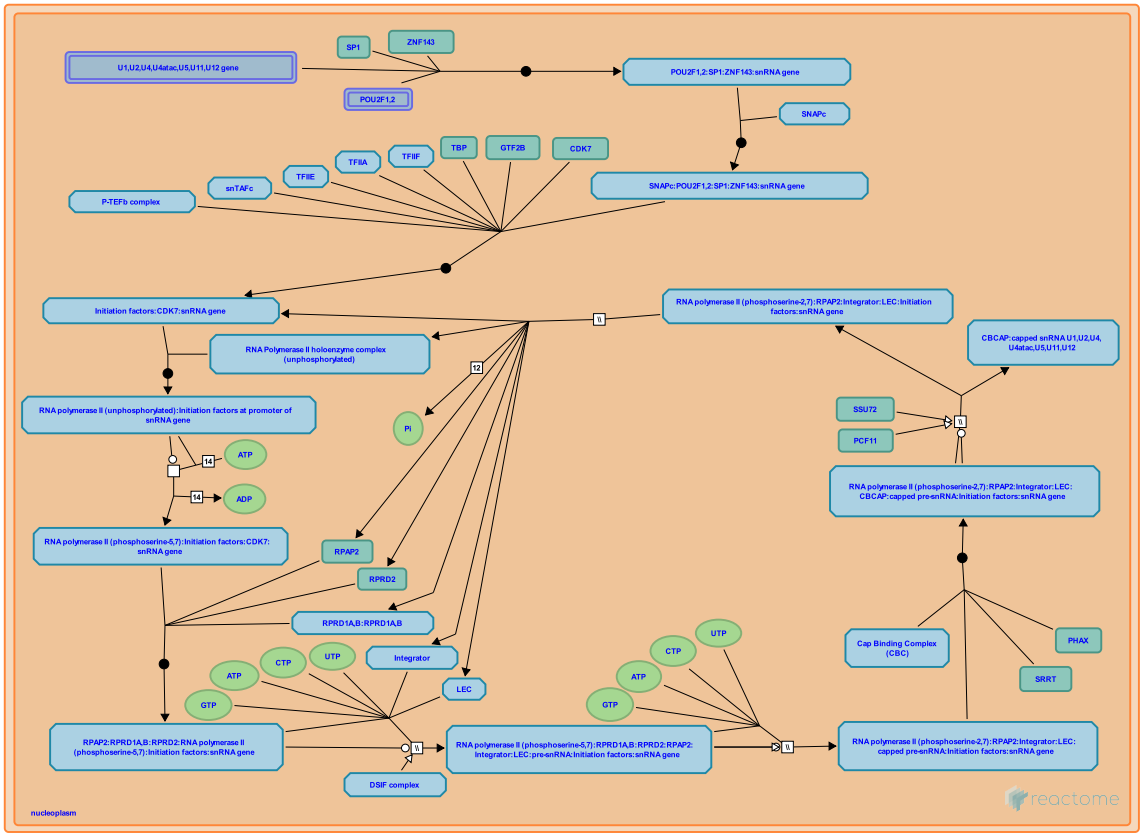
RNA polymerase II transcribes snRNA genes



Hernandez, N., May, B.

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

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.

23/04/2024

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. ↗

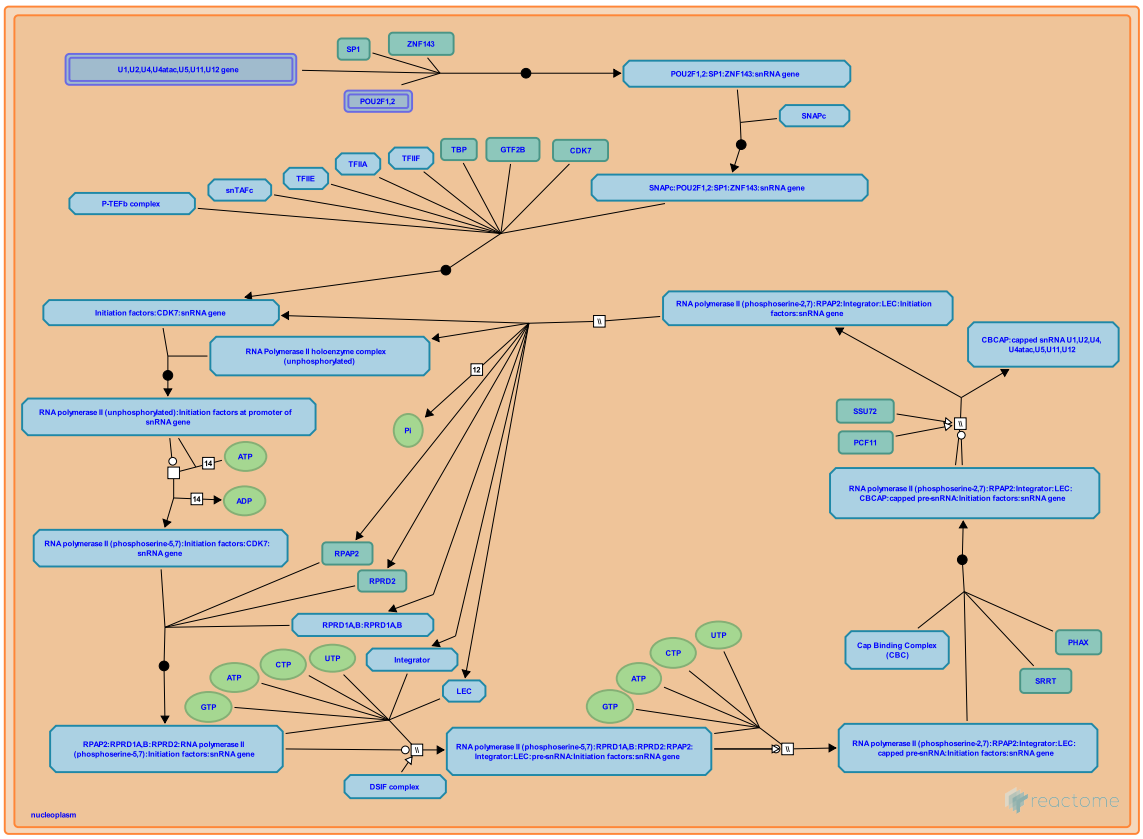
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

RNA polymerase II transcribes snRNA genes ↗

Stable identifier: R-HSA-6807505

Compartments: nucleoplasm



Small nuclear RNAs (snRNAs) play key roles in splicing and some of them, specifically the U1 and U2 snRNAs, are encoded by multicopy snRNA gene clusters containing tandem arrays of genes, about 30 in the RNU1 cluster (Bernstein et al. 1985) and about 10-20 in the RNU2 cluster (Van Ardsell and Weiner 1984). Whereas U6 snRNA genes are transcribed by RNA polymerase III, U1,U2, U4, U4atac, U5, U11, and U12 genes are transcribed by RNA polymerase II. Transcription of the U1 and U2 genes has been most extensively studied and the other snRNA genes as well as other genes with similar promoter structures, for example the SNORD13 gene, are inferred to be transcribed by similar reactions. The snRNA genes transcribed by RNA polymerase II are distinguished from mRNA-encoding genes by the presence of a proximal sequence element (PSE) rather than a TATA box and the presence of the Integrator complex rather than the Mediator complex (reviewed in Egloff et al. 2008, Jawdeker and Henry 2008).

The snRNA genes are among the most rapidly transcribed genes in the genome. The 5' transcribed region of the U2 snRNA gene is largely single-stranded during interphase and metaphase (Pavelitz et al. 2008) and chromatin within the transcribed region is cleared of nucleosomes (O'Reilly et al. 2014). Transcriptional activation of the RNA polymerase II transcribed snRNA genes begins with binding of transcription factors to the distal sequence element (DSE) of the promoter (reviewed in Hernandez 2001, Egloff et al. 2008, Jawdeker and Henry 2008). The factors, which include POU2F1 (Oct-1), POU2F2 (Oct-2), ZNF143 (Staf) and Sp1, promote binding of the SNAPc complex (also known as PTF and PBP) to the PSE. SNAPc helps clear the gene of nucleosomes (O'Reilly et al. 2014) and recruits initiation factors (TFIIA, TFIIB, TFIIE, TFIIF, and snTAFc:TBP) which recruit RNA polymerase II. Phosphorylation of the C-terminal domain (CTD) of RNA polymerase II (reviewed in Egloff and Murphy 2008) by CDK7 recruits RPAP2 and the Integrator complex, which is required for later processing of the 3' end of the pre-snRNA transcript (reviewed in Chen and Wagner 2010, Baillat and Wagner 2015). The Little Elongation Complex (LEC) also appears to bind around the time of transcription initiation (Hu et al. 2013). As transcription proceeds, RPAP2 dephosphorylates serine-5 and P-TEFb phosphorylates serine-2 of the CTD. As transcription reaches the end of the snRNA gene serine-7 of the CTD is phosphorylated. These marks serve to bind protein complexes and are required for 3' processing of the pre-snRNA (reviewed in Egloff and Murphy 2008). After transcription proceeds through the conserved 3' processing sequence of the pre-snRNA the Integrator complex cleaves the pre-snRNA. Transcription then terminates downstream in a less well characterized reaction that requires elements of the polyadenylation system.

Literature references

Pavelitz, T., Elco, CP., Bailey, AD., Weiner, AM. (2008). Human U2 snRNA genes exhibit a persistently open transcriptional state and promoter disassembly at metaphase. *Mol. Cell. Biol., 28*, 3573-88.

Laitem, C., Murphy, S., Dienstbier, M., O'Reilly, D., Zaborowska, J., Kuznetsova, OV. (2014). Human snRNA genes use polyadenylation factors to promote efficient transcription termination. *Nucleic Acids Res., 42*, 264-75.

Eissenberg, JC., Smith, ER., Lin, C., Hu, D., Shilatifard, A., Gao, X. et al. (2013). The little elongation complex functions at initiation and elongation phases of snRNA gene transcription. *Mol. Cell, 51*, 493-505.

Murphy, S., O'Reilly, D., Egloff, S. (2008). Expression of human snRNA genes from beginning to end. *Biochem. Soc. Trans., 36*, 590-4.

Van Arsdell, SW., Weiner, AM. (1984). Human genes for U2 small nuclear RNA are tandemly repeated. *Mol. Cell. Biol. , 4*, 492-9.

Editions

2015-11-02	Authored, Edited	May, B.
2016-02-19	Reviewed	Hernandez, N.

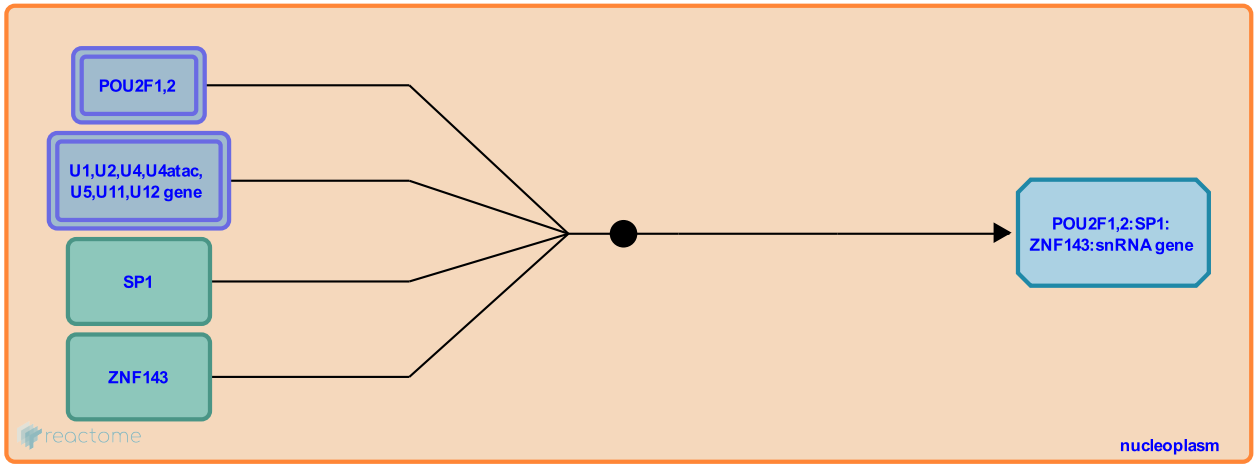
POU2F1 (OCT1) or POU2F2 (OCT2), SP1, and ZNF143 (STAF) bind the DSE of snRNA gene (U1, U2, U4, U4atac, U5, U11, U12)

Location: RNA polymerase II transcribes snRNA genes

Stable identifier: R-HSA-6807496

Type: binding

Compartments: nucleoplasm



An octamer binding factor, POU2F1 (Oct-1) or POU2F2 (Oct-2), SP1, ZNF143 (Staf) and possibly other transcription factors bind the distal sequence element (DSE) in the promoter of the snRNA gene (Murphy et al. 1992, Strom et al. 1996, Murphy 1997, Hovde et al. 2002). These upstream transcription factors enhance subsequent binding of the SNAPc complex to the downstream proximal sequence element (PSE) of the promoter.

Followed by: SNAPc binds PSE of snRNA gene (U1, U2, U4, U4atac, U5, U11, U12)

Literature references

Hovde, S., Brooks, A., Strong, K., Geiger, JH. (2002). Crystallization of the Oct-1/SNAP190 peptide/DNA complex. *Acta Crystallogr. D Biol. Crystallogr., 58*, 511-2.

Yoon, JB., Gerster, T., Murphy, S., Roeder, RG. (1992). Oct-1 and Oct-2 potentiate functional interactions of a transcription factor with the proximal sequence element of small nuclear RNA genes. *Mol Cell Biol, 12*, 3247-61.

Myslinski, E., Krol, A., Carbon, P. (1998). ZNF76 and ZNF143 are two human homologs of the transcriptional activator Staf. *J Biol Chem, 273*, 21998-2006.

Tanaka, M., Lai, JS., Herr, W. (1992). Promoter-selective activation domains in Oct-1 and Oct-2 direct differential activation of an snRNA and mRNA promoter. *Cell, 68*, 755-67.

Hovde, S., Henry, RW., Gu, L., Brooks, A., Hinkley, CS., Strong, K. et al. (2002). Activator recruitment by the general transcription machinery: X-ray structural analysis of the Oct-1 POU domain/human U1 octamer/SNAP190 peptide ternary complex. *Genes Dev., 16*, 2772-7.

Editions

2015-11-02	Authored, Edited	May, B.
2016-02-19	Reviewed	Hernandez, N.

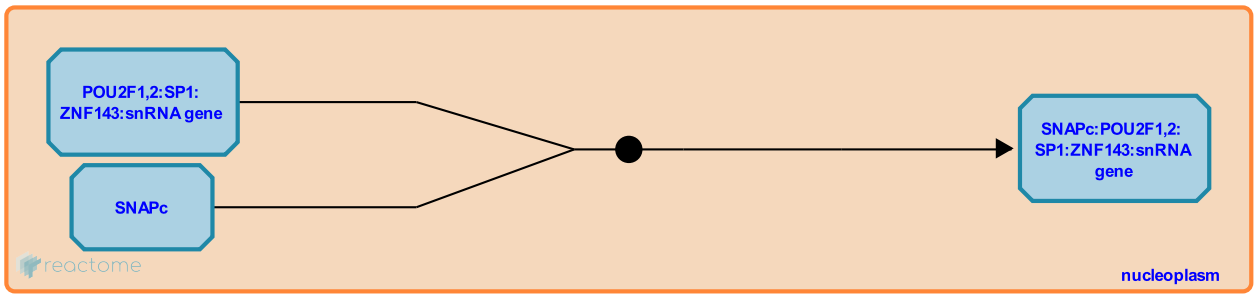
SNAPc binds PSE of snRNA gene (U1, U2, U4, U4atac, U5, U11, U12)

Location: RNA polymerase II transcribes snRNA genes

Stable identifier: R-HSA-6810239

Type: binding

Compartments: nucleoplasm



Transcription factors at the distal sequence element (DSE) recruit the SNAPc complex to bind the proximal sequence element (PSE) (Sadowski et al. 1993, Henry et al. 1995, Mittal et al. 1996, Ford and Hernandez 1997, Ford et al. 1998, Hovde et al. 2002, Jawdekar et al. 2006, James Faresse et al. 2012). Binding of SNAPc distinguishes snRNA promoters from promoters of mRNA-encoding genes, which have TATA or other elements rather than PSEs (Henry et al. 1995).

Preceded by: POU2F1 (OCT1) or POU2F2 (OCT2), SP1, and ZNF143 (STAF) bind the DSE of snRNA gene (U1, U2, U4, U4atac, U5, U11, U12)

Followed by: General transcription factors bind SNAPc:POU2F1:ZNF143:snRNA gene

Literature references

Hovde, S., Brooks, A., Strong, K., Geiger, JH. (2002). Crystallization of the Oct-1/SNAP190 peptide/DNA complex. *Acta Crystallogr. D Biol. Crystallogr., 58*, 511-2.

Mittal, V., Cleary, MA., Hernandez, N., Herr, W. (1996). The Oct-1 POU-specific domain can stimulate small nuclear RNA gene transcription by stabilizing the basal transcription complex SNAPc. *Mol. Cell. Biol., 16*, 1955-65.

Hovde, S., Henry, RW., Gu, L., Brooks, A., Hinkley, CS., Strong, K. et al. (2002). Activator recruitment by the general transcription machinery: X-ray structural analysis of the Oct-1 POU domain/human U1 octamer/SNAP190 peptide ternary complex. *Genes Dev., 16*, 2772-7.

Jawdekar, GW., Henry, RW., Hovde, SL., Jelencic, B., Feig, M., Hanzlowsky, A. et al. (2006). The unorthodox SNAP50 zinc finger domain contributes to cooperative promoter recognition by human SNAPC. *J. Biol. Chem., 281*, 31050-60.

Ford, E., Hernandez, N. (1997). Characterization of a trimeric complex containing Oct-1, SNAPc, and DNA. *J. Biol. Chem., 272*, 16048-55.

Editions

2015-11-08	Authored, Edited	May, B.
2016-02-19	Reviewed	Hernandez, N.

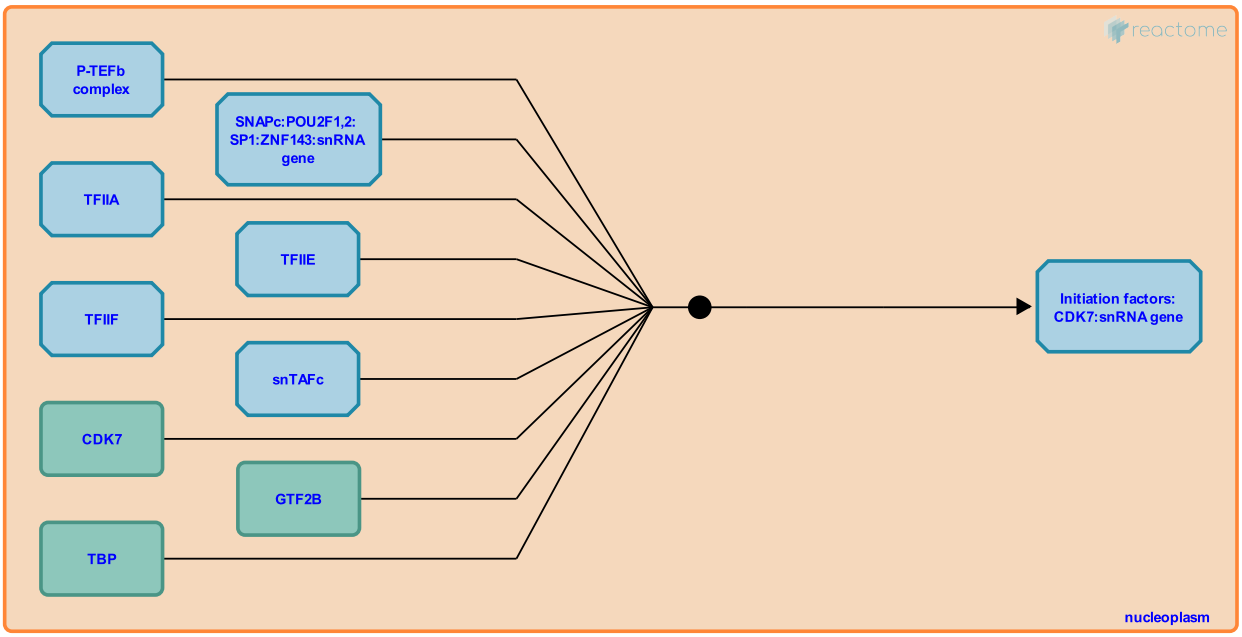
General transcription factors bind SNAPc:POU2F1:ZNF143:snRNA gene ↗

Location: RNA polymerase II transcribes snRNA genes

Stable identifier: R-HSA-6810234

Type: binding

Compartments: nucleoplasm



The promoter of an snRNA gene binds the basal transcription factors TFIIA, TFIIB (GTF2B), TFIIE, and TFIIF (Bernues et al. 1993, Kuhlman et al. 1999). Rather than the TFIID complex found at promoters of mRNA-encoding genes, a unique complex containing TBP (Sadowski et al. 1993) and snTAFc is present at promoters of snRNA genes (Zaborowska et al. 2012). The P-TEFb complex is also observed at snRNA genes, however, it seems to play a role more in 3' processing than in elongation (Medlin et al. 2005). CDK7 is also present and phosphorylates the C-terminal domain of RNA polymerase II (Glover-Cutter et al. 2009).

Preceded by: SNAPc binds PSE of snRNA gene (U1, U2, U4, U4atac, U5, U11, U12)

Followed by: RNA polymerase II binds initiation factors at promoter of snRNA gene (U1, U2, U4, U4atac, U5, U11, U12)

Literature references

Larochelle, S., Shokat, K., Zhang, C., Bentley, DL., Erickson, B., Fisher, RP. et al. (2009). TFIIH-associated Cdk7 kinase functions in phosphorylation of C-terminal domain Ser7 residues, promoter-proximal pausing, and termination by RNA polymerase II. *Mol. Cell. Biol., 29*, 5455-64. ↗

Zhang, F., Peterlin, BM., Medlin, J., Murphy, S., Scurry, A., Taylor, A. (2005). P-TEFb is not an essential elongation factor for the intronless human U2 snRNA and histone H2b genes. *EMBO J., 24*, 4154-65. ↗

Polycarpou-Schwarz, M., Simmen, KA., Egly, JM., Bernués, J., Mattaj, IW., Gunderson, SI. et al. (1993). Common and unique transcription factor requirements of human U1 and U6 snRNA genes. *EMBO J., 12*, 3573-85. ↗

Roeder, RG., Murphy, S., Zaborowska, J., Taylor, A. (2012). A novel TBP-TAF complex on RNA polymerase II-transcribed snRNA genes. *Transcription, 3*, 92-104. ↗

Henry, RW., Lobo, SM., Sadowski, CL., Hernandez, N. (1993). Targeting TBP to a non-TATA box cis-regulatory element: a TBP-containing complex activates transcription from snRNA promoters through the PSE. *Genes Dev, 7*, 1535-48. ↗

Editions

2015-11-08	Authored, Edited	May, B.
2016-02-19	Reviewed	Hernandez, N.

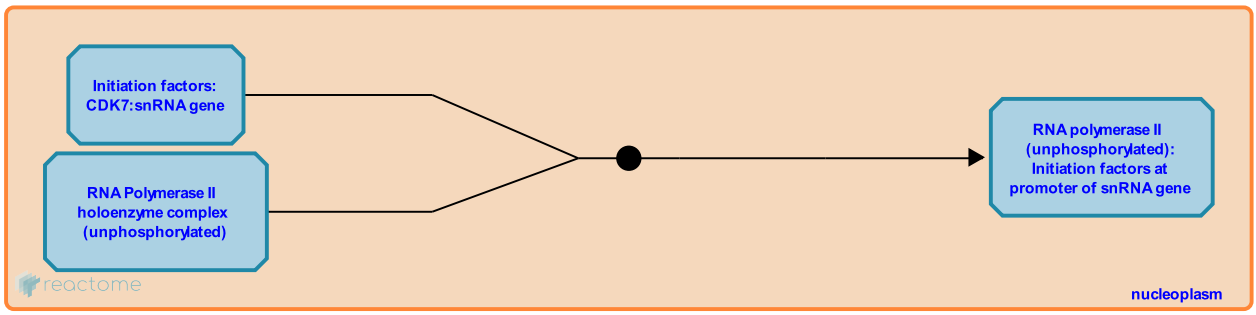
RNA polymerase II binds initiation factors at promoter of snRNA gene (U1, U2, U4, U4atac, U5, U11, U12) ↗

Location: RNA polymerase II transcribes snRNA genes

Stable identifier: R-HSA-6810238

Type: binding

Compartments: nucleoplasm



The basal initiation factors TFIIA, TFIIB, TFIIE, TFIIF, and TBP:snTAFc recruit unphosphorylated RNA polymerase II to the promoter of the (U1, U2, U4, U5) snRNA gene (Gunderson et al. 1990, Kuhlman et al. 1999, Zaborowska et al. 2012).

Preceded by: General transcription factors bind SNAPc:POU2F1:ZNF143:snRNA gene

Followed by: CDK7 phosphorylates serine-5 and serine-7 of heptad repeats in C-terminal domain of RNA polymerase II at snRNA promoter

Literature references

Burgess, RR., Gunderson, SI., Knuth, MW. (1990). The human U1 snRNA promoter correctly initiates transcription in vitro and is activated by PSE1. *Genes Dev., 4*, 2048-60. ↗

Roeder, RG., Murphy, S., Zaborowska, J., Taylor, A. (2012). A novel TBP-TAF complex on RNA polymerase II-transcribed snRNA genes. *Transcription, 3*, 92-104. ↗

Kuhlman, TC., Reinberg, D., Cho, H., Hernandez, N. (1999). The general transcription factors IIA, IIB, IIF, and IIE are required for RNA polymerase II transcription from the human U1 small nuclear RNA promoter. *Mol. Cell. Biol., 19*, 2130-41. ↗

Editions

2015-11-08	Authored, Edited	May, B.
2016-02-19	Reviewed	Hernandez, N.

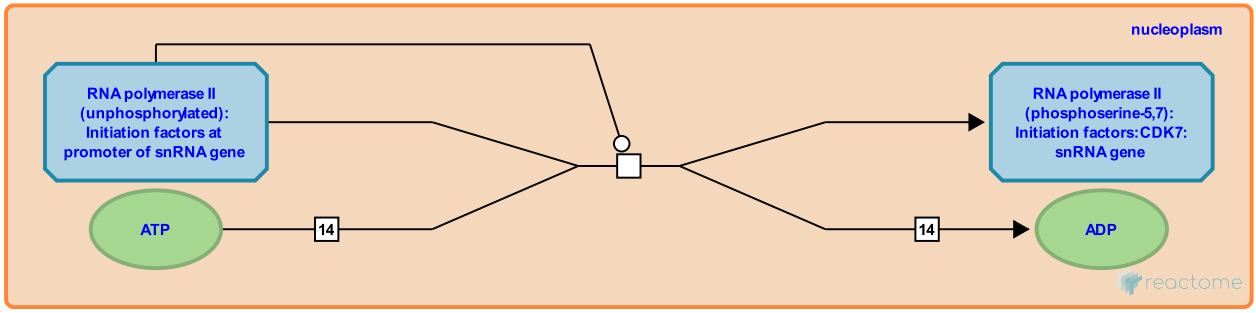
CDK7 phosphorylates serine-5 and serine-7 of heptad repeats in C-terminal domain of RNA polymerase II at snRNA promoter ↗

Location: RNA polymerase II transcribes snRNA genes

Stable identifier: R-HSA-6810233

Type: transition

Compartments: nucleoplasm



CDK7 phosphorylates serine-5 residues of heptad repeats (consensus YSPTSPS) in the C-terminal domain (CTD) of the large subunit (POLR2A) of RNA polymerase II. Serine-7 residues of the heptad repeats are also phosphorylated at promoters of snRNA genes (Egloff et al. 2007) and CDK7 is required for phosphorylation of serine-7 in vivo (Glover-Cutter et al. 2009). P-TEFb and DNA-PK are able to phosphorylate serine-7 in vitro (Glover-Cutter et al. 2009, Egloff et al. 2010). Impairment of CTD phosphorylation does not appear to affect transcription of snRNA genes but rather impairs 3' processing of the pre-snRNA (Medlin et al. 2003, Jacobs et al. 2004).

Preceded by: RNA polymerase II binds initiation factors at promoter of snRNA gene (U1, U2, U4, U4atac, U5, U11, U12)

Followed by: RPAP2 binds RNA polymerase II phosphorylated at serine-7 residues of heptad repeats in the C-terminal domain

Literature references

Larochelle, S., Shokat, K., Zhang, C., Bentley, DL., Erickson, B., Fisher, RP. et al. (2009). TFIIH-associated Cdk7 kinase functions in phosphorylation of C-terminal domain Ser7 residues, promoter-proximal pausing, and termination by RNA polymerase II. *Mol. Cell. Biol., 29*, 5455-64. ↗

Uguen, P., Murphy, S., Bentley, DL., Taylor, A., Medlin, JE. (2003). The C-terminal domain of pol II and a DRB-sensitive kinase are required for 3' processing of U2 snRNA. *EMBO J., 22*, 925-34. ↗

Tanzhaus, K., Chapman, RD., Murphy, S., Pitts, L., O'Reilly, D., Eick, D. et al. (2007). Serine-7 of the RNA polymerase II CTD is specifically required for snRNA gene expression. *Science, 318*, 1777-9. ↗

Ogiwara, I., Weiner, AM., Jacobs, EY. (2004). Role of the C-terminal domain of RNA polymerase II in U2 snRNA transcription and 3' processing. *Mol. Cell. Biol., 24*, 846-55. ↗

Murphy, S., Dienstbier, M., Szczepaniak, SA., Egloff, S., Taylor, A., Knight, S. (2010). The integrator complex recognizes a new double mark on the RNA polymerase II carboxyl-terminal domain. *J. Biol. Chem., 285*, 20564-9. ↗

Editions

2015-11-08	Authored, Edited	May, B.
2016-02-19	Reviewed	Hernandez, N.

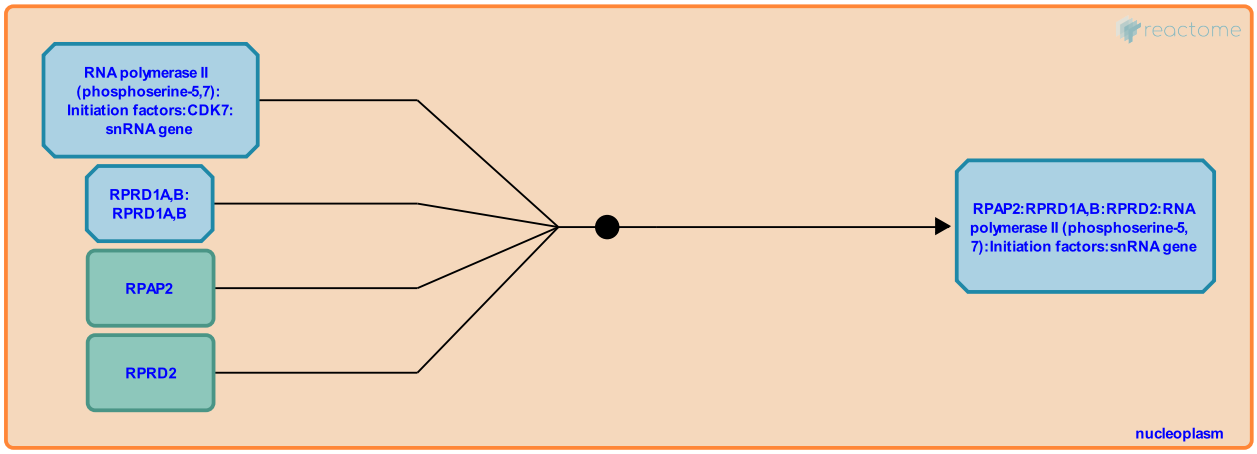
RPAP2 binds RNA polymerase II phosphorylated at serine-7 residues of heptad repeats in the C-terminal domain ↗

Location: RNA polymerase II transcribes snRNA genes

Stable identifier: R-HSA-6810235

Type: binding

Compartments: nucleoplasm



The protein phosphatase RPAP2 binds RNA polymerase II phosphorylated at serine-7 of the C-terminal domain (CTD) (Egloff et al. 2012). RPRD1A and RPRD1B bind RNA polymerase II with RPAP2 and appear to act as scaffolds for the complex (Ni et al. 2011, Ni et al. 2014).

Preceded by: CDK7 phosphorylates serine-5 and serine-7 of heptad repeats in C-terminal domain of RNA polymerase II at snRNA promoter

Followed by: Pre-snRNA transcript initiation, Integrator binding, LEC binding

Literature references

Laitem, C., Murphy, S., Kiss, T., Zaborowska, J., Egloff, S. (2012). Ser7 phosphorylation of the CTD recruits the RPAP2 Ser5 phosphatase to snRNA genes. *Mol. Cell, 45*, 111-22. ↗

Mosley, AL., Young, P., Li, J., Murphy, S., Olsen, JB., Zhong, G. et al. (2014). RPRD1A and RPRD1B are human RNA polymerase II C-terminal domain scaffolds for Ser5 dephosphorylation. *Nat. Struct. Mol. Biol., 21*, 686-95. ↗

Guo, H., Marcon, E., Young, P., Li, J., Ruan, ED., Olsen, JB. et al. (2011). Control of the RNA polymerase II phosphorylation state in promoter regions by CTD interaction domain-containing proteins RPRD1A and RPRD1B. *Transcription, 2*, 237-42. ↗

Editions

2015-11-08	Authored, Edited	May, B.
2016-02-19	Reviewed	Hernandez, N.

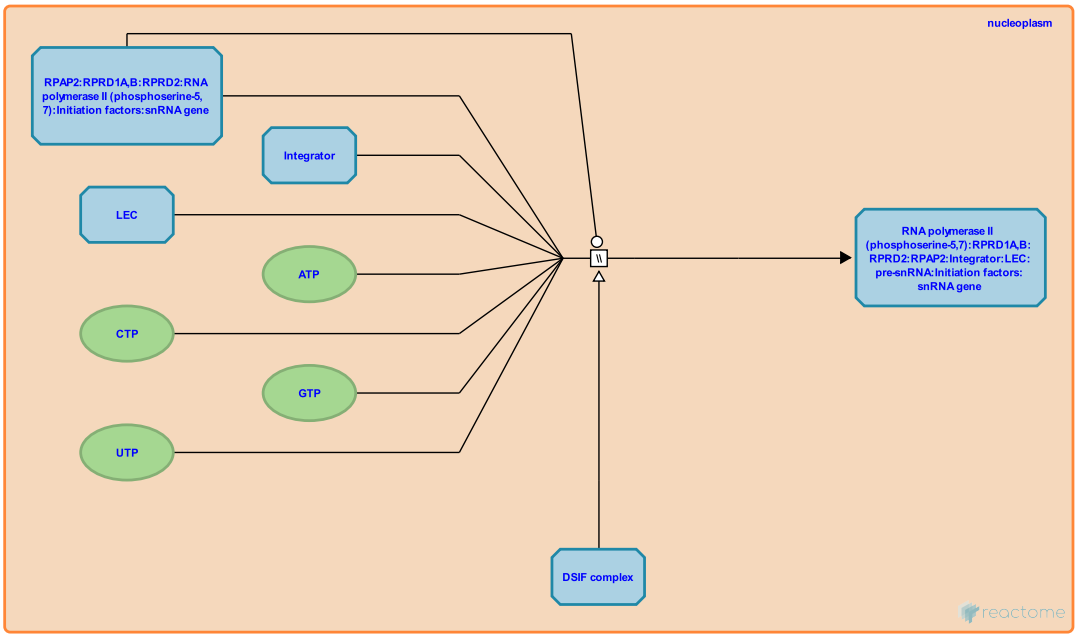
Pre-snRNA transcript initiation, Integrator binding, LEC binding ↗

Location: RNA polymerase II transcribes snRNA genes

Stable identifier: R-HSA-6814549

Type: omitted

Compartments: nucleoplasm



In an unknown order of events, RNA polymerase II initiates transcription and the Integrator complex (Baillat et al. 2005) and Little Elongation Complex (LEC, Hu et al. 2013) are recruited to phosphorylated RNA polymerase II (Egloff et al. 2010). The Integrator complex interacts with RPAP2, which binds phosphoserine-7 of the C-terminal domain (CTD) of RNA polymerase II and is required for recruitment of Integrator (Egloff et al. 2007, Egloff et al. 2012). RPAP2 interacts with the putative scaffold proteins RPRD1A and RPRD1B at the CTD (Ni et al. 2011, Ni et al. 2014) and DSIF is required for recruitment of Integrator (Skaar et al. 2015). The Integrator complex does not seem to play a significant role in subsequent elongation of the pre-snRNA transcript but is critical for processing of the 3' end of the pre-snRNA.

Preceded by: RPAP2 binds RNA polymerase II phosphorylated at serine-7 residues of heptad repeats in the C-terminal domain

Followed by: Pre-snRNA is elongated and capped with 7-methylguanosine

Literature references

Eissenberg, JC., Smith, ER., Lin, C., Hu, D., Shilatifard, A., Gao, X. et al. (2013). The little elongation complex functions at initiation and elongation phases of snRNA gene transcription. *Mol. Cell, 51*, 493-505. ↗

Tanzhaus, K., Chapman, RD., Murphy, S., Pitts, L., O'Reilly, D., Eick, D. et al. (2007). Serine-7 of the RNA polymerase II CTD is specifically required for snRNA gene expression. *Science, 318*, 1777-9. ↗

Laitem, C., Murphy, S., Kiss, T., Zaborowska, J., Egloff, S. (2012). Ser7 phosphorylation of the CTD recruits the RPAP2 Ser5 phosphatase to snRNA genes. *Mol. Cell, 45*, 111-22. ↗

Mosley, AL., Young, P., Li, J., Murphy, S., Olsen, JB., Zhong, G. et al. (2014). RPRD1A and RPRD1B are human RNA polymerase II C-terminal domain scaffolds for Ser5 dephosphorylation. *Nat. Struct. Mol. Biol., 21*, 686-95. ↗

Murphy, S., Dienstbier, M., Szczepaniak, SA., Egloff, S., Taylor, A., Knight, S. (2010). The integrator complex recognizes a new double mark on the RNA polymerase II carboxyl-terminal domain. *J. Biol. Chem., 285*, 20564-9. ↗

Editions

2015-11-21	Authored, Edited	May, B.
2016-02-19	Reviewed	Hernandez, N.

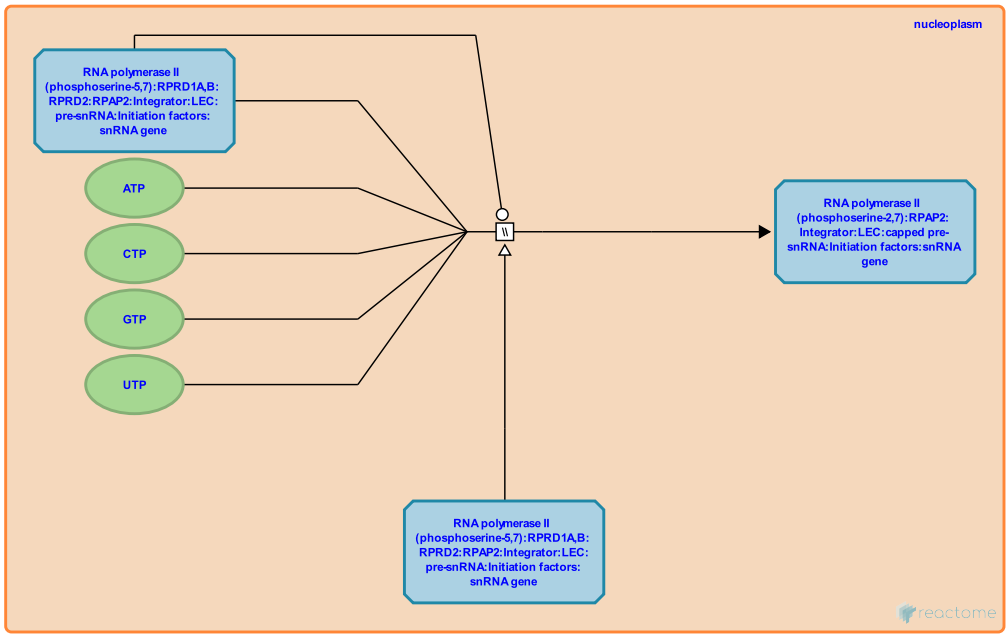
Pre-snRNA is elongated and capped with 7-methylguanosine ↗

Location: RNA polymerase II transcribes snRNA genes

Stable identifier: R-HSA-6814559

Type: omitted

Compartments: nucleoplasm



A 7-methylguanosine triphosphate group is added to the 5' end of the pre-snRNA during transcription elongation (Mattaj 1986). The capping enzyme and cap methyltransferase involved in mRNA capping may also be responsible for this reaction. In the case of mRNA capping, the capping enzyme is targeted to the pre-mRNA by interaction with the phosphorylated C-terminal domain (CTD) of RNA polymerase II (McCracken et al. 1997). During elongation, the phosphorylation pattern of the CTD also changes: serine-5 is dephosphorylated by RPAP2 (Egloff et al. 2012) interacting with RPRD1A and RPRD1B (Ni et al. 2011, Ni et al. 2014) and serine-2 is phosphoryated by P-TEFb. Serine-7 is also phosphorylated, possibly, however the responsible kinase is not certain. The order of the capping and phosphorylation events is unknown.

Preceded by: Pre-snRNA transcript initiation, Integrator binding, LEC binding

Followed by: CBCAP complex binds 7-methylguanosine cap of snRNA

Literature references

Siderovski, D., Hessel, A., Fong, N., Bentley, DL., Foster, S., Yankulov, K. et al. (1997). 5'-Capping enzymes are targeted to pre-mRNA by binding to the phosphorylated carboxy-terminal domain of RNA polymerase II. *Genes Dev., 11*, 3306-18. ↗

Mattaj, IW. (1986). Cap trimethylation of U snRNA is cytoplasmic and dependent on U snRNP protein binding. *Cell, 46*, 905-11. ↗

Laitem, C., Murphy, S., Kiss, T., Zaborowska, J., Egloff, S. (2012). Ser7 phosphorylation of the CTD recruits the RPAP2 Ser5 phosphatase to snRNA genes. *Mol. Cell, 45*, 111-22. ↗

Mosley, AL., Young, P., Li, J., Murphy, S., Olsen, JB., Zhong, G. et al. (2014). RPRD1A and RPRD1B are human RNA polymerase II C-terminal domain scaffolds for Ser5 dephosphorylation. *Nat. Struct. Mol. Biol., 21*, 686-95. ↗

Guo, H., Marcon, E., Young, P., Li, J., Ruan, ED., Olsen, JB. et al. (2011). Control of the RNA polymerase II phosphorylation state in promoter regions by CTD interaction domain-containing proteins RPRD1A and RPRD1B. *Transcription, 2*, 237-42. ↗

Editions

2015-11-21	Authored, Edited	May, B.
2016-02-19	Reviewed	Hernandez, N.

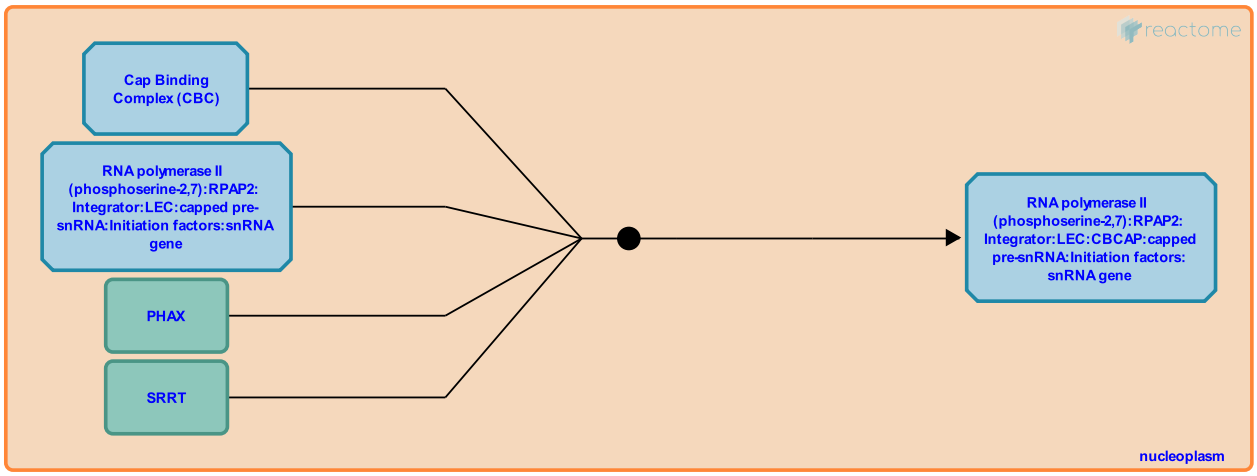
CBCAP complex binds 7-methylguanosine cap of snRNA ↗

Location: RNA polymerase II transcribes snRNA genes

Stable identifier: R-HSA-6814885

Type: binding

Compartments: nucleoplasm



As the capped pre-snRNA continues to be elongated, the CBCAP complex comprising NCBP1 (CBP80), NCBP2 (CBP20), SRRT (ARS2) and PHAX binds the 7-methylguanosine cap (Hallais et al. 2013). The CBCAP complex enhances 3' processing of the pre-snRNA (Hallais et al. 2013) and participates in export of the snRNA from the nucleus to the cytosol, where the snRNA is further modified and assembled with proteins into pre-snRNPs.

Preceded by: Pre-snRNA is elongated and capped with 7-methylguanosine

Followed by: Integrator complex processes the 3' end of snRNA

Literature references

Benbahouche, Nel H., Lener, D., Vandermoere, F., Bertrand, E., Verheggen, C., Clerici, M. et al. (2013). CBC-ARS2 stimulates 3'-end maturation of multiple RNA families and favors cap-proximal processing. *Nat. Struct. Mol. Biol., 20*, 1358-66. ↗

Editions

2015-11-27	Authored, Edited	May, B.
2016-02-19	Reviewed	Hernandez, N.

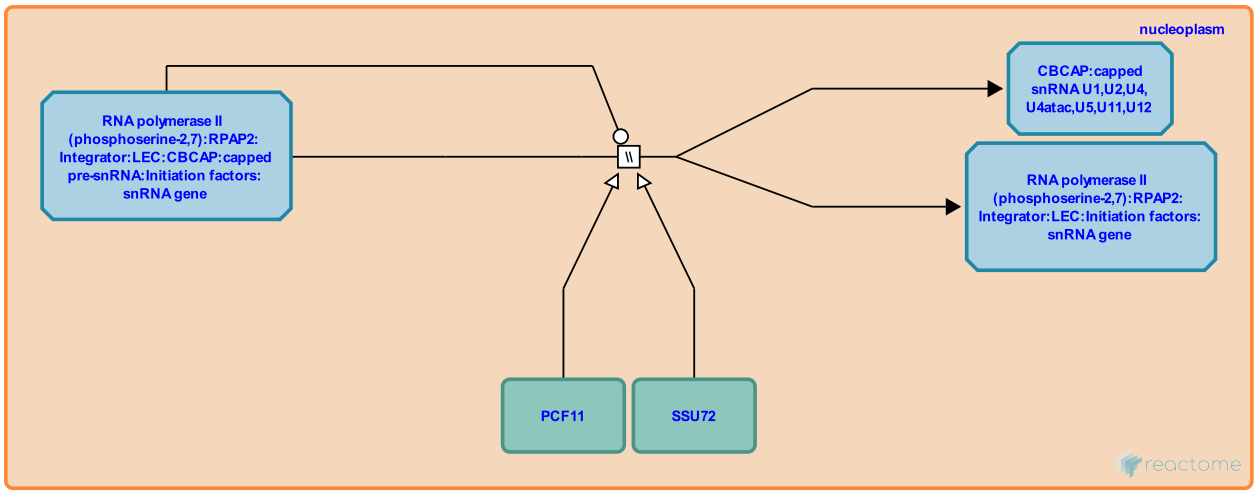
Integrator complex processes the 3' end of snRNA ↗

Location: RNA polymerase II transcribes snRNA genes

Stable identifier: R-HSA-6814555

Type: omitted

Compartments: nucleoplasm



Transcription of the pre-snRNA extends through a conserved region, the 3' box, and terminates downstream. The heterodimeric subunits INTS9 and INTS11 within the Integrator complex form an endoribonuclease that cleaves the pre-snRNA at a location 5' to the 3' box (Baillat et al. 2005, Abrecht and Wagner 2012, Skaar et al. 2015), releasing the capped snRNA bound to the cap binding complex. Factors that bind the 5' cap of the pre-snRNA enhance processing at the 3' end (Hallais et al. 2013) and polyadenlyation factors PCF11 and SKU72 are required for transcription termination (O'Reilly et al. 2014). The remainder of the transcript downstream of the cleavage site is presumably degraded by exoribonuclease.

Preceded by: CBCAP complex binds 7-methylguanosine cap of snRNA

Followed by: Dephosphorylation and dissociation of RNA polymerase II at 3' end of snRNA gene

Literature references

Wagner, EJ., Albrecht, TR. (2012). snRNA 3' end formation requires heterodimeric association of integrator subunits. *Mol. Cell. Biol., 32*, 1112-23. ↗

Laitem, C., Murphy, S., Dienstbier, M., O'Reilly, D., Zaborowska, J., Kuznetsova, OV. (2014). Human snRNA genes use polyadenylation factors to promote efficient transcription termination. *Nucleic Acids Res., 42*, 264-75. ↗

Wu, X., Hughes, SH., Florens, LA., Saraf, A., Skaar, JR., Pagano, M. et al. (2015). The Integrator complex controls the termination of transcription at diverse classes of gene targets. *Cell Res., 25*, 288-305. ↗

Baillat, D., Cooch, N., Shilatifard, A., Shiekhattar, R., Näär, AM., Hakimi, MA. (2005). Integrator, a multiprotein mediator of small nuclear RNA processing, associates with the C-terminal repeat of RNA polymerase II. *Cell, 123*, 265-76. ↗

Benbahouche, Nel H., Lener, D., Vandermoere, F., Bertrand, E., Verheggen, C., Clerici, M. et al. (2013). CBC-ARS2 stimulates 3'-end maturation of multiple RNA families and favors cap-proximal processing. *Nat. Struct. Mol. Biol., 20*, 1358-66. ↗

Editions

2015-11-21	Authored, Edited	May, B.
2016-02-19	Reviewed	Hernandez, N.

Dephosphorylation and dissociation of RNA polymerase II at 3' end of snRNA gene ↗

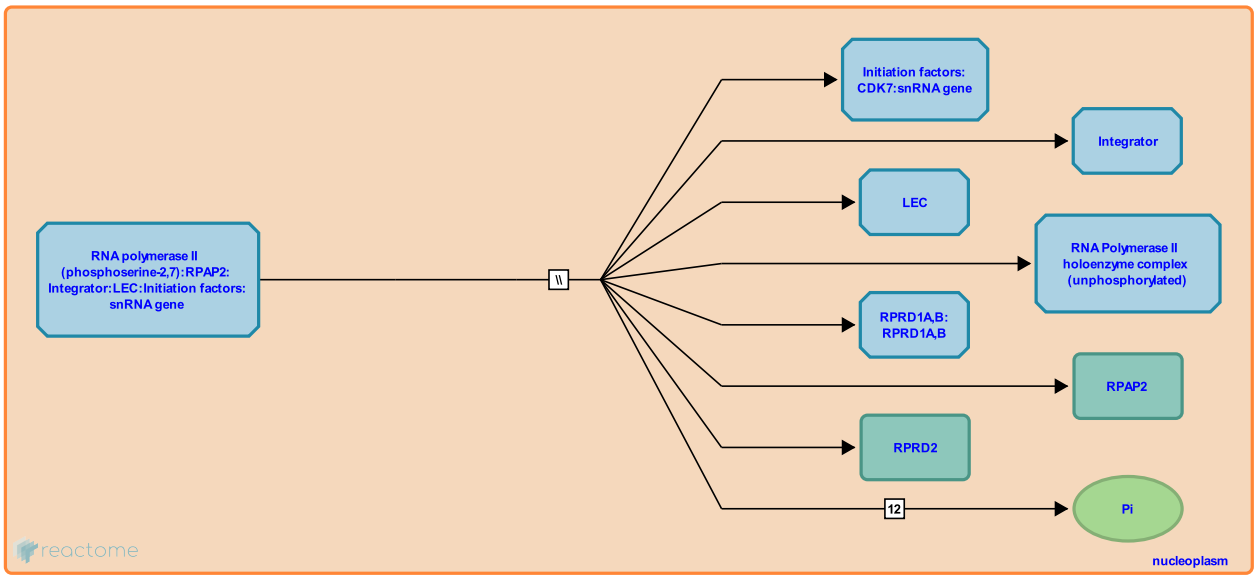
Location: RNA polymerase II transcribes snRNA genes

Stable identifier: R-HSA-6814554

Type: omitted

Compartments: nucleoplasm

Inferred from: Hypophosphorylation of RNA Pol II CTD by FCP1P protein (Homo sapiens)



Like RNA polymerase II at mRNA-encoding genes, RNA polymerase II at snRNA genes is believed to be dephosphorylated at the C-terminal domain (CTD) in order to begin another round of transcription. RNA polymerase II and factors bound to its C-terminal domain (CTD) dissociate and RNA polymerase II dissociates from the 3' end of the snRNA gene. The order of events is unclear.

Preceded by: Integrator complex processes the 3' end of snRNA

Editions

2015-11-21	Authored, Edited	May, B.
2016-02-19	Reviewed	Hernandez, N.

Table of Contents