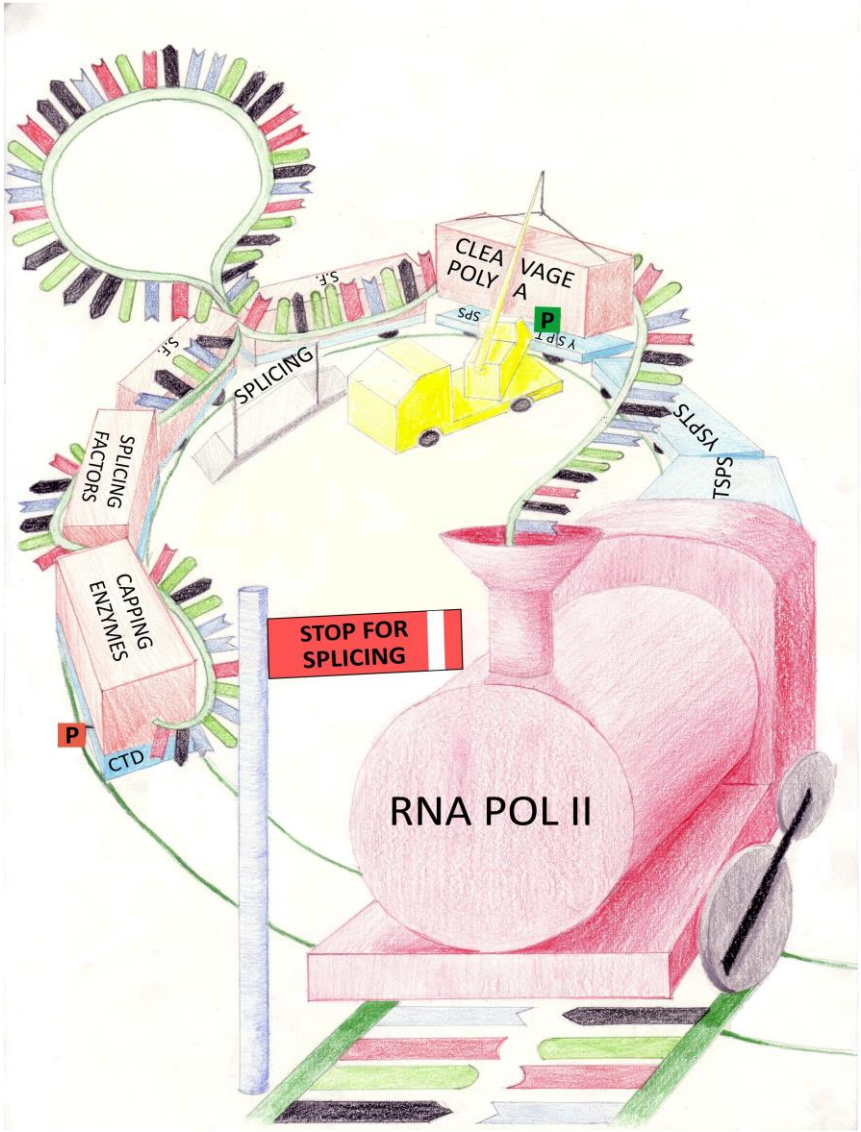
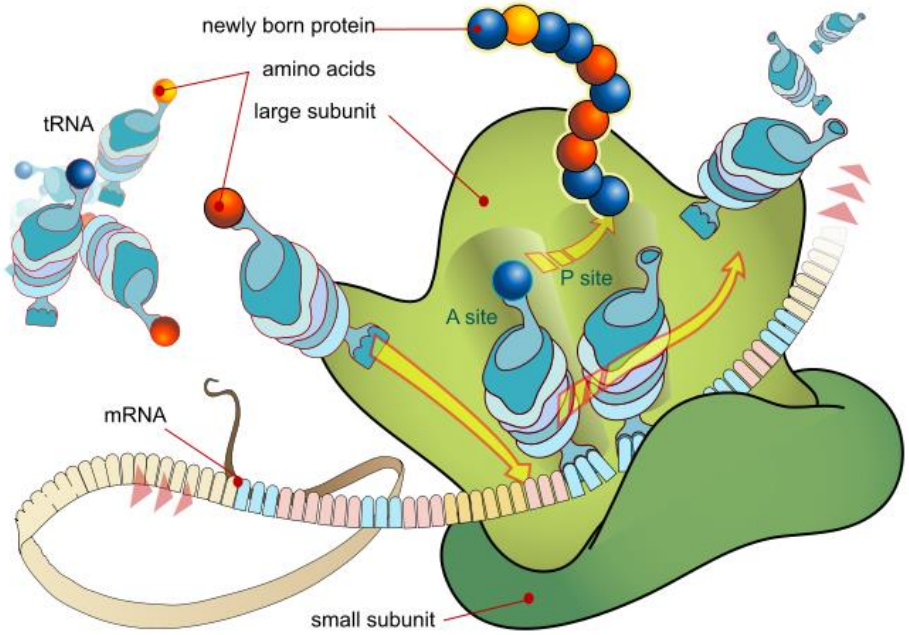
RNA MACHINERIES



TRANSCRIPTION - RNAP^{+}
SPLICING - SPLICEOSOME
3'end FORMATION - CPA



TRANSLATION - RIBOSOME^{+}

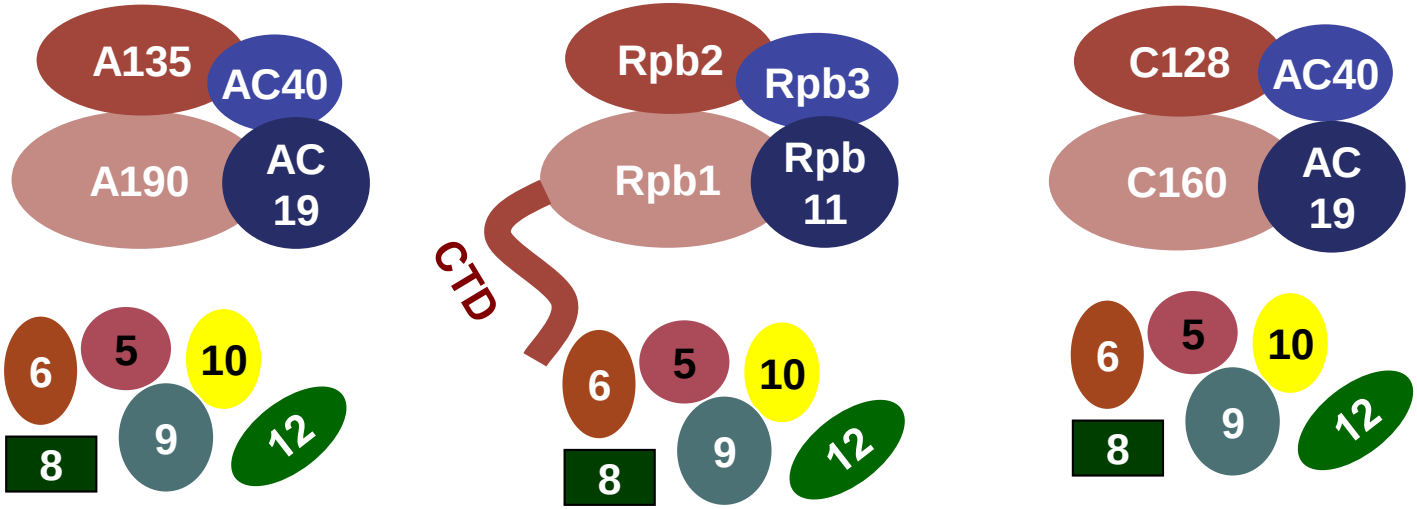
RNA POLYMERASES

RNA Pol I

RNA Pol II

RNA Pol III

Core subunits (similar in all)



Common subunits (same in all)

+ 4 others **+ 2 others** **+ 5 others**

RNAs:

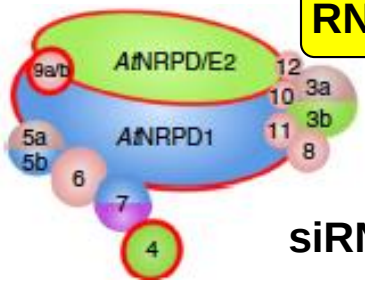
ribosomal RNA 35S precursor contains 18S, 5.8S and 25S rRNAs

mRNA , most snRNAs (U1, U2, U3, U4, U5, U11, U12, U4atac), snoRNAs, microRNAs, telomerase RNA, ncRNAs

tRNA, 5S rRNA, U6 snRNA, U6atac snRNA, 7SK RNA, 7SL RNA, RNase P RNA, RNase MRP RNA

Additional plant Polymerases

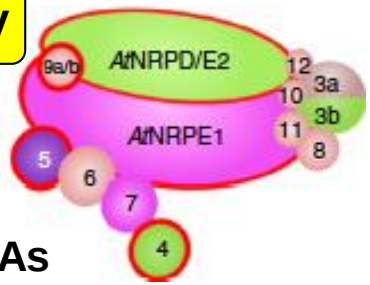
RNA Pol IV



siRNAs

Involved in transcriptional gene silencing

RNA Pol V

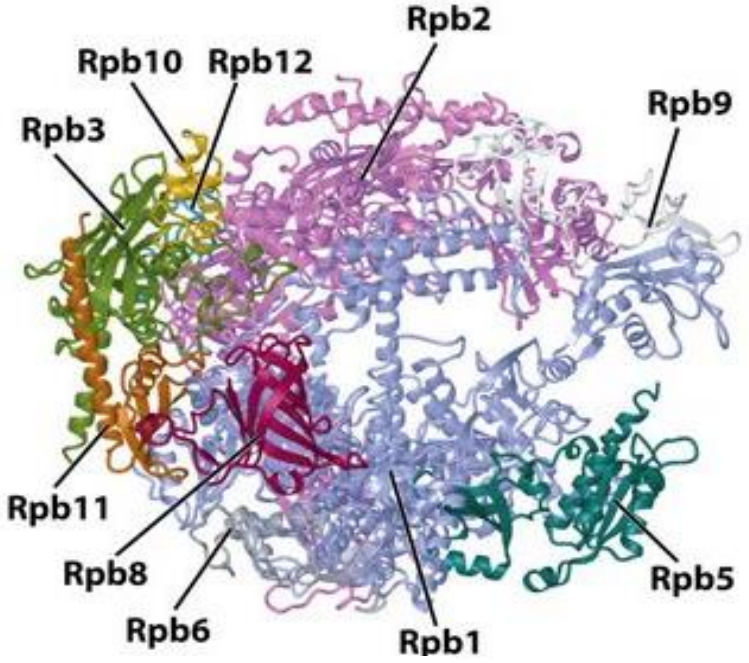


lncRNAs

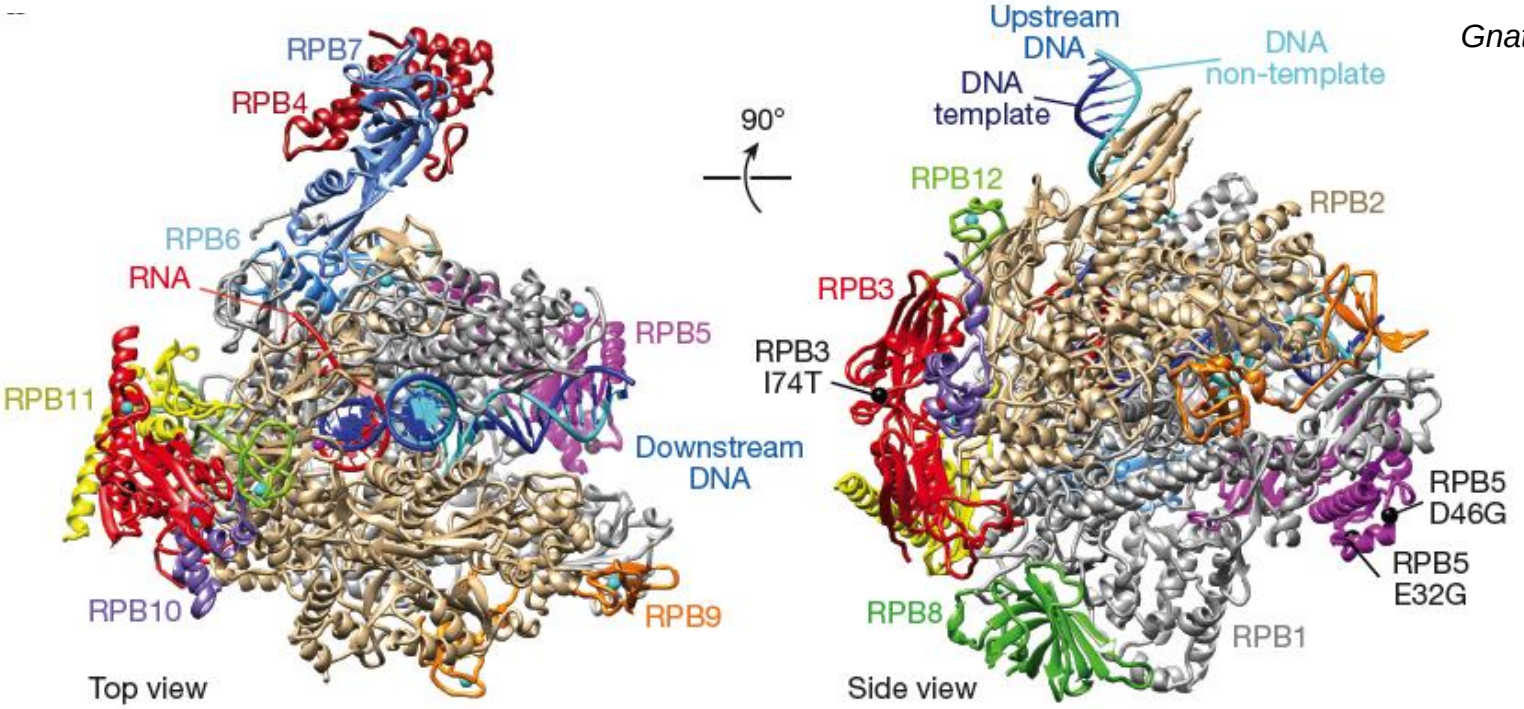
Zbigniew Dominski, *lectures* 2008

Yeast Pol II

- 12 subunits
- core by specific **Rpb1-3**, **9** and **11**
- **Rpb5-6, 8, 10** and **12** - shared by Pol I-III
- specific subcomplex **Rpb4/7** not essential
- associated factors RAP74, RAP30 (TFIIF)



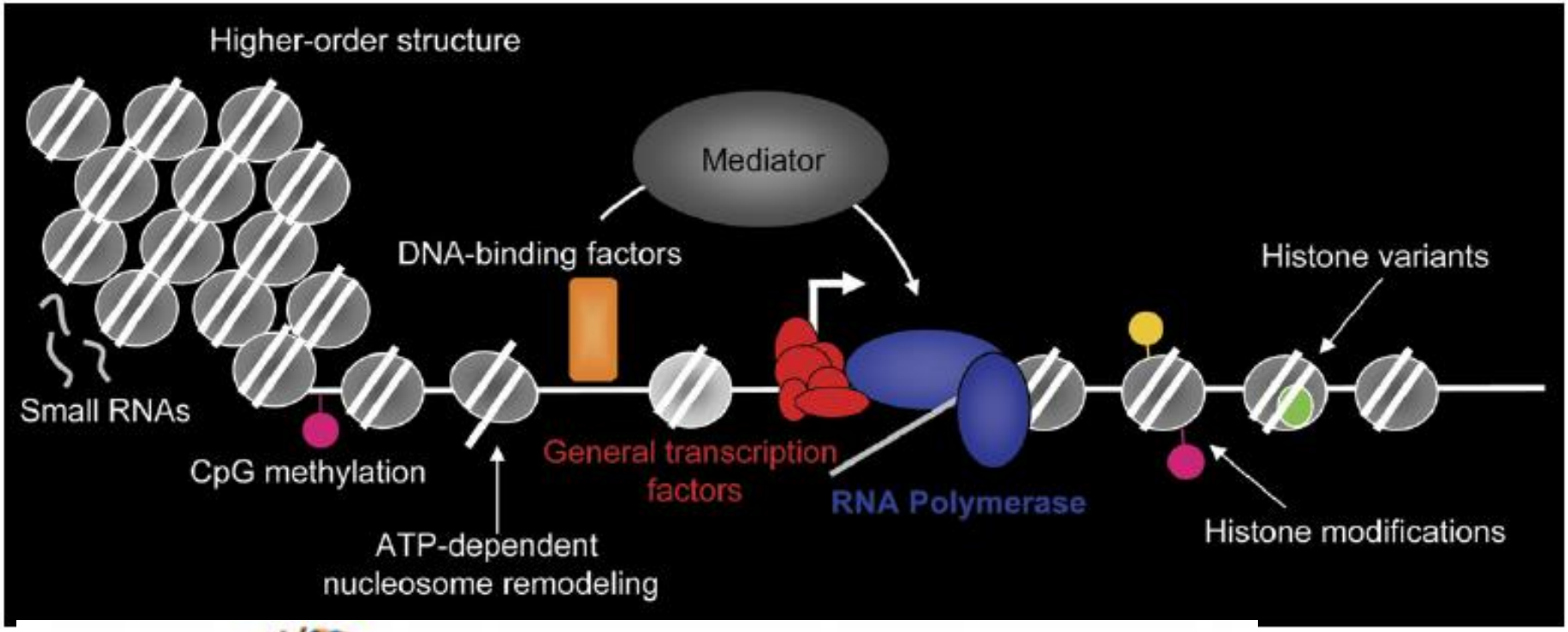
Mammalian Pol II

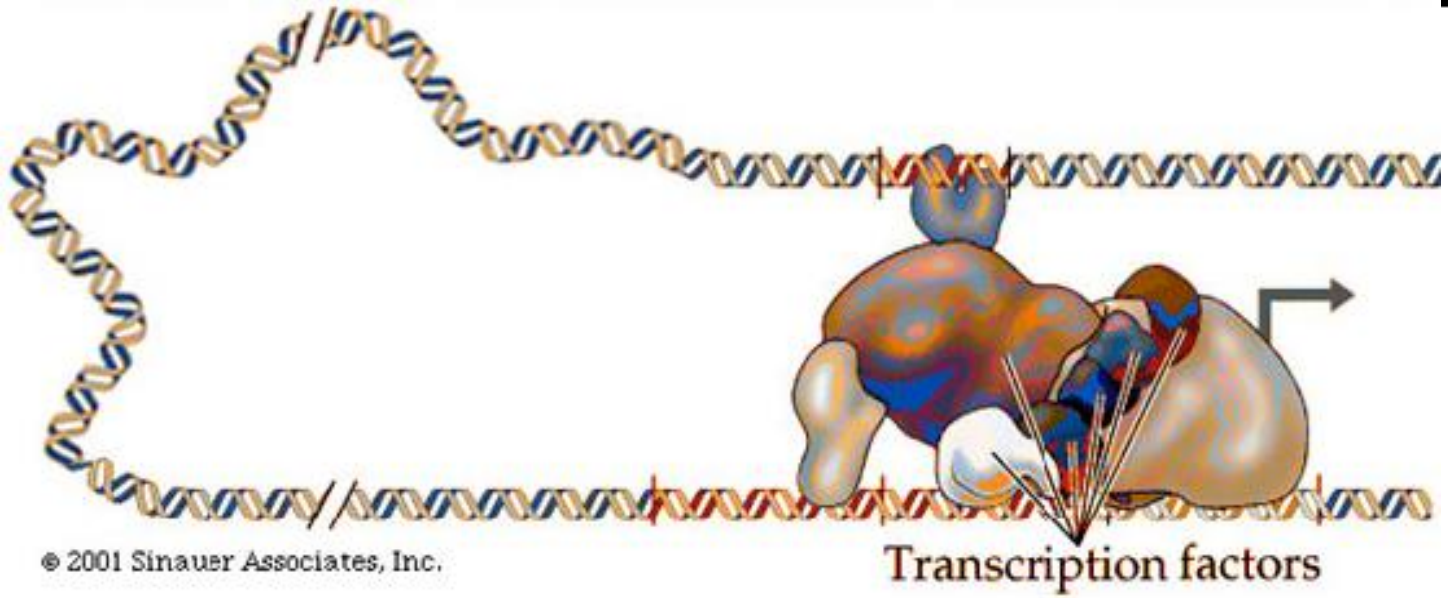


Gnatt et al, Science, 2001

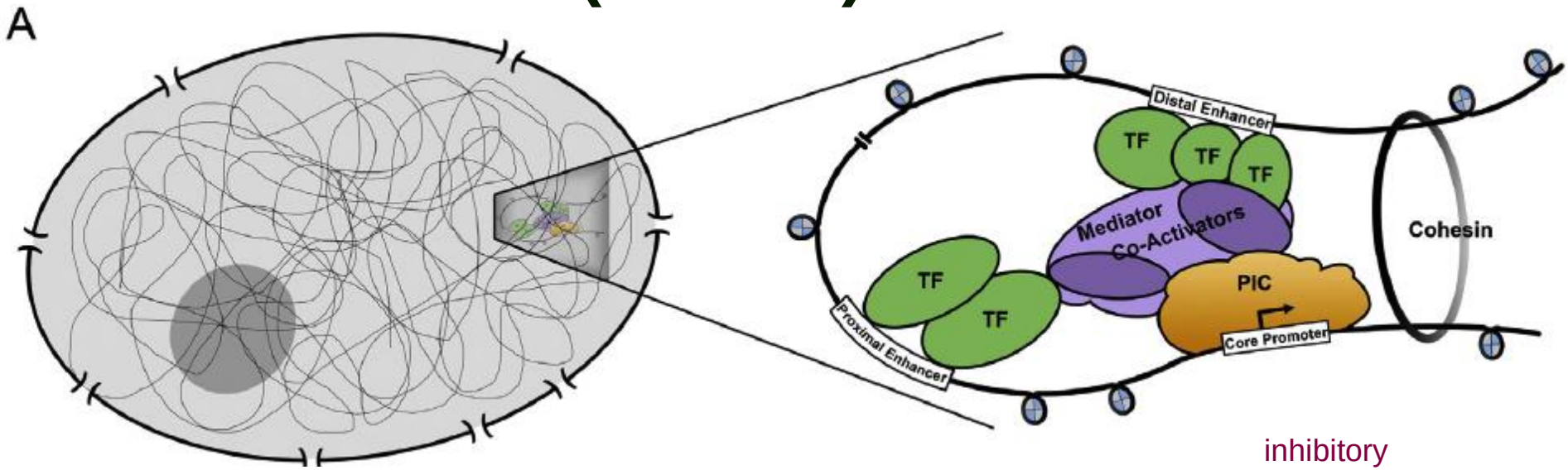
Berneckyet al, 2016, Nature

Pol II (RNAPII) in the cell

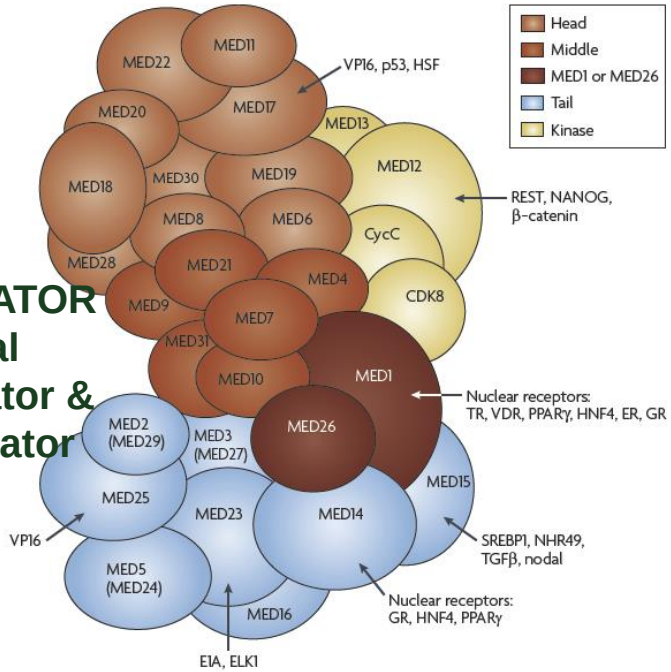




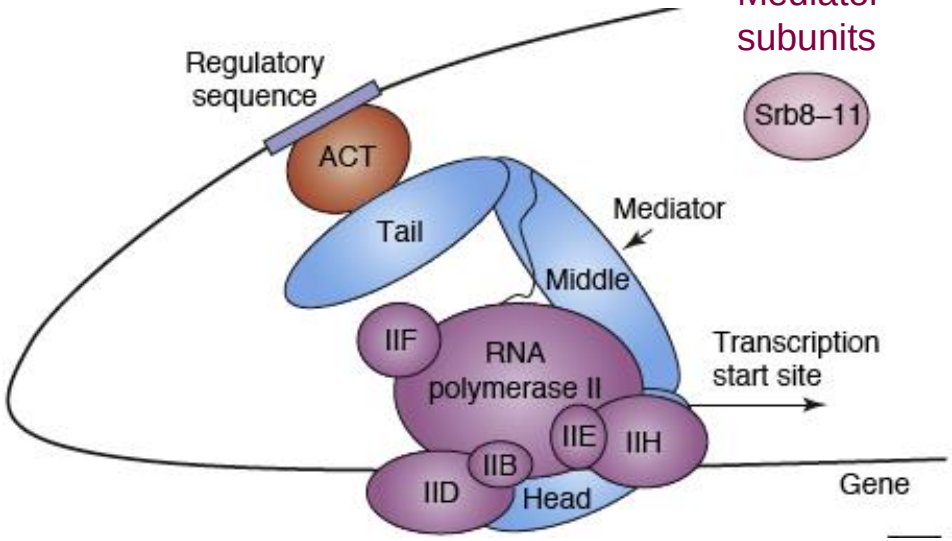
Pol II (RNAPII) in the cell



MEDIATOR central activator & integrator



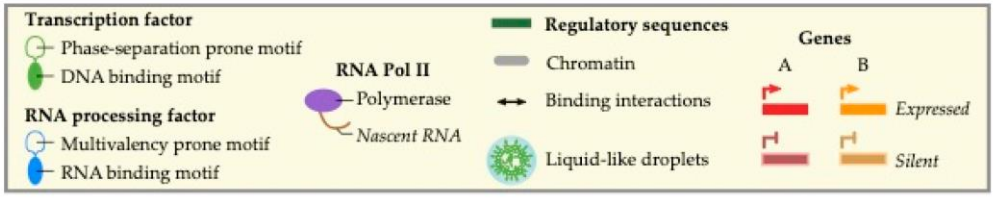
inhibitory Mediator subunits

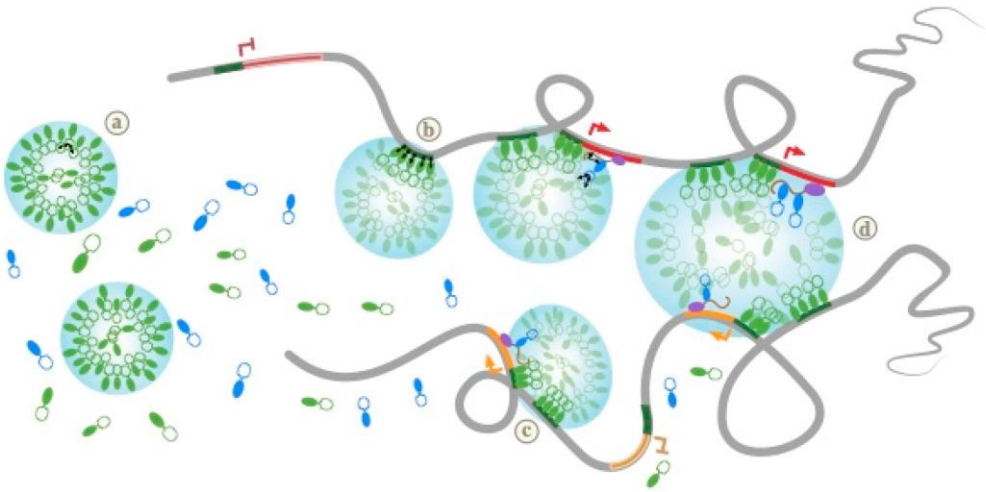


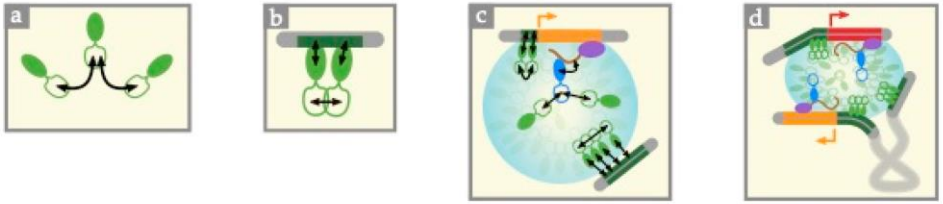
ACT - trx activator
II B D E H F – trx factors

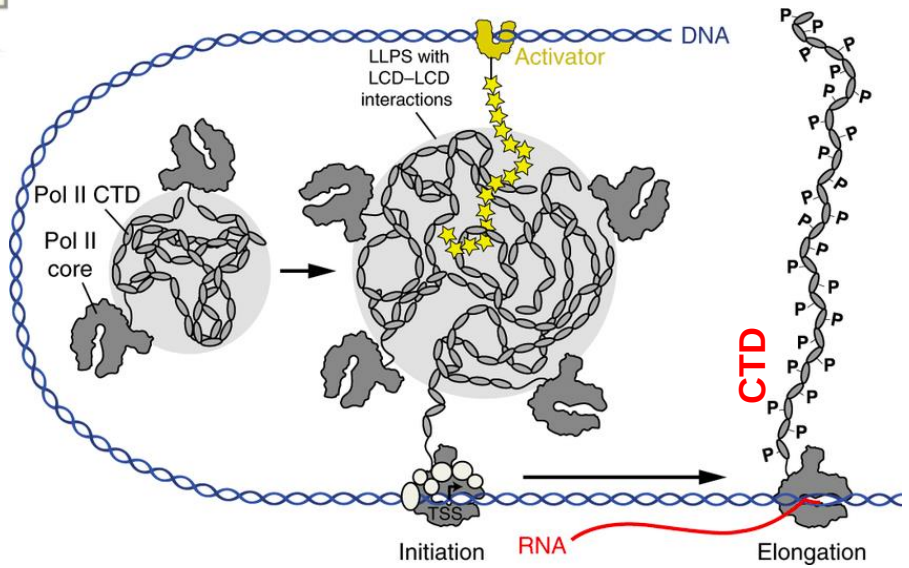
Bjorklund and Gustafsson, 2005, TiBS; Danino et al. BBA, 2015

Pol II (RNAPII) in the cell









LLPS, droplets

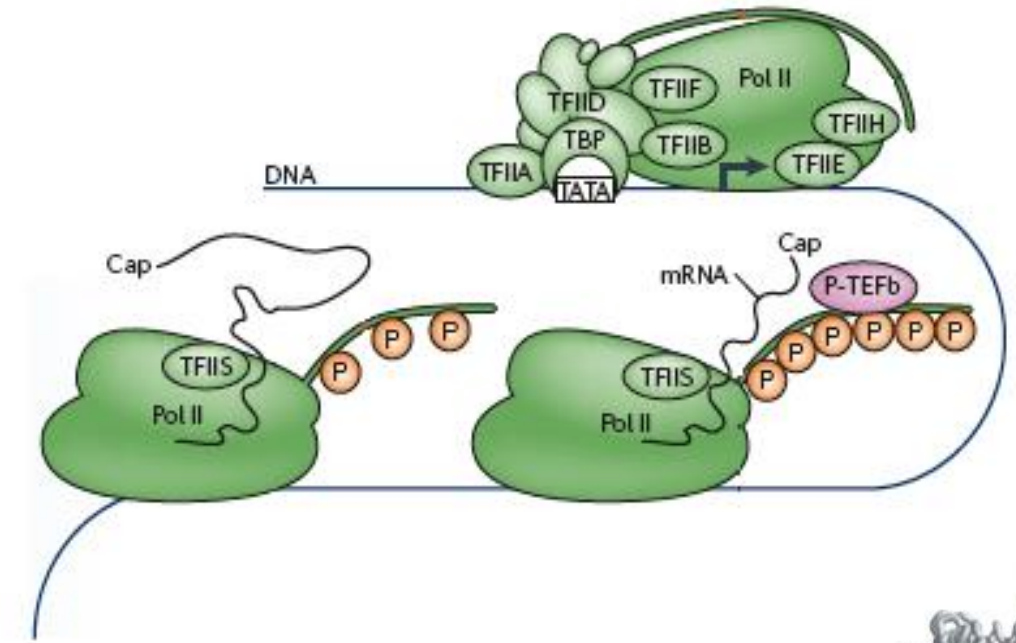
Liquid-like phase separation
Transcriptional condensates are formed by phase-separation self-assembly driven by IDR (Intrinsically Disordered Region)-containing proteins (e.g. CTD in Pol II)

CTD-driven phase separation

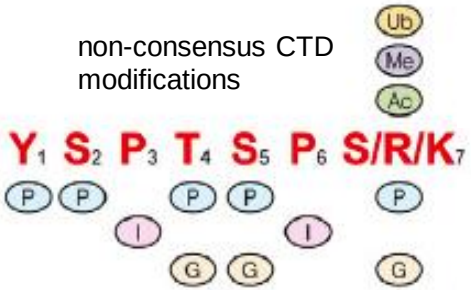
Activators recruit/nucleate Pol II hubs near promoters. Initiation-coupled CTD phosphorylation removes individual Pol II enzymes for transcription elongation.

Lesne et al.,2019 Genes
Boehning et al, 2018, Nat Struct Mol Biol

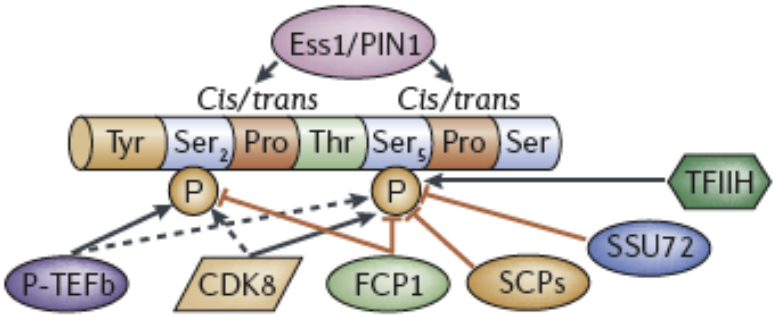
Pol II C-terminal domain (CTD)



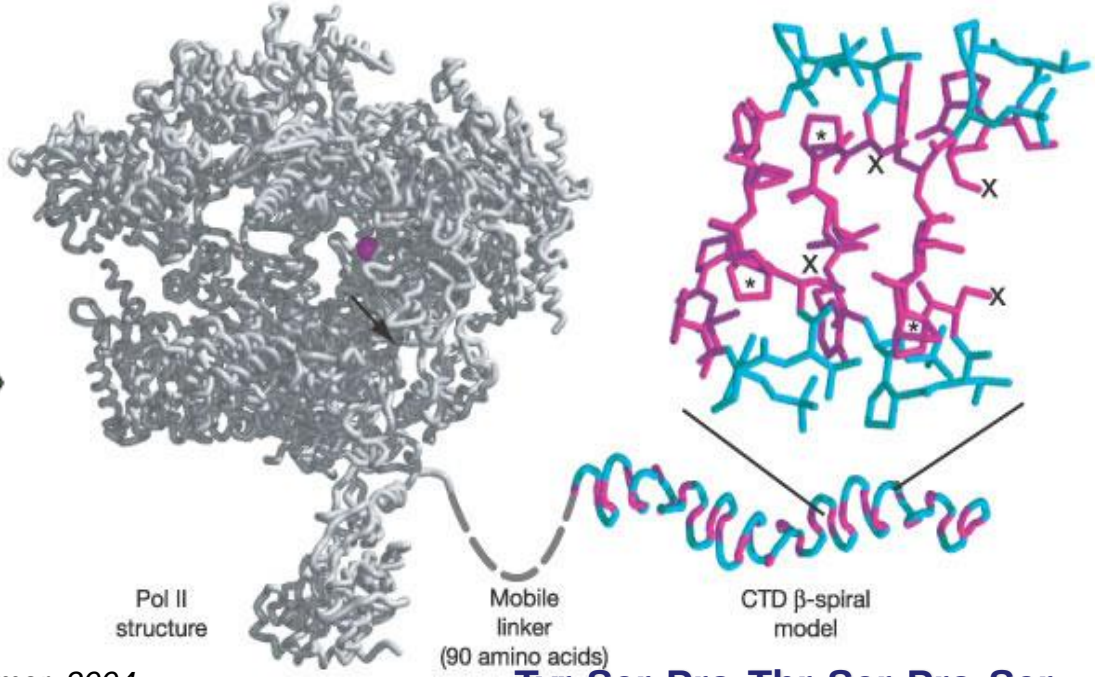
Goodrich and Kugel, Nat. Rev. Mol. Biol., 2006



26 (yeast) - 52 (human) repeats



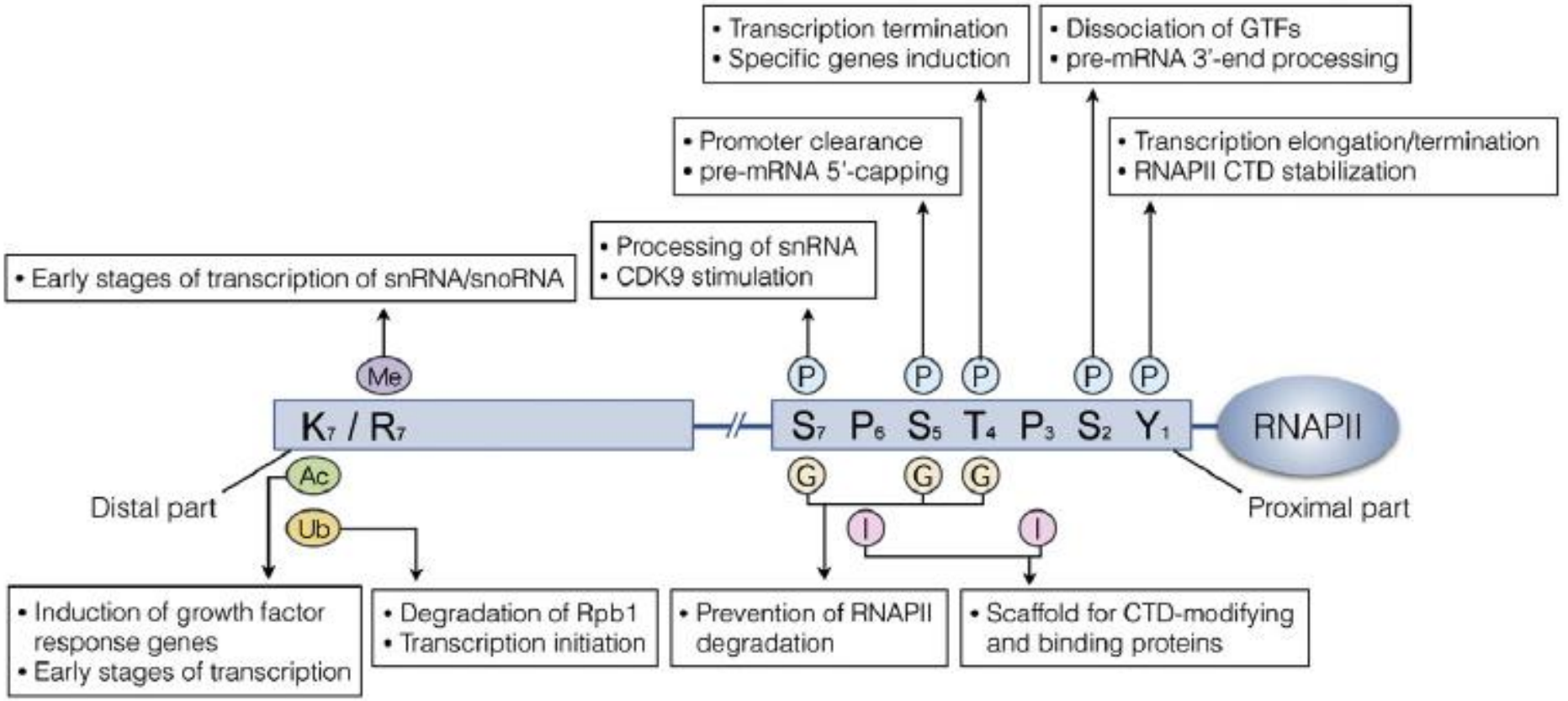
Saunders et al, 2006, Nat.Rev.Mol.Cel.Biol



Meinhart and Cramer, 2004

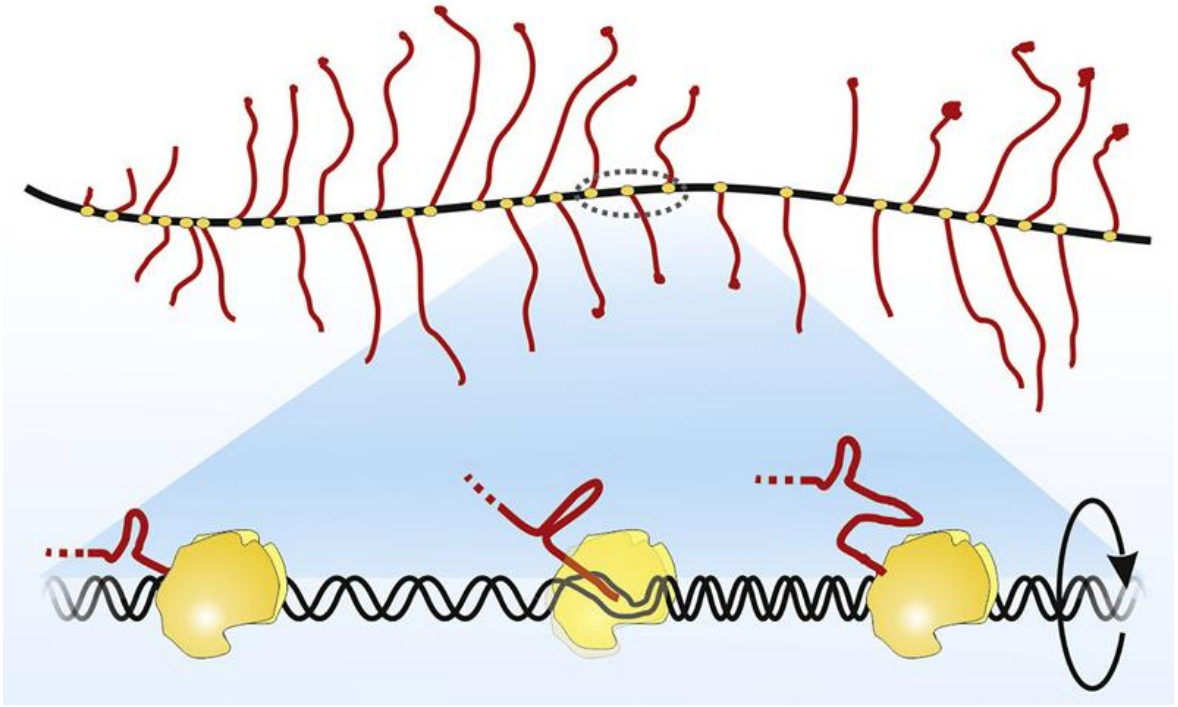
$Tyr_1Ser_2Pro_3Thr_4Ser_5Pro_6Ser_7$

CTD CODE



Srivastava and Ahn, Biotechnol Adv 2015

NASCENT TRANSCRIPTS

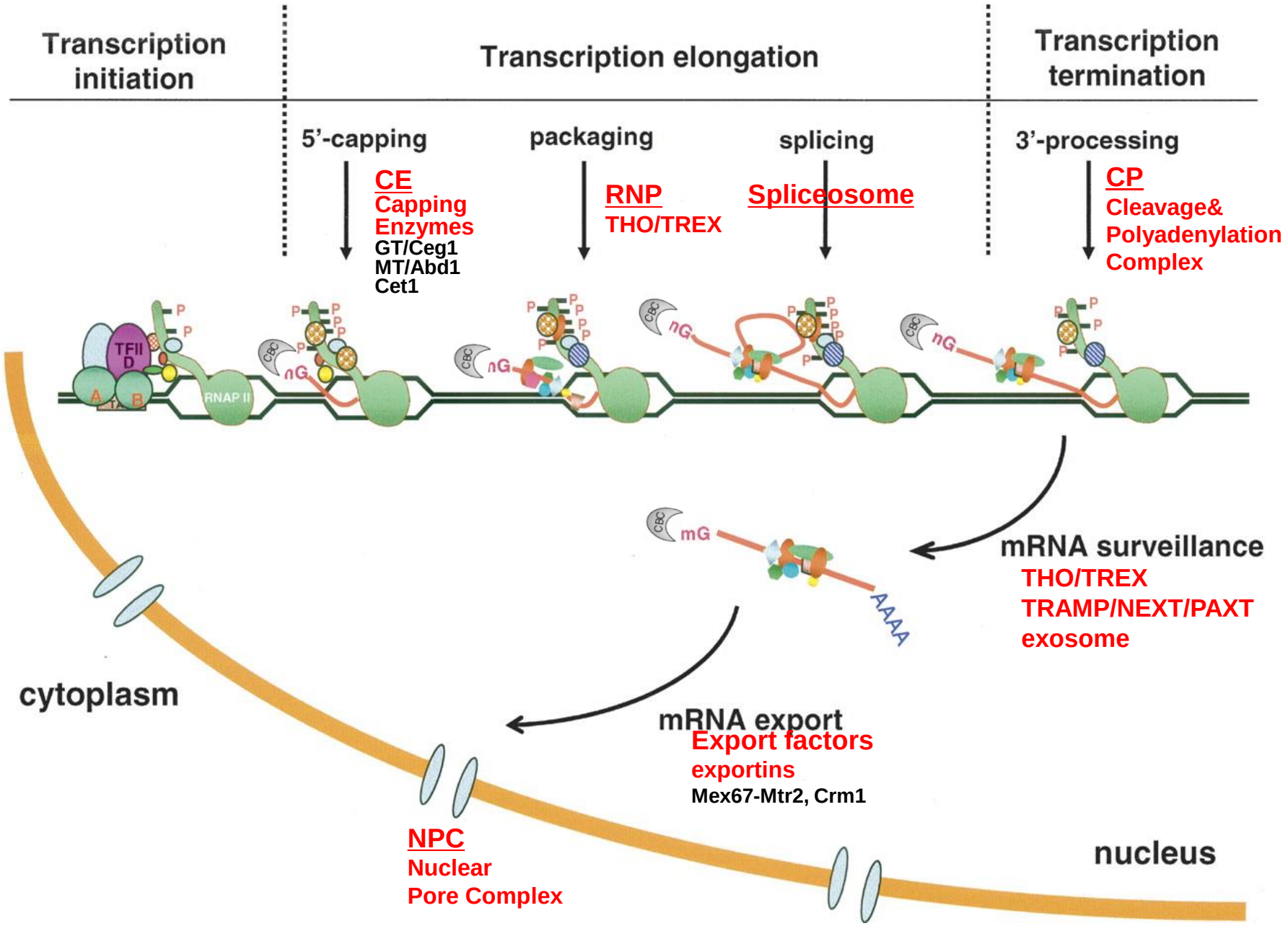


Nascent transcript = during formation, newly formed, still bound by Pol II

- nascent RNAs couple RNA processing with transcription elongation and chromatin modification
- nascent RNAs modulate binding of proteins to regulatory elements (chromatin)
- regulatory effects of nascent transcripts can be enhanced by gene looping
- high concentrations of nascent RNAs can initiate formation of nuclear bodies
- sometimes the function is conferred by nascent transcription (activity) and not the transcript itself

Turowski et al., Mol Cell, 2020

CO-TRANSCRIPTIONAL PROCESSES

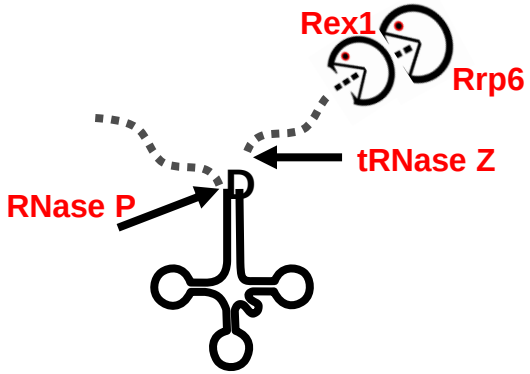


Li and Manley, Genes Dev, 2006

POST-TRANSCRIPTIONAL PROCESSES

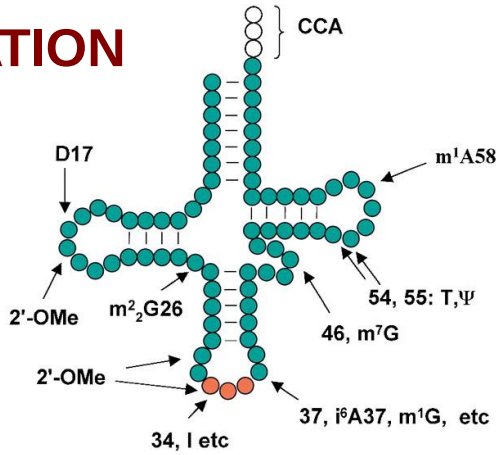
tRNA PROCESSING

- 5’ end by RNAse P
- 3’ end by tRNase Z or
- by exonuclease Rex1 and Rrp6



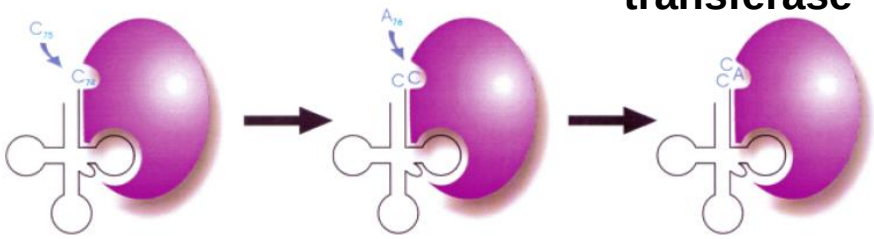
tRNA MODIFICATION

by RNA modifying enzymes



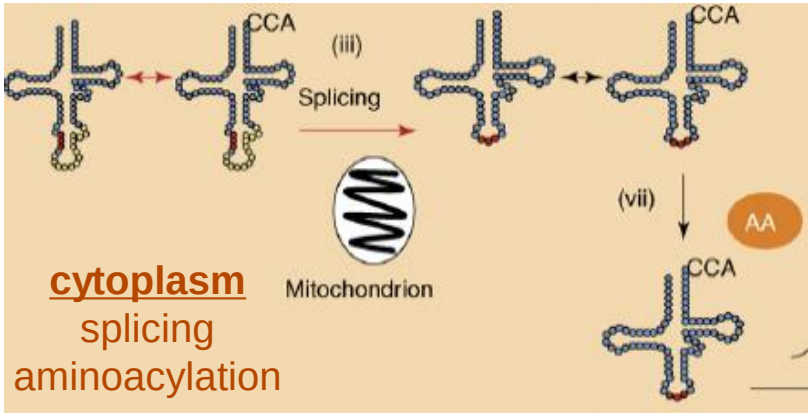
tRNA CCA ADDITION

by tRNA nucleotidyl-transferase



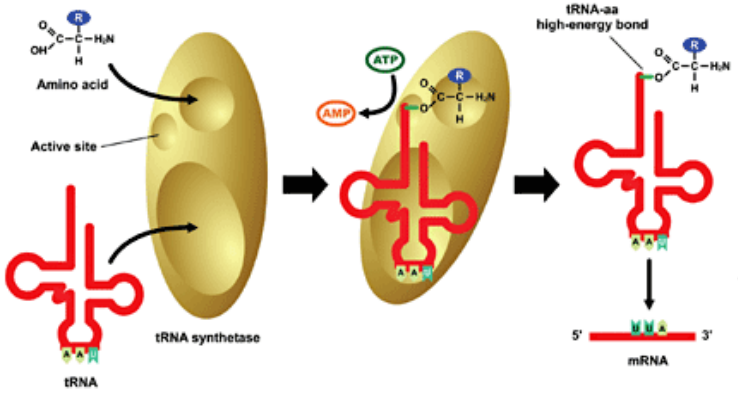
tRNA SPLICING

In the cytoplasm on the mitochondrial membrane *(YEAST!!)*



Hopper and Shaheen, TiBS,2008

tRNA AMINOACYLATION



by tRNA aminoacyl synthetases

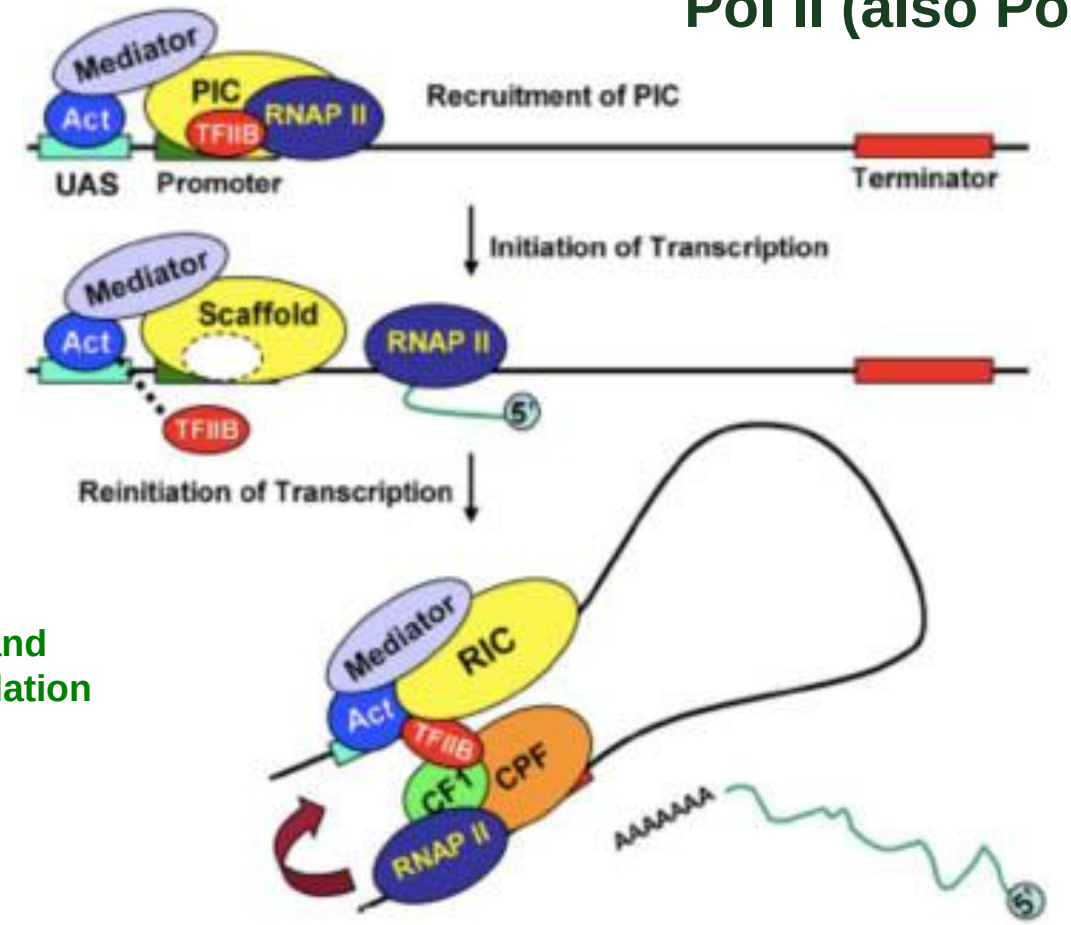
GENE LOOPING

Pol II (also Pol I)

PIC Preinitiation Complex

Scaffold transcription factors (TFIID, A, E, H)

CF1, CPF Cleavage and Polyadenylation Complex



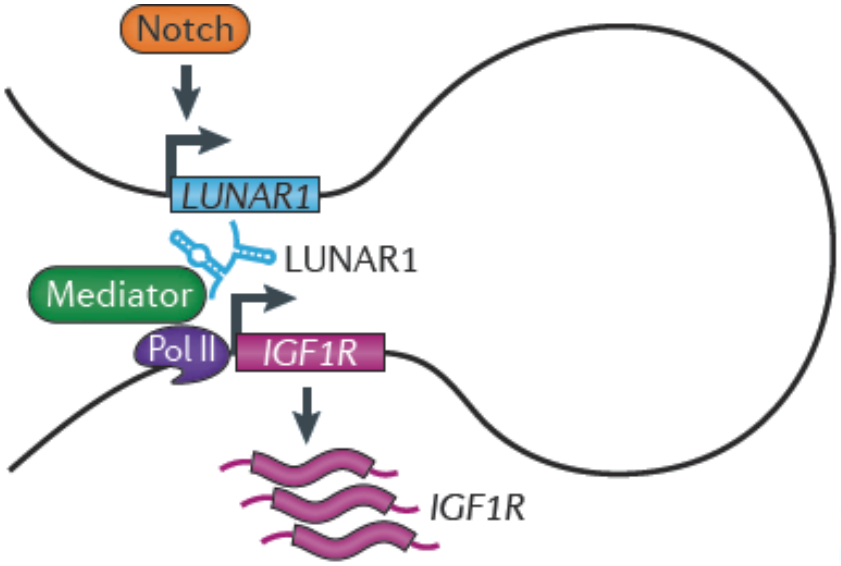
Ansari and Hampsay, GDev, 2005; El Kaderi et al., JBC, 2009

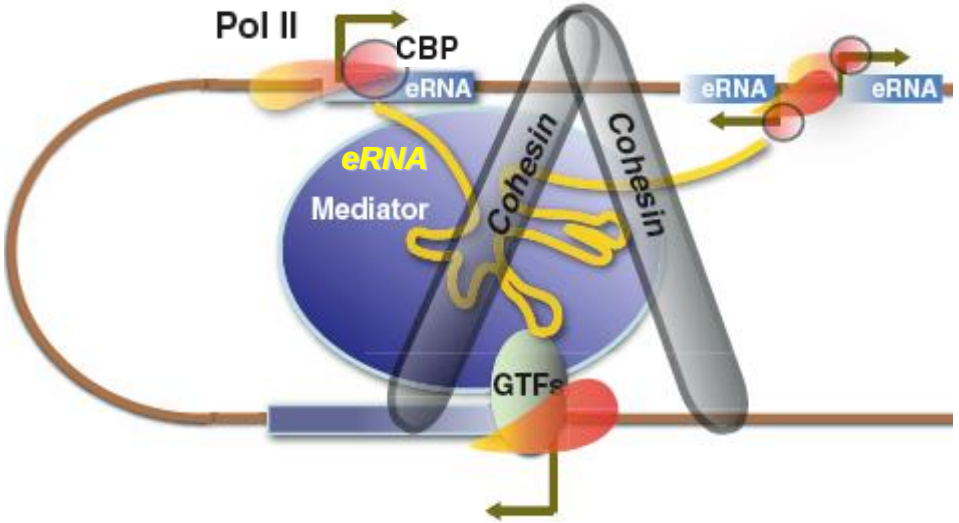
Loop formation requires interaction between factors at the promoter (THIIB) and terminator (Rna15 from CF1) /in mammals: transcription factors, nuclear receptors, insulators, chromatin remodellers, Polycomb, architectural proteins/

Loop function: facilitation of transcription reinitiation of PolII, but also repression of gene expression (PcG, DNA methylation)

GENE LOOPING

via Mediator and enhancer RNAs (eRNAs)



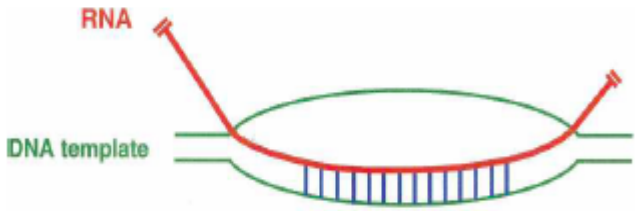


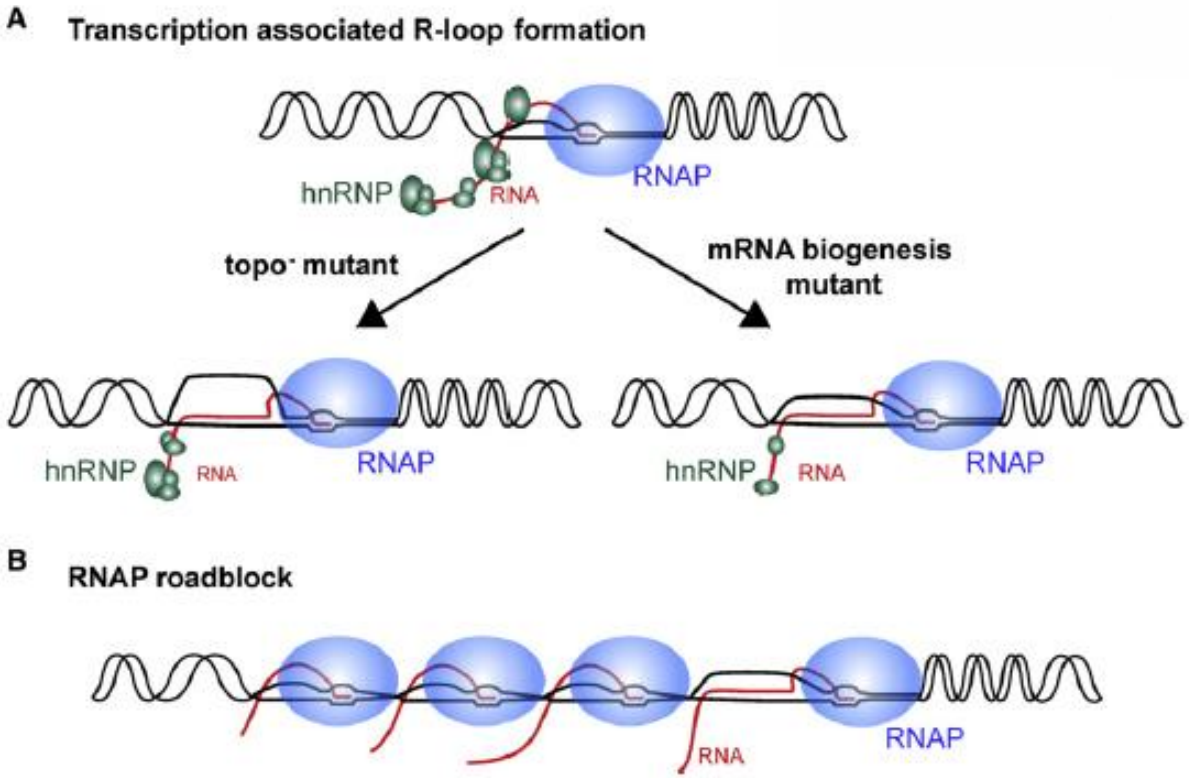
Some eRNAs (e.g. *LUNAR1* near the IGF1R locus) **mediate chromosome looping between enhancers and nearby genes via Mediator or MLL protein complexes**

Quinn and Chang, Nat Rev Genet 2015;
Lai and Shiekhattar, Curr Op Gene Dev 2014

R-LOOPs

DNA::RNA hybrids formed during transcription before RNP packaging





R-loops

- accumulate in RNP biogenesis mutants (*tho*, *sen1*, mRNA export)

- negative effects: polymerase stalling, termination defects, replication fork stalling, DNA damage, genetic instability

- prevented by topoisomerases, helicase Sen1, THO complex, resolution (cleavage) by RNase H

Aguilera and Garcia-Muse, Mol Cell, 2012

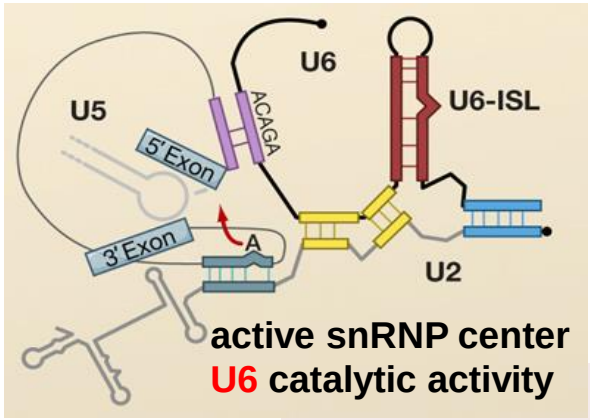
SPLICEOSOME

5 snRNAs: U1, U2, U4, U5, U6

Core Sm or LSM (U6) proteins **1.7 - 3 MDa**

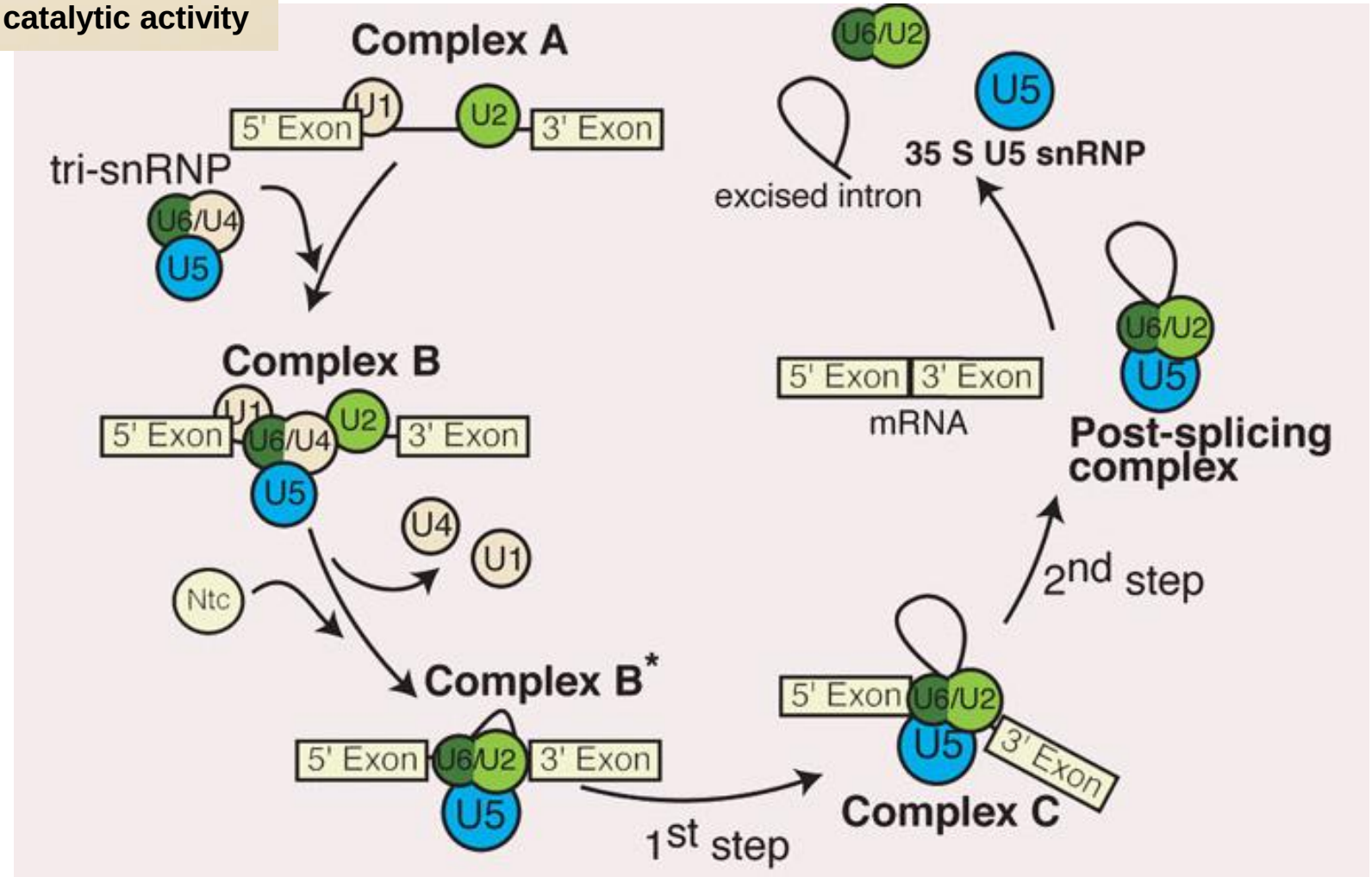
Specific snRNP proteins

Splicing factors



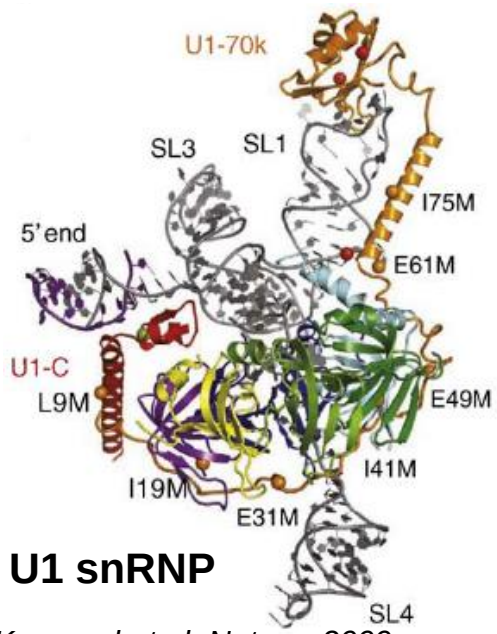
active snRNP center

U6 catalytic activity



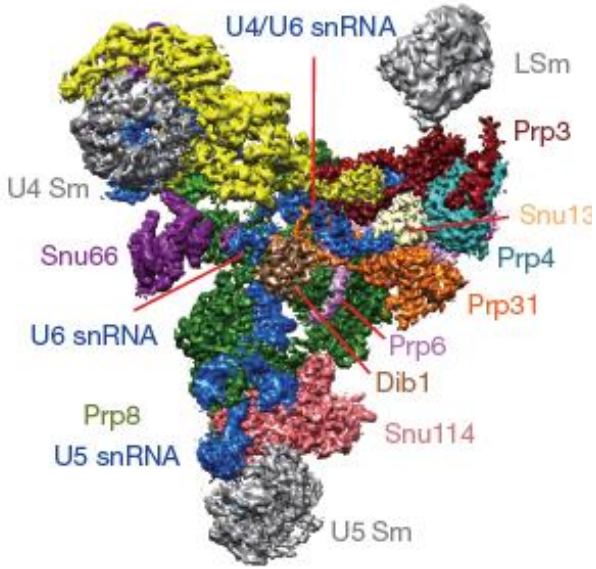
Warf and Berglund, 2010, TiBS; Reddy, Ann.Rev.PlantBiol., 2007

SPLICEOSOME
Cryo- EM



U1 snRNP

Krummel et al, Nature, 2009

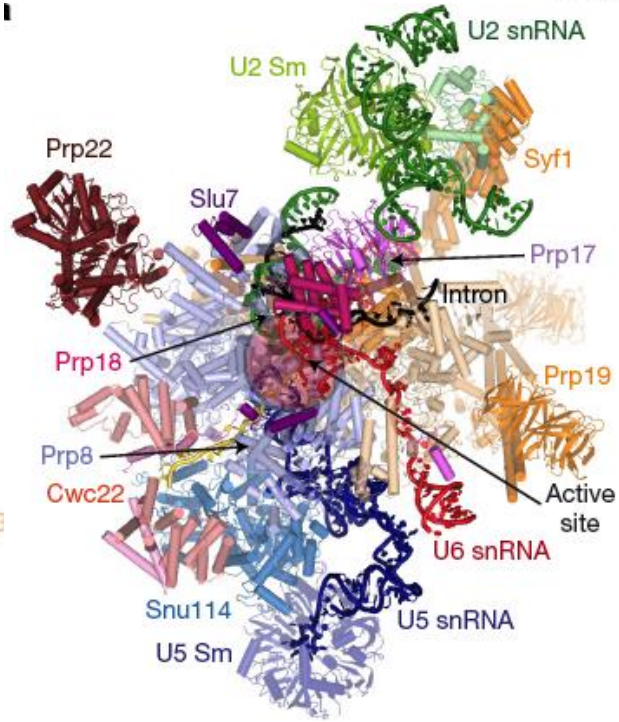


U4/U6.U5 tri-snRNP

Nguyen1, Galej et al, Nature, 2016*

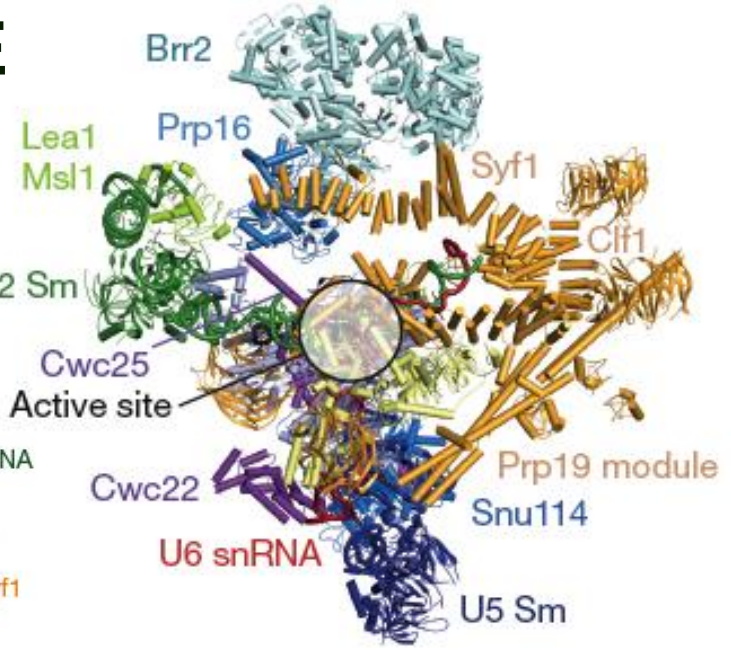
C complex yeast

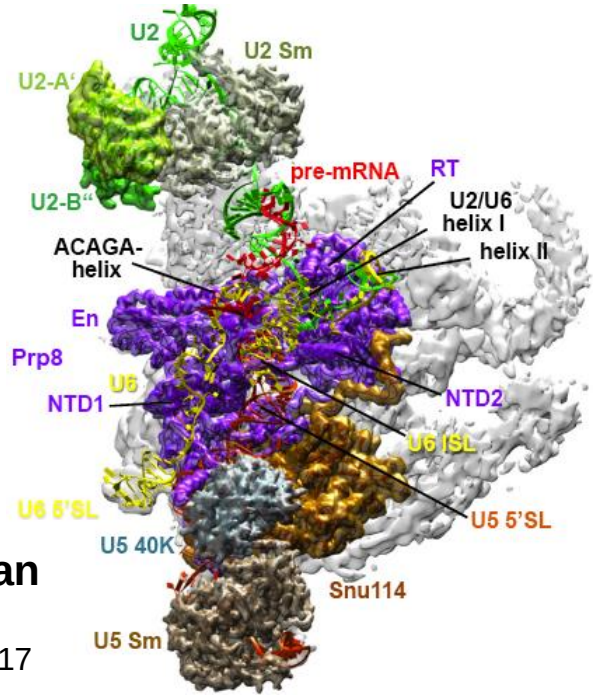
Galej et al, Nature, 2016



C* complex yeast

Fica et al, Nature, 2017



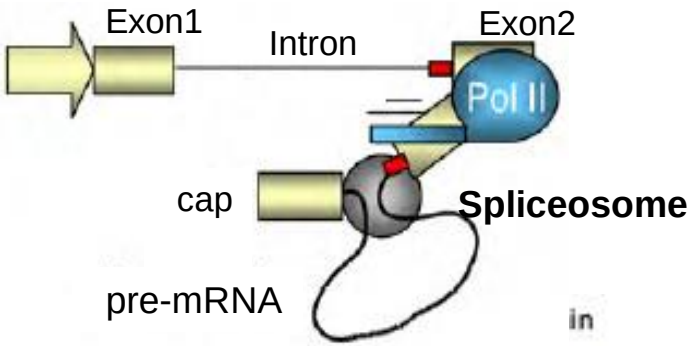


C* complex human

second step

Bertramet al, Nature, 2017

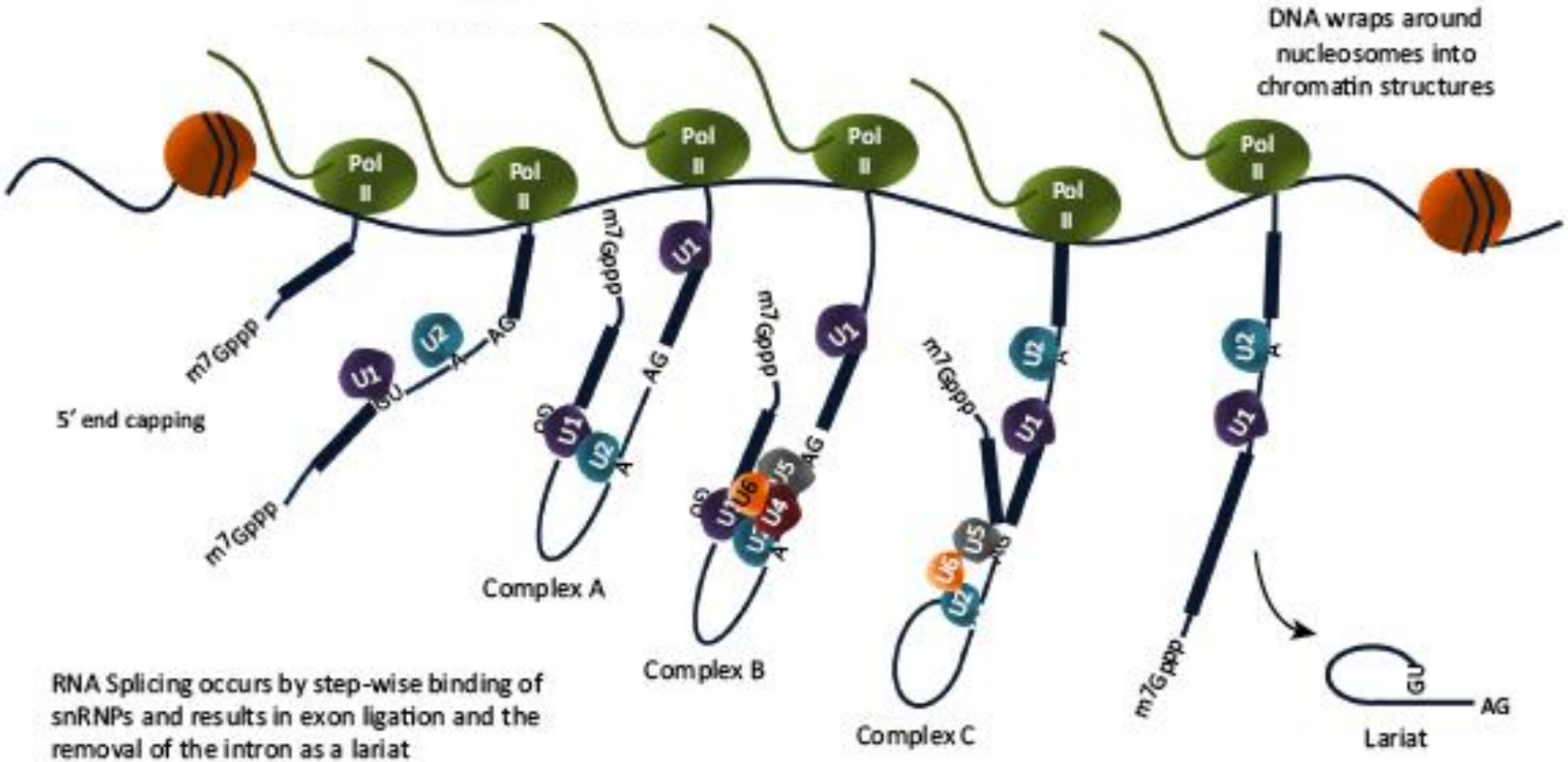
SPLICING: co-transcriptional process



- **spliceosome assembly (Ser5-P)**
- **majority of splicing (up to 70-80%)**

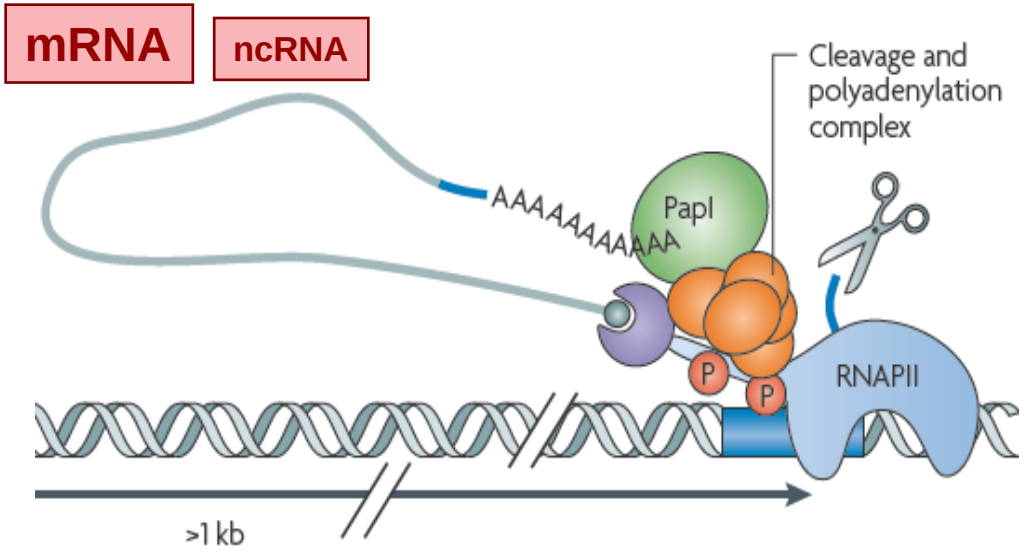
Munoz *et al.*, *TiBS*, 2009

in



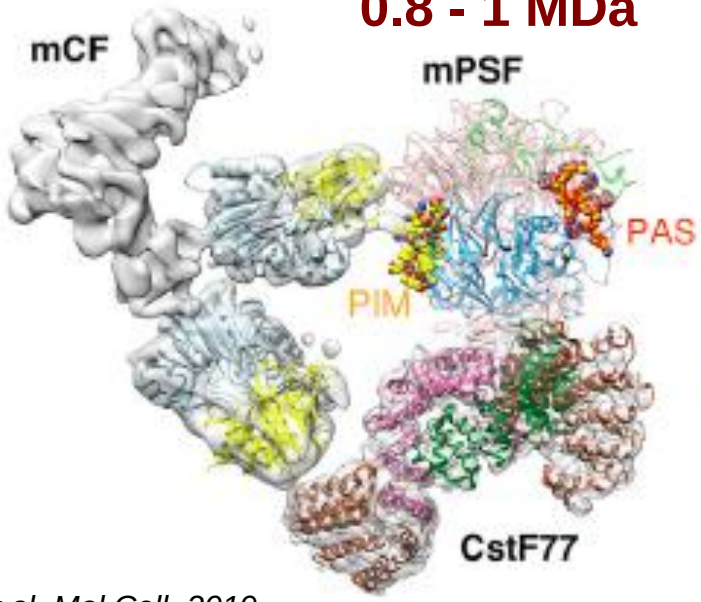
Wong *et al.*, *TiG*, 2014

CPA Cleavage and Polyadenylation

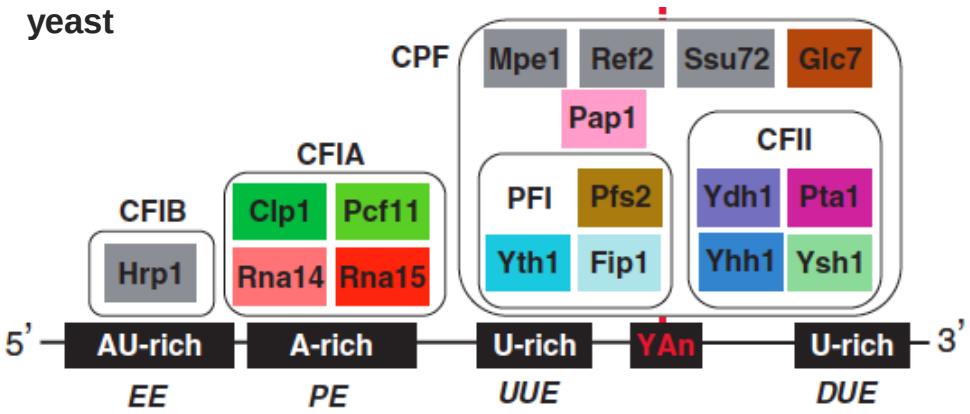


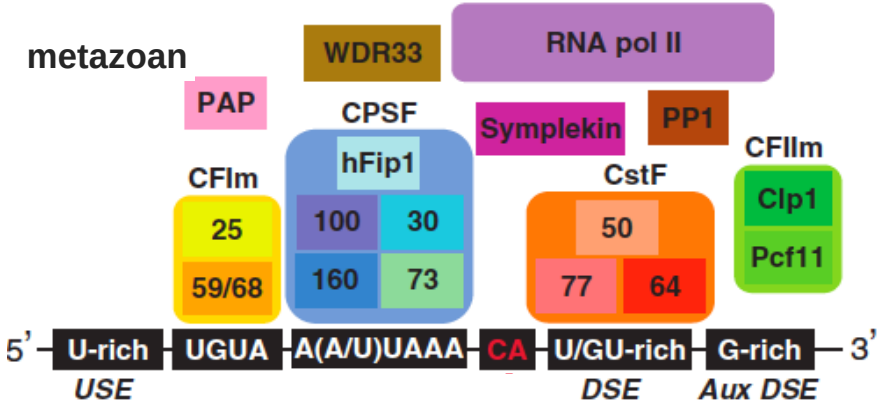
Jacquier, Nat. Rev. Genet, 2009

0.8 - 1 MDa



Zhang et al, Mol Cell, 2019

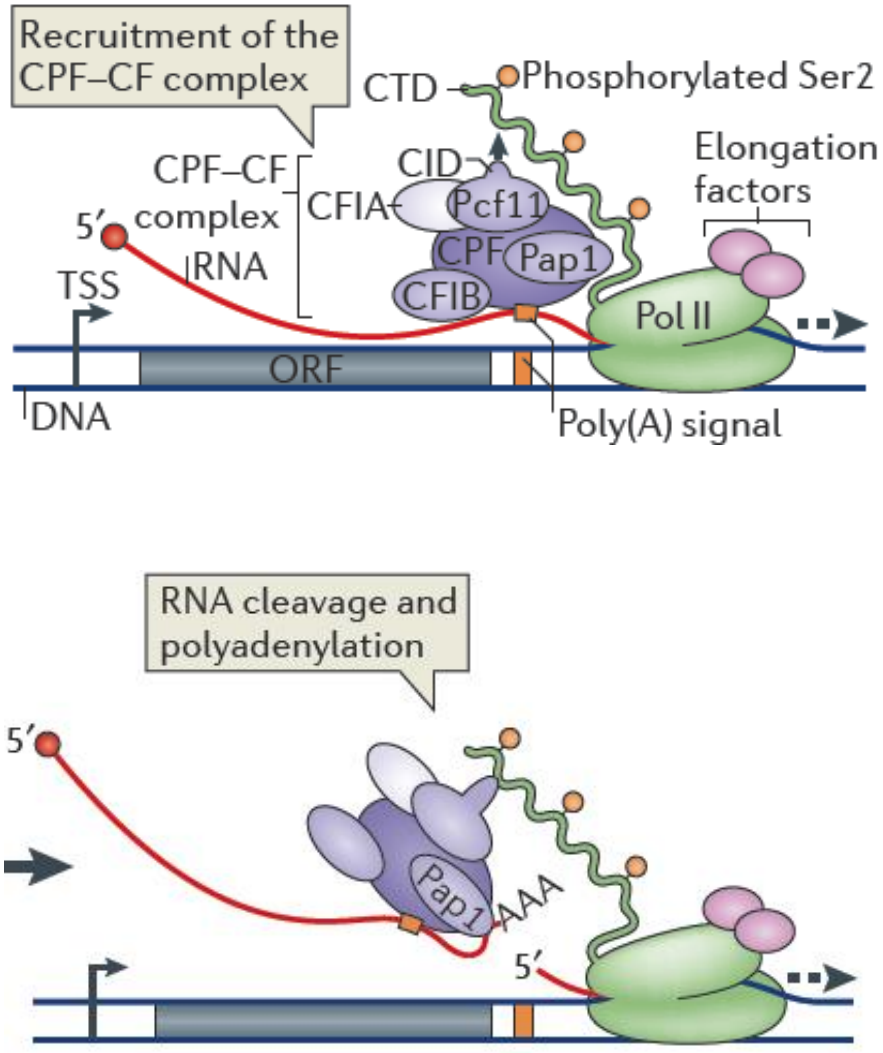




Cleavage by CPSF-73 (human), Brr5/Ysh1 (yeast)

Millevoi and Vagner, NAR, 2008

CPA: mRNA 3’ end formation
transcription termination at mRNA genes



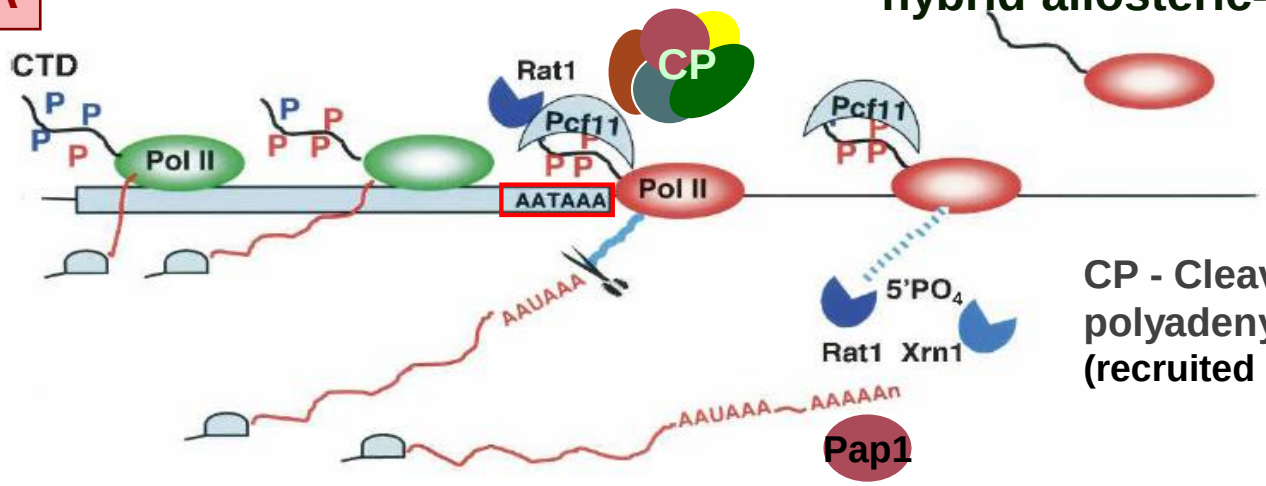
Poruua, Libri, Nat Rev Mol Cell Biol, 2015

POL II TRANSCRIPTION TERMINATION

mRNA

ncRNA

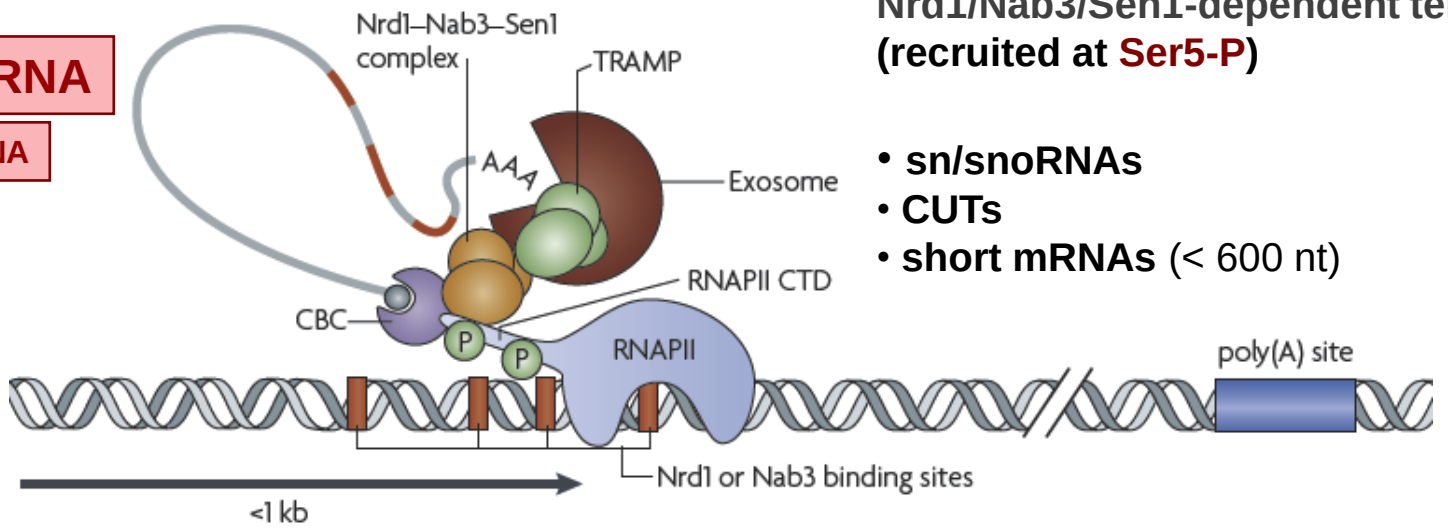
hybrid allosteric- torpedo model



CP - Cleavage and polyadenylation complex (recruited at Ser2-P CTD)

ncRNA

mRNA



Nrd1/Nab3/Sen1-dependent termination (recruited at Ser5-P)

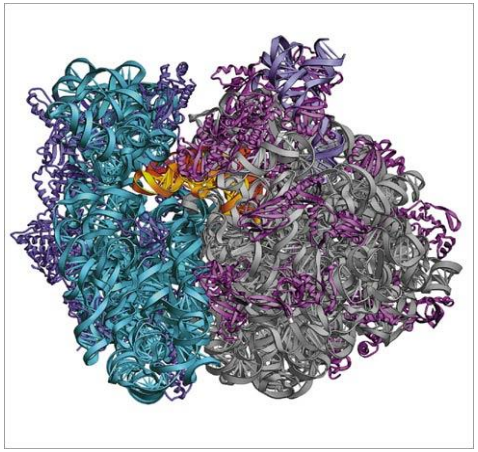
- **sn/snoRNAs**
- **CUTs**
- **short mRNAs** (< 600 nt)

Luo and Bentley, Gene Dev, 2006

Jacquier, Nat. Rev. Genet 2009

Lecture on transcription termination by Michał Koper

RIBOSOME



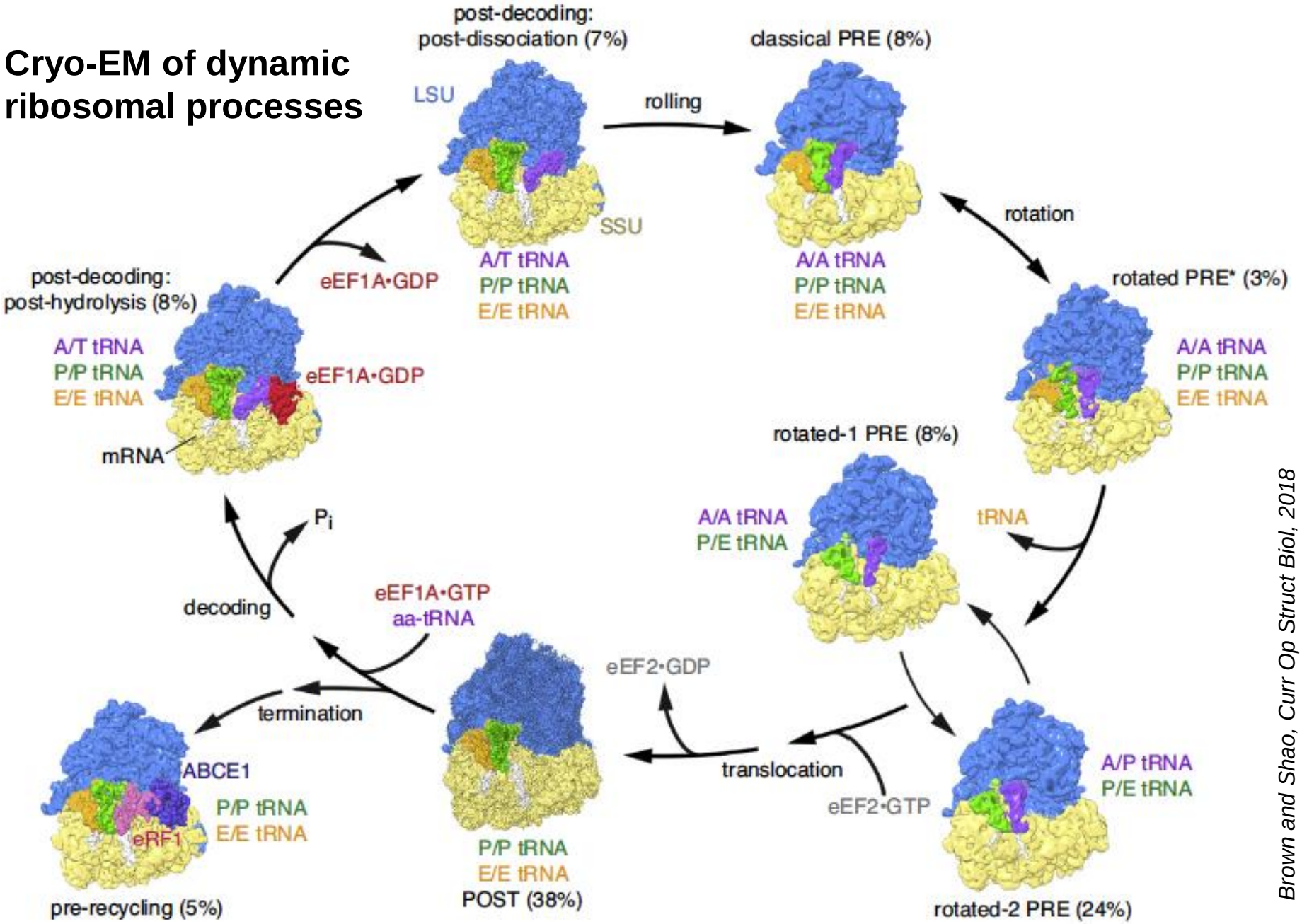
3.3 (yeast) – 4.3 (humans) MDa

Ribosome is a ribozyme

- No ribosomal protein with a peptidyl transferase (PT) activity
- Drugs (chloramphenicol) that inhibit PT bind to the 25S rRNA (PT loop)
- Mutations that provide resistance to these drugs map to the PT loop
- Nearly all (99%) of proteins can be stripped from the large subunit and it still retains the PT activity
- Only RNA chains are close enough to the PT center (structure)
- Ribosomal proteins are important for ribosome stability and integrity, but NOT for catalysis

TRANSLATION CYCLE

Cryo-EM of dynamic ribosomal processes



Brown and Shao, Curr Op Struct Biol, 2018