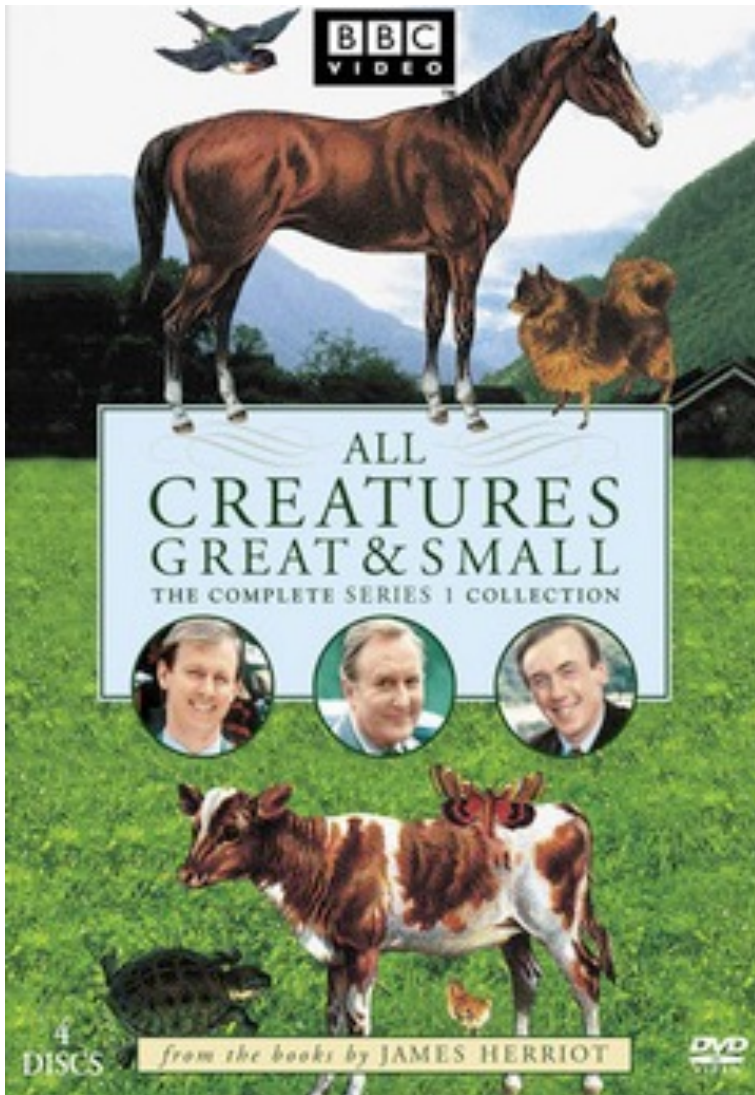


All RNAs great and small

lecture 3



RNA enzymes and complexes

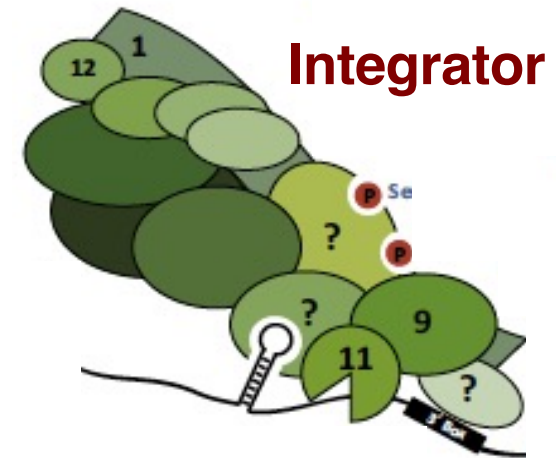
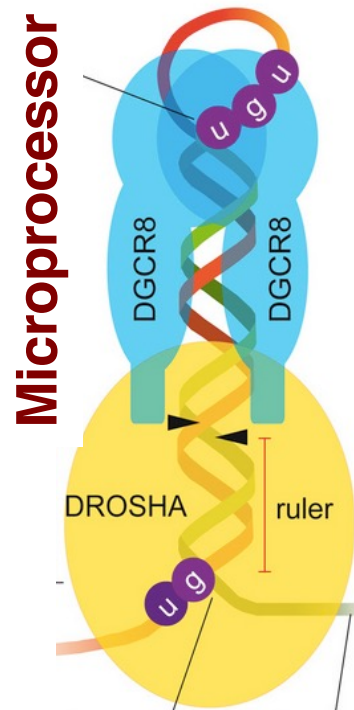
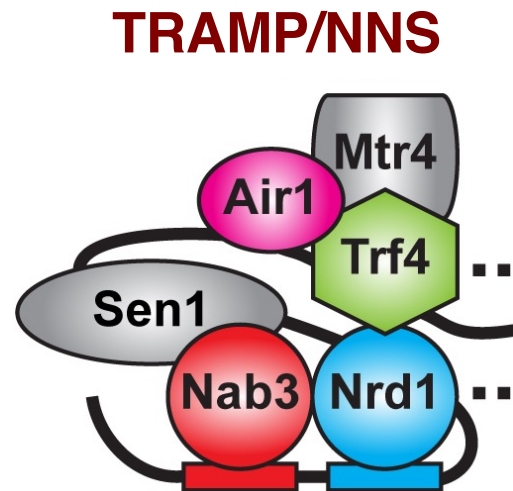
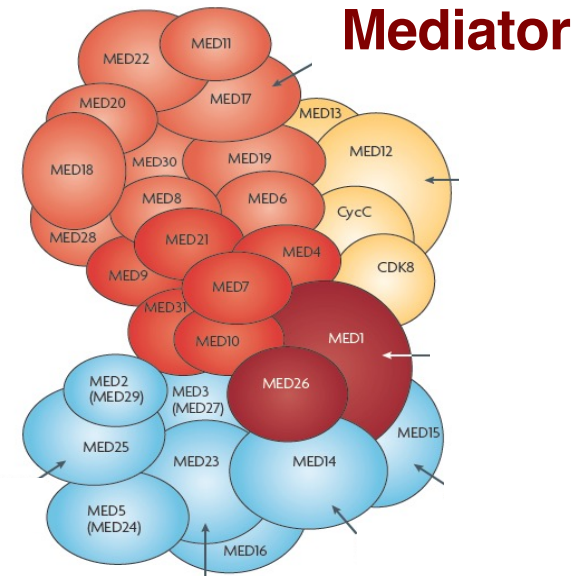
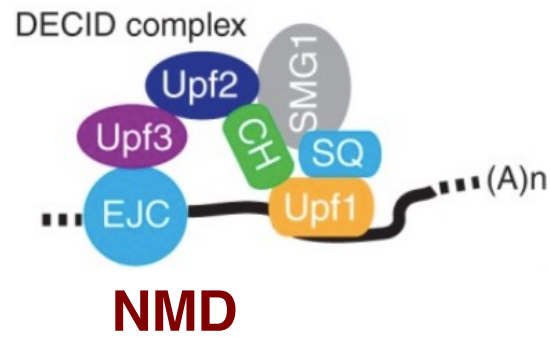
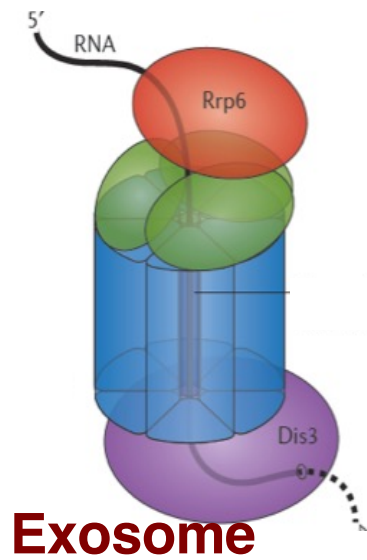
RNA granules

RNA decay

Institute of Genetics and Biotechnology
University of Warsaw



RNA enzymes and complexes



RNA processing and decay machinery: RNases

Protein	Function	Characteristics
<u>Exonucleases 5'→3'</u>		
Xrn1	cytoplasmic, mRNA degradation	processive
Rat1/XRN2	nuclear, pre-rRNA, sn/snoRNA, pre-mRNA processing and degradation	
Rrp17/hNOL12	nuclear, pre-rRNA processing	
<u>Exosome 3'→5' multisubunit exo/endo complex</u>		
Rrp44/Dis3	catalytic subunit	subunits organized as in bacterial PNPase Exo/PIN domains, processive
Rrp4, Rrp40	pre-rRNA, sn/snoRNA processing, mRNA degradation participates in NMD, ARE-dependent, non-stop decay	
Rrp41-43, 45-46		
Mtr3, Ski4		
Mtr4	nuclear helicase cofactor	DEAD box
Rrp6 (Rrp47)	nuclear exonuclease (Rrp6 BP, cofactor)	RNase D homolog, processive
Ski2,3,7,8	cytoplasmic exosome cofactors. SKI complex	helicase, GTPase
<u>Other 3'→5' and 5'→3'</u>		
Rex1-4	3'-5' exonucleases, rRNA, snoRNA, tRNA processing	RNase D homolog
DXO	5'-3' exonuclease in addition to decapping	
ERI1	3'-5' exonuclease, rRNA processing, histone mRNA decay	
<u>mtEXO 3'→5'</u> mitochondrial degradosome RNA degradation in yeast		
Suv3/ Dss1	helicase/ 3'-5' exonuclease	DExH box/ RNase II homolog
<u>Deadenylation</u>		
Ccr4/NOT/Pop2	major deadenylase complex (Ccr, Caf, Pop, Not proteins)	Ccr4- Mg ²⁺ dependent endonuclease
Pan2p/Pan3	additional deadenylases (polyA tail length)	RNase D homolog, poly(A) specific nuclease
PARN	mammalian deadenylase	RNase D homolog, poly(A) specific nuclease
<u>Endonucleases</u>		
RNase III		
-Rnt1	pre-rRNA, sn/snoRNA processing, mRNA degradation	dsRNA specific
-Dicer, Drosha	siRNA/miRNA biogenesis, functions in RNAi	PAZ, RNA BD, RNase III domains
Ago2 Slicer	mRNA cleavage in RNAi	
SMG6	mRNA cleavage in NMD	PIN domain
RNase P	5' tRNA end processing	RNP complex
RNase MRP	pre-rRNA processing	RNP complex, similar to RNase P
RNase L	rRNA degradation in apoptosis	oligo 2-5A dependent (ppp(A ₂ 'p) _n A)
ELAC2/Trz1	3' tRNA endonuclease	PDE motif and Zn ²⁺ binding motif
Utp24 Nob1 Las1	pre-rRNA processing at sites A0, D and C2	

Eukaryotic auxiliary decay factors

Protein

Function / Characteristics

5' → 3' decay: decapping

Dcp1/Dcp2	Dcp2- pyrophosphatase catalytic activity, Nudix domain, Dcp1- protein binding
Hedls/Ge-1/Edc4	decapping cofactor, WD40 domain
Edc1,2,3	decapping enhancers, stimulate cap binding/catalysis, Edc1-2 (yeast), Edc3 (all eukaryotes)
Dhh1	DexD/H ATPase, decapping activator by translation repression
Lsm1-7	decapping activator, heptameric complex, binds mRNA 3' end-U rich tracts
Pat1	decapping activator by translation repression
DXO	pyrophosphohydrolase, 5' decapping endonuclease, deNADding, 5'OH hydrolase

TRAMP complex: exosome cofactors, nuclear RNA QC, polyadenylation-dependent degradation.

Trf4/Trf5 (hTRF4-2)	nuclear alternative poly(A) polymerases
Mtr4 (hMTR4)	DEAD box helicase
Air1/Air2 (ZCCHC7)	RNA binding proteins

NEXT and PAXT complexes: exosome cofactors, nuclear RNA QC

hMTR4	DEAD box helicase
RMB7/ZCCHC8	NEXT RNA binding proteins
ZFC3H1	PAXT RNA binding protein
PABPN1	PAXT nuclear polyA binding protein

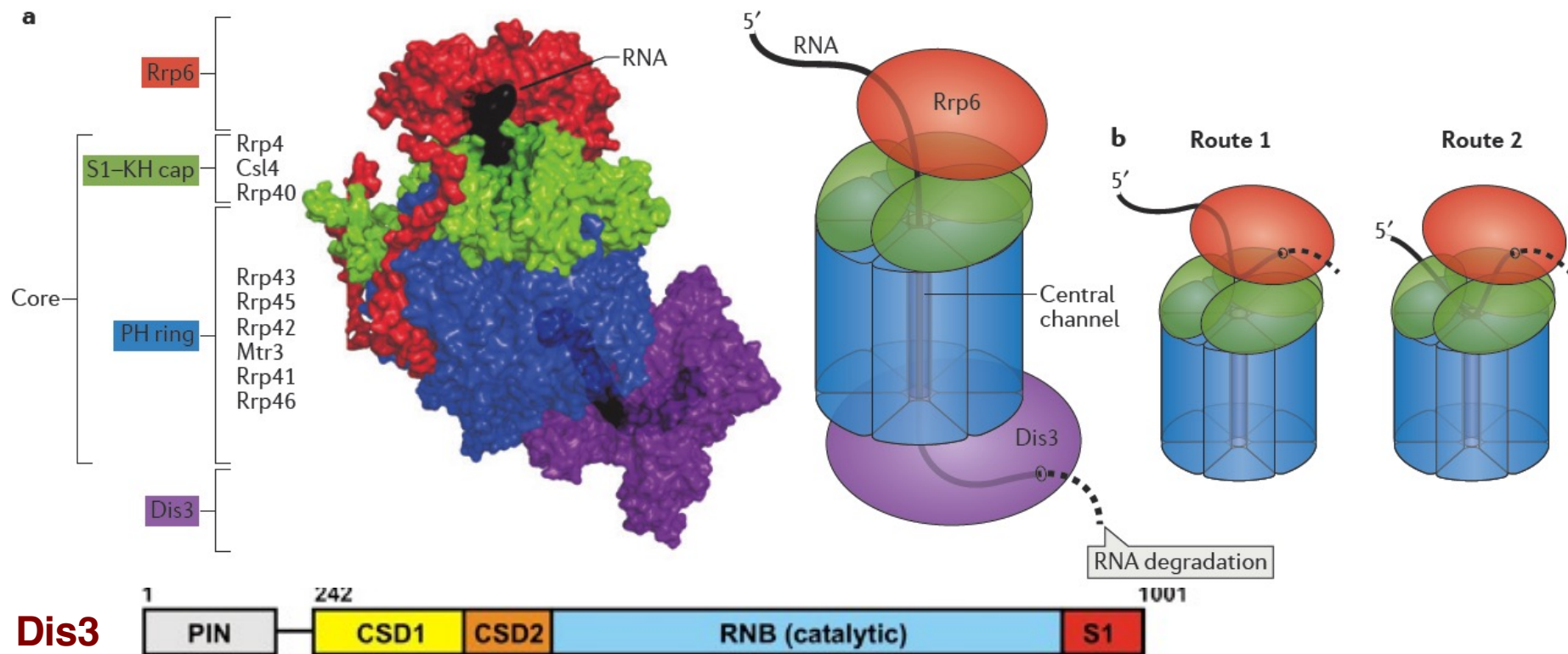
Nrd1-Nab3-Sen1 complex: PolII termination of ncRNAs, TRAMP-dependent degradation

Nrd1	Pol II C-terminal domain (CTD) binding, RNA binding
Nab3	RNA binding
Sen1	RNA helicase

CBCA-NEXT, CBCA-PAXT and RESTRICTOR complexes: nuclear RNA QC

CBC	CBCA	nuclear cap binding complex
ARS2		RNA binding, Pol II transcription, termination, RNA decay
ZC3H18		NEXT, zinc finger protein
ZFCH1		PAXT nuclear polyA binding protein
ZC3H4, WDR82		RESTRICTOR Pol II termination, RNA Decay by NEXT and exosome complexes

EXOSOME: 3'→5' decay machinery



- 3'→5' exo/endo nuclease complex
- 10 core components (RNA BP)
- catalytically active exo hydrolytic **Dis3/Rrp44** (RNase II)
- **PIN** domain with endo activity
- nuclear cofactors- RNA BP Rrp47, nuclease **Rrp6** (RNase D), RNA helicase **Mtr4**
- cytoplasmic cofactors- **Ski2-3-8 complex** (RNA helicase Ski2), GTPase Ski7
- substrates- processing and/or degradation of almost all RNAs

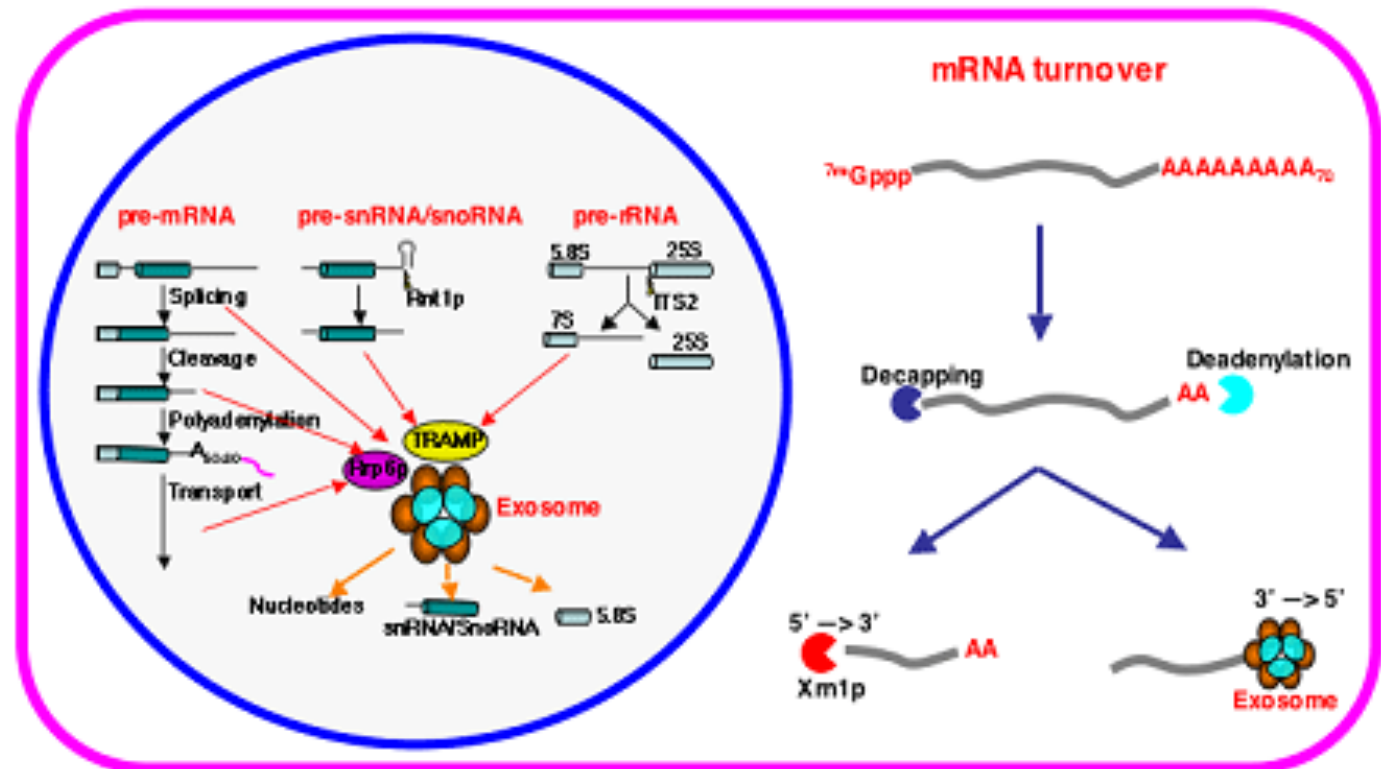
EXOSOME: 3'→5' decay machinery: functions

NUCLEAR: Rrp6 and core components have partly separate functions

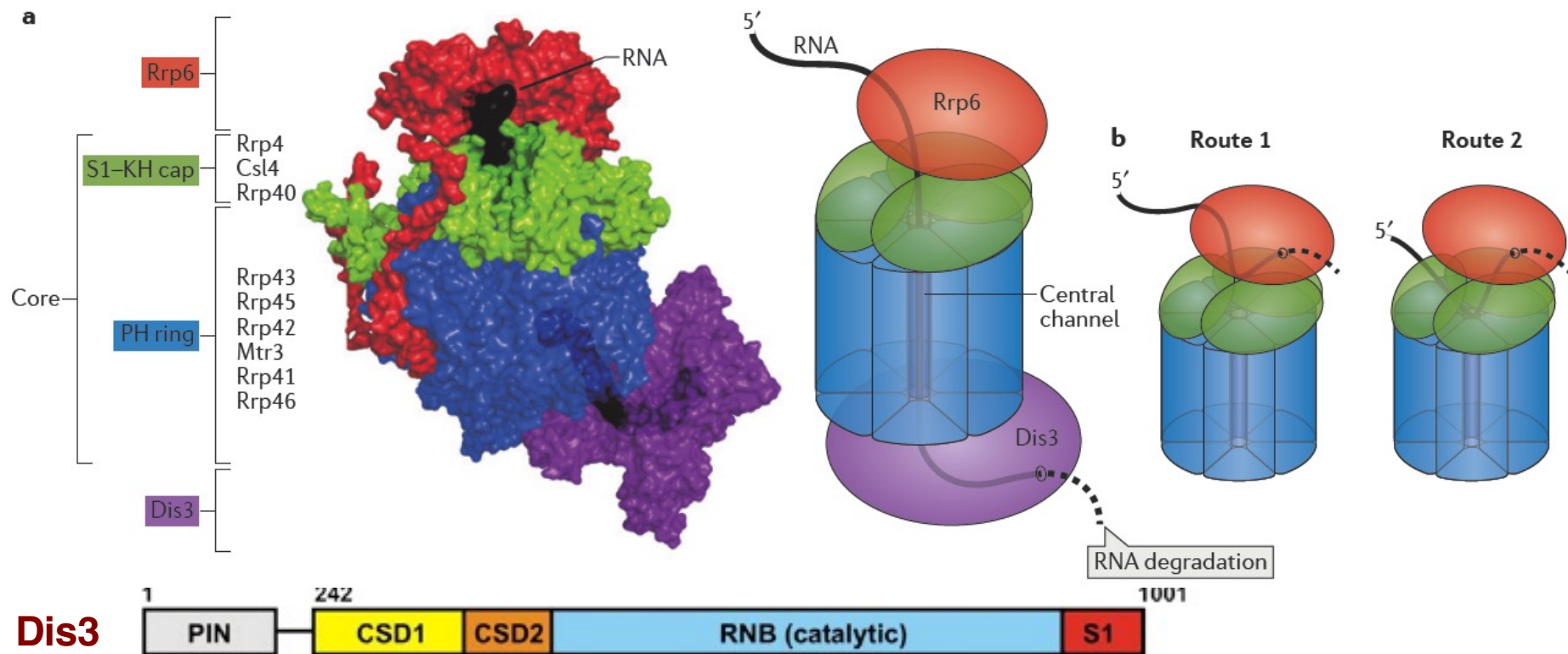
- 3' -end processing of 5.8S rRNA, sn/snoRNAs, tRNAs, SRP RNA
- degradation of pre-mRNAs, tRNAs, sn/snoRNAs
- degradation of other ncRNAs: CUTs, PROMPTS

CYTOPLASMIC:

- generic mRNA decay
- specialised mRNA decay pathways: NMD, NSD, NO-GO decay, ARE-dependent decay



EXOSOME: 3'→5' decay machinery



- 3'→5' exo/endo nuclease complex
- 10 core components (RNA BP)
- catalytically active exo hydrolytic **Dis3/Rrp44** (RNase II)
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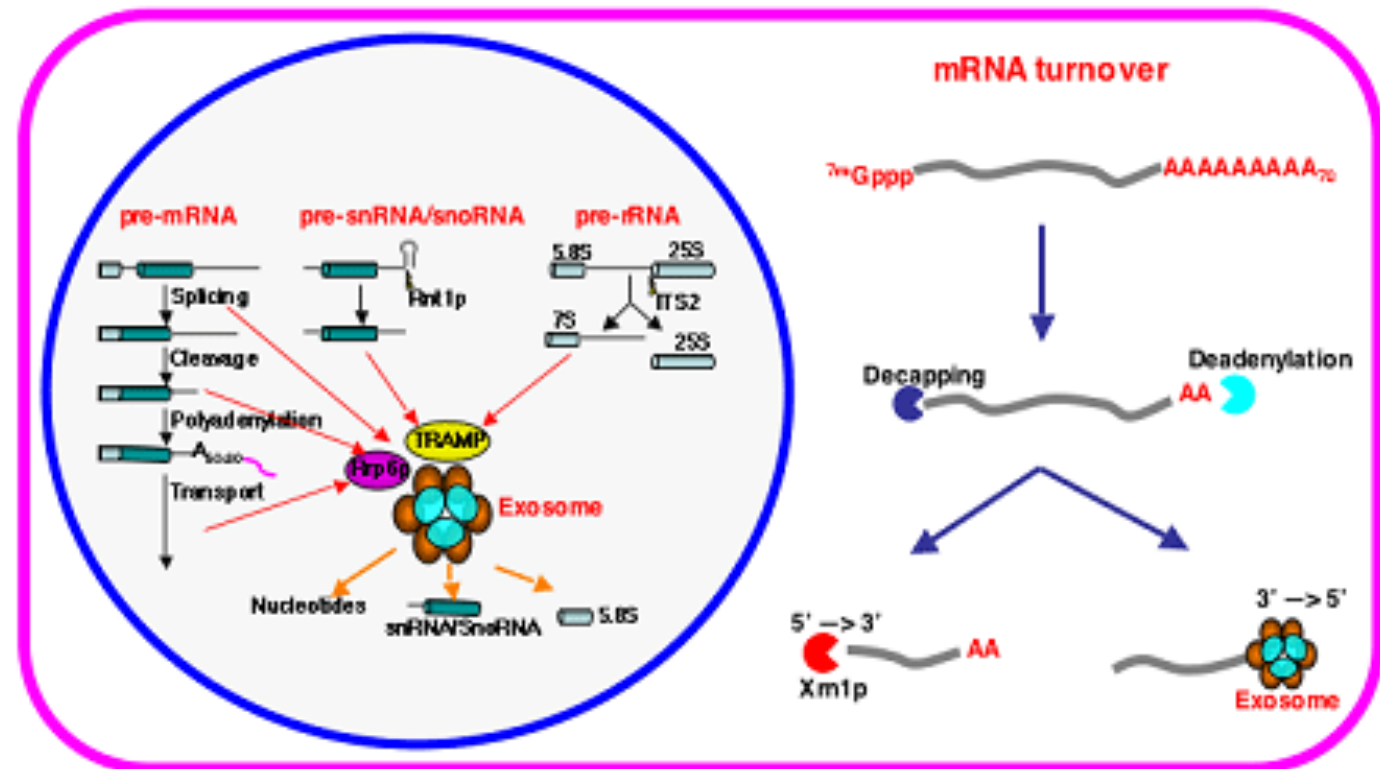
EXOSOME: 3'→5' decay machinery: functions

NUCLEAR: Rrp6 and core components have partly separate functions

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- degradation of other ncRNAs: CUTs, PROMPTS

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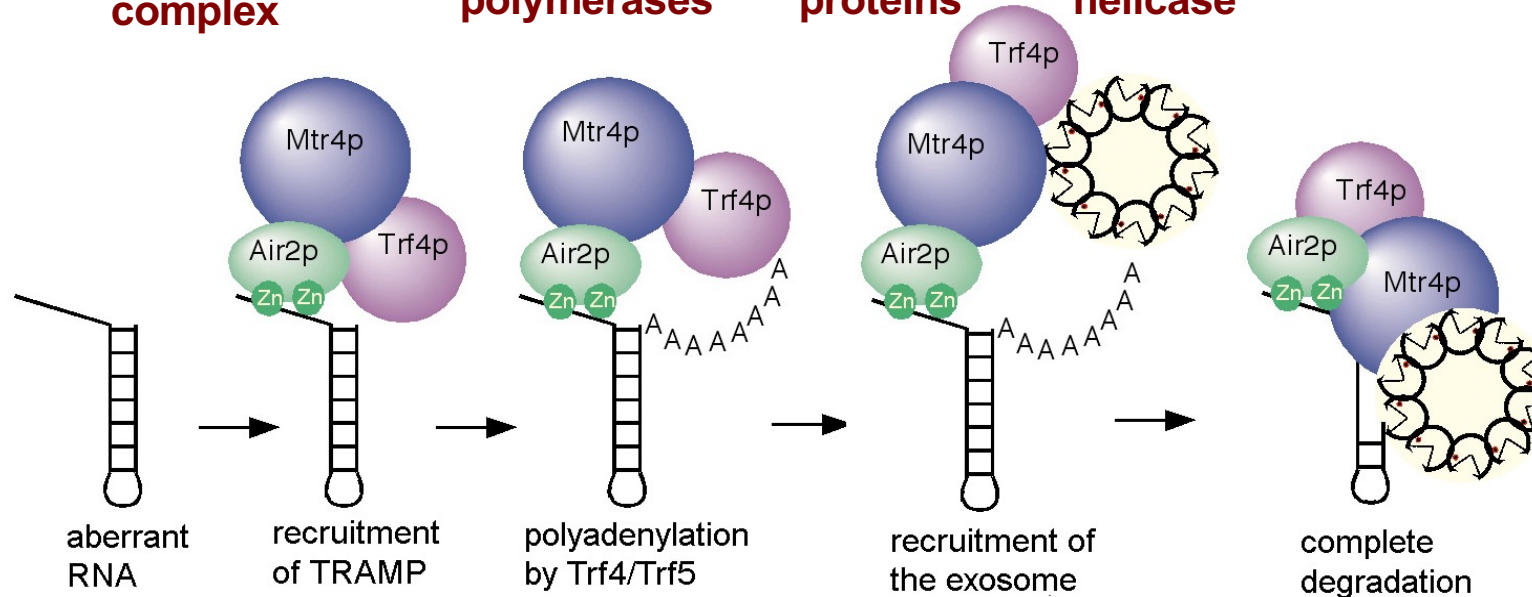
- generic mRNA decay
- specialised mRNA decay pathways: NMD, NSD, NO-GO decay, ARE-dependent decay



TRAMP – exosome cofactor

yeast

TRAMP = Trf4/5 + Air1/2 + Mtr4
 polyadenylation complex poly(A) polymerases RNA binding proteins RNA DEVH helicase



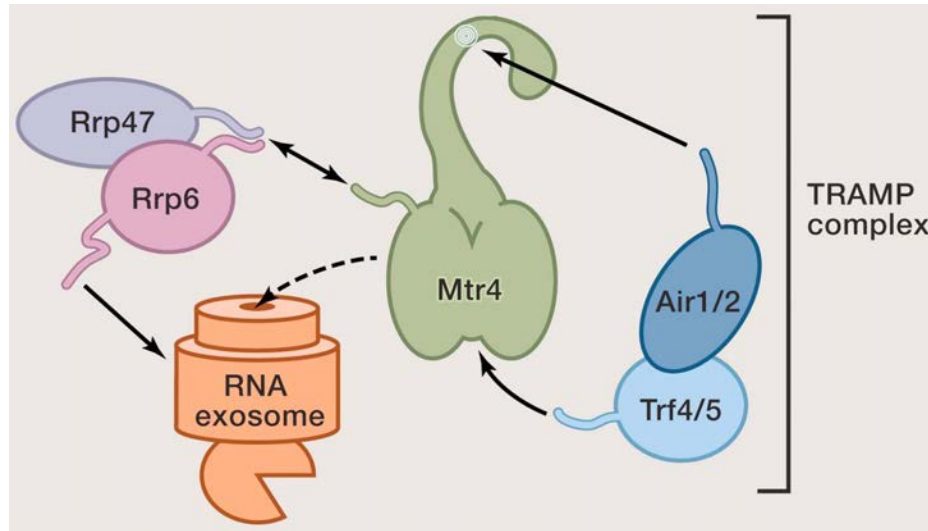
Polyadenylation-mediated nuclear discard pathway for defective RNAs

- hypomodified tRNAs, pre-tRNAs
- ncRNAs:
 - sn/snoRNAs, rRNAs
 - CUTs (Cryptic Unstable Transcripts)
- some mRNAs

TRAMP interacts with

- exosome via Mtr4
- Nrd1/Nab3/Sen1 complex

TRAMP + Exosome = nuclear RNA surveillance



Mtr4 – DEAH box RNA helicase

Air1/2 – RNA binding proteins

Trf4/5 – poly(A) polymerases

Substrate specificity conferred by Trf4/5

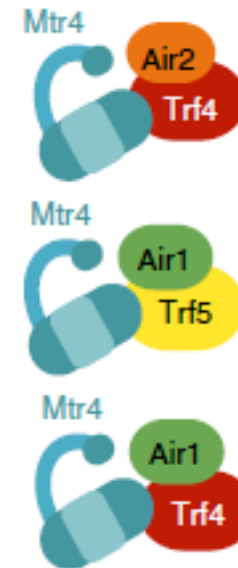
Air1/2 are highly redundant

SUBSTRATES

TRAMP 4-2: mRNA, ncRNA

TRAMP 5-1: pre-rRNA

TRAMP 4-1: mRNA, introns



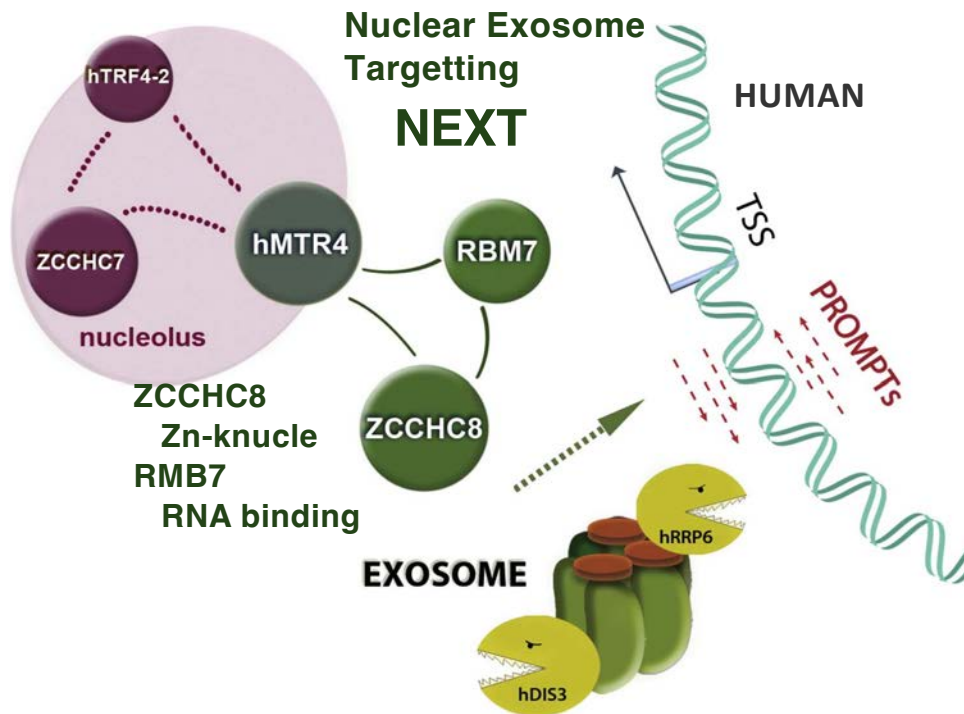
TRAMP

- interacts with the exosome via Mtr4 - role in degradation
- role in sn/snoRNA 3' end processing together with the exosome
- interacts with Nrd1/Nab3 complex - role in ncRNA Pol II termination
- role in transcription silencing in *S. cerevisiae* and *S. pombe* (Cid14)

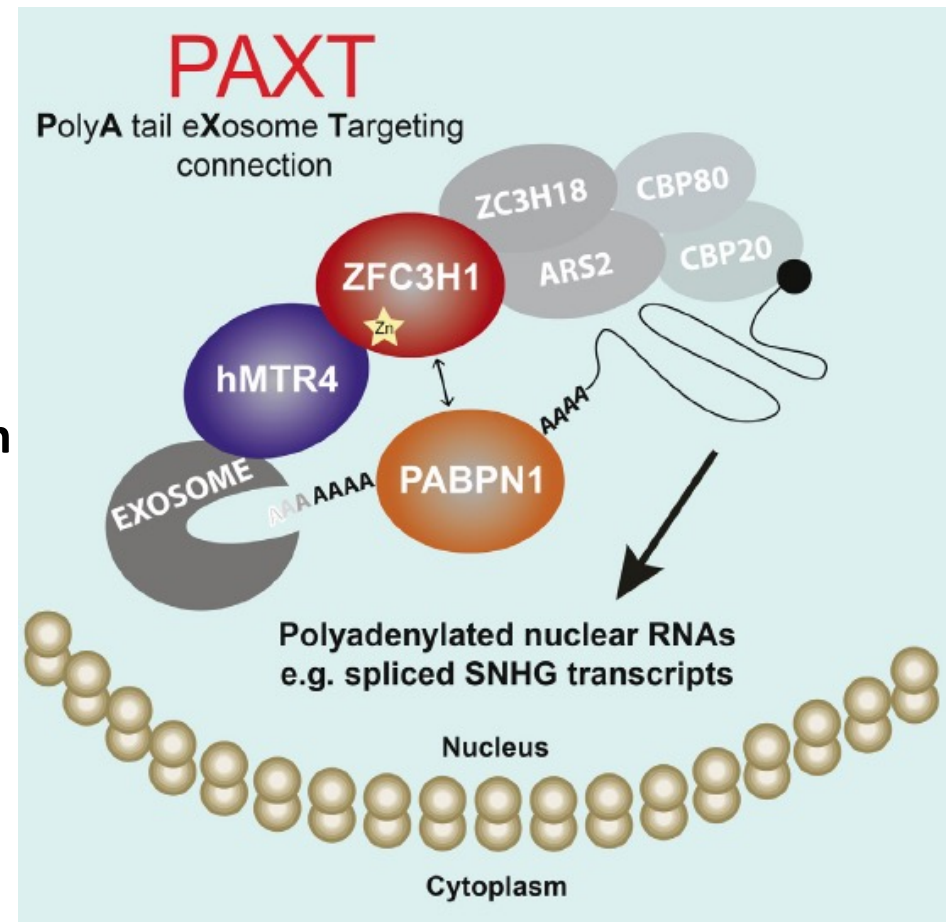
NEXT and PAXT - exosome cofactors

mammals

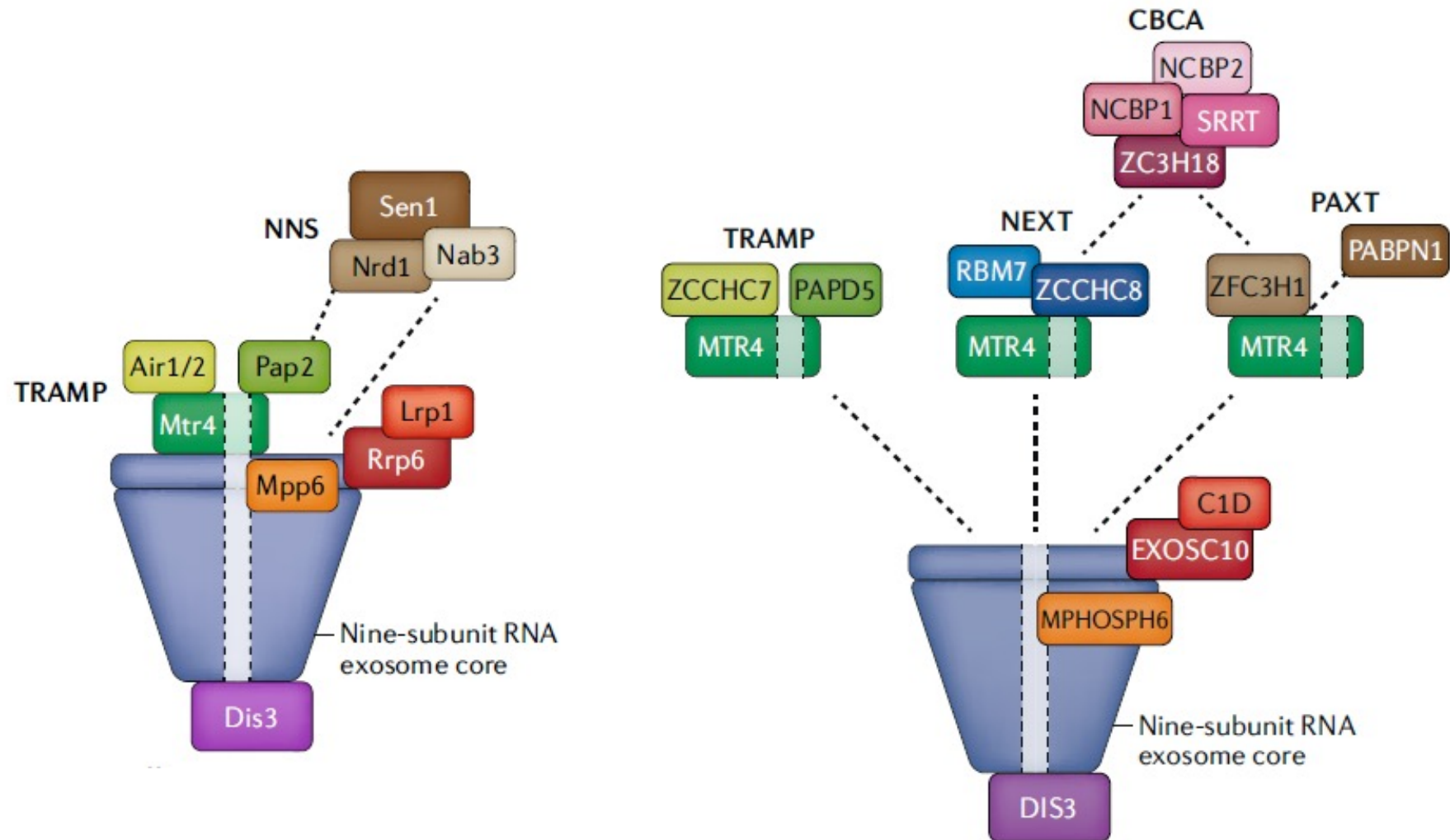
MTR4- associated complexes



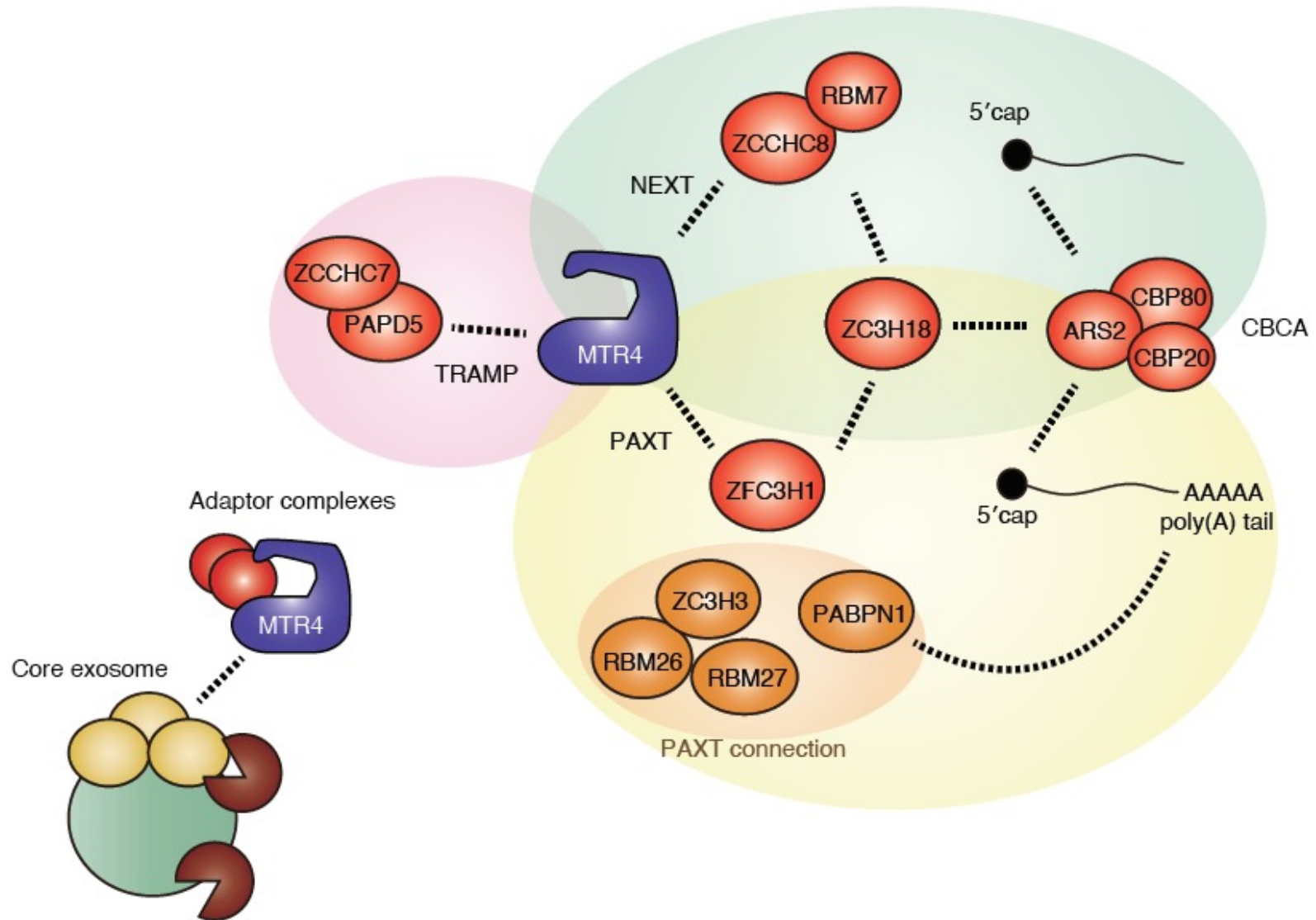
- ZFC3H1 (Zn-knuckle protein) links MTR4 with PABPN1 in PAXT
- ZFC3H1/PABPN1 and RBM7/ZCCHC8 interact with MTR4 in a mutually exclusive manner
- PAXT and NEXT direct distinct RNA species for nuclear exosome degradation
- PAXT targets tend to be longer and more extensively polyadenylated than NEXT targets



EXOSOME with TRAMP, NEXT and PAXT



EXOSOME with TRAMP, NEXT and PAXT

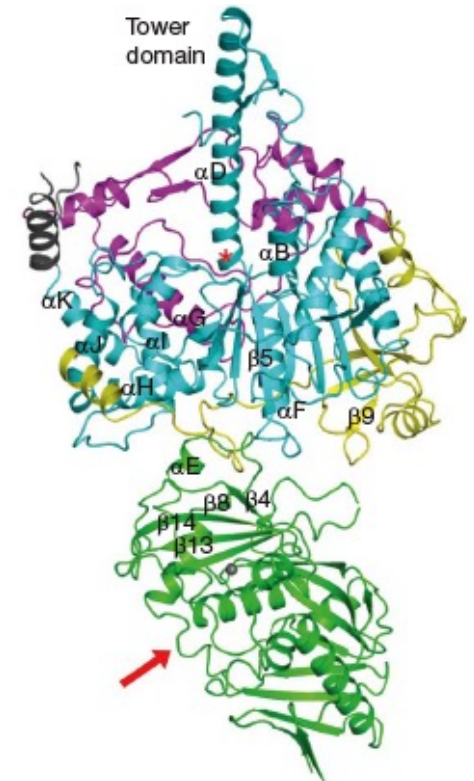


XRN family: 5' → 3' processive exonucleases



Kastenmayer and Green, 2000, PNAS

Crystal structure of *S. pombe* Rat1/Rai1 complex



Xiang et al, 2009, Nature

NUCLEAR Rat1/XRN2

with Rai1 activator (5' -ppp pyrophosphohydrolase and phosphodiesterase-decapping nuclease)

- 5' -end processing of 5.8S and 25S rRNAs, snoRNAs
- degradation of pre-mRNAs, tRNAs, sn/snoRNAs
- degradation of some ncRNAs: CUTs
- transcription termination of Pol I and II (*torpedo mechanism*)

CYTOPLASMIC XRN1

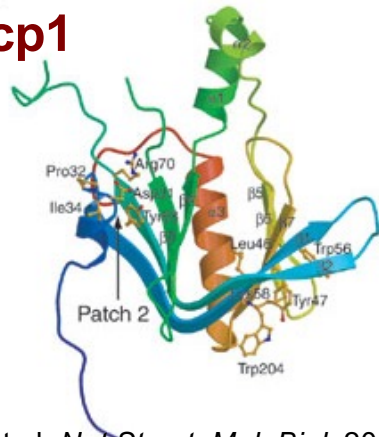
- generic mRNA decay
- specialised mRNA decay pathways: NMD, NSD, NO-GO decay, ARE-dependent decay
- degradation of miRNA-dependent mRNA cleavage products (*in plants*)
- degradation of some ncRNAs: CUTs, SUTs, XUTs

XRN1 and Rat1/XRN2 have deNADding and deFADding activity

Sharma et al, Nat Comm 2022; NAR 2022

DCP/NUDT- decapping enzymes

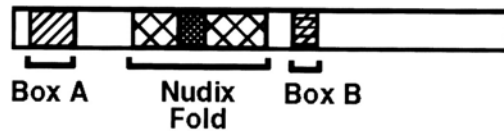
Dcp1



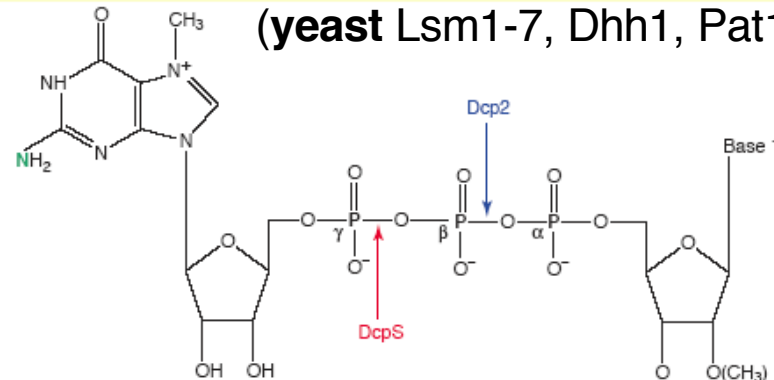
She et al. *Nat. Struct. Mol. Biol.*, 2004

- Dcp1/Dcp2 complex participates in mRNA 5' decay
- catalyses the reaction $m^7GpppX\text{-mRNA} \rightarrow m^7GDP + 5'p\text{-mRNA}$
- Dcp2 is the catalytic subunit (pyrophosphatase Nudix domain)
- Dcp1 is required for activity *in vivo*, interacts with other proteins
- Dcp1/Dcp2p is regulated by Pab1 and activating factors

Dcp2



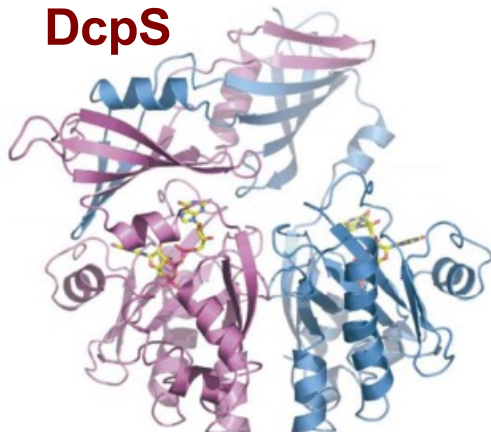
Wang et al. *PNAS*, 2002



(yeast *Lsm1-7*, *Dhh1*, *Pat1*, *Edc1-3*, *Upf1-3*)

NUDT proteins (22): *in vivo* decapping **Nudt16, Nudt3 (mammals)**
in vivo deNADding **Nudt12 (mammals)**

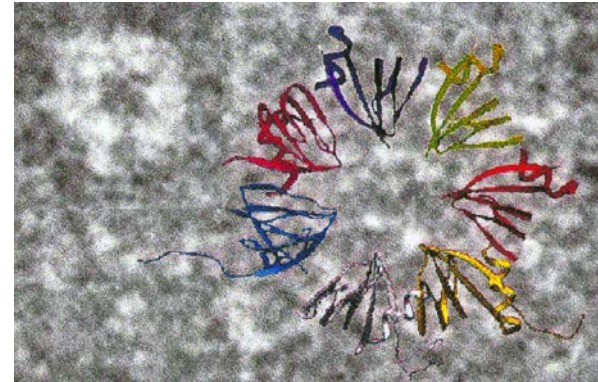
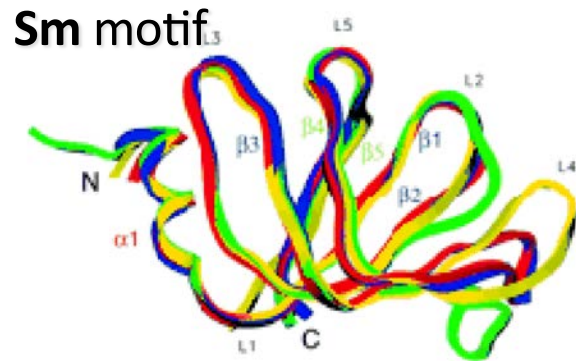
DcpS



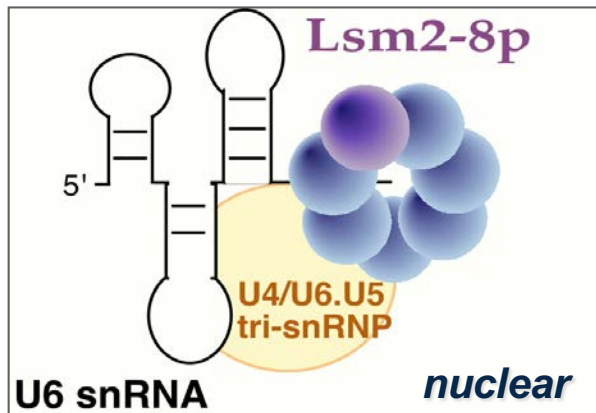
- DcpS: HIT pyrophosphatase („histidine triad” on the C-terminus)
 - catalyses the cleavage of $m^7GDP \rightarrow m^7GMP + P_i$ remaining after decapping during mRNA 5' decay
 - cooperates with the exosome during mRNA 3' decay
- ($m^7GpppX\text{-oligoRNA} \rightarrow m^7GMP + pp\text{-oligoRNA}$)
- functions as an asymmetric dimer

Gu et al., *M. Cell*, 2004

LSM proteins

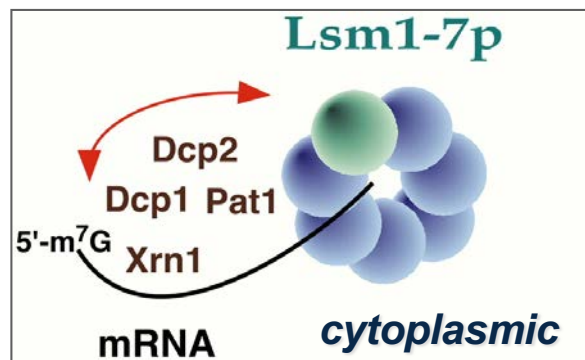


Achsel et al, EMBO J, 2001



Involved in pre-mRNA splicing

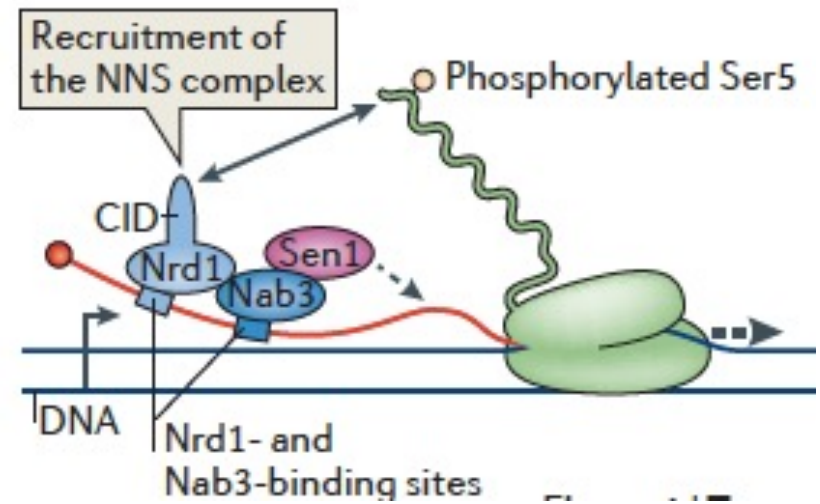
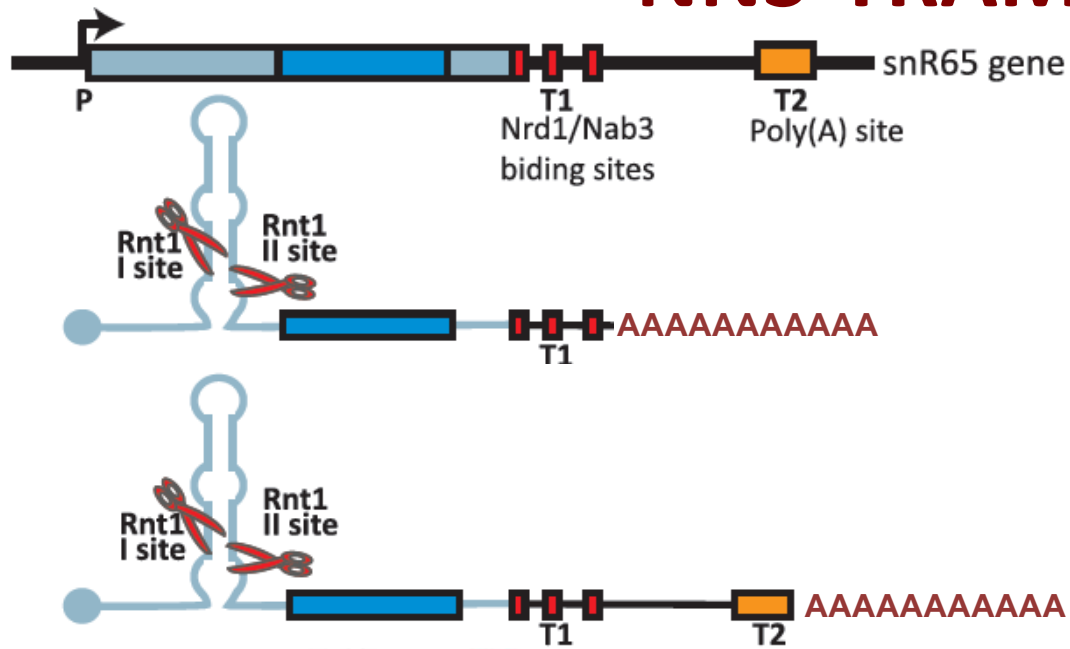
- associates with U6 snRNA
- required for U6 RNA accumulation and U6 snRNP biogenesis
- interacts with the U4/U6.U5 tri-snRNP



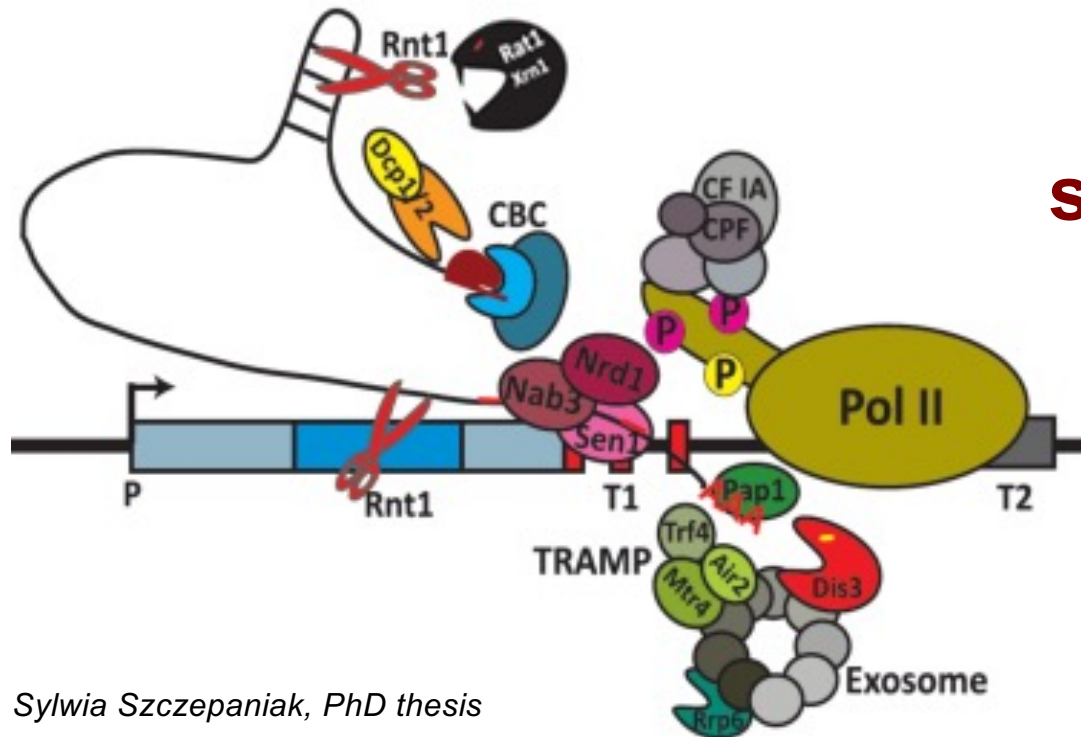
Functions in mRNA decapping and decay

- activator of decapping
- interacts with components of the mRNA decapping and degradation machinery (XRN, DCP, Pat1)

NNS-TRAMP-exosome



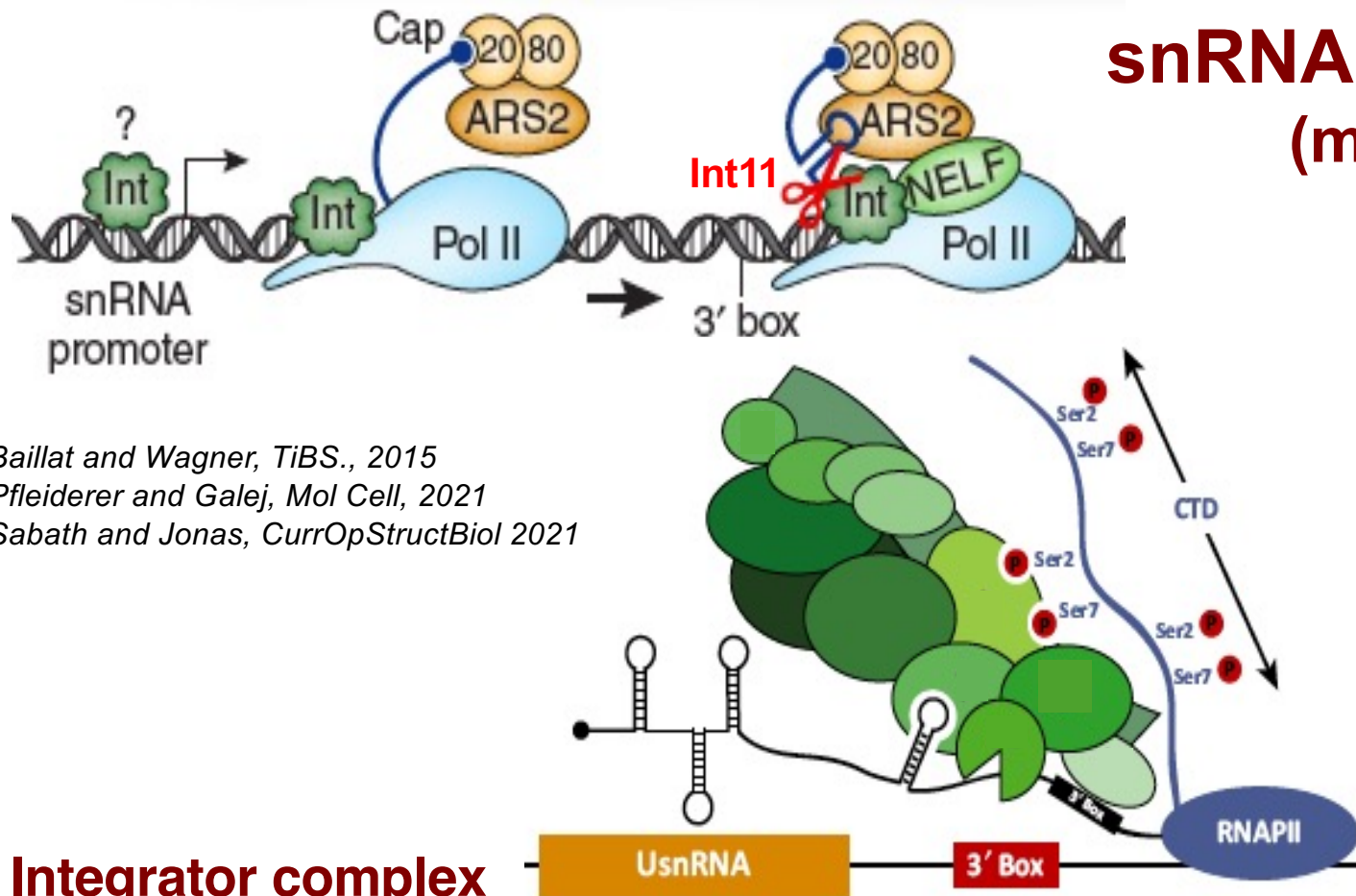
Poruua, Libri, Nat Rev Mol Cell Biol, 2015



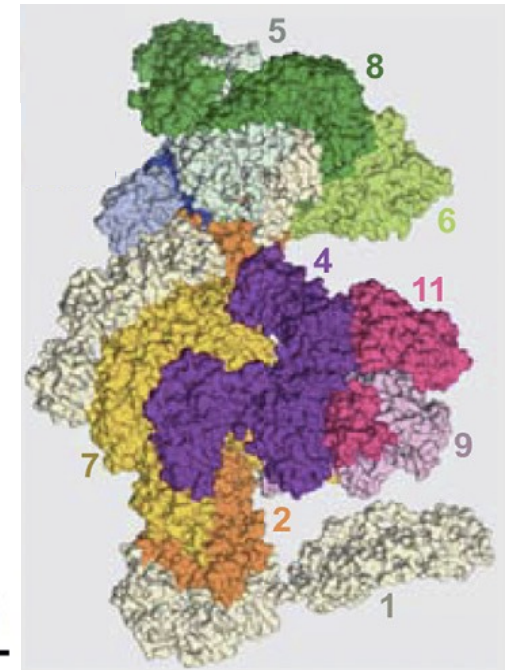
sn/snoRNA processing (yeast)

INTEGRATOR

snRNA processing (metazoa)



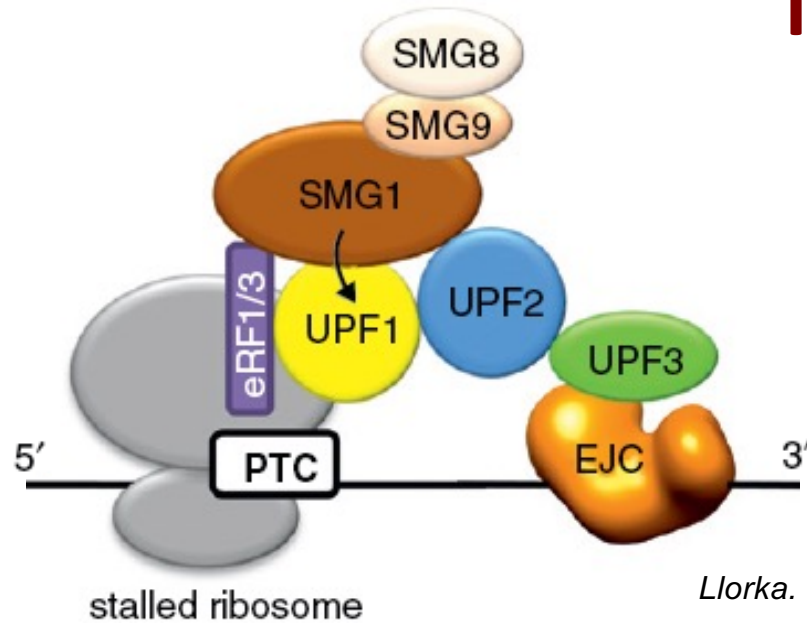
Baillat and Wagner, *TiBS.*, 2015
 Pfeleiderer and Galej, *Mol Cell*, 2021
 Sabath and Jonas, *CurrOpStructBiol* 2021



Integrator complex

- recruited contrancriptionally to snRNA promoter
- interacts with Pol II CTD (**Ser7-P/Ser2-P** dyad)
- cleaves pre-snRNA at 3'box (endonuclease **Int11**)
- involved in transcription termination at snRNA genes
- contributes to transcription termination at mRNA genes (intronless in particular)
- promotes transcription elongation by nascent transcript cleavage (PolII release)

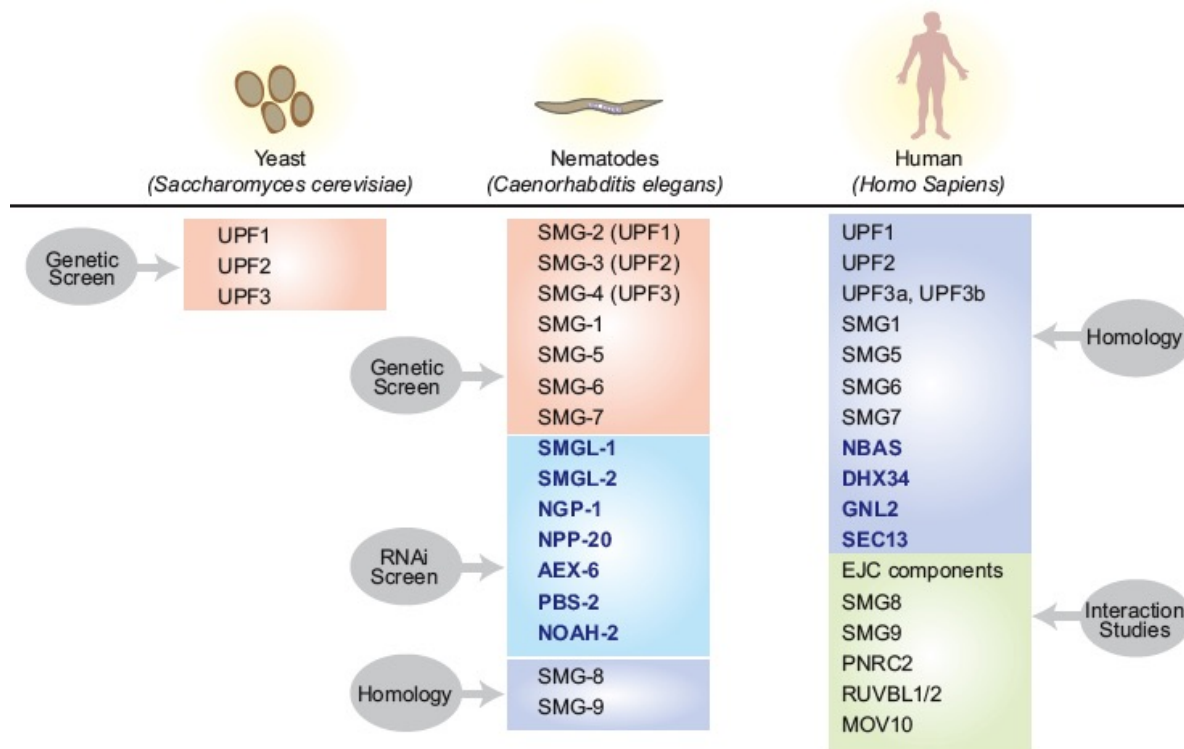
NMD factors



SURF complex
SMG1-UPFs-SMGs-
Release Factors

DECID (decay inducing)
phosphoSMG1-UPFs-EJC

Llorca. Cur. Op. Chem. Biol. 2013



Hug et al., NAR, 2016

XRN family: 5'→3' processive exonucleases



Kastenmayer and Green, 2000, PNAS

Crystal structure of *S. pombe*
Rat1/Rai1 complex



NUCLEAR

Rat1/XRN2 with Rai1 activator (5' -ppp pyrophosphohydrolase and phosphodiesterase-decapping nuclease)

- 5' -end processing of 5.8S and 25S rRNAs, snoRNAs
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- degradation of some ncRNAs: CUTs
- transcription termination of Pol I and II (*torpedo mechanism*)

CYTOPLASMIC XRN1

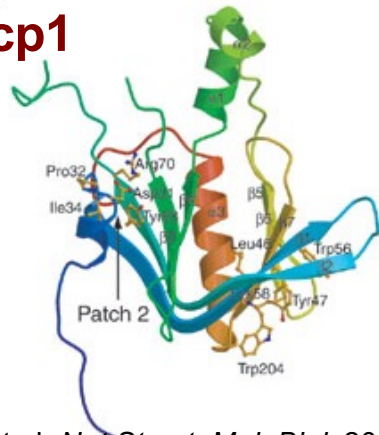
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- degradation of miRNA-dependent mRNA cleavage products (*in plants*)
- degradation of some ncRNAs: CUTs, SUTs, XUTs

Yeast Rat1 and Xrn1 have also deNADding activity

Xiang et al, 2009, Nature

DCP/NUDT- decapping enzymes

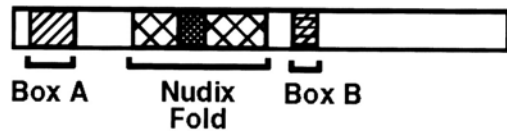
Dcp1



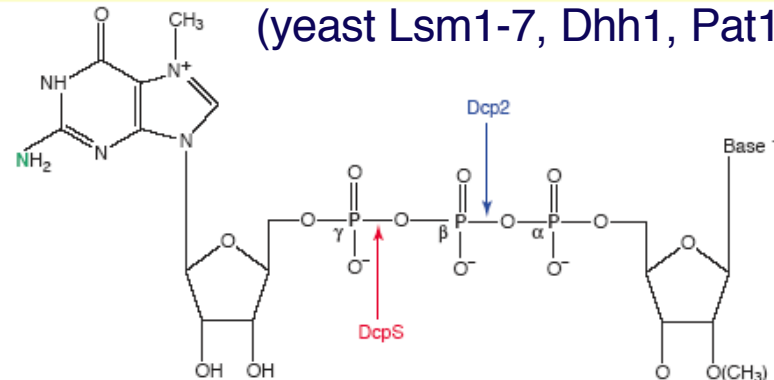
She et al. *Nat. Struct. Mol. Biol.*, 2004

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- Dcp1 is required for activity *in vivo*, interacts with other proteins
- Dcp1/Dcp2p is regulated by Pab1 and activating factors

Dcp2



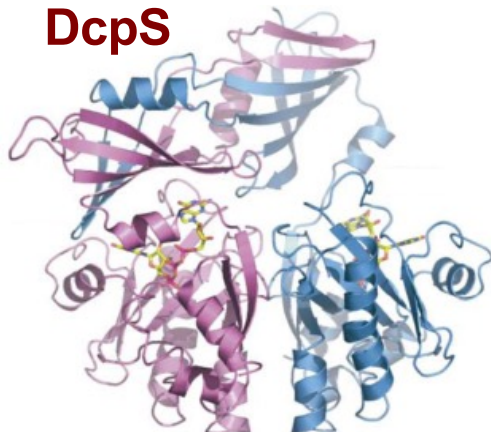
Wang et al. *PNAS*, 2002



(yeast *Lsm1-7*, *Dhh1*, *Pat1*, *Edc1-3*, *Upf1-3*)

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in vivo deNADding **Nudt12 (mammals)**

DcpS



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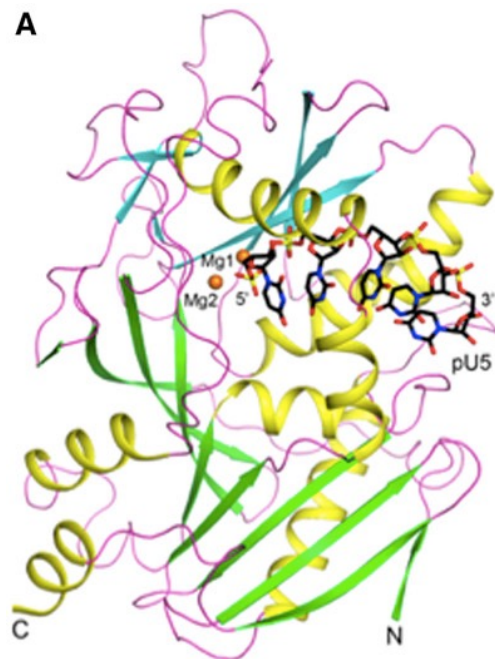
Gu et al., *M. Cell*, 2004

DXO/Rai1 family

Cellular activities

cap surveillance

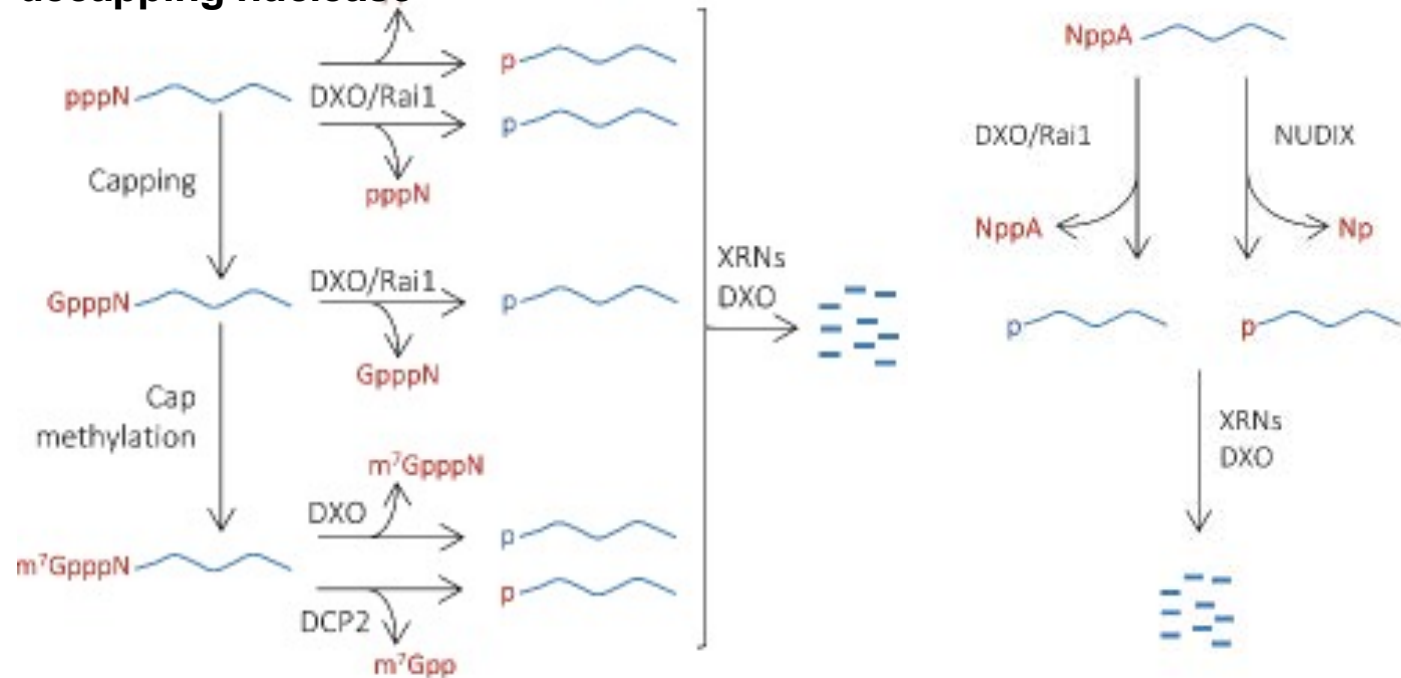
deNADding



pyrophosphohydrolase
decapping nuclease

5' -3' exonuclease

deNADding
nuclease



ACTIVITY	SUBSTRATE	MmDXO	At DXO1
5'-3' exoribonuclease	p-RNA	+++	+
Pyrophosphohydrolase	ppp-RNA	+++	-
Decapping (unmethylated cap)	Gppp-RNA	+++	-
Decapping (mature cap)	m ⁷ Gppp-RNA	+++	-
DeNADding	NppA-RNA	++++	+++

Additional activities:

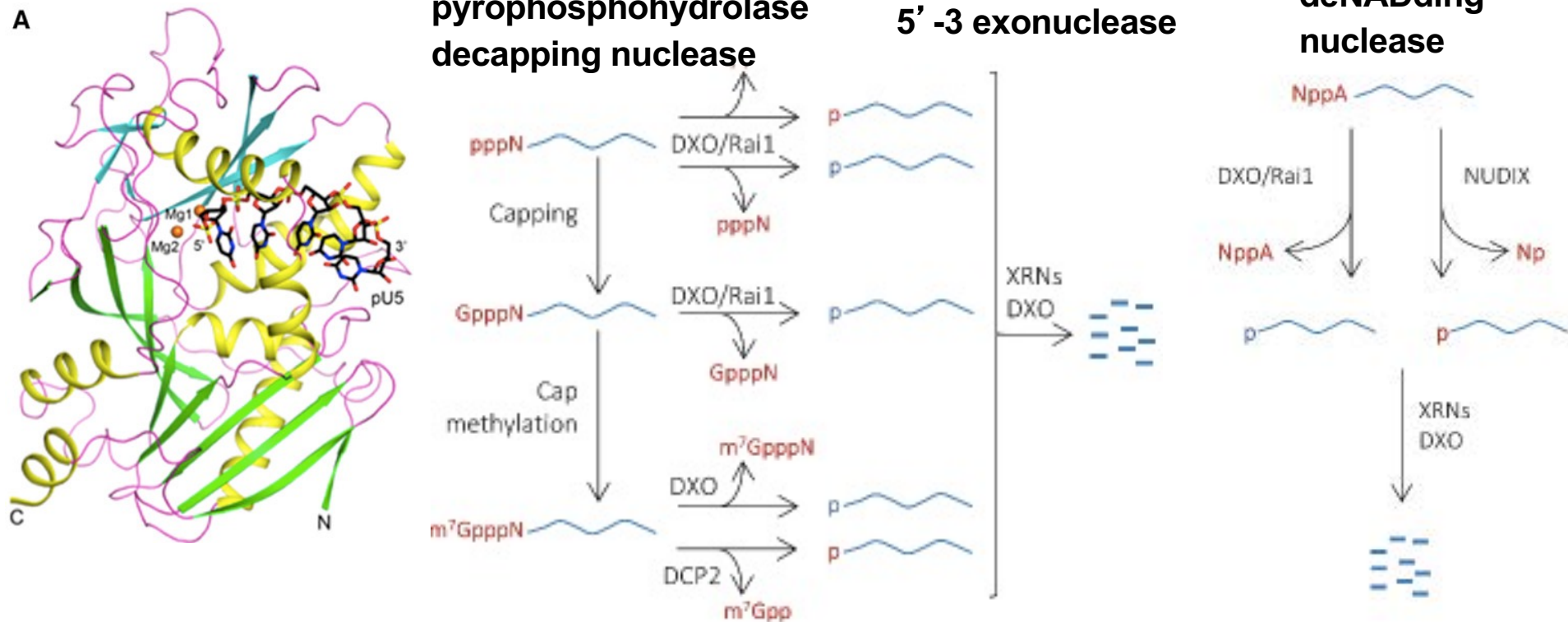
- 5' OH RNA hydrolase
- FAD and CoA decapping nuclease

DXO/Rai1 family

Cellular activities

cap surveillance

deNADding



ACTIVITY	SUBSTRATE	MmDXO	At DXO1
5'-3' exoribonuclease	p-RNA	+++	+
Pyrophosphohydrolase	ppp-RNA	+++	-
Decapping (unmethylated cap)	Gppp-RNA	+++	-
Decapping (mature cap)	m ⁷ Gppp-RNA	+++	-
DeNADding	NppA-RNA	++++	+++

Additional activities:

- 5' OH RNA hydrolase

- FAD and CoA

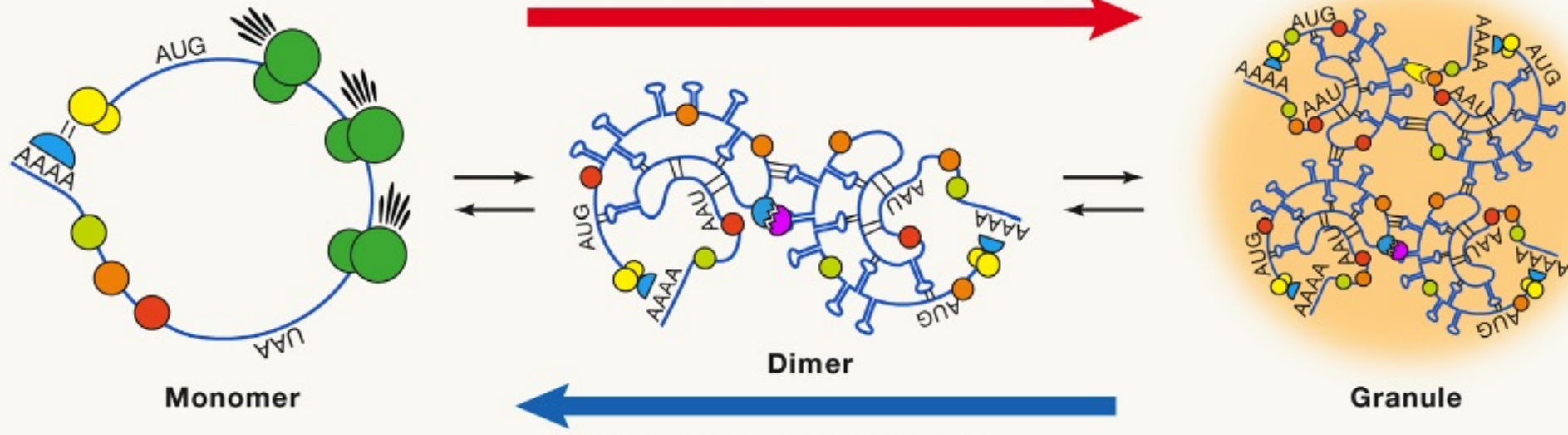
decapping nuclease

RNP granule assembly

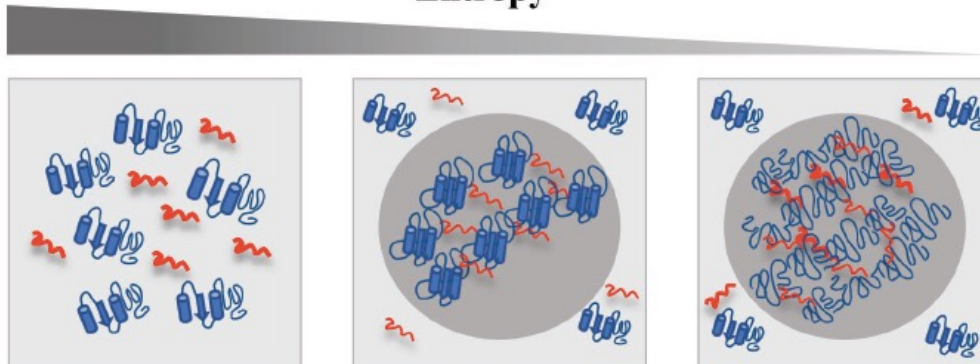
by protein-protein and RNA-RNA interactions

Assembly promoted by:

- Longer RNA length
- High local concentrations
- RNAs with increased ability to interact
- Multivalent RNA-binding proteins



Entropy



Energy

Phase transition

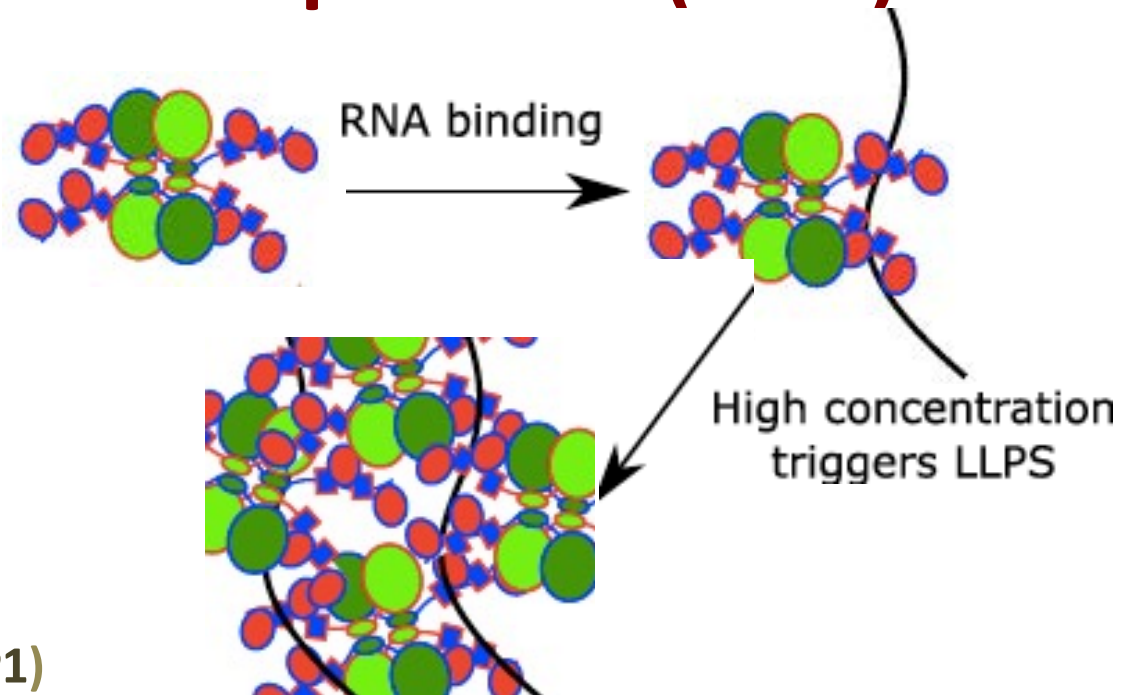
Droplets, MLOs (Membraneless Organelles)

Liquid-Liquid Phase Separation (LLPS)

Formed by unstructured protein domains around RNAs

IDR - Intrinsic Disordered Domains

PLD - Prion-Like Domains

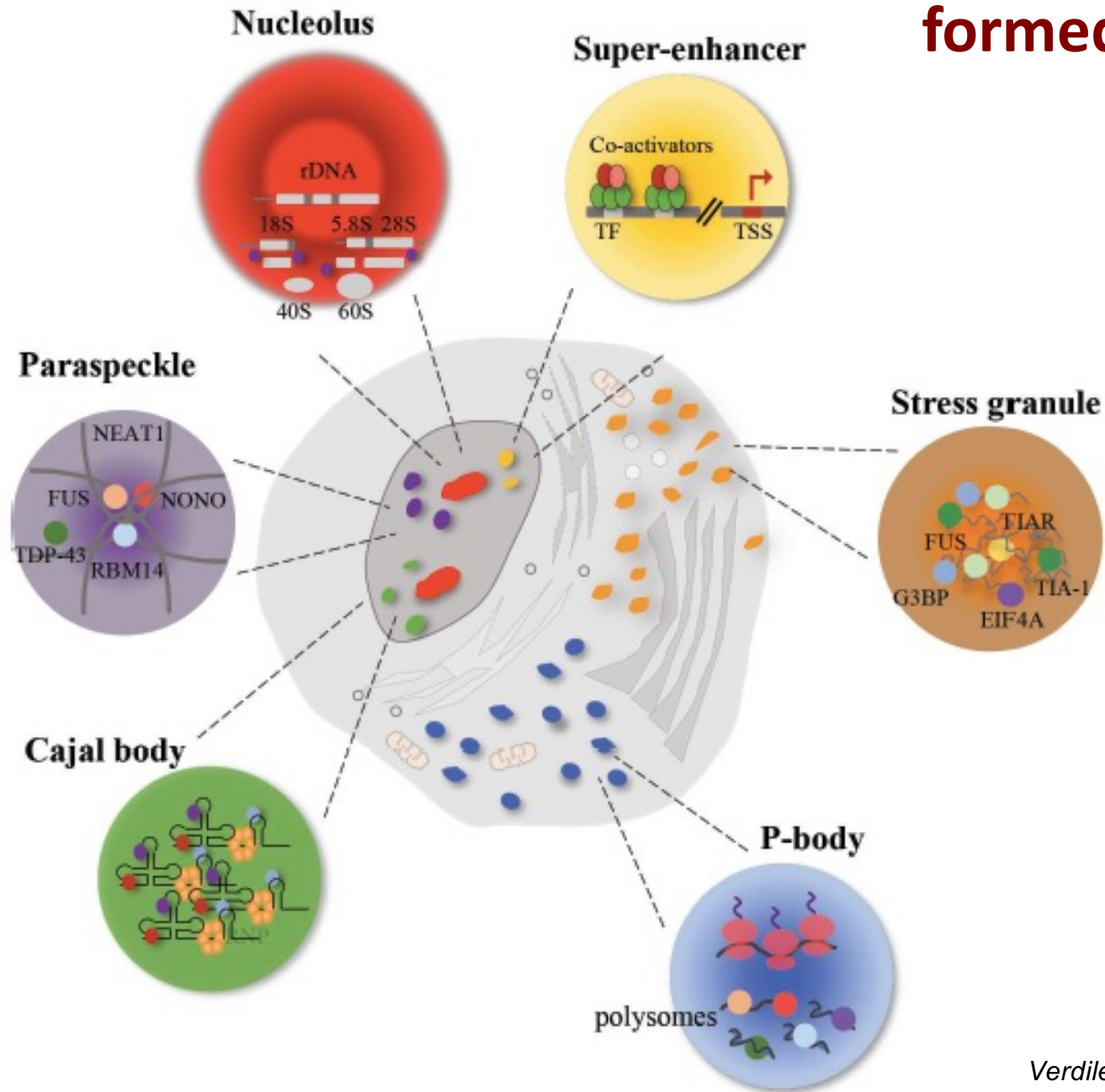


Organize several cellular processes:

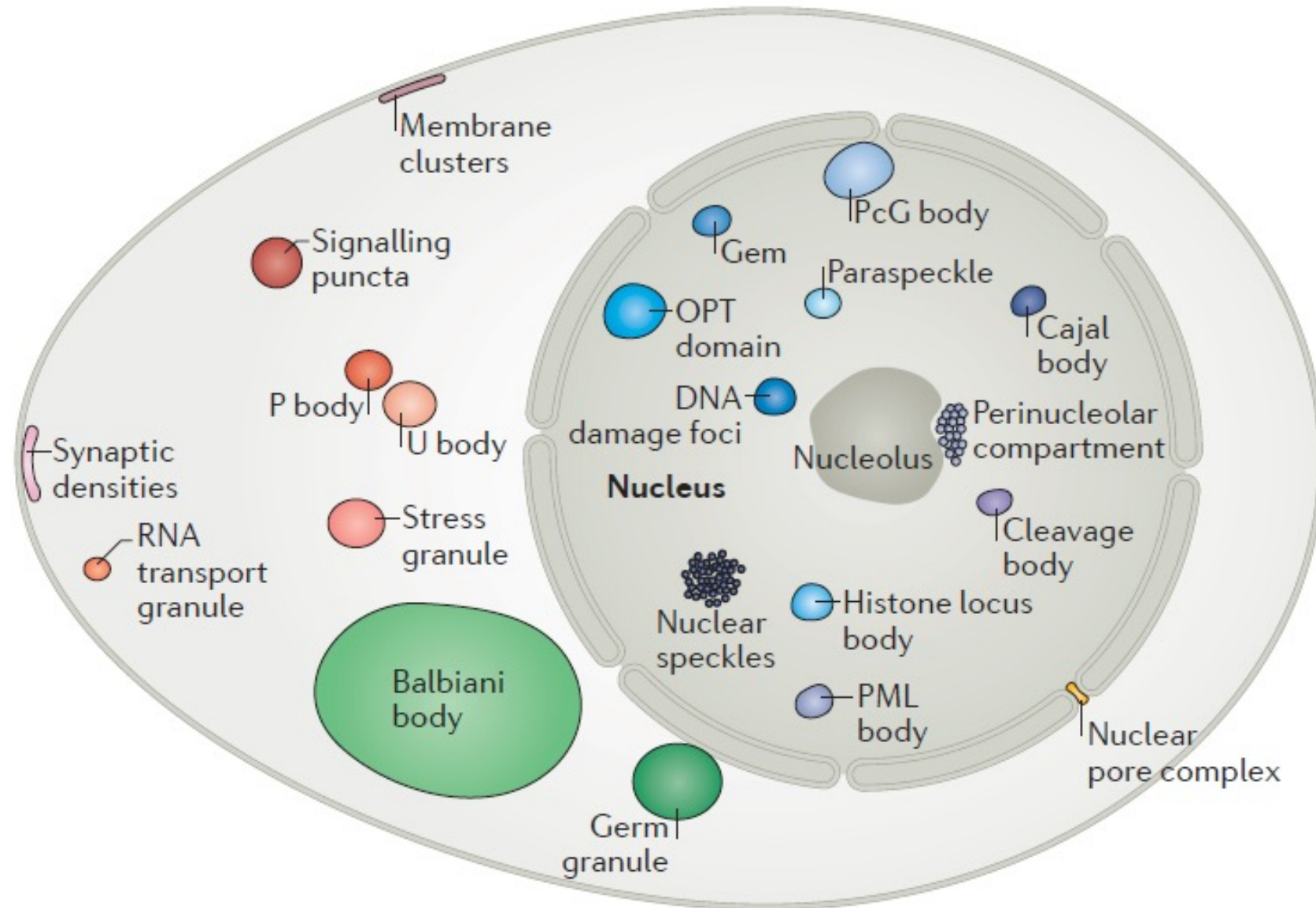
- Heterochromatin structure (HP1)
- Transcription (Mediator, Pol II CTD)
- Processing (nucleolus, spliceosome, SR proteins, Cajal bodies)
- RNA retention and storage
(Nuclear speckles, Paraspeckles, P-bodies, Stress Granules)
- RNA decay (degradosome)
- Protein modification and degradation (autophagosome, proteasome)

Membraneless Organelles

formed by LLPS

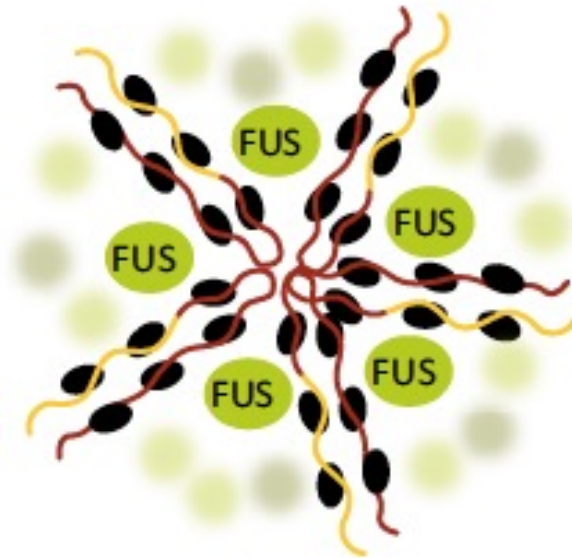
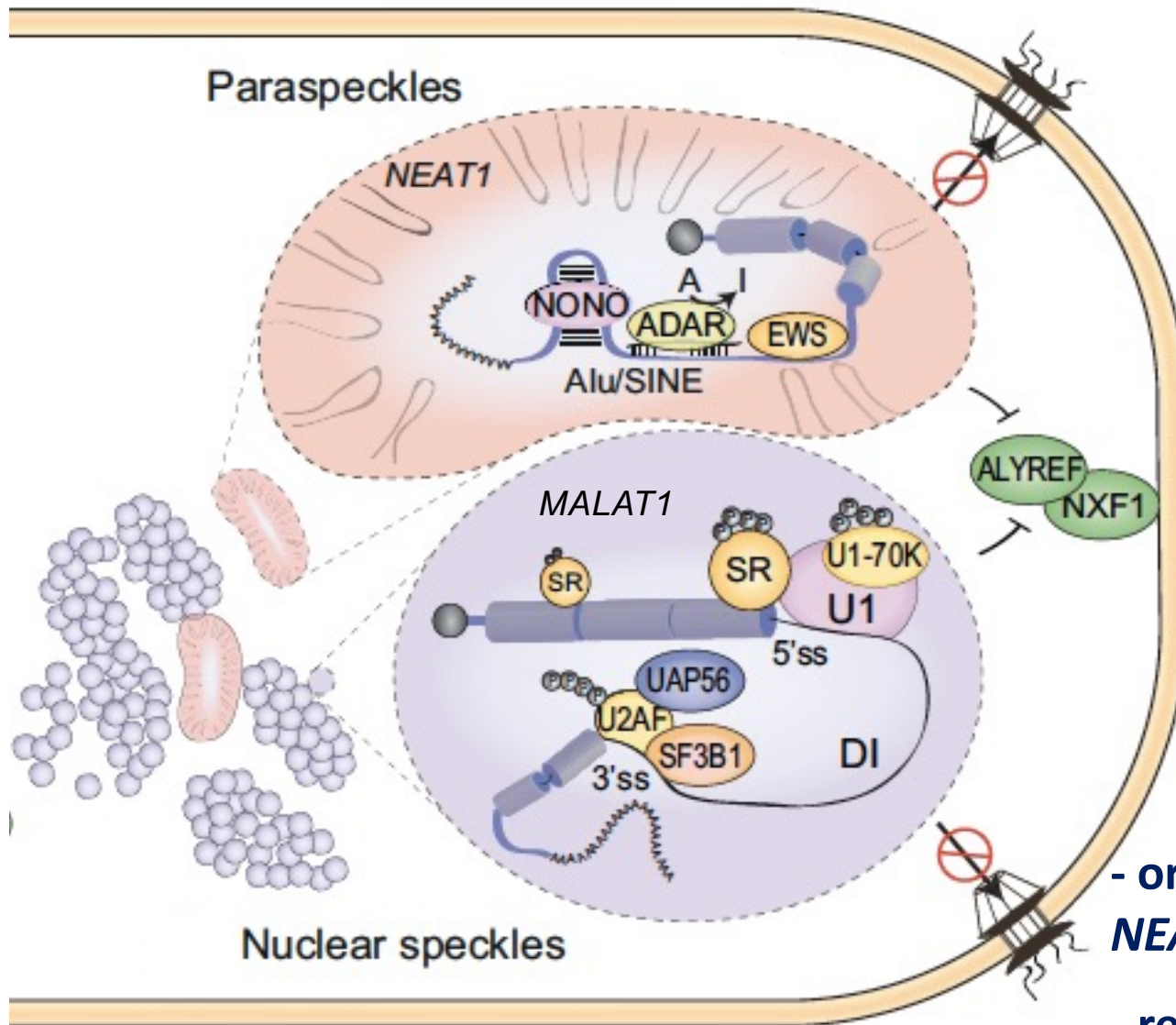


Cellular Condensates



Paraspeckles

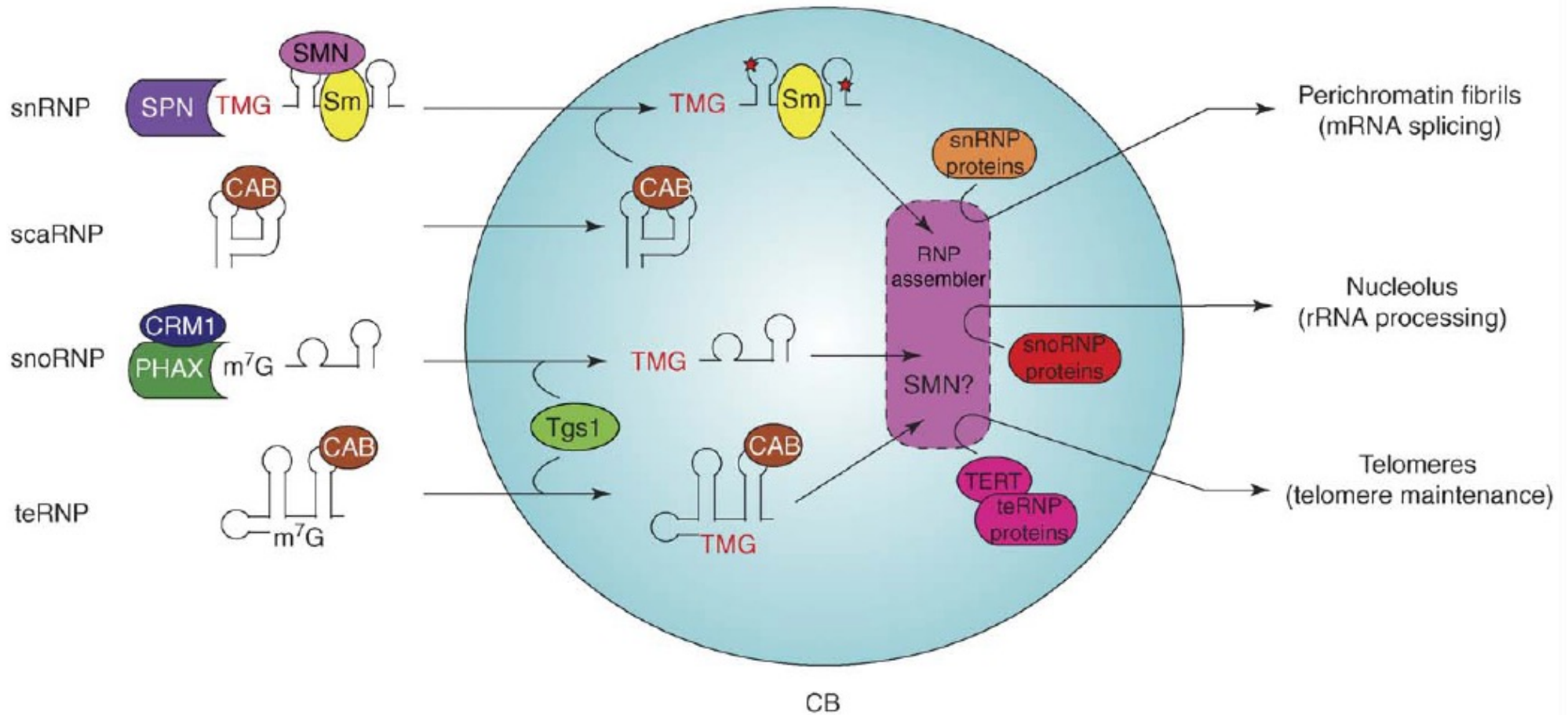
Nuclear speckles



- organized around lncRNAs:
NEAT1 (PS) or *MALAT1* (NS)

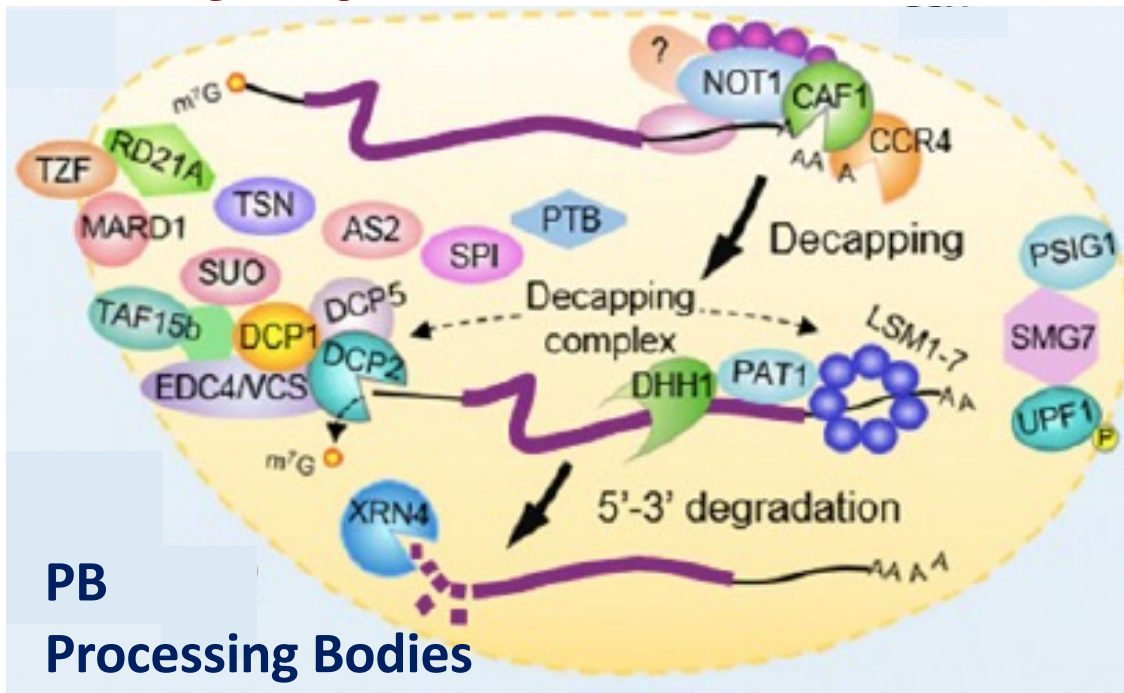
- regulate gene expression
by mRNA nuclear retention

Cajal bodies



- contain CB-specific scaRNA
- sites of snRNA modification (capping, 2'O-Me, pseudoU) and RNA processing

Cytoplasmic P-bodies and Stress Granules

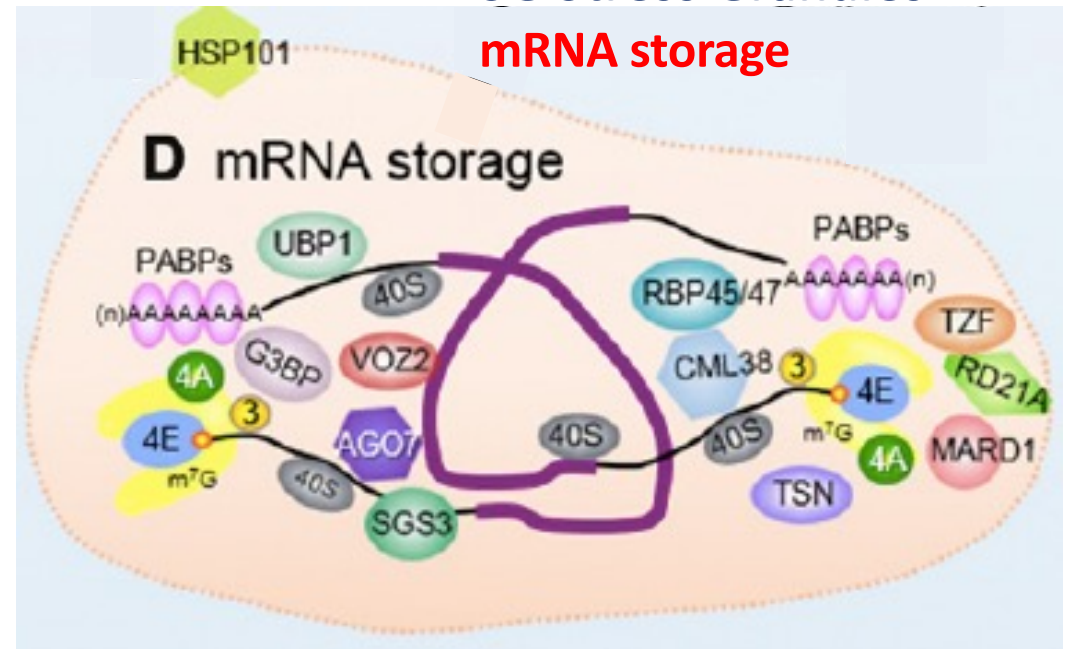


mRNA storage
mRNA decay

SG: global translation halts upon stress, mRNAs bound to the translational machinery and other proteins form SGs.
PB: translationally stalled mRNAs devoid of initiation factors shuttle to PBs.

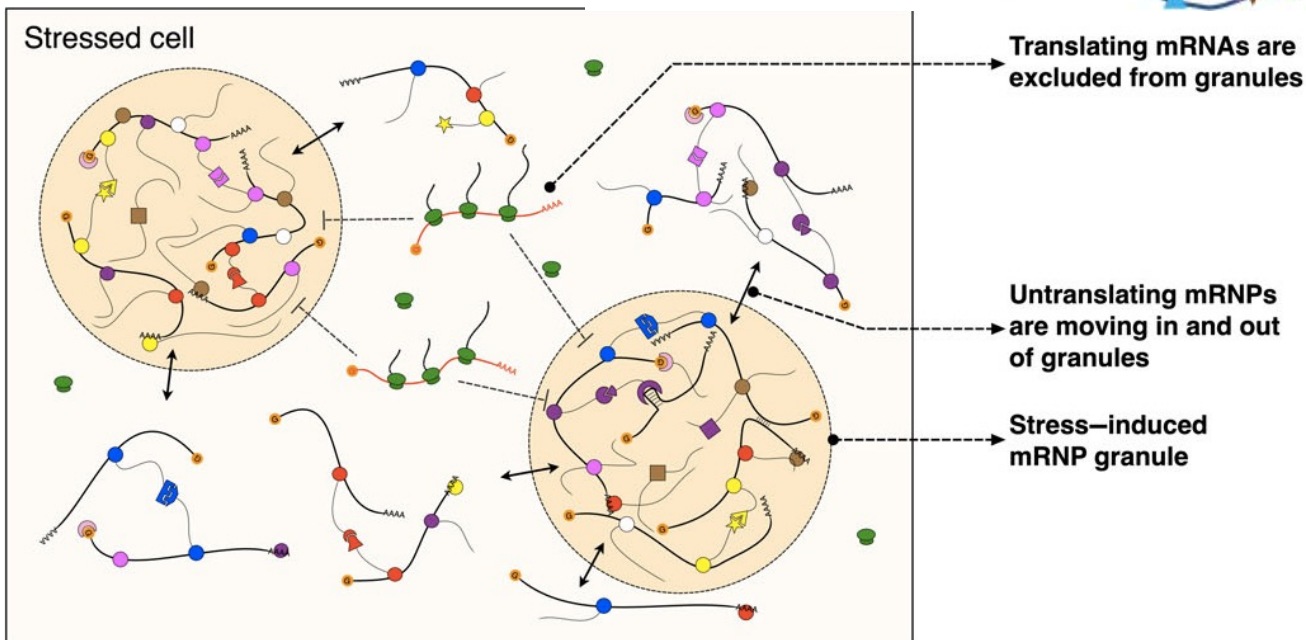
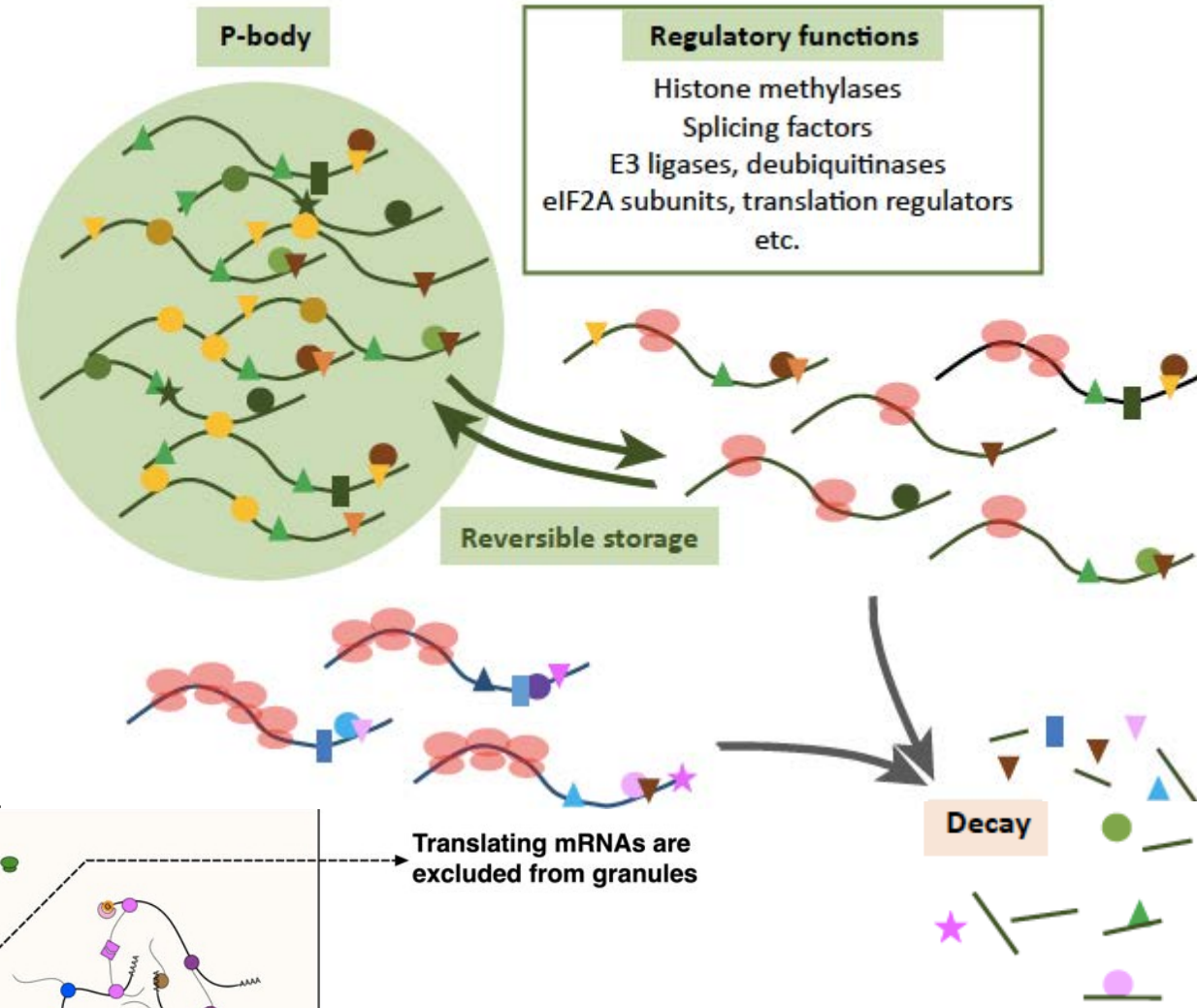
Dynamic biomolecular condensates
Form by phase separation of RNAs and proteins
Role in translational control and proteome buffering upon translational arrest (PB) and stress (SG)

SG Stress Granules



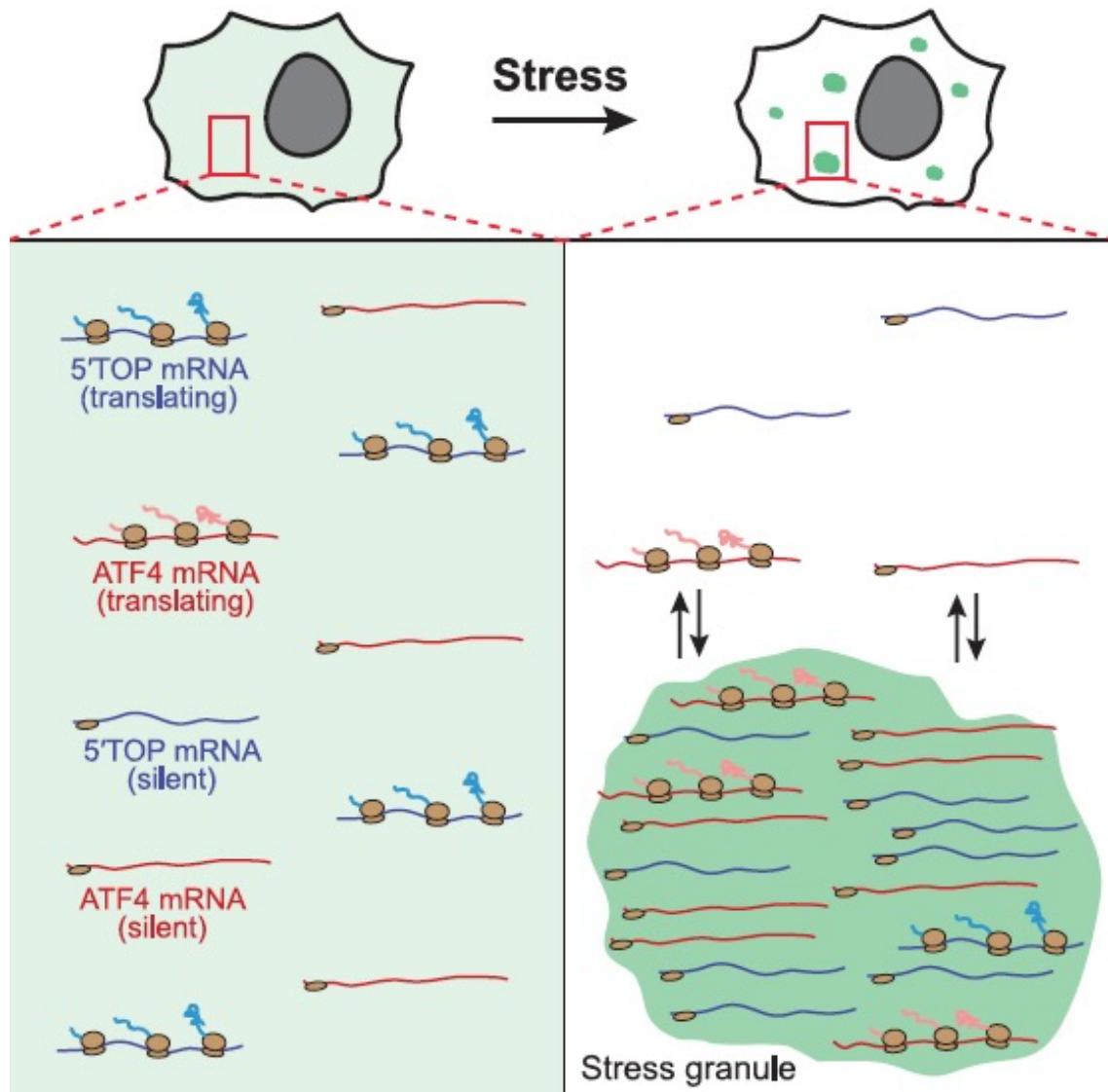
mRNA storage

PB SG mRNPs



Guzikowski et al, WIREsRNA, 2019;
Standart and Weil, TiG, 2018

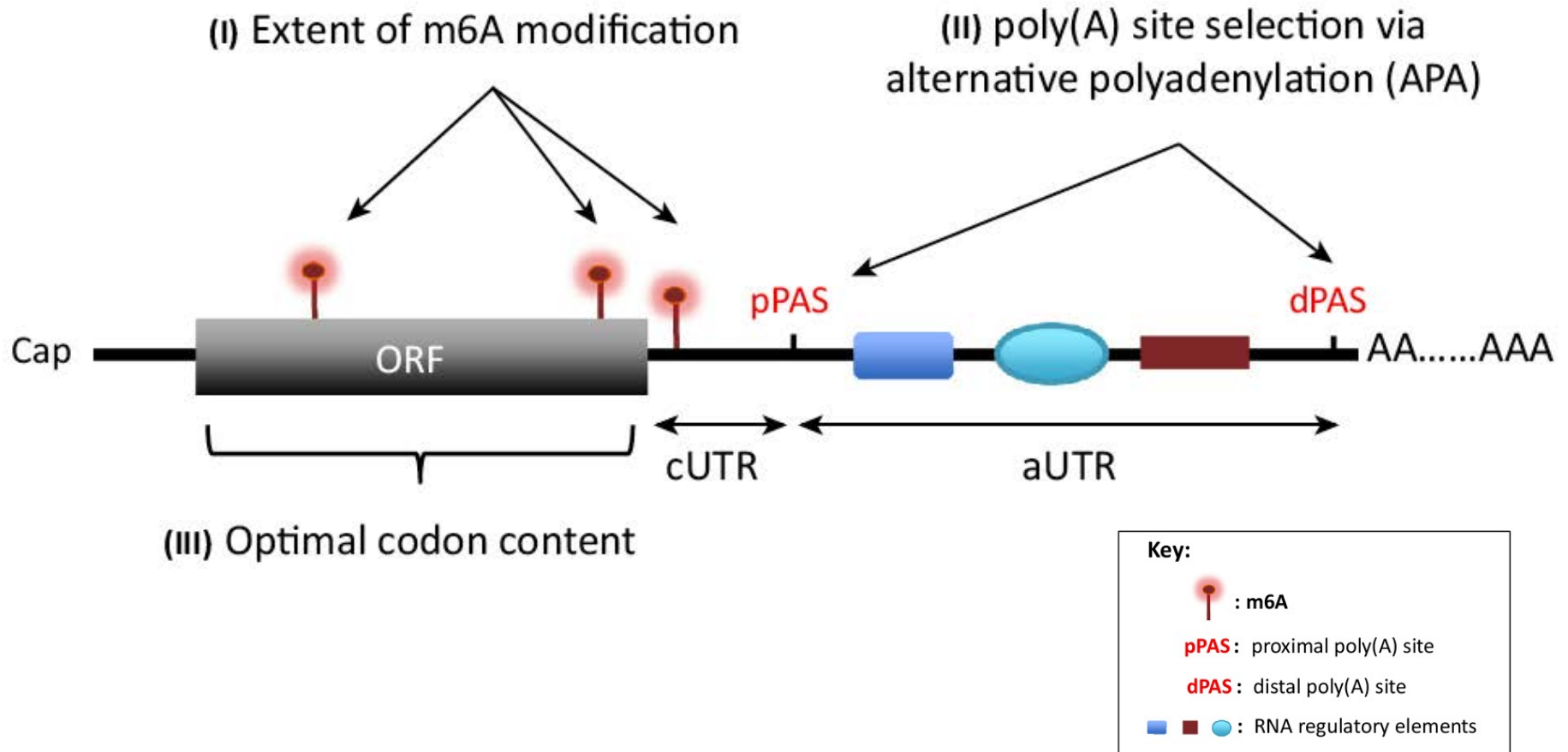
Translation in SGs



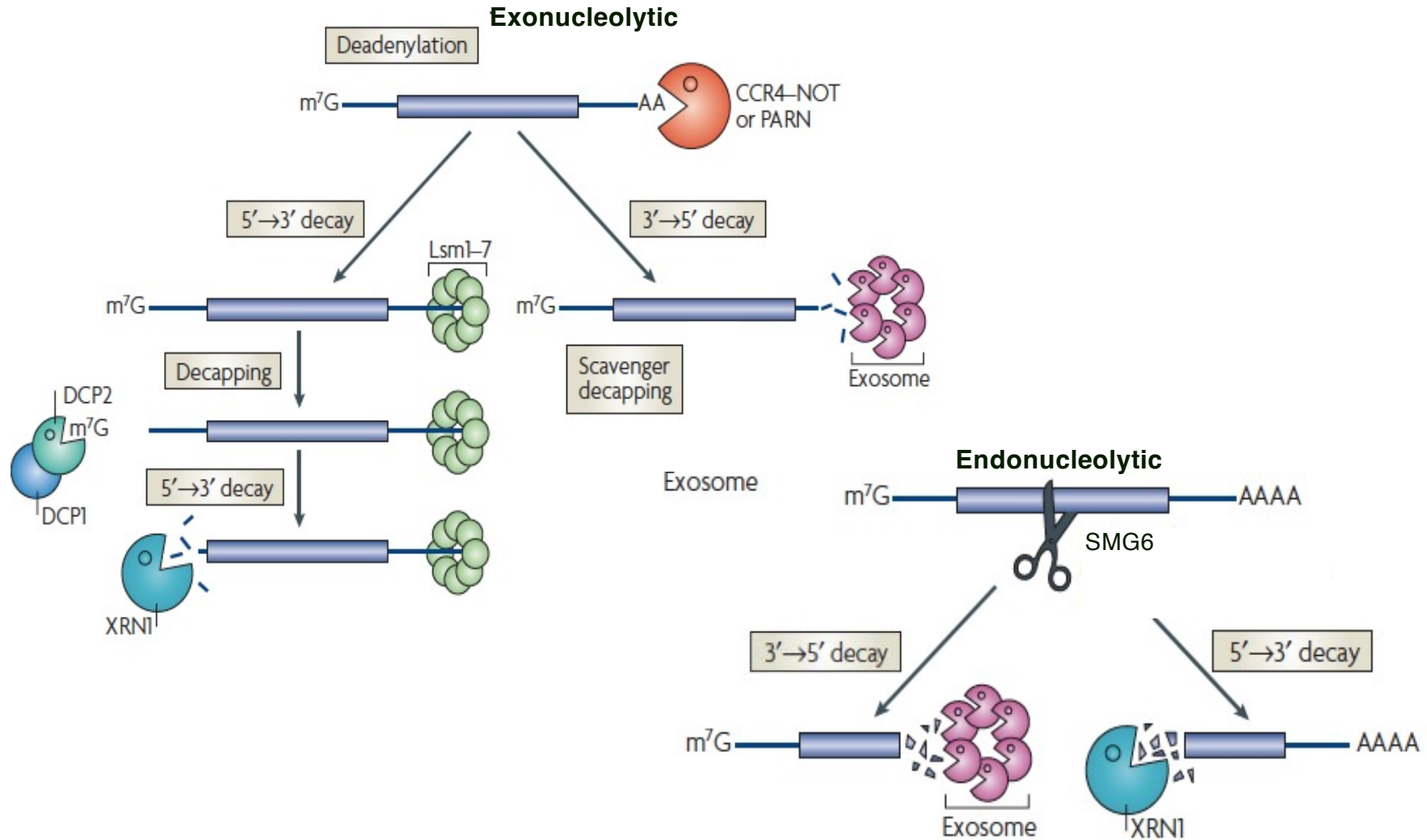
- nontranslating mRNAs are preferentially recruited to SGs
- mRNAs in SGs can undergo translation (complete cycle)
- translating mRNAs can enter, leave, or stably localize to SGs
- translation in SGs mainly, but not only, occurs on mRNAs enhanced under stress
(shown using single-molecule mRNA imaging, SunTag)

mRNA STABILITY

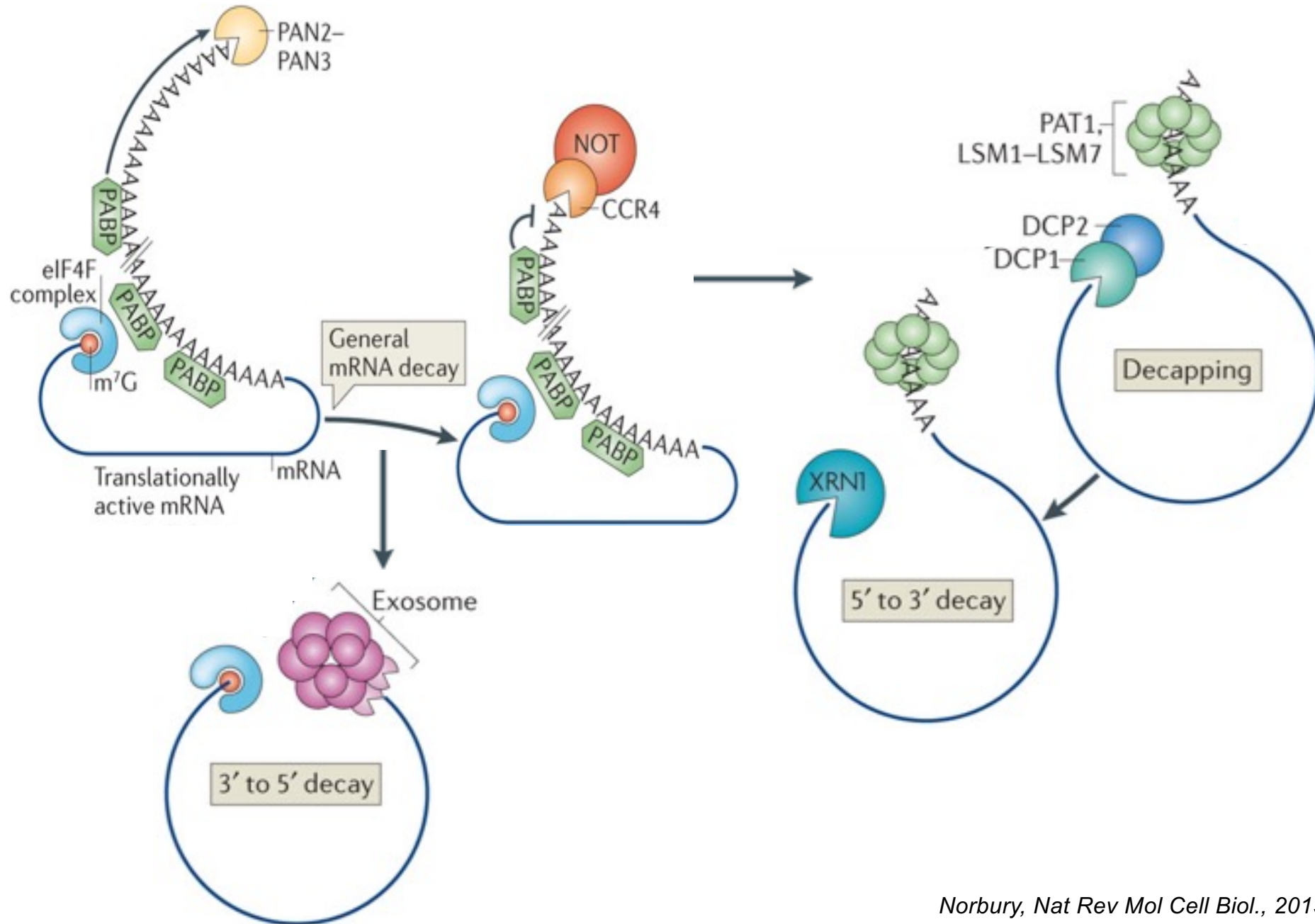
Elements *in cis*:



mRNA general decay in the cytoplasm

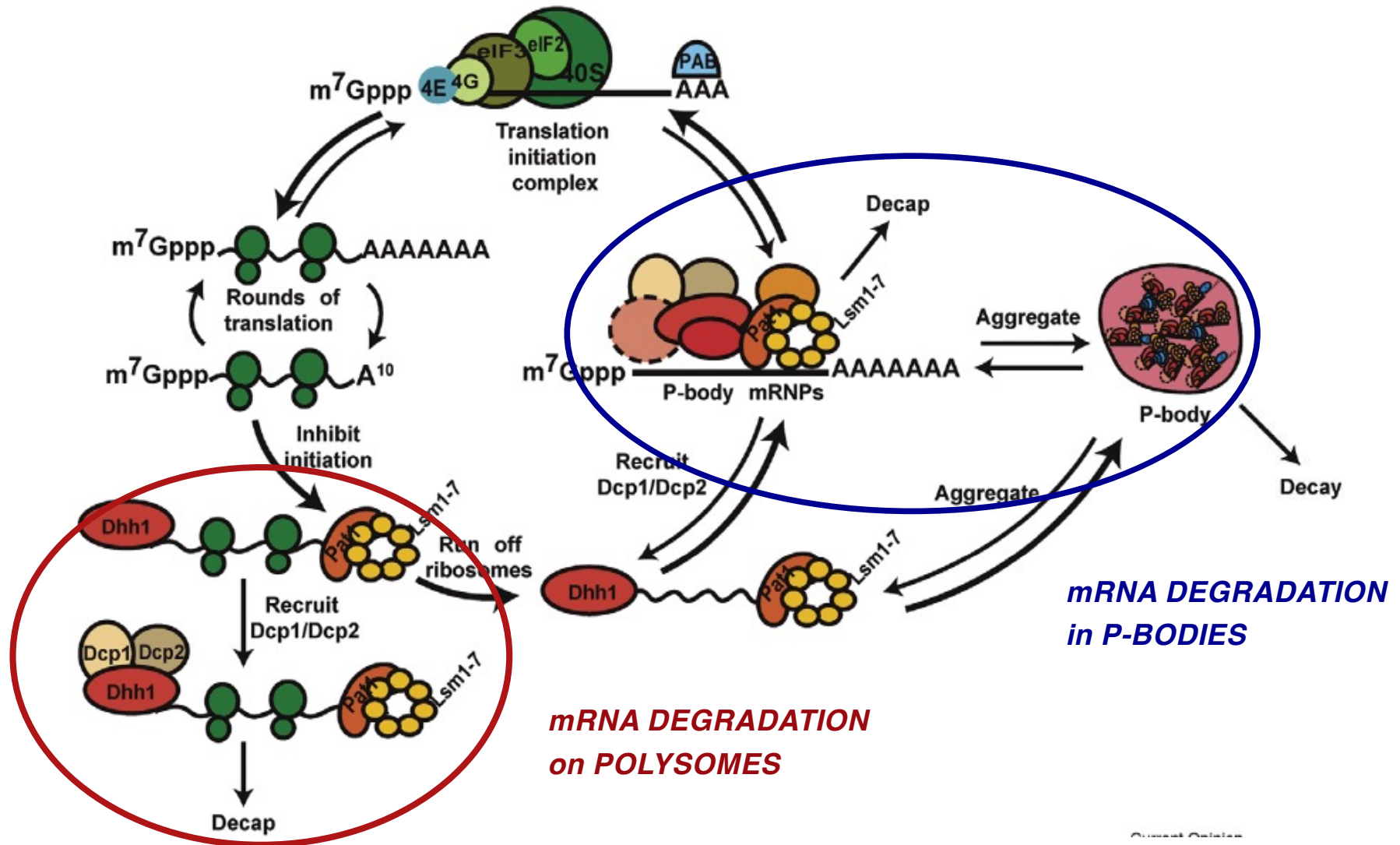


mRNA degradation in the cytoplasm



mRNA degradation in the cytoplasm

Balagopal and Parker, Curr. Op. Cell Biol., 2009



**DEADENYLATION → RELEASE OF RIBOSOMES → RELEASE OF TRANSLATION FACTORS
 → RECRUITMENT OF DECAY FACTORS → RNA DECAY**

RNA decay in the nucleus

mRNA 5'-3' decay



Lsm2-8p complex
(stimulates decapping)

Rat1p and cofactors
(5'-3' exonuclease)

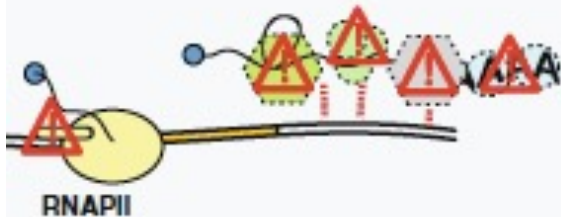
mRNA 3'-5' decay



nuclear exosome
(3'-5' exonuclease)

TRAMP
(exosome cofactor)

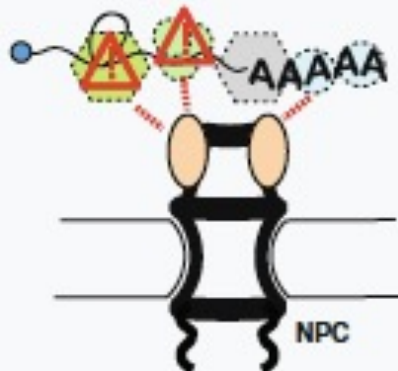
mRNA retention at gene locus



nuclear exosome
(3'-5' exonuclease)

Sac3/Thp1/Sus1 complex
(mRNP components)

anchoring of mRNP



Mlp1/Mlp2/Pml39
(NPC components)

Unspliced pre-mRNAs

3'-end unprocessed pre-mRNAs

Unpackaged mRNAs

(wrong mRNPs)

mRNAs retained in the nucleus

(export defect)

Transcripts retained at chromatin

Aberrant ncRNAs

Unmodified tRNAs

Excessive rRNAs and tRNAs

mRNA quality control decay in the cytoplasm

NMD – Nonsense Mediated Decay (mRNAs with premature STOP codon)

NGD – No-Go Decay (ribosome stuck on an obstacle)

NSD – Non-Stop Decay (mRNAs with no STOP codon)

Problems with a stalling ribosome during translation

(A) Improper termination



UPF1
(UPF2/3
EJC)

NMD
SMG6 (Endonuclease)
Exosome, Xrn1

UPFs facilitate
degradation of
truncated (unfolded)
products

(B) A lack of termination



Dom34/Pelota
Hbs1/hHsb1

NSD
Exosome
Ski
complex

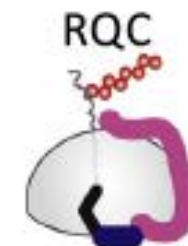


(C) Ribosome stall

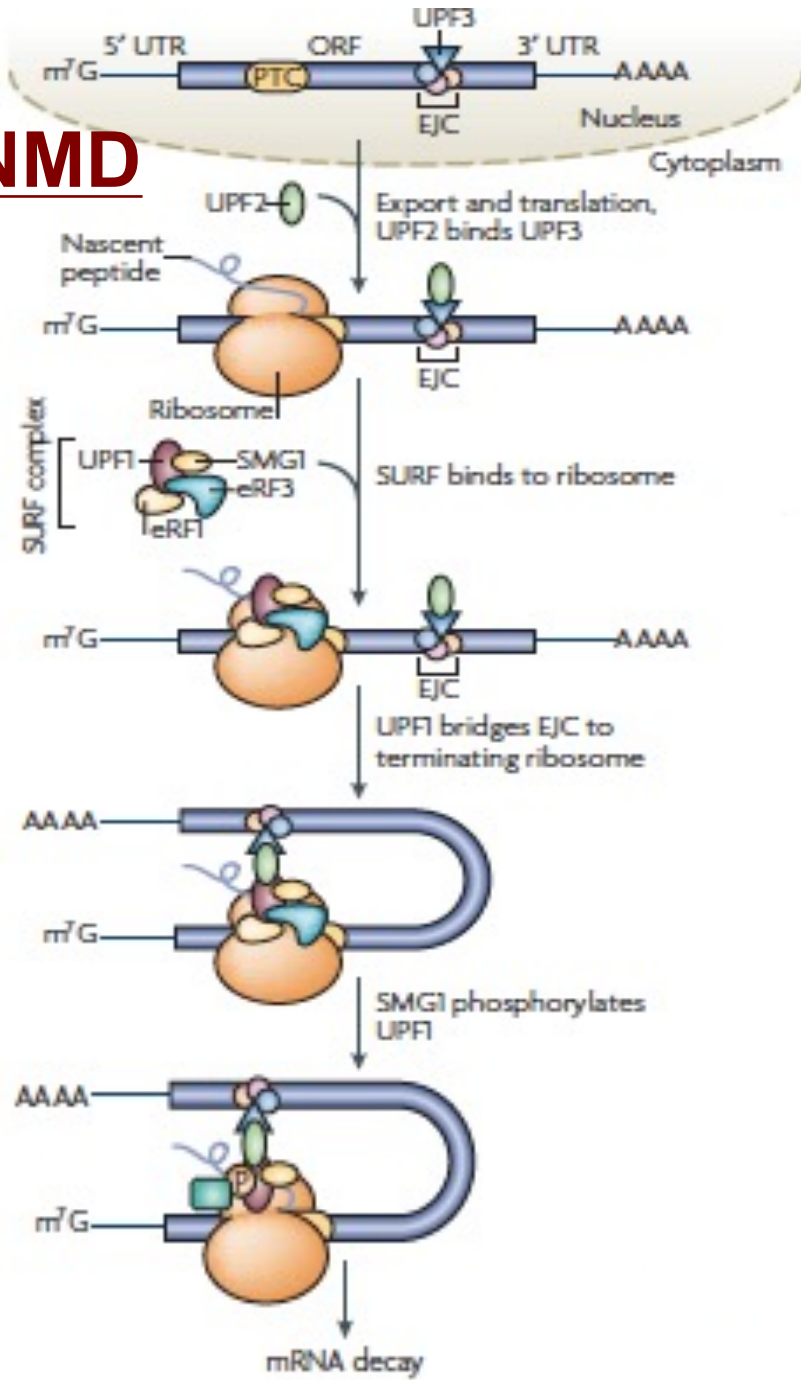


Dom34/Hbs1?
(Rack1, Hel2?)

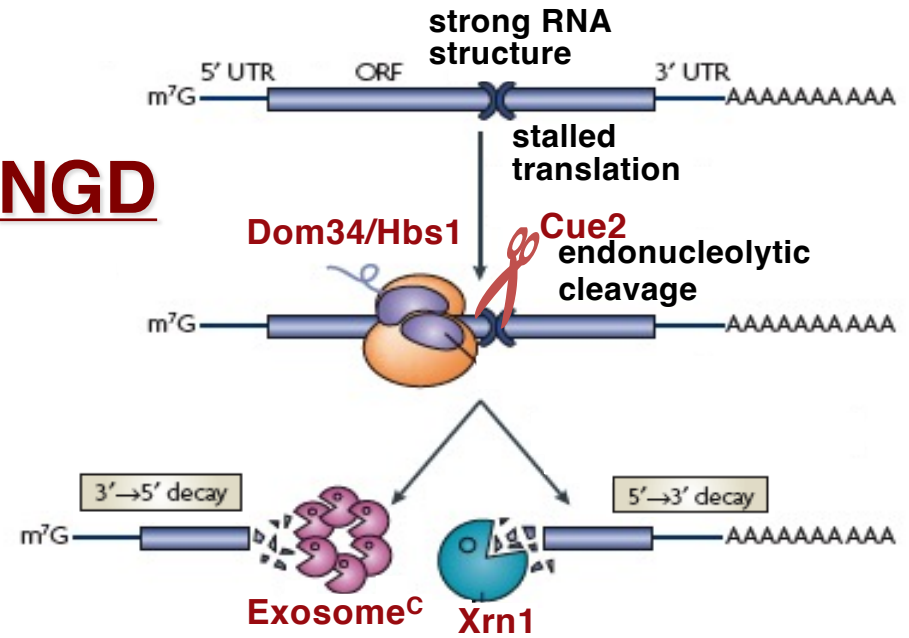
NGD
Endonucleolytic
cleavage



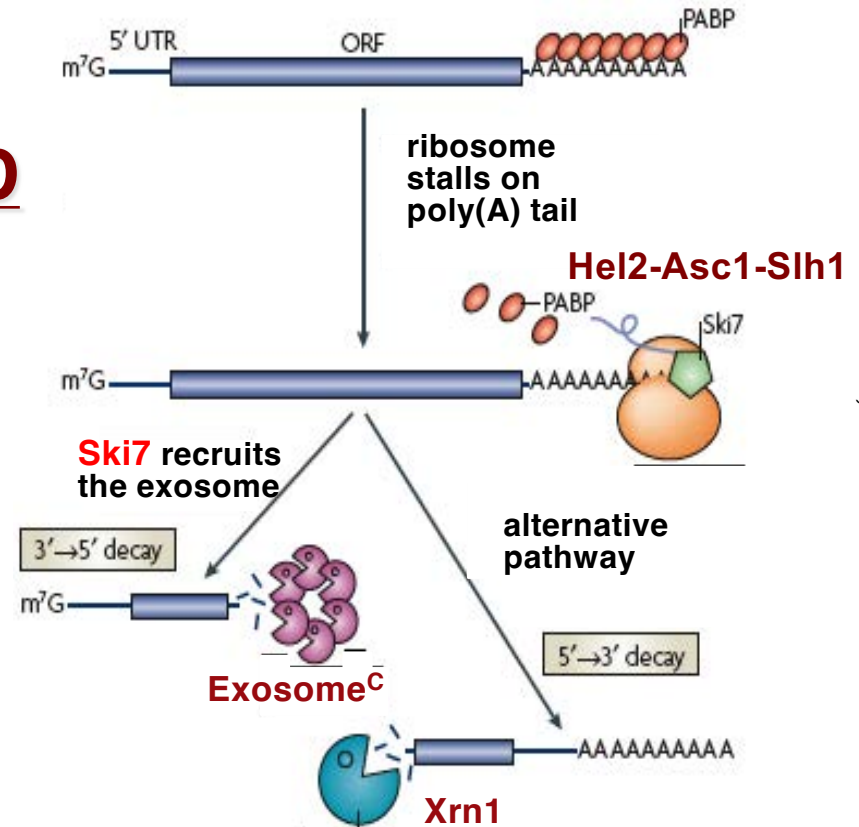
NMD



NGD



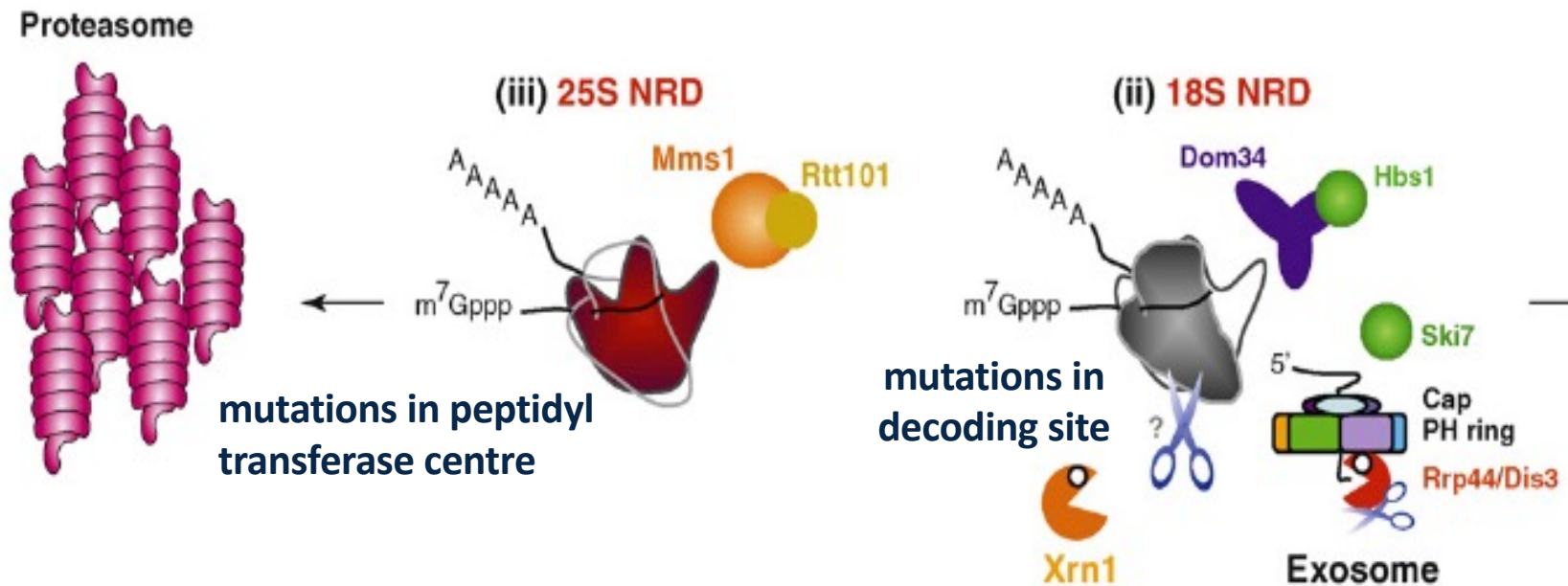
NSD



rRNA surveillance

NRD- Nonfunctional rRNA Decay

Mature aberrant ribosomes are eliminated in the cytoplasm



Mms1, Rtt101-
subunits of E3 ubiquitin ligase complex

Dom34::Hbs1
factors involved in NGD and NSD

18S NRD

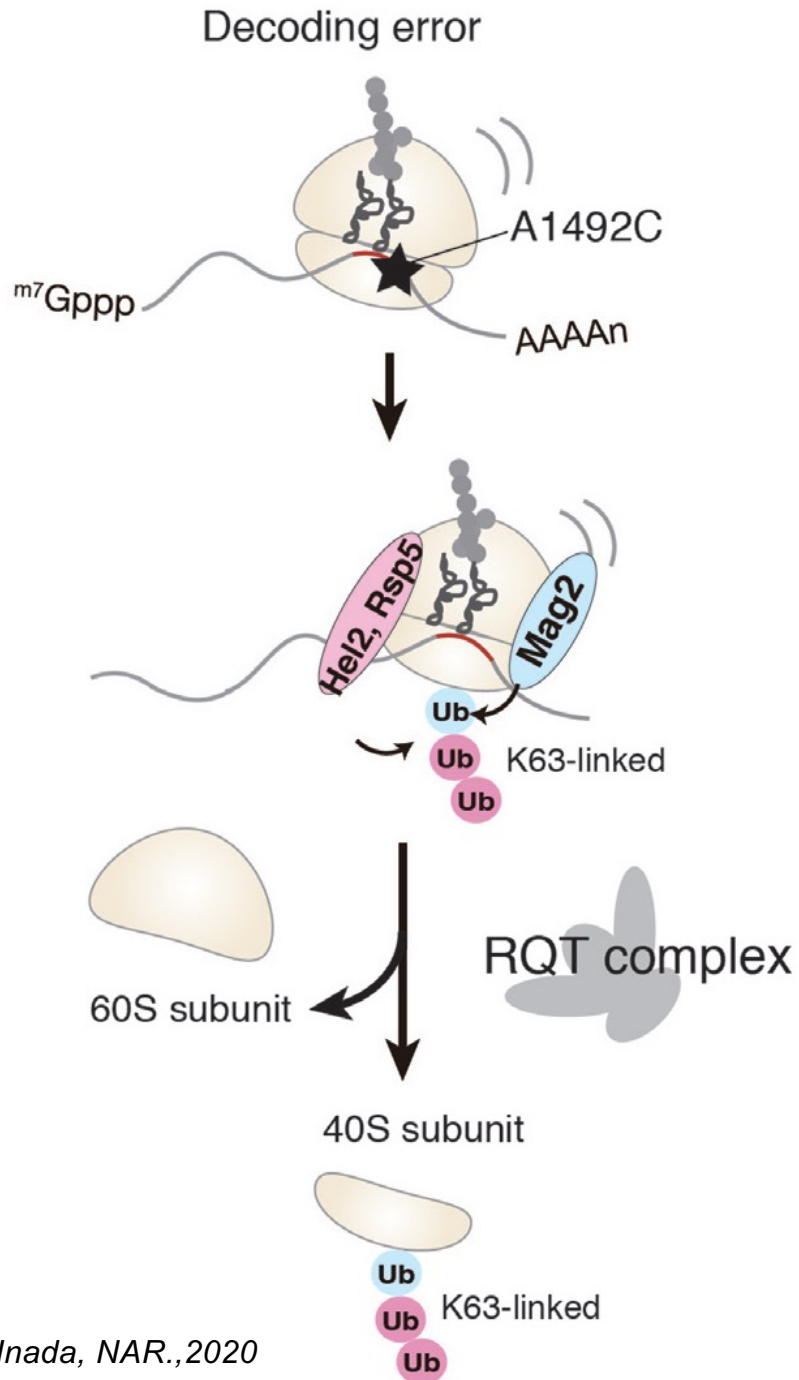
Ribosome stalling due to decoding error
Recognition of the stalled ribosome

Ribosome ubiquitination
K212 of RPS3 is monoubiquitinated by Mag2 followed by polyubiquitination by Hel2 or Rsp5

Ribosome dissociation
Subunit dissociation by the Ski2-like RNA helicase Slh1 in the RQT complex

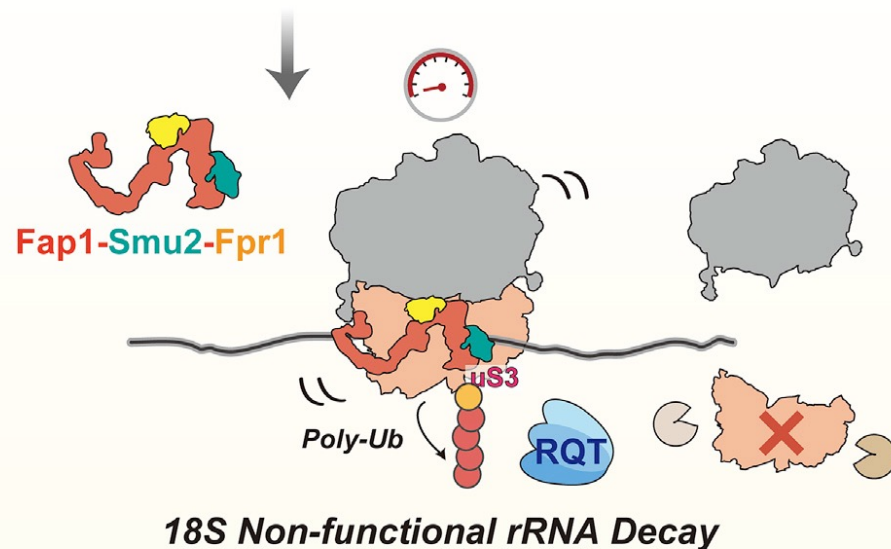
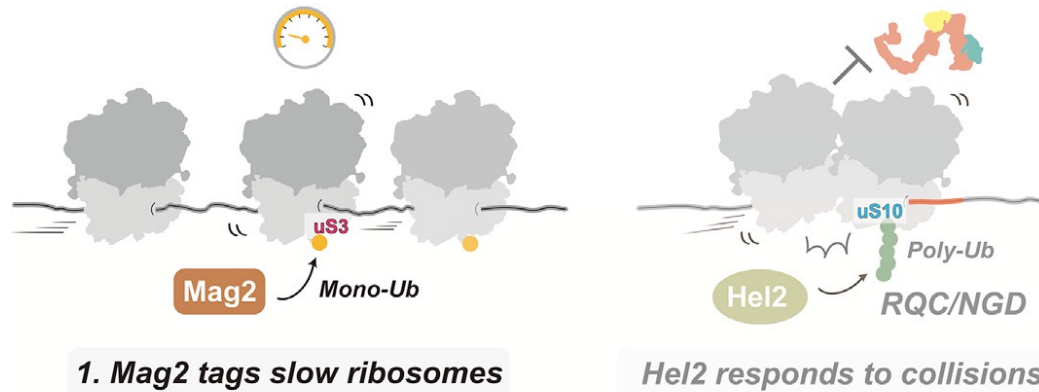
18s rRNA degradation
by Xrn1 or exosome

Factors involved in 18S NRD
are also involved in RQC



rRNA SURVEILLANCE

18S NRD versus RQC



2. Fap1 senses individual stalled 80S ribosomes

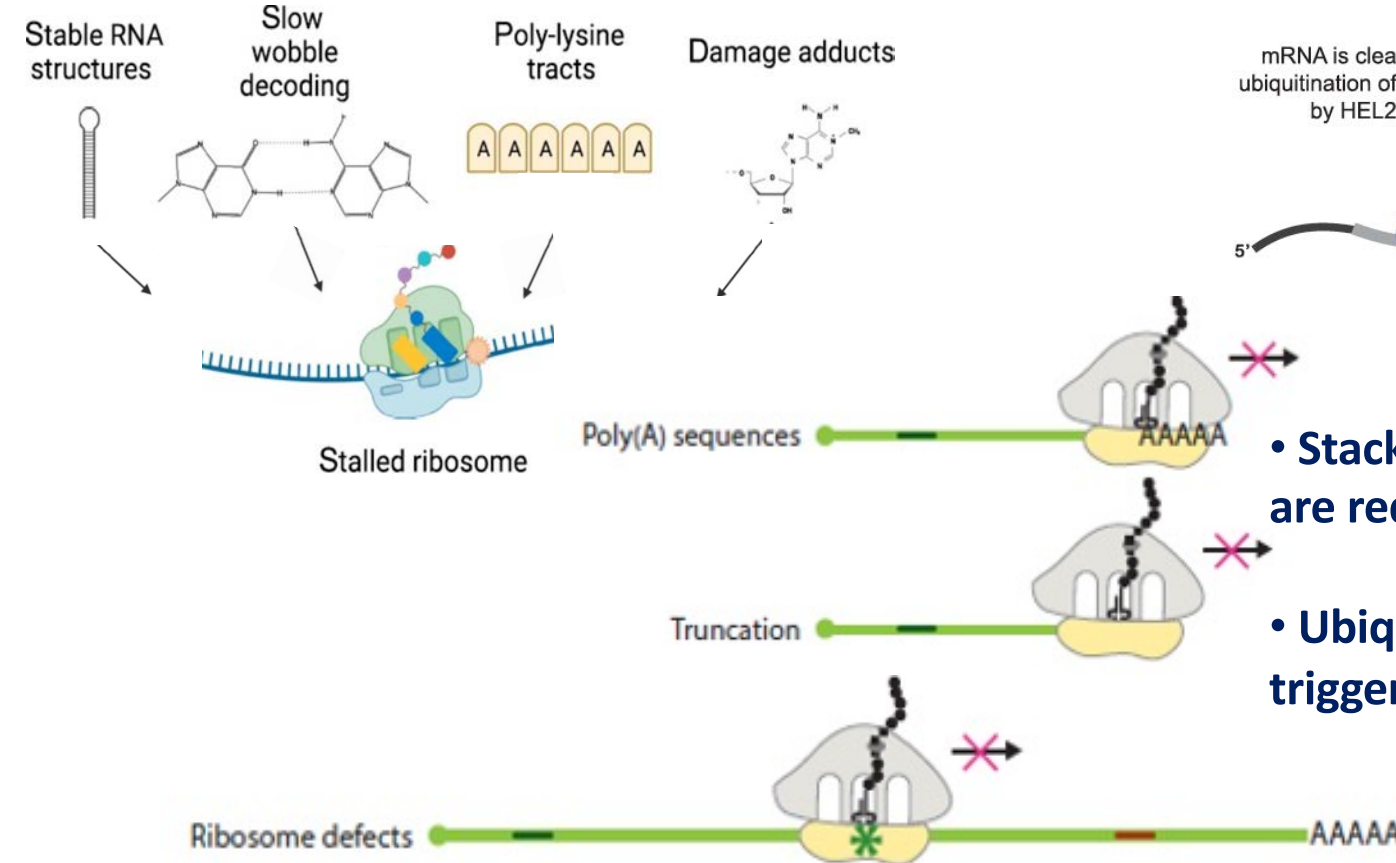
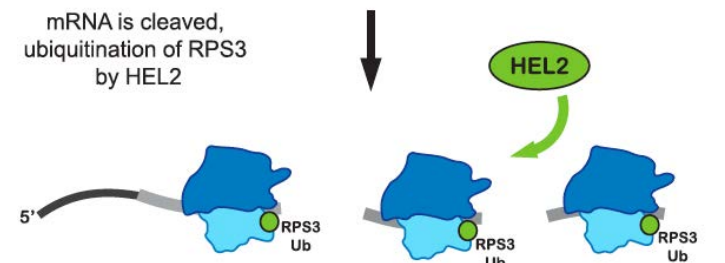
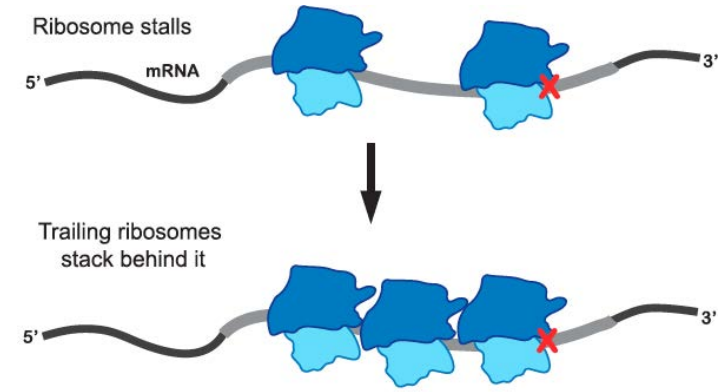
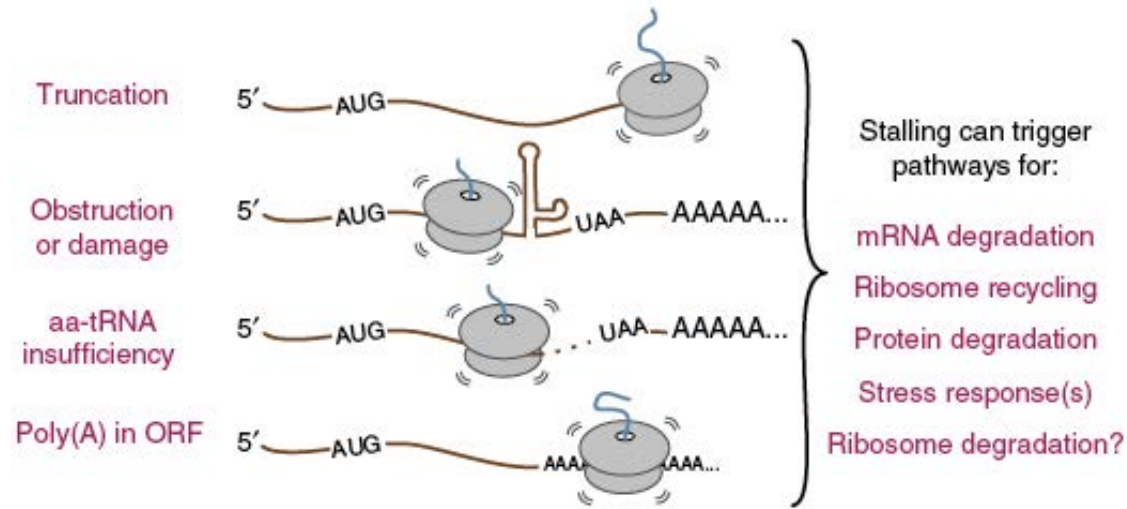
18S NRD

- detects non functional ribosomes (mutation in decoding center 18S rRNA)
- or stalled monosomes
- stalled ribosomes recognized by Mag2 E3 ligase, RPS3 monoUb Fap1 E3 ligase, RPS3 polyUb
- non-functional ribosomes are degraded

RQC

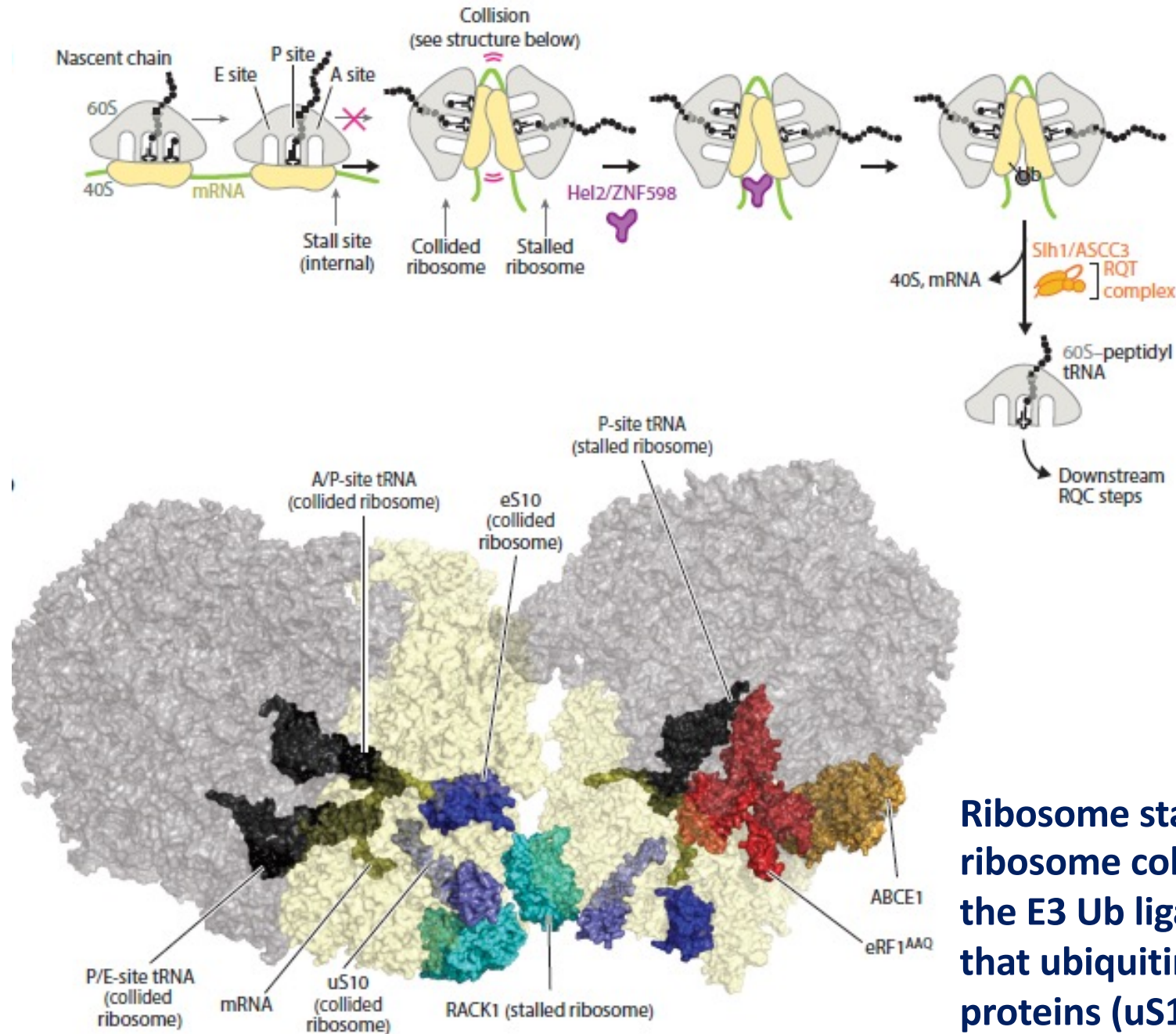
- detects collided ribosomes
- stalled disome recognized by Hel2 E3 ligase, RPS10 polyUb
- ribosomes are released and recycled

Ribosome stalling



- Stacked or colliding ribosomes are required to elicit NGD
- Ubiquitination of RPS3 by HEL2 triggers RQC

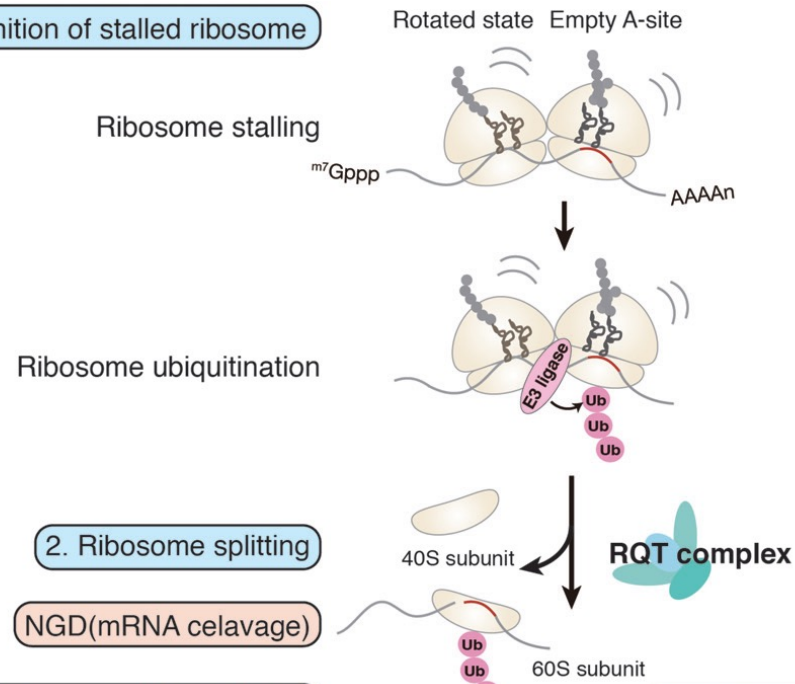
Ribosome stalling and collision



Ribosome stalling leads to ribosome collision recognized by the E3 Ub ligase Hel2/ZNF589 that ubiquitinates ribosomal proteins (uS10, eS19, uS3)

RIBOSOME QC (RQC)

1. Recognition of stalled ribosome

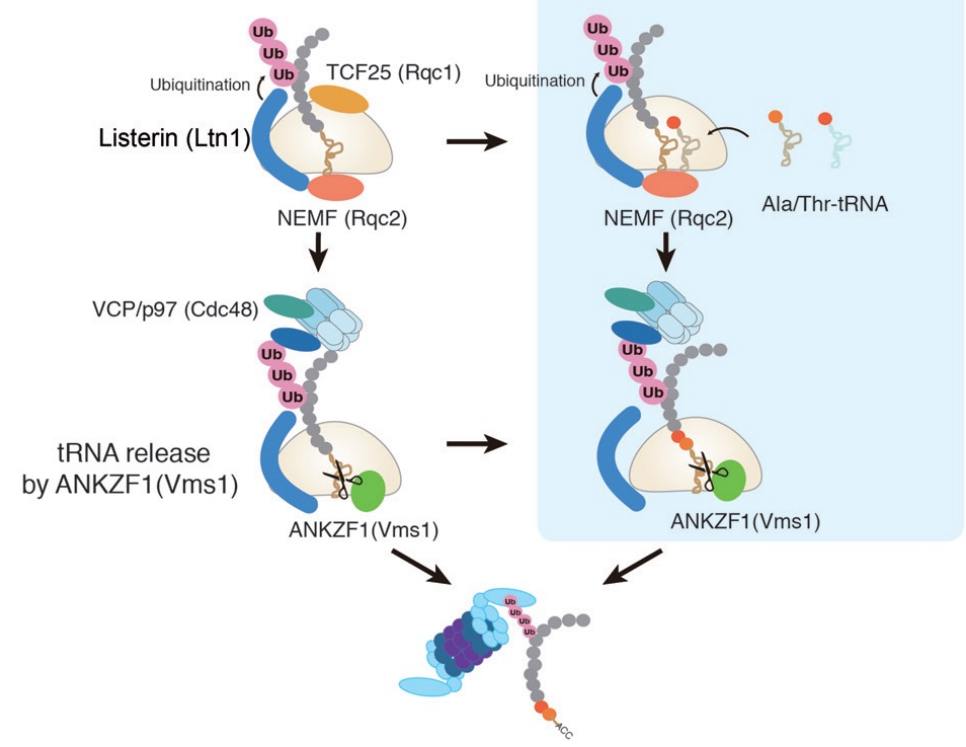


2. Ribosome splitting

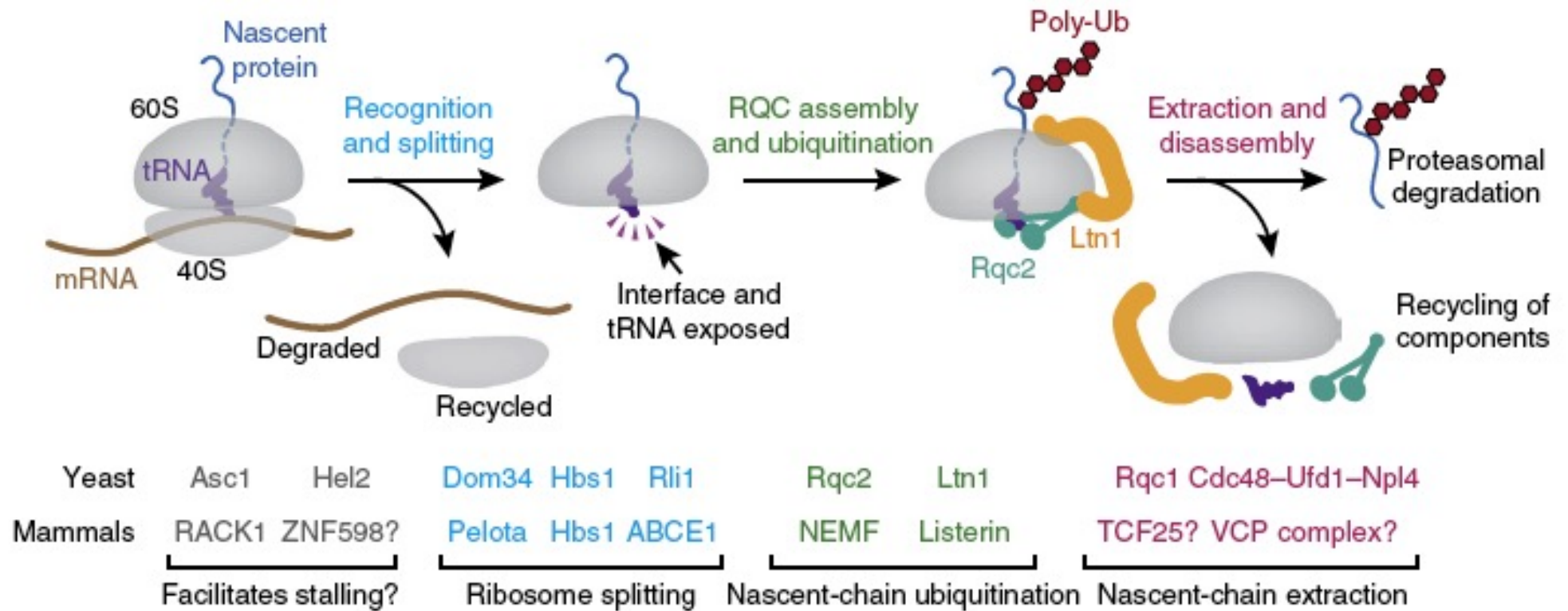
NGD(mRNA celavage)

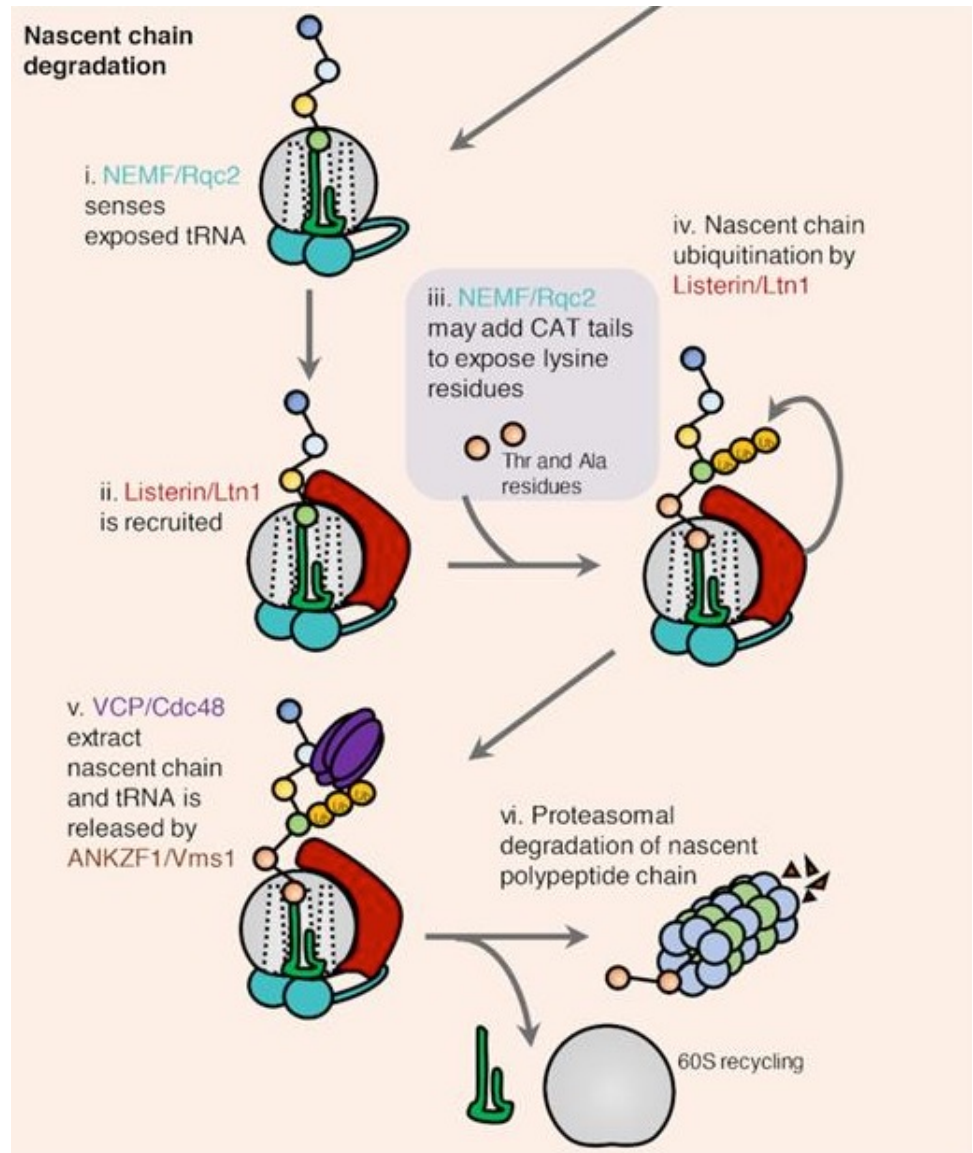
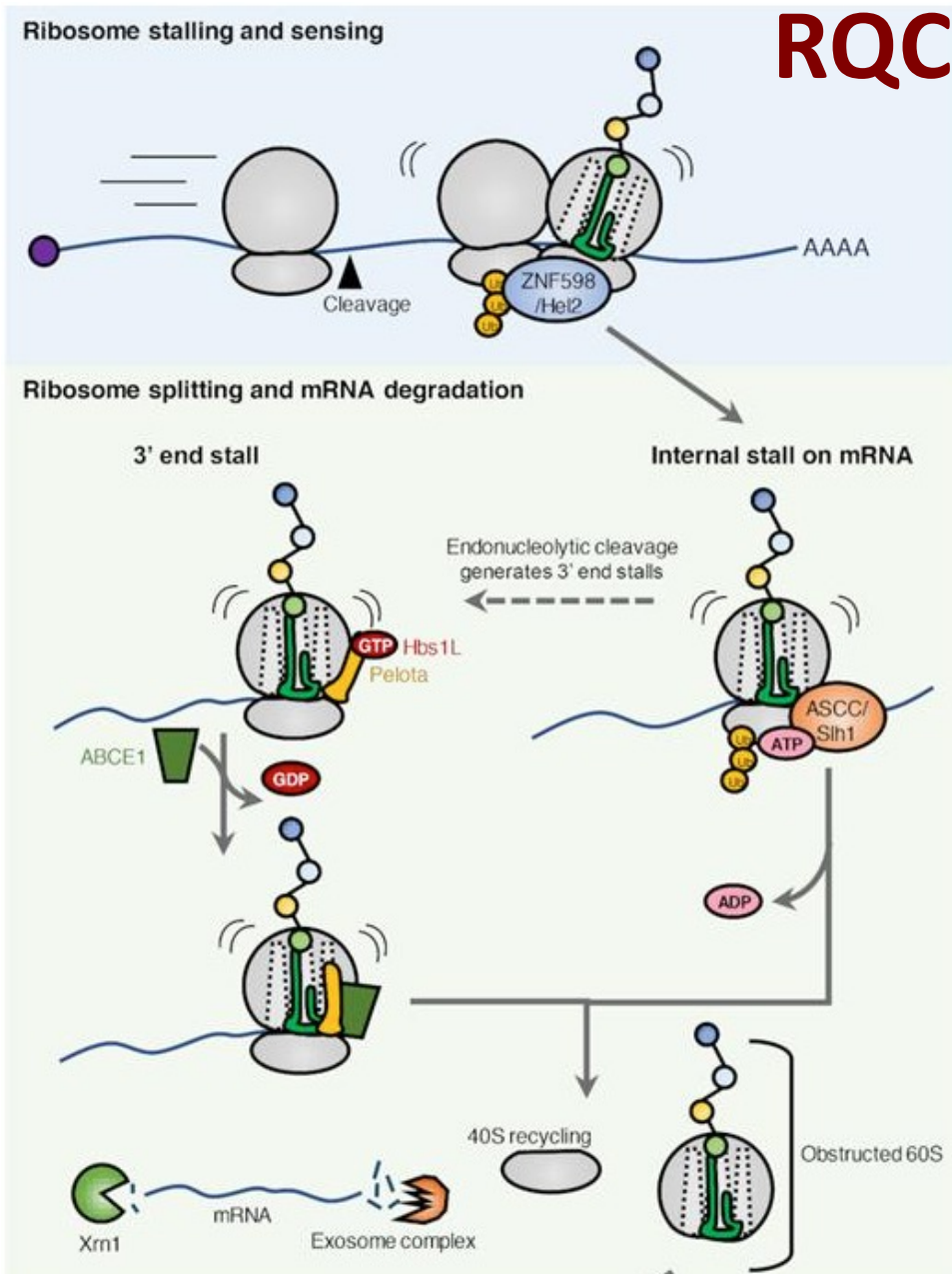
3. Proteasomal degradation

4. CAT-tailing by NEMF (Rqc2)



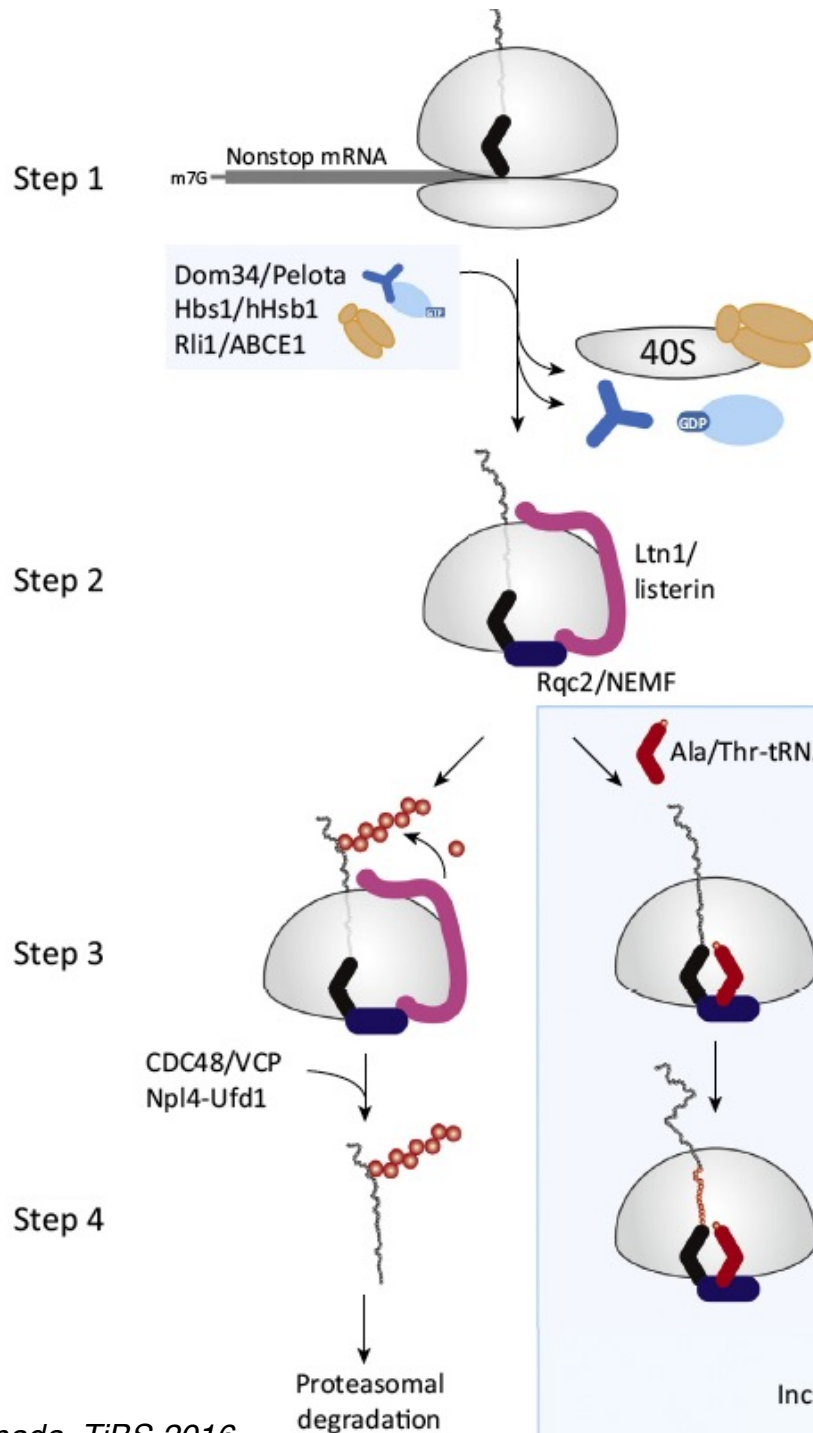
RQC pathway





- Ribosome stalling
- Ribosome collision
- Recognition by E3 Ub ligase Hel2/ZNF589
- Ubiquitination of ribosomal proteins (uS10, eS19, uS3)

RQC mechanism



Dom34-Hbs1-Rli1 or Hel2-Asc1-Slh1

facilitate subunit dissociation of stalled ribosomes

RQC proteins assemble on 60S

- Ltn1 Ub ligase ubiquitinates the nascent peptide
- Rqc2, Cdc48 and cofactors remove nascent peptide for proteasomal degradation
- Alternative pathways: via addition of CAT-tail (Ala and Thr extension)

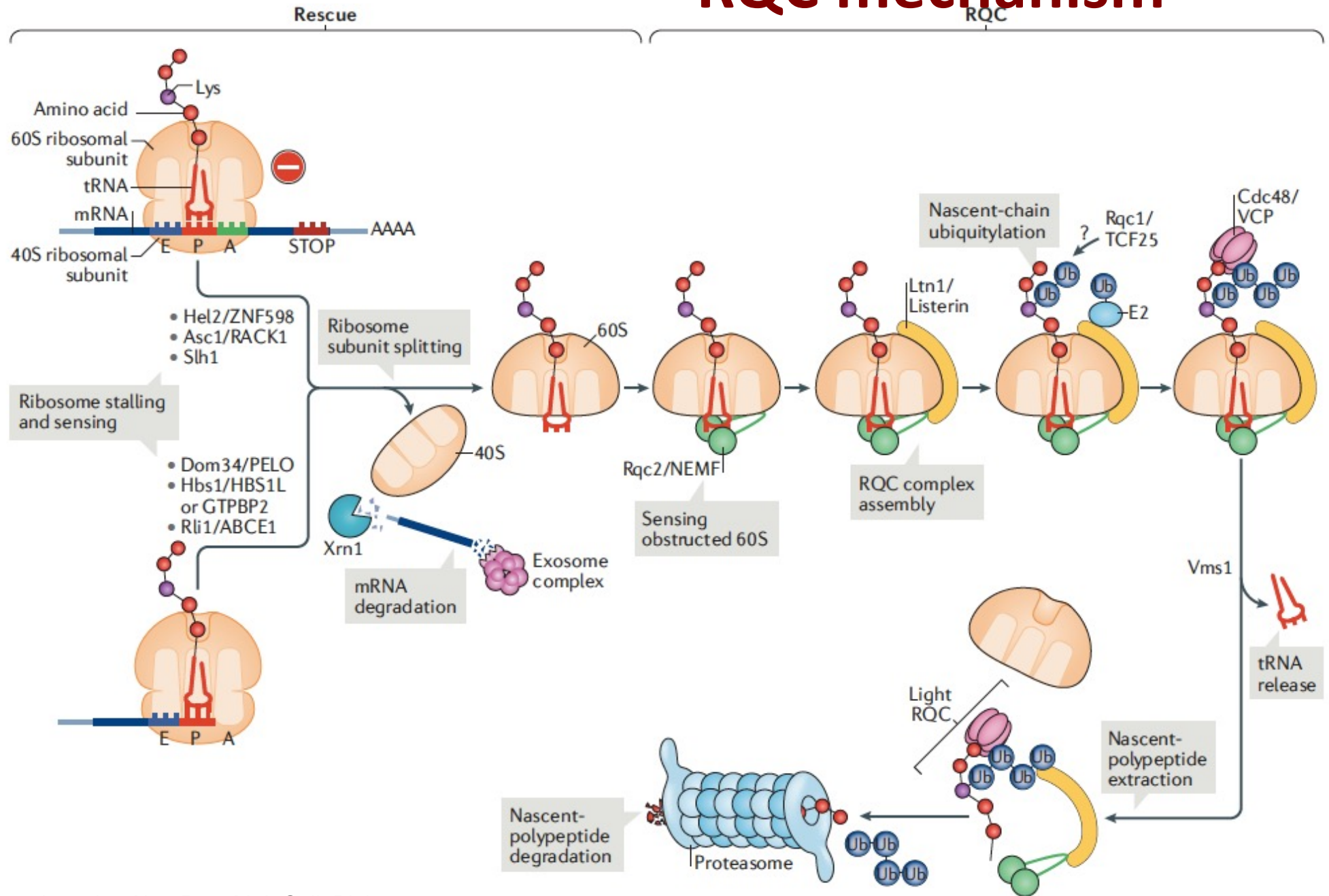
CATylation

The canonical RQC is preferred but if ubiquitylation of the nascent polypeptide fails, CAT tail is added by Rqc2 to extract the trapped polypeptide

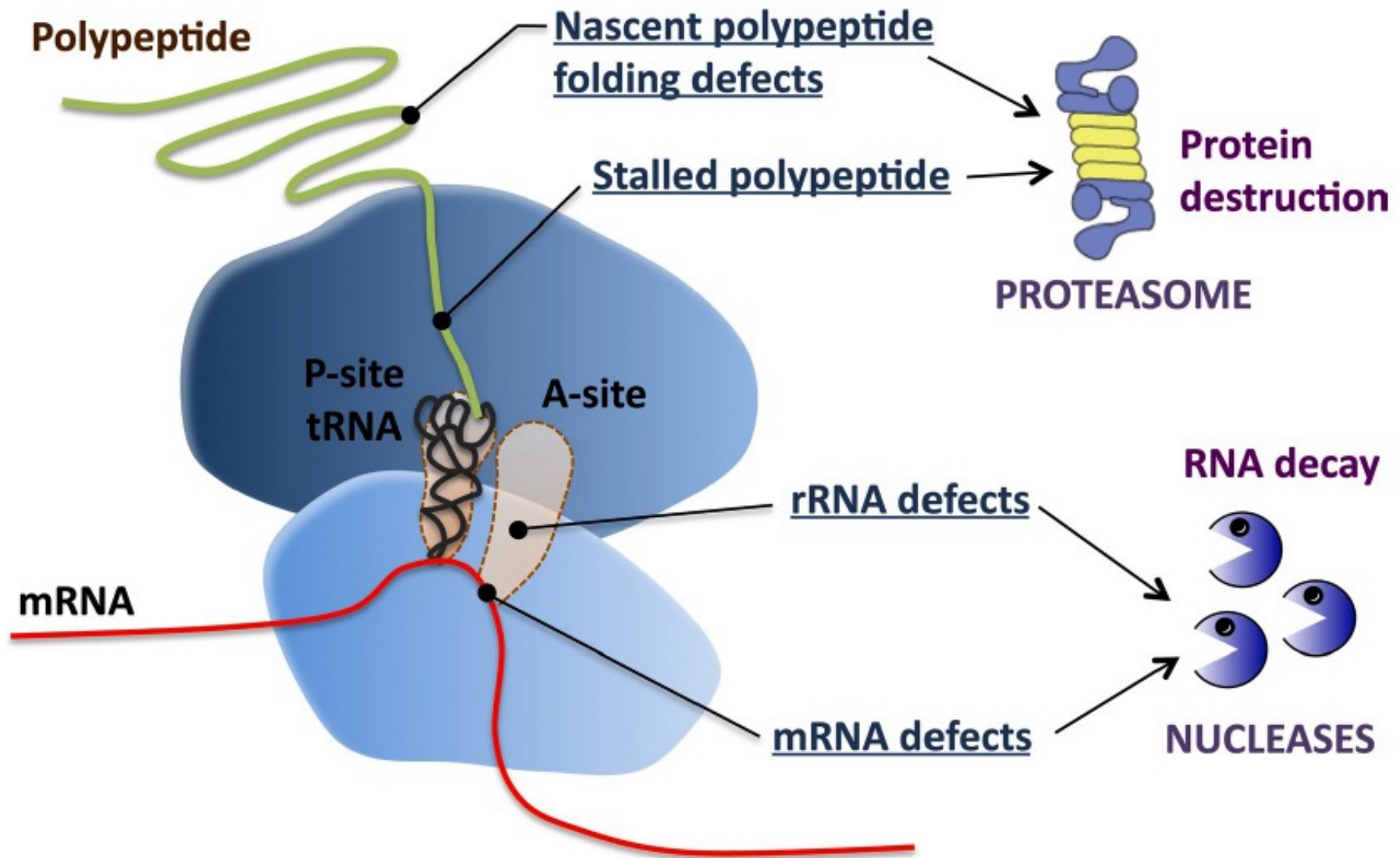
CATylation results in

- Ltn1-dependent degradation of aberrant proteins
- nascent chain aggregation
- activation of stress signaling
- nascent chain proteolysis

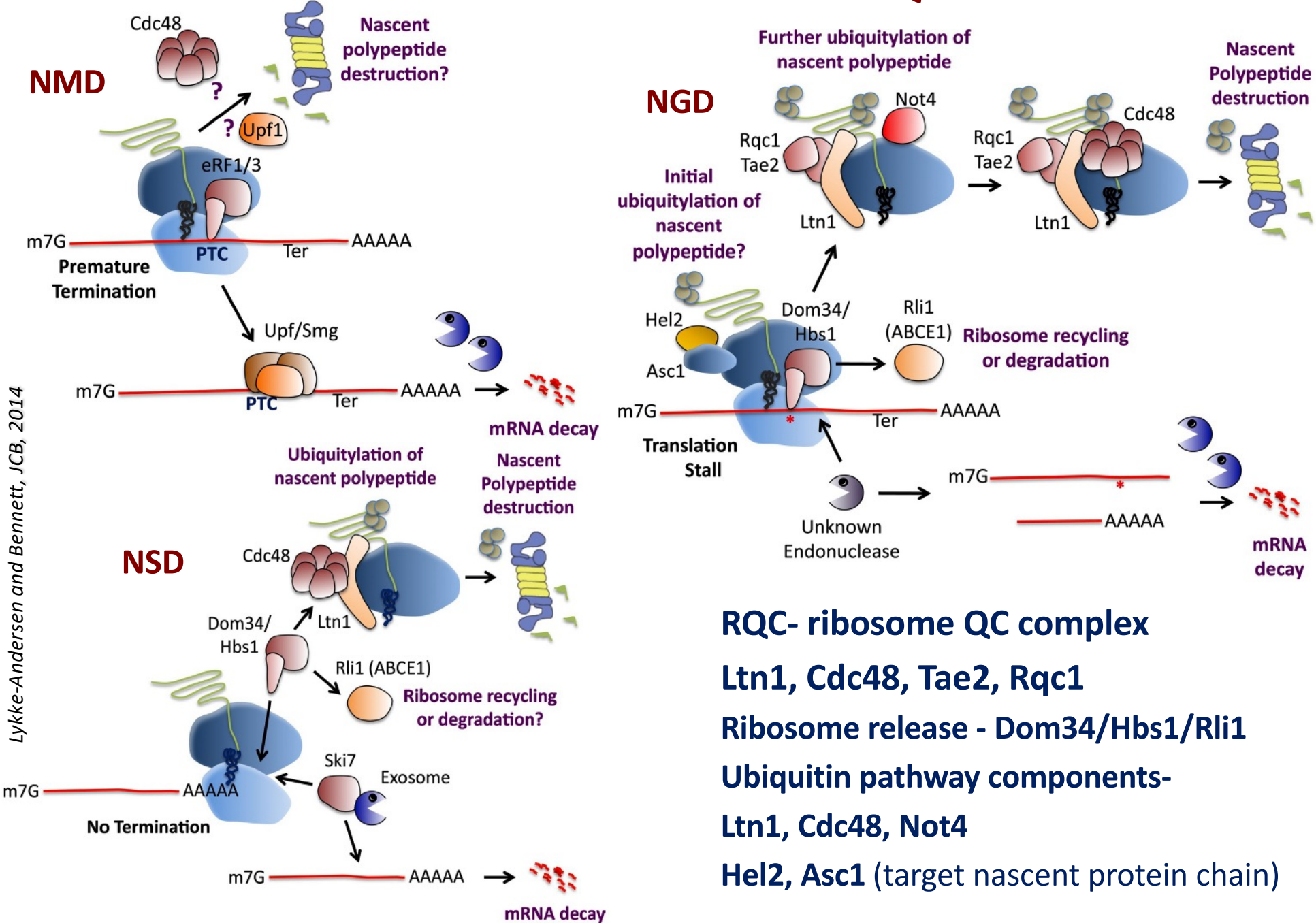
RQC mechanism



Co-translational protein and mRNA QC



Co-translational QC



Lykke-Andersen and Bennett, JCB, 2014

- RQC- ribosome QC complex
- Ltn1, Cdc48, Tae2, Rqc1
- Ribosome release - Dom34/Hbs1/Rli1
- Ubiquitin pathway components- Ltn1, Cdc48, Not4
- Hel2, Asc1 (target nascent protein chain)

NEXT LECTURE:

Global analyses of RNAs and RNPs