

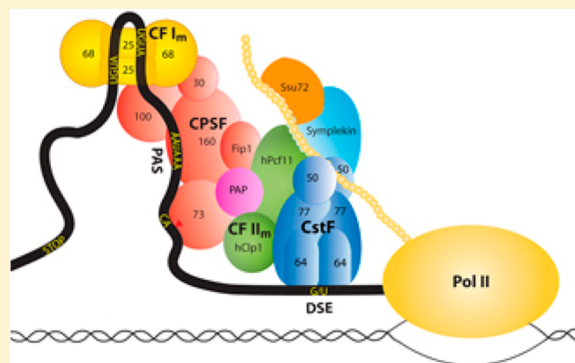
Structure and Function of Pre-mRNA 5'-End Capping Quality Control and 3'-End Processing

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ABSTRACT: Messenger RNA precursors (pre-mRNAs) are produced as the nascent transcripts of RNA polymerase II (Pol II) in eukaryotes and must undergo extensive maturational processing, including 5'-end capping, splicing, and 3'-end cleavage and polyadenylation. This review will summarize the structural and functional information reported over the past few years on the large machinery required for the 3'-end processing of most pre-mRNAs, as well as the distinct machinery for the 3'-end processing of replication-dependent histone pre-mRNAs, which have provided great insights into the proteins and their subcomplexes in these machineries. Structural and biochemical studies have also led to the identification of a new class of enzymes (the DXO family enzymes) with activity toward intermediates of the 5'-end capping pathway. Functional studies demonstrate that these enzymes are part of a novel quality surveillance mechanism for pre-mRNA 5'-end capping. Incompletely capped pre-mRNAs are produced in yeast and human cells, in contrast to the general belief in the field that capping always proceeds to completion, and incomplete capping leads to defects in splicing and 3'-end cleavage in human cells. The DXO family enzymes are required for the detection and degradation of these defective RNAs.



In eukaryotes, mRNA precursors (pre-mRNAs) are transcribed by RNA polymerase II (Pol II) from the genome and must undergo extensive cotranscriptional processing to become mature mRNAs. The typical progression of pre-mRNA maturation involves 5'-end capping, splicing, and 3'-end cleavage and polyadenylation. The integrity and precision of each of these steps are critical for generating stable, functional mRNAs. Moreover, recent studies have demonstrated the importance of alternative splicing, alternative polyadenylation (APA), and RNA editing in producing an incredibly diverse, often cell-specific mRNA library that contributes to the biological complexity of higher eukaryotes.

5'-end capping occurs very early during Pol II transcription, typically after the synthesis of ~20 nucleotides of the pre-mRNA. Capping has been linked to splicing and 3'-end processing of the pre-mRNA, and the export of the mature mRNA. In addition, the 5'-end cap is directly recognized by the eukaryotic translation initiation factor eIF-4E, which is essential for mRNA translation by the ribosome.

A majority of pre-mRNAs acquire a poly(A) tail after 3'-end processing, which is important for the export of the mature mRNAs from the nucleus to the cytoplasm. The poly(A) tail also promotes the translation of the mRNAs and protects them from degradation. In comparison, 3'-end processing of replication-dependent histone pre-mRNAs involves only the cleavage reaction, and these mRNAs do not carry a poly(A) tail. Instead, a conserved stem-loop structure at their 3'-end

supports many of the functions that are associated with the poly(A) tail.

This review will focus on recent advances (within the past ~5 years) in structural and functional studies of pre-mRNA 3'-end processing, and the newly reported structures are summarized in Table 1. There are also many other excellent reviews on these topics, some of which are listed here.^{1–8} In addition, a novel quality surveillance mechanism for 5'-end capping was discovered recently and will be reviewed here, as well. Other aspects of pre-mRNA processing, such as splicing, APA,^{9–11} and poly(A) length regulation,^{12,13} and other mechanisms of mRNA quality control and decay, such as nonsense-mediated decay and no-go decay, will not be covered here because of space limitations.

■ CANONICAL PRE-MRNA 3'-END PROCESSING

Key sequence elements in the 3'-untranslated regions (UTRs) of pre-mRNAs are recognized for 3'-end processing. In mammals, the major sequence elements include a hexanucleotide poly(A) signal (PAS, oftentimes AAUAAA) 10–30 nucleotides upstream of the cleavage site,¹⁴ the cleavage site itself (oftentimes after a CA dinucleotide), and a U- or G/U-rich downstream sequence element (DSE) (Figure 1). In

Received: December 26, 2013

Revised: March 7, 2014

Published: March 11, 2014



Table 1. Recently Published Structures of Protein Factors Involved in Pre-mRNA 3'-End Processing or 5'-End Capping Quality Surveillance

protein factor	subdomains	Protein Data Bank entries	refs
CPSF			
archaeal CPSF-73	metallo- β -lactamase, β -CASP	2YCB, 2XR1	21, 22
archaeal CPSF-73–RNA complex	metallo- β -lactamase, β -CASP	3AF6	20
CPSF-30–NS1A complex	CPSF-30: zinc fingers 2 and 3; NS1A: effector	2RHK	29
CstF			
Rna14–Rna15 complex	Rna14: full length; Rna15: hinge	4EBA, 4E8S, 4E6H	37
Rna14–Rna15 complex	Rna14: monkeytail; Rna15: hinge	2L9B	40
CstF-50	homodimerization	2XZ2	39
Rna15	RRM	2X1B	44
Rna15–RNA complex	RRM	2X1A, 2X1F	44
Rna15–Hrp1–RNA complex	Rna15: RRM; Hrp1: RRM	2KM8	43
CF I_m			
CF I _m 25	full length	3BAP, 2CL3, 3BHO, 2J8Q	50, 51
CF I _m 25–RNA complex	full length	3MDG, 3MDI	52
CF I _m 25–CF I _m 68 complex	CF I _m 25: full length; CF I _m 68: RRM	3Q2S	53
CF I _m 25–CF I _m 68–RNA complex	CF I _m 25: full length; CF I _m 68: RRM	3Q2T	53
CF I _m 25–CF I _m 59 complex	CF I _m 25: full length; CF I _m 59: RRM	3N9U	unpublished (2010)
PAP			
PAP γ	core	4LT6	74
PAP–Fip1 complex	PAP: full length; Fip1: NTD fragment	3C66	23
PAPD1		3PQ1	77
cytoplasmic polyadenylation			
CPE-binding protein (CPEB)	ZZ domain	2M13	86
symplekin-Ssu72			
symplekin	NTD	3ODR, 3ODS, 3GS3, 3O2T	88, 146
Ssu72	full length	3OMW, 3OMX, 3FDF	147
Ssu72–Pol II CTD pSer5 complex	full length	3P9Y	98
symplekin–Ssu72 complex	Symplekin: NTD; Ssu72: full length	3O2S	88
symplekin–Ssu72–Pol II CTD pSer5 complexes	Symplekin: NTD; Ssu72: full length	3O2Q, 4IMJ, 4IMI	88, 97
symplekin–Ssu72–Pol II CTD pSer7 complexes	Symplekin: NTD; Ssu72: full length	4H3H, 4H3K	99
histone mRNA 3'-end processing			
SLBP–RNA complex	RBD fragment	2KJM	148
SLBP–3'hExo–RNA complex	SLBP: RBD; 3'hExo: full length	4L8R	112
SLBP–SLIP1 complex	SLBP: fragment; SLIP1: full length	4JHK	106
mRNA 5'-end capping quality surveillance			
DXO–RNA complexes	full length	4J7L, 4J7M	143
DXO–m ⁷ GpppG complex	full length	4J7N	143
Dxo1	full length	4GPU, 4GPS	142
Dom3Z (DXO)	full length	3FQI	140
Dom3Z–GDP complex	full length	3FQJ	140
Rai1	full length	3FQG	140
Rat1–Rai1 complex		3FQD	140

addition, auxiliary sequence elements can be recognized, which may also help alter the site of 3'-end processing by APA.

A large protein machinery is responsible for 3'-end processing in mammals, which consists of several subcomplexes such as cleavage and polyadenylation specificity factor (CPSF), cleavage stimulation factor (CstF), cleavage factor I (CF I_m), CF II_m, and other protein factors such as poly(A) polymerase (PAP), symplekin, and Ssu72 (Figure 1). CPSF-73 (the 73 kDa subunit of CPSF) is the endoribonuclease for the cleavage reaction. CPSF-160 recognizes the PAS, and CstF-64 recognizes the DSE. This large machinery ensures the fidelity of 3'-end processing, supports APA in response to specific molecular and cellular environments, and is also connected to the DNA damage response.¹⁵ Moreover, many protein factors in the machinery communicate with other transcription processes, such as Pol II initiation and termination. A

proteomic study identified more than 90 protein factors that may be associated with the pre-mRNA, although the exact roles of many of these proteins in 3'-end processing remain to be established.¹⁶

Similarly, pre-mRNA 3'-end processing in yeast also involves a large protein machinery. Many of the protein factors have homologues in the mammalian machinery, although the subcomplexes in yeast can have compositions and functions different from those of the subcomplexes in mammals. For example, yeast CF IA contains Rna14 and Rna15, the homologues of mammalian CstF-77 and CstF-64, respectively. CF IA also contains Clp1 and Pcf11, which belong to CF II_m in mammals (Figure 1). CF II in yeast contains Ysh1, Ydh1, and Yhh1, which are homologues of CPSF-73, CPSF-100, and CPSF-160, respectively. CF II also contains Pta1, the homologue of symplekin, while the other two subunits of

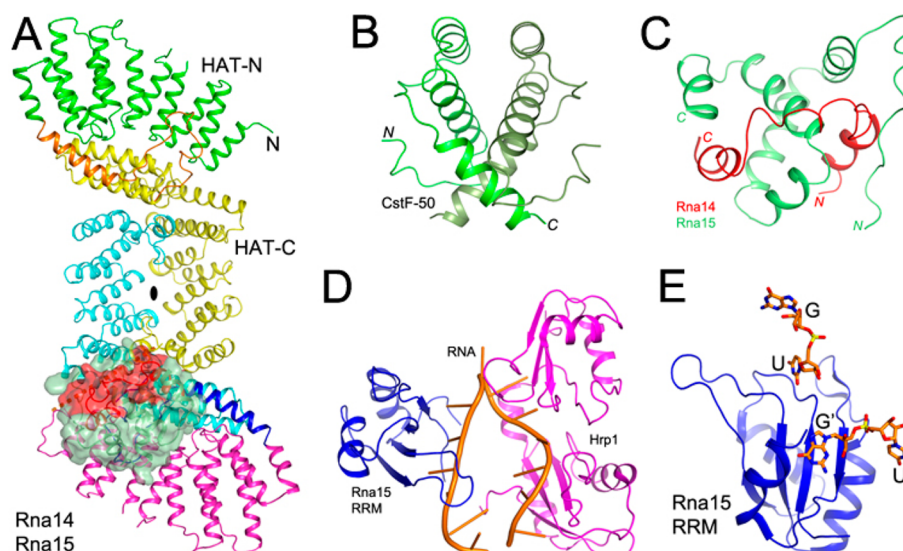


Figure 3. Recently published structures of the CstF subunits and their homologues. (A) Structure of the *K. lactis* Rna14–Rna15 dimer (PDB entry 4EBA).³⁷ Only one copy of the complex between the Rna14 C-terminal Pro-rich segment (red) and the Rna15 hinge region (pale green) is ordered (shown as a molecular surface). (B) Structure of the *Drosophila* CstF-50 N-terminal domain dimer (PDB entry 2XZ2).³⁹ (C) Structure of the heterodimer of the Pro-rich segment of Rna14 (red) with the hinge region of Rna15 (pale green) (PDB entry 2L9B).⁴⁰ (D) Structure of the yeast Rna15 RRM (blue)–Hrp1 (magenta)–RNA (orange) complex (PDB entry 2KM8).⁴³ (E) Structure of the yeast Rna15 RRM–RNA complex (PDB entry 2X1F).⁴⁴ The binding site at the top (RNA labeled GU) mediates specific recognition. The RNA in front of the β -sheet (labeled G'U') is related by crystal symmetry to the GU RNA and is not specifically recognized.

and/or decay.^{18,19} Recently published structures of CPSF-73 homologues from two different archaeal species revealed the presence of two type II K homology (KH) RNA-binding motifs at the N-terminus, as well as the formation of a homodimer via the C-terminal region of the metallo- β -lactamase domain (Figure 2A). The RNA is likely recognized by the KH domains in one monomer and cleaved by the active site in the other monomer.^{20–22} This mechanism may be unique to archaea as mammalian CPSF-73 and its yeast homologue Ysh1 do not contain KH domains at the N-terminus.

Fip1, the yeast homologue of hFip1, tethers PAP to the processing machinery, which recognizes an intrinsically unstructured segment in Fip1 near its N-terminus (Figure 2B).²³ PAP mutants that retain polymerase activity but cannot bind Fip1 are nonetheless lethal, indicating that the Fip1–PAP interaction serves an essential function in yeast. An N-terminal deletion mutant of Fip1 in which this binding site is disrupted cannot complement the loss of wild-type Fip1, but the mutant is fully functional if it is fused directly to PAP.²⁴

CPSF-30 is targeted by the C-terminal effector domain of the nonstructural protein (NS1A) from the influenza A family of viruses,^{25–27} and the viral polymerase stabilizes this complex.²⁸ NS1A binding inhibits host antiviral responses such as production of type I interferon and activation of dendritic cells. The effector domain of NS1A is recognized by the second and third zinc fingers of CPSF-30, in a 2:2 heterotetrameric complex (Figure 2C).²⁹ Single-site mutations of NS1A residues in the interface prevent binding to CPSF-30, and an influenza virus carrying such a mutation in NS1A cannot inhibit interferon- β pre-mRNA processing and is attenuated in cells.

Arabidopsis thaliana CPSF-30 (AtCPSF-30) binds the A-rich near upstream element (NUE, which contains the AAUAAA motif) that is present in a subset of pre-mRNAs, located 10–30 nucleotides upstream of the cleavage site.³⁰ Binding of RNA by AtCPSF-30 is mostly mediated through the first of its three zinc fingers.³¹ AtCPSF-30 also possesses endonuclease activity,

which is mediated by its third zinc finger and inhibited by the N-terminal region of AtFip1(V), a plant homologue of Fip1.³¹ Loss of AtCPSF-30 results in an enhanced tolerance to oxidative stress because of the overexpression of proteins with thioredoxin- and glutaredoxin-like domains.³² The nuclease activity of AtCPSF-30 itself is redox-sensitive, as the third zinc finger contains a disulfide bond that stabilizes the overall structure of the protein.³³ Some of these properties may be unique to AtCPSF-30 as it is localized in the cytoplasm in the absence of other CPSF subunits.³⁴

CstF. CstF contains three subunits: CstF-50, CstF-64, and CstF-77. CstF-50 has a WD40 domain in the C-terminal region. CstF-64 has a RNA recognition module (RRM) at the N-terminus, followed by a hinge region, a Pro/Gly-rich region, and a small C-terminal domain (CTD). CstF-77 contains a HAT domain in the N-terminal region, followed by a Pro-rich region.

The crystal structure of the HAT domain of CstF-77 revealed a dimeric association, providing the first evidence that CstF may function as a dimer.^{35,36} The recently published crystal structure of the *Kluyveromyces lactis* Rna14–Rna15 complex also showed a dimeric association of this heterodimer into a heterotetramer, mediated by the HAT domain of Rna14 (Figure 3A).³⁷ Mutation of two residues in the HAT domain dimer interface caused a temperature-sensitive phenotype in yeast, and the cell extract was defective in cleavage and polyadenylation.³⁸ The structure of the N-terminal segment of CstF-50 is also a dimer (Figure 3B).³⁹ Overall, the structures as well as biochemical studies support a stable, dimeric association of the CstF complex. While Rna14 and Rna15 are dimeric in the CF IA complex in yeast, Clp1 and Pcf11 may actually be monomeric, giving an overall 2:2:1:1 stoichiometry for the complex.³⁸

The interactions between Rna14 and Rna15 are mediated by the C-terminal Pro-rich region of Rna14 and the hinge region of Rna15 (Figure 3C).^{37,40} The formation of the CstF-64–

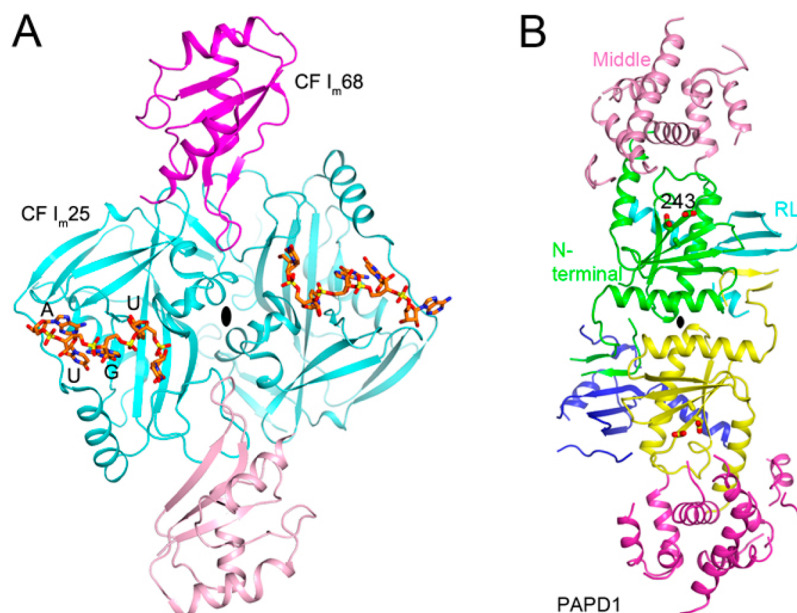


Figure 4. Structures of CF I_m and PAPP1. (A) Structure of the human CF I_m 25 (cyan)–CF I_m 68 (magenta)–UGUA RNA (orange) complex dimer (PDB entry 3Q2T).⁵³ (B) Structure of the human mitochondrial PAPP1 D325A mutant dimer (PDB entry 3PQ1).⁷⁷ The domains are shown in different colors. The catalytic residues are shown as stick models.

CstF-77 complex is also important for the nuclear localization of CstF.⁴¹ CstF-77 contains a poly(A) site within its intron 3, and the usage of this site depends on the expression levels of CstF-77, resulting in a negative feedback mechanism.⁴²

The amino acid sequences of the RRM of CstF-64 and Rna15 are ~50% identical, but the RRM displays distinct sequence preferences for RNA. CstF-64 recognizes the G/U-rich DSE, while Rna15 recognizes the A-rich positioning element (PE) in yeast. This distinct preference for Rna15 may be due to Hrp1, which constitutes CF IB but does not have a counterpart in the mammalian machinery. A crystal structure of the Rna15 RRM–Hrp1–RNA complex showed that the A-rich RNA interacts with the surface of the RRM β -sheet (Figure 3D),⁴³ which is the canonical mode of RNA recognition for RRM. On the other hand, a crystal structure of Rna15 RRM in complex with U-rich RNA, in the absence of Hrp1, shows that the RRM has a second, noncanonical RNA binding surface, which involves conserved loops above the β -sheet of the RRM (Figure 3E).⁴⁴ The interaction between Hrp1 and the Rna14–Rna15 dimer has also been studied by NMR, and a model for the Rna14–Rna15–Hrp1–RNA complex has been proposed.⁴⁵

The regulation of the RNA preference of Rna15 by Hrp1 may have important functional relevance. If there are two copies of Rna15 and only one copy of Hrp1 in the yeast 3'-end processing machinery, the two copies of Rna15 may bind to two different sequence elements in the transcript, one being A-rich and the other U- or G/U-rich. This may explain why 3'-end processing is enhanced by the addition of U-rich sequences between the PE and the cleavage site in the absence of Hrp1.⁴⁴ Whether CstF-64 has a binding partner that is functionally homologous to Hrp1 to facilitate an A-rich sequence preference has not been determined. Musashi1, a mammalian homologue of Hrp1, with a similar RNA binding mode,⁴⁶ is known to bind to the 3'-UTR of mRNAs but exerts its control at the translation level rather than the transcription level. Such regulation of the RNA preference of CstF-64 could also be important for its function in APA.

A second isoform of CstF-64 in mammals, CstF-64 τ , was originally thought to be restricted to the testis and brain, although recent studies suggest that it is more widely expressed.⁴⁷ CstF-64 τ may complement the function of CstF-64. Moreover, a dimeric CstF complex could include one copy each of CstF-64 and CstF-64 τ , which could be another mechanism for regulating 3'-end processing and APA. In addition, a family of splicing variants of CstF-64 has been identified, known as β CstF-64, which may have roles in APA in neuronal cells.⁴⁸

CF I_m . CF I_m is comprised of two subunits: CF I_m 25 and CF I_m 68. CF I_m 25 has a Nudix nucleotide hydrolase fold but lacks hydrolase activity. CF I_m 68 is the most common second subunit, but there are alternative 59 and 72 kDa subunits. These three proteins contain an N-terminal RRM, a central Pro/Gly-rich region, and a C-terminal Arg/Ser-, Arg/Asp-, and Arg/Glu-rich segment. CF I_m binds UGUA elements and is typically positioned 40–50 nucleotides upstream of the cleavage site.⁴⁹

Several crystal structures have been reported for this complex over the past few years, which have greatly enhanced our understanding of its molecular mechanism.^{50–54} The structures show that CF I_m is a heterotetramer, with a central CF I_m 25 dimer and two CF I_m 68 monomers bound to opposite sides of the CF I_m 25 dimer (Figure 4A).^{53,54} The two Nudix domains in the CF I_m 25 dimer are arranged antiparallel to each other, which would require the two UGUA *cis* elements of the pre-mRNA to make a 180° turn to bind to them simultaneously (Figure 1). The two RRM of CF I_m 68 enhance RNA binding by ~3-fold and promote RNA loop formation but are dispensable.

CF I_m has a key role in APA^{49,55,56} and in the export of mRNA from the nucleus.⁵⁷ Knockdown of the 25 and 68 kDa subunits in HEK293 cells increased the extent of global use of proximal poly(A) sites. On the other hand, knockdown of CF I_m 59 has no effect on poly(A) site choice. Therefore, the CF I_m 25–CF I_m 68 complex promotes the selection of distal

poly(A) sites, producing mRNAs with an extended 3'-UTR that may be subject to specific 3'-UTR-mediated regulation. CF I_m68 interacts with the nuclear export machinery through the Thoc5 protein of the TREX complex and the nuclear export receptor NXF1/TAP and shuttles between the nucleus and the cytoplasm.⁵⁸ Knockdown of Thoc5 also promotes the usage of proximal poly(A) sites.⁵⁹

CF I_m68 is recruited by the capsid protein of HIV⁶⁰ and helps the virus to evade host innate immune recognition.⁶¹ A C-terminal deletion of CF I_m68 promotes HIV-1 capsid disassembly.⁶²

CF II_m. CF II_m comprises two subunits: hClp1 and hPcf11. hClp1 contains three domains: N-terminal, central, and C-terminal domains. The central domain contains a Walker A P-loop motif and can bind ATP. hPcf11 contains a Pol II C-terminal domain (CTD) interaction domain (CID) at the N-terminus, two zinc fingers, a short sequence between the two zinc fingers that interacts with Clp1,⁶³ and other sequence motifs. Their homologues in yeast, Clp1 and Pcf11, belong to CF IA and interact with Rna14 and Rna15. An equivalent interaction between CF II_m and CstF in mammalian cells has not been demonstrated. In addition to the Clp1–Pcf11 interface identified from earlier studies,⁶³ there may be a “distant” binding site for Pcf11 on Clp1.^{64,65}

hClp1 exhibits ATP hydrolase activity and plays an important role in pre-tRNA splicing^{66–68} as well as pre-mRNA 3'-end processing. Yeast Clp1 does not have ATP hydrolase activity but still requires ATP binding for its function. Yeast cells carrying Clp1 mutations in the ATP binding pocket, which induce a conformational change but do not occlude ATP binding, are not viable.^{65,69} The correct conformation of Clp1 induced by ATP binding may be essential for interactions with other protein factors in the machinery, including Ssu72, Ysh1, Pta1, and Rna14. Clp1 may therefore be an important structural protein in the machinery, which is supported by the observation that reconstitution of CF IA from individual components requires Clp1.⁶⁴ Clp1 may contribute to gene looping and transcriptional directionality at bidirectional promoters, possibly through its interaction with Ssu72.

hClp1 may also compete with the mRNA nuclear export factor Aly (Yra1 in yeast) for binding to hPcf11, and yeast Clp1 can displace Yra1 from Pcf11 in affinity experiments.⁷⁰ Recombinant Yra1 inhibits *in vitro* CF IA-mediated cleavage and polyadenylation reactions.⁷¹

PAP. CPSF stimulates the activity of PAP so that it processively extends the poly(A) tail, the length of which is regulated by the nuclear poly(A)-binding protein (PABPN1).⁷² Once the tail reaches ~250 nucleotides, PABPN1 interferes with this stimulation. PABPN1 can also stimulate PAP and cause hyperadenylation, which can mediate RNA degradation by the exosome.⁷³

A recently published structure of the human PAP γ core,⁷⁴ from the γ clade of mammalian PAPs, confirms the three-domain core structure shared among the canonical PAPs, with N-terminal, middle, and C-terminal domains (Figure 2B).

Noncanonical PAPs have very weak conservation of sequence with respect to that of canonical PAPs and lack the C-terminal domain in the core.^{75,76} Some of these enzymes catalyze the oligo- or polyuridylation of their substrates and are also known as poly(U) polymerases (PUPs) or terminal uridylylate transferases (TUTs or TUTases). The structure of human mitochondrial PAPD1 reveals a dimer of this enzyme, involving a RL (RNA-binding domain-like) domain unique to

this enzyme (Figure 4B), and biochemical studies suggest that dimerization is required for PAPD1 activity.⁷⁷ PAPD1 can use all four nucleotides as substrates *in vitro*, and how it achieves nucleotide specificity in the mitochondria is currently not known. Structures of other noncanonical PAPs (TUTs) have also been reported.⁷⁶

Cytoplasmic Polyadenylation. Cytoplasmic polyadenylation is important for the post-transcriptional control of gene expression through the reactivation of deadenylated and dormant but otherwise intact cytoplasmic mRNAs, which is directed by the presence of a cytoplasmic polyadenylation element (CPE) in the 3'-UTR of the mRNAs.^{78,79} The CPE is bound by the regulatory cytoplasmic element binding protein (CPEB), which in turn interacts with many other proteins to regulate cytoplasmic polyadenylation and mRNA translation. This CPEB complex contains competing deadenylase (PARN) and PAP (Gld2) enzymes to regulate the length of the poly(A) tail.⁸⁰ CPEB-dependent protein synthesis plays a key role in synapse formation and long-term memory persistence in sensory neuron–motor neuron cultures,⁸¹ and CPEB prion-like multimerization is associated with changes in synapse persistence.⁸²

Many protein factors can affect the expression of their target mRNA by binding to CPEB and freeing the mRNA for polyadenylation and translation.⁷⁹ For example, translation of the mRNA for tumor suppressor p53 is promoted by the interaction between CPEB and noncanonical PAP Gld4⁸³ and inhibited by overexpression of CPEB in the absence of Gld2.⁸⁴ Another tumor suppressor protein, parafibromin, also exerts control over cell fate through its interaction with CPEB⁸⁵ and affects the translation of multiple genes.

CPEB also recruits several protein factors of the canonical, nuclear 3'-end processing machinery, including CPSF and symplekin, for cytoplasmic polyadenylation. A recent solution structure of the C-terminal zinc-binding domain of CPEB reveals a structural similarity to ZZ-type zinc fingers, which are known to facilitate protein–protein interactions with sumoylated proteins.⁸⁶ Both symplekin and CPSF are known to be sumoylated, suggesting a possible mechanism for how CPEB recognizes these factors.

Symplekin–Ssu72–Pol II CTD Complex. Symplekin is a scaffold protein and mediates interactions among many proteins in the 3'-end processing machinery. The yeast homologue, Pta1, shares very weak sequence conservation with symplekin but has generally equivalent protein partners. The N-terminal domain (NTD) of symplekin/Pta1 interacts with Ssu72, a central region with CstF-64/Pti1 (a yeast homologue of Rna15), and a C-terminal domain with CPSF-73/Ysh1.^{87–89}

Ssu72 is a Pol II CTD phosphatase and has functions in 3'-end processing as well as gene looping,⁹⁰ which helps to maintain correct transcription directionality and prevents transcription of certain noncoding RNAs from bidirectional promoters.⁹¹ The Pol II CTD contains heptapeptide repeats (26 in yeast and 52 in humans) with the Tyr1-Ser2-Pro3-Thr4-Ser5-Pro6-Ser7 consensus sequence, and the phosphorylation state of the CTD regulates the function of Pol II.^{92–94} Ssu72 is a well-characterized pSer5 phosphatase and has recently been reported to have pSer7 phosphatase activity, as well.^{95,96}

The recent crystal structure of the symplekin NTD in complex with Ssu72 and a Pol II CTD pSer5 peptide defines the detailed interactions in this ternary complex (Figure 5A).⁸⁸ Although the NTD–Ssu72 interface is ~25 Å from the active

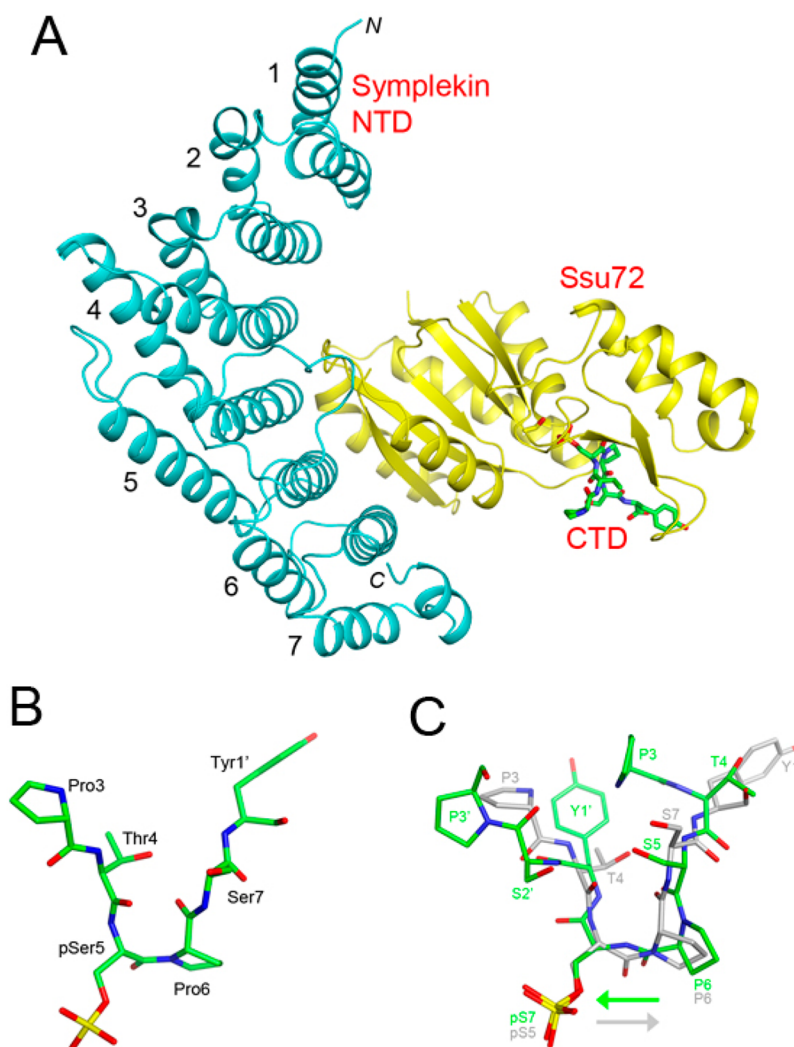


Figure 5. Structures of human symplekin NTD–Ssu72–Pol II CTD phosphopeptide complexes. (A) Structure of the human symplekin NTD (cyan)–Ssu72 (yellow)–Pol II CTD pSer5 phosphopeptide (green) complex (PDB entry 3O2Q).⁸⁸ The seven pairs of antiparallel helices are labeled. (B) Mode of binding of the Pol II CTD pSer5 peptide in the active site of Ssu72. (C) Overlay of the modes of binding of the Pol II CTD pSer7 peptide (green) and the pSer5 peptide (gray) in the active site of Ssu72 (PDB entry 4H3H).⁹⁹ The directions of the polypeptide backbones are denoted by the arrows. The primed numbers indicate residues in the second CTD repeat.

site of Ssu72, the NTD can stimulate the phosphatase activity of Ssu72, indicating that symplekin is not just a passive scaffold in the 3'-end processing machinery.

The structure also reveals that the pSer5–Pro6 peptide bond of the Pol II CTD assumes the *cis* configuration in the active site of Ssu72 (Figure 5B), the first time that a protein phosphatase (or protein kinase) has been shown to recognize the *cis* configuration of the substrate. Subsequent structures of another ternary complex (with pThr4 and pSer5)⁹⁷ as well as an Ssu72–phosphopeptide binary complex⁹⁸ confirmed this finding. The peptidyl-prolyl isomerase Pin1 enhances the dephosphorylation activity of Ssu72.⁸⁸ The symplekin NTD can regulate the function of Ssu72 in transcription-coupled 3'-end processing with the HeLa cell nuclear extract.⁸⁸ Studies in yeast show that the Pta1 NTD can inhibit 3'-end processing, and binding of Ssu72 to the NTD relieves this inhibition.⁸⁷

The binding mode of the pSer5 peptide in the active site of Ssu72 contrasts with its reported pSer7 phosphatase activity, as it could require that the pSer7–Tyr1 peptide bond be in the *cis* configuration. The crystal structure of the symplekin NTD–Ssu72–Pol II CTD pSer7 peptide ternary complex showed that

the peptide, with all its amide bonds in the *trans* configuration, is bound in the reverse orientation compared to that of the pSer5 peptide in the active site of Ssu72 (Figure 5C).⁹⁹ The substrate and the general acid for catalysis are misaligned in this complex. *In vitro* assays using peptide substrates indicate that the pSer7 phosphatase activity is ~4000-fold weaker than the pSer5 phosphatase activity. On the other hand, assays with the entire CTD as the substrate, using antibodies to monitor dephosphorylation, showed no differences between the two activities. The reason behind this discrepancy is currently not known. A CTD peptide phosphorylated at Ser2, Ser5, and Ser7 is bound exclusively with pSer5 in the active site, suggesting that Ssu72 has a higher affinity for pSer5 than for pSer7.⁹⁹

■ REPLICATION-DEPENDENT HISTONE PRE-MRNA 3'-END PROCESSING

Metazoan replication-dependent (also known as canonical) histone proteins H1, H2A, H2B, H3, and H4 are involved in *de novo* chromatin packaging during DNA replication, while variant histones, notably, H3.3, H2A.Z, CENP-A, macroH2A, and H1.0, are important for chromatin remodeling, centromere

3'hExo belongs to the DEDD family of 3'-5' exonucleases and prefers single-stranded RNA as the substrate. The activity of 3'hExo requires two Mg²⁺ cations coordinated by four invariant acidic residues (DEDD) in its active site. In addition to the nuclease domain, 3'hExo also contains an N-terminal SAP domain, previously characterized as a nucleic acid binding motif.¹⁰⁹ 3'hExo trims up to two nucleotides from the 3'-end of histone mRNAs after cleavage, and it also participates in the rapid decay of histone mRNAs at the end of the S phase.¹¹⁰ In addition to its roles in histone mRNA metabolism, 3'hExo is critical for trimming the 3'-end of the 5.8S rRNAs¹¹¹ and regulating microRNA homeostasis.

The recently published crystal structure of the human SLBP RBD-3'hExo-SL ternary complex provided the first molecular insights into the architecture of this complex (Figure 6B).¹¹² The stem adopts the conformation of A-form RNA, and three of the four bases of the loop are flipped out. The SLBP RBD interacts with the 5'-flanking sequence, the 5'-arm of the stem, and the loop of SL. The SAP domain of 3'hExo interacts with the loop, and the nuclease domain with the 3'-arm and flanking sequence. In particular, the last nucleotide of the SL is located in the active site of the nuclease domain, explaining how 3'hExo can trim the last two nucleotides of the histone mRNA after cleavage.

The observed binding mode is consistent with most of the mutagenesis data on this complex. Only the guanine base in the second base pair of the stem is specifically recognized, by the side chain of Arg181 in SLBP (Figure 6D), which explains why this nucleotide is invariant in all metazoans. The structure indicates that SLBP and 3'hExo primarily recognize the shape, rather than the sequence, of the SL.

There are no direct contacts between the SLBP RBD and 3'hExo in the ternary complex (Figure 6C). The cooperative binding between the two proteins observed earlier likely results from the induced-fit behavior of the SL, as there are large conformational differences between the SL in the complex versus that free in solution.¹¹² Therefore, binding of one protein induces a conformation of the SL that promotes the binding of the other protein.

HDE and U7 snRNP. HDE recruits the U7 snRNP through base pairing with the 5'-extension of U7 snRNA.¹⁰¹ The heptameric Sm ring of U7 snRNP contains Sm proteins B, D3, E, F, and G that are found in spliceosomal snRNPs as well as two unique subunits, Sm-like proteins Lsm10 and Lsm11. Lsm11 is a 40 kDa protein in humans, which is substantially larger than the typical Sm protein (~13 kDa). It has a unique N-terminal segment that is mostly unstructured but is essential for histone pre-mRNA processing via the recruitment of other processing factors, including the zinc finger protein ZFP100 and FLASH (see below).

Other Processing Factors. Similar to polyadenylated mRNAs, CPSF-73 is the endoribonuclease for the cleavage reaction of replication-dependent histone pre-mRNAs.¹⁰² The cleavage site is also typically located after a CA dinucleotide, located five (in vertebrates) or four (in fruit fly and sea urchin) nucleotides downstream of the stem.¹⁰³ The 5'-end-capped and 3'-end-cleaved histone mRNA, accompanied by SLBP and 3'hExo, is then exported into the cytoplasm by the antigen peptide transporter.

Besides CPSF-73, several other protein factors in the canonical 3'-end processing machinery are also important for histone pre-mRNA 3'-end processing, including CPSF-100, symplekin, CstF-64, and CstF-77.^{113,114} These proteins form

the heat labile factor (HLF), discovered in the 1980s as an essential component of the histone pre-mRNA 3'-end processing machinery,¹¹⁵ and are recruited to the machinery through FLASH.

FLASH (FLICE-associated huge protein) was initially identified as a 220 kDa proapoptotic protein that is part of the death-inducing signaling complex (DISC).¹¹⁶ Only a small segment of ~140 residues at the N-terminus of FLASH, especially a Leu-Asp-Leu-Tyr motif, is required for recruiting the various protein factors for histone pre-mRNA processing.¹¹⁷⁻¹²¹ This segment also has tight interactions with Lsm11, which brings FLASH to the 3'-end of histone pre-mRNAs.

The central region of FLASH recruits arsenite resistance protein 2 (ARS2).¹²² ARS2 directly binds to histone mRNAs and interacts with the nuclear cap-binding complex (CBC).¹²³ The CBC-ARS2 complex can stimulate the 3'-end processing of histone mRNAs, presumably through CBC's interactions with the negative elongation factor (NELF) and SLBP.¹²³⁻¹²⁵

The 100 kDa zinc finger protein (ZFP100) interacts with both SLBP and U7 snRNP and is crucial for efficient 3'-end processing.¹²⁶ It contains a poorly conserved N-terminal domain and a C-terminal domain that is comprised of 18 C2H2-type zinc fingers. Overexpression of ZFP100 greatly enhances the 3'-end processing of a reporter RNA that mimics histone pre-mRNAs, while overexpression of the components of the U7 snRNP alone does not, indicating that ZFP100 is the limiting factor for histone pre-mRNA processing. The primary role of ZFP100 is probably to bridge the SLBP-SL complex with the U7 snRNP-HDE complex, thereby stabilizing the overall processing machinery.

Phosphorylation of Thr4 in the Pol II CTD is required for histone 3'-end processing.¹²⁷ It is also required for Pol II transcription elongation.¹²⁸ The kinase that phosphorylates Thr4 is CDK9, which also targets NELF.^{127,129} CDK9 is recruited to histone genes by the nuclear protein ataxia-telangiectasia locus (NPAT), the expression of which is negatively regulated by p53.¹³⁰ It remains unclear how the Pol II CTD communicates with the integral components of the histone pre-mRNA 3'-end processing machinery.

Cell Cycle Regulation of Histone Pre-mRNA 3'-End Processing. The demand for histones during the S phase of the cell cycle is enormous, and an estimated 10⁸ molecules of each of the five histones are synthesized within a period of several hours.¹³¹ Levels of histone mRNA increase by 35-fold at the beginning of the S phase, through transcription activation (3.5-fold increase) and enhanced pre-mRNA processing (10-fold increase). At the conclusion of the S phase, or through inhibition of DNA synthesis in the S phase, levels of histone mRNA are reduced back to the G1 phase baseline.

SLBP is a key factor in the regulation of histone mRNA levels, and the level of this protein correlates with those of histone mRNAs during the cell cycle. In late G1 phase, inhibition of protein degradation and activation of translation synergistically increase the level of SLBP.¹³² At the end of the S phase, several residues in the N-terminal segment of SLBP (including Ser20, Ser23, Thr60, and Thr61) are phosphorylated, which facilitates its polyubiquitination and rapid clearance by the ubiquitin-proteasome system.^{107,108} Pin1 may also have a role in facilitating the phosphorylation of Ser20 and Ser23, and the dephosphorylation of Thr171.¹⁰⁸

On the other hand, artificial inhibition of DNA replication in the S phase has little effect on the cellular levels of SLBP,

indicating the existence of other mechanism(s) for regulating histone levels.

■ A NOVEL QUALITY SURVEILLANCE MECHANISM FOR MRNA 5'-END CAPPING

The 5'-end 7-methylguanosine (m^7G) cap is a significant contributor to mRNA splicing, nuclear export, translation, stability, and other processes.^{133,134} The cap is added cotranscriptionally and attached to the terminal nucleotide of the RNA by an unusual 5'-5' triphosphate linkage. Capping proceeds in three steps: conversion of 5'-end-triphosphorylated RNA (pppRNA, the primary transcript of Pol II) to diphosphorylated RNA (ppRNA), coupling to GMP to produce capped RNA (GpppRNA), and methylation to produce $m^7GpppRNA$ (Figure 7). A mature, methylated cap is essential for recognition by the cap-binding complex, CBC and eIF-4E, which coordinate many of the functions attributed to the cap.^{135,136}

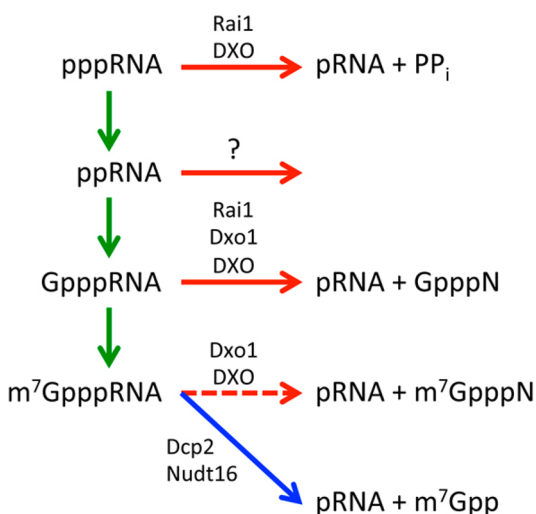


Figure 7. Reactions for pre-mRNA 5'-end capping and quality control. Reactions in the capping pathway are denoted by the green arrows. The intermediates in the capping pathway are recognized by the DXO family enzymes (Rai1, Dxo1, and DXO) for degradation (red arrows). The fate of the ppRNA is currently not known, although it may be possible that Rai1 and DXO also mediate its degradation. The reaction catalyzed by the classical decapping enzymes (Dcp2 and Nudt16) is denoted by the blue arrow. DXO and Dxo1 can also remove the mature cap but generate a different product (dashed red arrow).

Removal of the cap (decapping) is a regulated process catalyzed by at least two Nudix hydrolase enzymes, Dcp2 and Nudt16,^{137,138} which release m^7GDP (m^7Gpp) and 5'-end-monophosphorylated RNA (pRNA) (Figure 7). Six additional Nudix proteins possessing decapping activity *in vitro* have also been reported,¹³⁹ although the functional role of these putative decapping enzymes in cells remains to be determined.

Until recently, it was generally accepted in the field that capping always proceeds to completion, and a quality control mechanism was not known (or deemed necessary). However, if there are defects in 5'-end capping, the intermediates of the capping pathway (pppRNA, ppRNA, and GpppRNA) could accumulate in cells, because Dcp2 and Nudt16 predominantly function on mature $m^7GpppRNA$ and have minimal activity on these intermediates.¹³⁷ They are also protected against

degradation by 5'-3' exoribonucleases (XRN), which are only active against pRNA substrates.

A novel family of enzymes that possess RNA 5'-end pyrophosphohydrolase (PPH, releasing pyrophosphate PP_i), decapping, and/or distributive 5'-3' exoribonuclease activity was recently discovered. These enzymes include Rai1^{140,141} and Ydr370C/Dxo1¹⁴² in yeast and Dom3Z/DXO in mammals.¹⁴³ These decapping exonucleases (DXO family of enzymes) primarily act on incompletely capped mRNAs, converting them to substrates for degradation by XRN or their own exonuclease activity (Figure 7). These biochemical activities are strongly suggestive of a hitherto unrecognized mRNA 5'-end capping quality surveillance mechanism, helping to clear transcripts with incompletely capped 5'-ends. Functional studies in yeast and mammalian cells have confirmed the presence of defects in 5'-end capping and demonstrated the importance of the DXO family enzymes in this quality control mechanism.

Biochemical Properties of the DXO Family Enzymes.

The DXO activities were first identified, unexpectedly, from studies on yeast Rai1, the protein partner of the nuclear 5'-3' exoribonuclease Rat1.¹⁴⁰ The crystal structure of Rai1 revealed a large pocket lined with conserved residues, some of which coordinate a divalent metal ion at the bottom of the pocket. This indicated that Rai1 is an enzyme, although no catalytic activities were known for it at the time. Further studies demonstrated that Rai1 has PPH activity¹⁴⁰ and decapping activity toward GpppRNA, while it has much weaker activity toward the mature $m^7GpppRNA$.¹⁴¹ Moreover, the product of decapping is GpppN, the entire cap structure, in contrast to Dcp2 and Nudt16, which release m^7GDP (m^7Gpp) (Figure 7).

Rai1 has a weak sequence homologue in yeast, Dxo1 (Ydr370C). Biochemical studies showed that it has decapping activity (toward both GpppRNA and $m^7GpppRNA$) as well as a distributive 5'-3' exoribonuclease activity, although it lacks PPH activity.¹⁴²

The mammalian homologue of Rai1, DXO (previously known as Dom3Z), has all three activities, PPH, decapping (toward both GpppRNA and $m^7GpppRNA$), and exonuclease.¹⁴³ These activities would allow DXO to single-handedly detect and degrade incompletely capped mRNAs. $m^7GpppRNAs$ are protected from DXO degradation by cap-binding proteins *in vivo*, indicating that mature mRNAs are insensitive to DXO. Therefore, DXO is expected to function preferentially on incompletely capped pre-mRNAs.

Structural Basis for the DXO Activities. Biochemical studies showed that mammalian DXO possesses three, apparently distinct, catalytic activities: PPH, decapping, and exonuclease. On the other hand, the RNA body produced by these activities is the same, 5'-end-monophosphorylated RNA (pRNA). Crystal structures of mouse DXO in complex with 5'-end-monophosphorylated RNA oligos, 5-mer RNA (pU5) (Figure 8A), and 6-mer RNA with phosphorothioate linkages to inhibit hydrolysis [pU(S)6] as well as the m^7GpppG cap analogue (Figure 8B) have defined the binding modes of the RNA substrate/product and revealed the molecular mechanism for the different activities.¹⁴³

The pU5 oligo is bound in the DXO active site as a product, with its 5'-end phosphate group mimicking the scissile phosphate of the substrate. A second metal ion is bound in the active site in the presence of this oligo, and a terminal oxygen atom of the 5'-end phosphate group is a bridging ligand to both metal ions (Figure 8C). The pU(S)6 oligo is bound in the active site as a substrate, revealing the recognition pocket

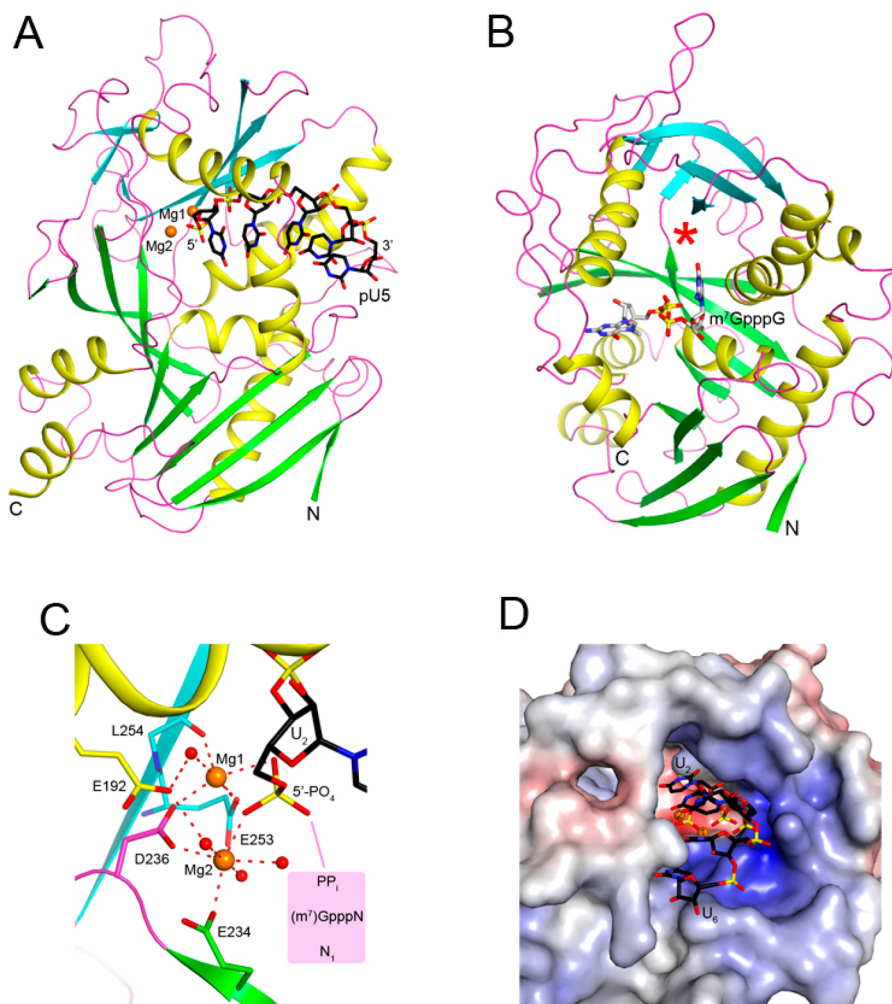


Figure 8. Molecular mechanism for the catalytic activities of DXO family enzymes. (A) Structure of mouse DXO in complex with pU5 oligo RNA (black stick models) (PDB entry 4J7L).¹⁴³ The two Mg²⁺ ions are shown as orange spheres. (B) Structure of mouse DXO in complex with the m⁷GpppG cap analogue (gray sticks) (PDB entry 4J7N). The expected location of the metal ions is indicated by the red star. The view is related to that of panel A by an ~60° rotation around the vertical axis. (C) Binding mode of the 5'-end phosphate group of pU5. This RNA is bound in the active site as the product. Binding of the pyrophosphate (PP_i), the cap structure [(m⁷)GpppN], or the first nucleotide (N₁) on the other side of the catalytic machinery explains the three catalytic activities. (D) The active site of DXO is located at the bottom of a deep pocket, which is large enough to accommodate only ssRNA.

for the first nucleotide (especially its 5'-phosphate) for the 5'-3' exonuclease activity. However, there are disruptions to the conformation of this oligo at the scissile bond caused by the incorporation of the phosphorothioate linkages and the fact that only one metal ion (Ca²⁺, to prevent hydrolysis) is present in the active site.

The structures demonstrate that the same active site machinery supports the three activities, and it is the distinct binding modes of the substrates that determine the outcome of the reaction. The 5'-end PP_i pyrophosphate, (m⁷)GpppN cap, or the first nucleotide is bound on the other side of the catalytic machinery from the RNA body (Figure 8C). An attack on the scissile phosphate group, likely by a water/hydroxide coordinated to one of the metal ions, then leads to the hydrolysis.

At the same time, different DXO family enzymes have distinct biochemical activity profiles. For example, Rai1 has PPH and GpppRNA decapping activities but no exonuclease activity, while DXO has all the activities (Figure 7). Further studies are needed to elucidate the molecular mechanisms of these differences.

The DXO family enzymes share four conserved sequence motifs.¹⁴² Motif I is an Arg residue and recognizes the 5'-phosphate group of the pRNA substrate and pppRNA. Motif II, GΦXΦE (where Φ is an aromatic or hydrophobic residue and X any residue), provides a ligand to the metal ion [Glu192 in mouse DXO (Figure 8C)]. Motif III, EhD (where h is a hydrophobic residue), is ligated to both metal ions in the pU5 complex [Glu234 and Asp236 (Figure 8C)]. Motif IV, EhK, provides a ligand to the metal ion (Glu253), and the Lys residue is likely to stabilize the transition state of the reaction.

The structures of the DXO family enzymes have a remote relationship to that of D-(D/E)XK nucleases,^{142,144,145} which include some viral and phage nucleases. However, there is little sequence conservation with these enzymes, and only the Asp residue of motif III (EhD) and motif IV (EhK) [the D-(D/E)XK motif] are shared among them. The level of structural conservation outside of these two motifs is much lower among these enzymes. The D-(D/E)XK enzymes also include some type II restriction endonucleases, such as HincII, EcoRV, EcoRI, BamHI, and BglI,¹⁴² but the level of structural conservation with the DXO family enzymes is much lower.

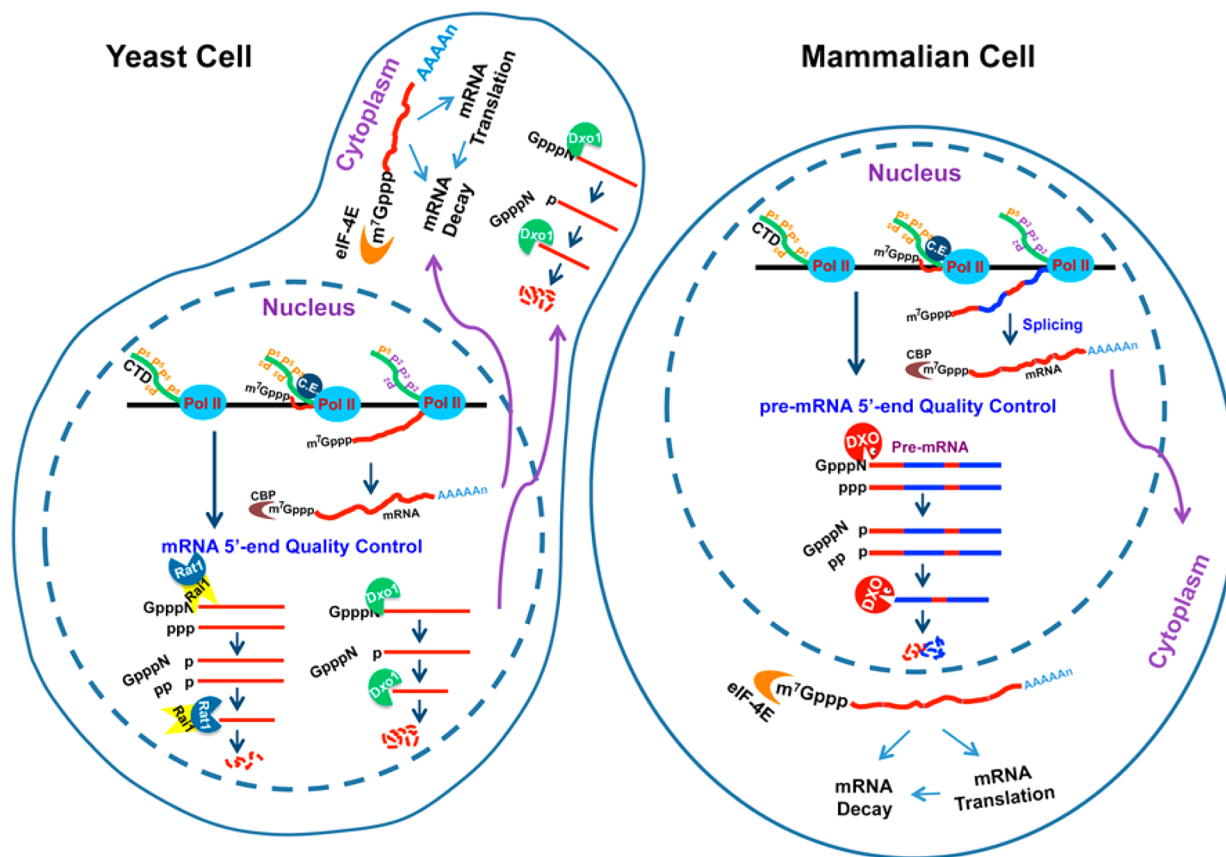


Figure 9. DXO family enzymes function in 5'-end capping quality control. In eukaryotes, pre-mRNAs are transcribed in the nucleus by Pol II and processed into mature mRNAs by the addition of a 5'-end cap, intron splicing, and 3'-end cleavage and polyadenylation. The mature mRNAs are exported to the cytoplasm for protein translation. In yeast cells, incompletely capped Pol II RNA transcripts are subjected to degradation by the Rai1–Rat1 decapping–exonuclease heterodimer, which detects and degrades 5'-end uncapped RNA or 5'-end unmethylated capped RNA in the nucleus. Dxo1, which is predominantly but not exclusively in the cytoplasm, decaps and degrades unmethylated capped Pol II transcripts. In mammalian cells, the incompletely capped Pol II RNA transcripts are substrates for DXO, which decaps and exonucleolytically degrades the defectively capped pre-mRNA prior to further splicing and 3'-end processing. Collectively, the DXO enzymes can hydrolyze the 5'-end of incompletely capped RNAs to expose the 5'-end of the RNA to subsequent exonucleolytic decay (by Dxo1 and DXO directly or by the Rai1–Rat1 heterodimer) in a 5'-end capping quality control mechanism to maintain RNA fidelity. CE is the capping enzyme and CBP the cap-binding protein.

For example, the active site of the DXO family enzymes is located at the bottom of a deep pocket (Figure 8D), which is consistent with their exonuclease, decapping, and PPH activity. In comparison, the active site of the type II enzymes is much more open, in line with their endonuclease activity.

Functions of DXO Family Enzymes in 5'-End Capping Quality Control. Functional studies in yeast cells harboring a deletion of Rai1 and/or Dxo1 reveal a role for these proteins in ensuring the integrity of mRNA 5'-end caps. Incompletely capped mRNAs were observed in *rail1Δ* cells following nutritional stress (glucose or amino acid starvation), suggesting that Rai1 is necessary for their detection and degradation.¹⁴¹ Moreover, incompletely capped mRNAs are detected under normal, nonstress growth conditions in *rail1Δdxo1Δ* doubly disrupted yeast strains.¹⁴² Collectively, these findings demonstrate that incompletely capped transcripts are normally generated in yeast cells (Figure 9), providing direct evidence that the capping process is less efficient than initially envisioned.

In addition, the fact that a double disruption of *Rai1* and *Dxo1*, but not individual disruptions, is required for the accumulation of incompletely capped mRNAs during nonstress conditions indicates that the Rai1 and Dxo1 proteins function redundantly in the surveillance mechanism to detect and

degrade incompletely capped transcripts. On the other hand, *Dxo1* cannot complement the loss of *Rai1* under nutritional stress conditions. It remains to be determined whether the incompletely capped transcripts are generated as a consequence of intrinsic stochastic inefficiency of the capping process or an indication that capping is normally a regulated process in which not all primary transcripts are destined to acquire a methylated cap.

Functional studies in human embryonic kidney 293T cells confirm the importance of DXO in ensuring mRNA 5'-end capping quality.¹⁴³ A decrease in the DXO level in these cells through shRNA knockdown results in a significant accumulation of unprocessed pre-mRNAs (with splicing and polyadenylation defects) with minimal changes in mature mRNA levels. These unprocessed pre-mRNAs harbor incompletely capped 5'-ends, while the mature mRNAs contain an m⁷G cap. These data indicate that incompletely capped pre-mRNAs do not undergo further processing (splicing or polyadenylation), while the normally capped pre-mRNAs are licensed to undergo processing (Figure 9).

While earlier studies had demonstrated a link between capping quality and splicing of the first intron, the accumulated pre-mRNAs in DXO knockdown cells show retention of all the introns tested, irrespective of their positions.¹⁴³ Therefore, the

data suggest that incompletely capped pre-mRNAs are inefficiently spliced at all introns. These pre-mRNAs also have compromised 3'-end processing, consistent with earlier reports that the cleavage step is facilitated by the 5'-end cap.

The reported findings demonstrate that incompletely capped transcripts are generated in mammalian cells and define a novel link between capping and pre-mRNA processing. They also indicate that the capping process may function as a critical checkpoint that determines whether a pre-mRNA should be further processed (Figure 9). DXO serves as a surveillance protein in a 5'-end capping quality control mechanism to clear incompletely capped pre-mRNAs.

■ FUTURE PERSPECTIVES

Structural, biochemical, and functional studies over the past few years have provided great new insights into pre-mRNA 3'-end processing in eukaryotes, and we are gaining a better understanding of the molecular mechanisms for the functions of various proteins in the 3'-end processing machineries in yeast and humans. However, this is still a burgeoning field of research, and there is much to learn about the architecture of these machineries and the regulation of their cellular functions, for example, in APA. It is also important to understand how the core machineries can acquire post-translational modifications and additional protein factors in response to specific cellular conditions or localizations. Further characterizations of the molecular mechanism and cellular functions of cytoplasmic polyadenylation will be another important area for research.

The discovery of the 5'-end capping quality surveillance mechanism has opened up a new field of research. For the first time, it is apparent that the capping step does not always proceed to completion. An important unanswered question is whether this is simply a consequence of the intrinsic inefficiency of the capping process or a regulated event to modulate subsequent pre-mRNA processing by controlling cap addition. If the latter is true, what are the components involved and how are the decisions about which pre-mRNAs are capped made? Regardless of how incompletely capped transcripts are generated, important future studies in this area also include defining the genomewide and cellular impacts of 5'-end capping quality surveillance, as well as the molecular mechanism of how the authenticity of the 5'-end cap influences pre-mRNA splicing and polyadenylation.

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Funding

This research is supported by grants from the National Institutes of Health (NIH) to L.T. (GM077175 and GM090059) and M.K. (GM067005). A.R.J. was also supported by the NIH training program in Cellular and Molecular Foundations of Biomedical Science (GM008798).

Notes

The authors declare no competing financial interest.

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