The International Journal of Biochemistry & Cell Biology 44 (2012) 1847–1851

Contents lists available at SciVerse ScienceDirect

The International Journal of Biochemistry & Cell Biology

journal homepage: www.elsevier.com/locate/biocel

Signalling Networks in Focus

Signals from noncoding RNAs: Unconventional roles for conventional pol III transcripts

Shanshan Hu[a], Jing Wu[a,b], Liang Chen[a], Ge Shan[a,*]

[a] School of Life Science, University of Science and Technology of China, 443 Huangshan Road, Hefei, Anhui Province 230027, China
[b] School of Life Science and Technology, Huazhong University of Science and Technology, 1037 Luoyu Road, Wuhan, Hubei Province 430074, China

ARTICLE INFO

Article history:
Received 14 May 2012
Received in revised form 6 July 2012
Accepted 9 July 2012
Available online 20 July 2012

Keywords:
Pol III
Noncoding RNA
tRNA
5S rRNA
7SL RNA

ABSTRACT

A range of noncoding RNAs are transcribed by pol III. A lot of them such as tRNA, 7SL RNA, 7SK RNA, 5S RNA, MRP RNA, Y RNAs, H1 RNA, and vault RNAs are considered as "house keeping" RNAs essential for eukaryotic cells. In recent years, researchers started to recognize the existence of unconventional functions of many pol III transcripts other than classical "house keeping" roles. Therefore, these ncRNAs could now be viewed as molecules with functional regulatory signals as well as cellular building blocks. These noncoding RNAs, all transcribed by pol III, may assemble regulatory networks with analogy to signaling pathways in eukaryotic cells. In this review we discuss these unconventional roles of pol III transcripts.

1. Introduction

Eukaryotes possess three main RNA polymerases; pol I, II, and III. Each of the three RNA polymerases transcribes specific classes of genes. pol I transcribes only ribosomal RNA genes while pol II transcribes the protein-coding genes as well as many noncoding RNA (ncRNA) genes. Interestingly, a range of ncRNAs are transcribed by pol III, being mainly derived from three types of promoters (Fig. 1). pol III contains the largest number of subunits (17 subunits) among all three RNA polymerases. pol III transcripts include highly conserved ncRNAs involved in many important metabolic processes. Recently, researchers have begun to reveal their "unconventional" functions other than the classical "house-keeping" roles. Therefore, these so called "house-keeping" RNAs are more than functional building blocks in a majority of eukaryotic cells, but rather serve as molecules carrying signals for regulating cell physiology as well.

2. Key molecules and their functions with associated pathologies

2.1. tRNA

tRNAs transport amino acids into ribosomes and decipher triplets of nucleotides at each codon of mRNAs. Moreover, a "non-translational" function of some tRNAs is to serve as primers for reverse transcription for retroviruses (Mak and Kleiman, 1997).

Unexpectedly high levels of tRNAs has long been connected with cancers as well. Winter et al. (2000) demonstrated that tRNAs were overproduced consistently in human ovarian cancers. Moreover, overexpression of initiator $tRNAi^{Met}$ is oncogenic (Marshall et al., 2008). Overexpression of $tRNAi^{Met}$ not only promotes cell cycle but also allows immortalized fibroblasts to generate tumors in mice. These results indicate that $tRNAi^{Met}$ could be involved in tumorigenic transformation (Marshall et al., 2008).

In addition to the role of tRNA in tumor transformation, recent research suggests that tRNA can also inhibit caspase activation. Mei et al. (2010) reported that microinjection of tRNA in cells inhibited cytochrome c-induced apoptosis. Mitochondrial tRNAs along with cytosolic tRNAs bind to cytochrome c to impair the interaction of cytochrome c with Apaf-1, a caspase activator, and prevent the apoptosome formation (Mei et al., 2010). This finding raises the possibility that mitochondrial tRNAs may play a key role in determining cellular response to apoptotic stimuli.

2.2. 7SK RNA

7SK is a small nuclear RNA (snRNA) about 330 nucleotides (nt) in length. The 3′ end of 7SK RNA binds strongly to LARP7/PIP7S to form snRNP, which may prevent 7SK RNA from degradation (Bayfield et al., 2010). The long 5′ stem–loop of 7SK RNA binds to the HEXIM1 protein (Lebars et al., 2010). 7SK snRNP utilizes HEXIM proteins (HEXIM1 or HEXIM2) to bind the positive

* Corresponding author. Tel.: +86 551 3606274.
E-mail addresses: shange@ustc.edu.cn, shange1@hotmail.com (G. Shan).

1357-2725/$ – see front matter © 2012 Elsevier Ltd. All rights reserved.
http://dx.doi.org/10.1016/j.biocel.2012.07.013

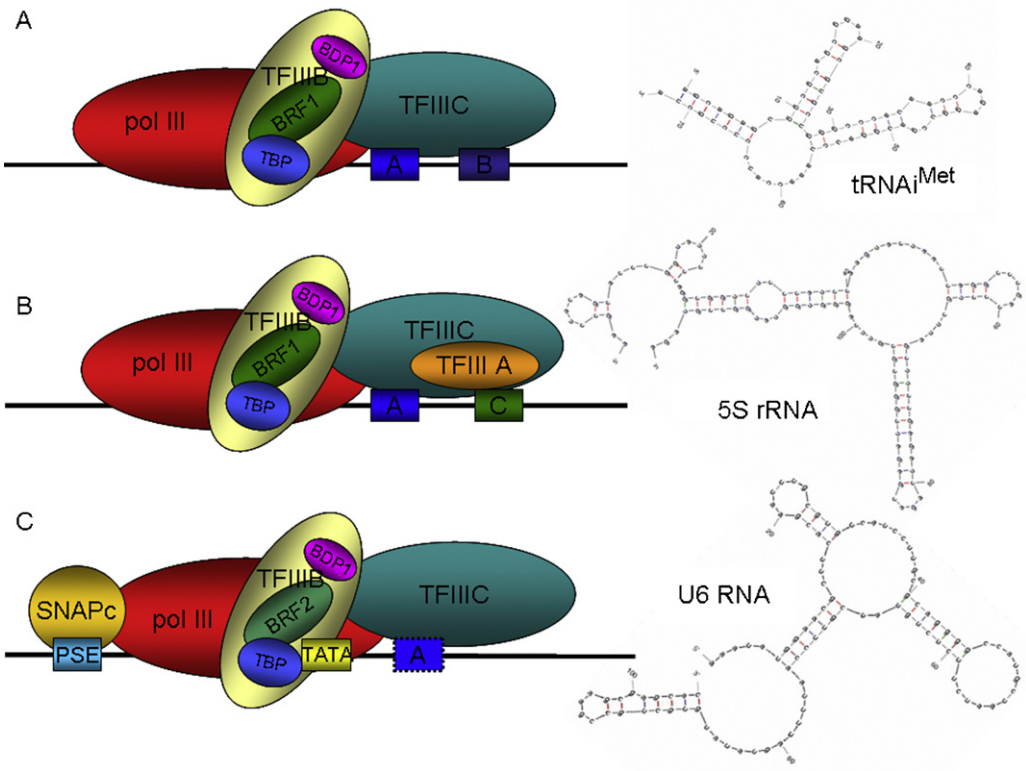

Fig. 1. Transcriptional machinery and structures of RNA pol III transcripts. pol III promoters have three types. (A) Most pol III-transcribed genes, for example, tRNA genes have sequence blocks A and B in the transcribed region. The A and B boxes are recognized by TFIIIC. TFIIIC recruits TFIIIB, which is composed of BDP1, BRF1 and TBP. Secondary structure of $tRNAi^{Met}$ was shown. (B) The second type internal promoters are characteristic of 5S rRNA gene, which needs the binding of an additional TFIIIA to a C site compared to the first type. Secondary structure of 5S rRNA was shown. (C) The third type internal promoters are characteristic of U6 snRNA genes. These promoters contain a TATA box, which is bound by TBP, and PSEs (proximal sequence elements), which is bound by SNAPc (small nuclear RNA activating protein complex) factor. Site A may or may not be present in this type of promoters. Secondary structure of U6 RNA was shown. RNA structures were predicted with mfold software (Zuker, 2003) with human sequences.

transcription elongation factor b (P-TEFb). P-TEFb has an activity of cyclin dependent kinase-9 when binding with some other proteins (Nguyen et al., 2001). Studies have demonstrated key functions of 7SK RNA in regulating pol II transcriptional activity (Nguyen et al., 2001; He et al., 2008). Although details are unclear, some research has shown that 7SK snRNP indirectly regulates the activity of P-TEFb (He et al., 2008). 7SK-HEXIM1-P-TEFb complex inhibits the cyclin dependent kinase-9 activity of P-TEFb, which then phosphorylates the C-terminal domain (CTD) of pol II. The phosphorylation status of CTD determines the transition of pol II from transcriptional initiation to elongation.

Treatments such as UV irradiation or low concentration of the transcriptional inhibitor actinomycin D promote the transcriptional transactivator, Tat, and increase transcriptional level of HIV-1 (He and Zhou, 2011). Tat binds 7SK snRNP containing P-TEFb, and this binding results in the release of P-TEFb from 7SK snRNP; Tat subsequently associates with P-TEFb, and then binds to the HIV transactivation response element, which is required for activating the transcription of HIV 5′ LTR (long terminal repeat) promoter. Thus, 7SK can affect the transcription of HIV genome (He and Zhou, 2011; Barrandon et al., 2008).

2.3. MRP RNA

MRP RNA is a RNA component of the RNase MRP (mitochondrial RNA processing) complex, which is an essential eukaryotic ribonucleoprotein endoribonuclease involved in many biochemical processes.

The central region of MRP RNA is important for transportation of MRP complex into mitochondria. Without the central region of MRP RNA, the MRP complex would not be present in mitochondria. However, the MRP complex is not mitochondria specific and most MRP complex is in the nucleolus. The nucleolar localization of MRP complex is mediated by its protein subunits (Martin and Li, 2007). MRP RNA plays an essential role in the enzymatic activity of RNase MRP complex at different cellular locations. RNase MRP is initially isolated from mouse mitochondria, which can cleave the mitochondrial RNA transcripts to generate primers for the replication of leading strand of mitochondrial DNA. The RNase MRP complex has the ability to specifically cleave the precursor of ribosomal RNA (rRNA) at the A3 site to form small 5.8S rRNA in the nucleus of *Saccharomyces cerevisiae* (Mattijssen et al., 2010).

In addition to pre-rRNA, CLB2 mRNA is another direct target for the RNase MRP complex. CLB2 mRNA normally disappears rapidly as the completion of mitosis, but RNase MRP mutations lead to increase of CLB2 mRNA level, which subsequently causes late anaphase delay. Tina Gill et al. (2004) demonstrated that RNase MRP complex specifically cleaved the 5′ UTR of CLB2 mRNA at the end of mitosis to remove the 5′cap to allow rapid 5′–3′ degradation by the Xrn1 nuclease. The result showed a new mechanism of mRNA degradation, which is crucial for controlling the cell cycle in *S. cerevisiae* (Gill et al., 2004). Similar function may exist in higher eukaryotic organisms since RNase MRP is highly conserved.

A more striking role of MRP RNA has been reported recently (Maida et al., 2009). The human telomerase reverse transcriptase catalytic subunit (TERT) was found to interact with MRP RNA, thus forming a ribonucleoprotein complex that has RNA-dependent RNA polymerase (RdRP) activity. The RdRP activity can produce double-stranded RNAs, which can then be processed into small interfering RNA in a Dicer-dependent manner (Maida et al., 2009).

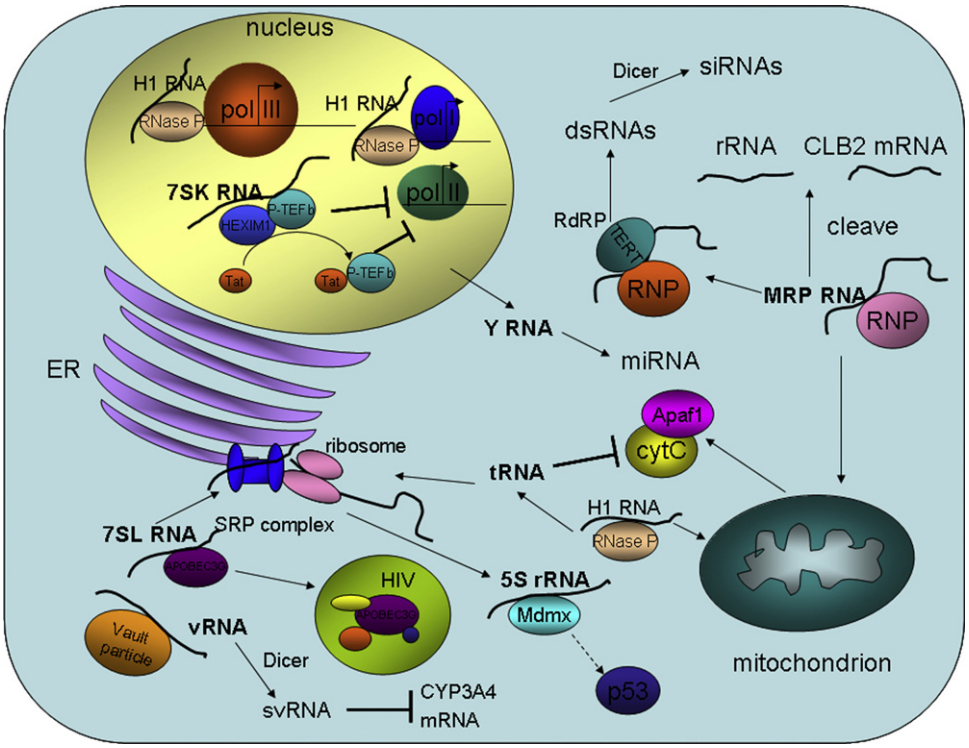

Fig. 2. Unconventional roles of pol III transcripts in nucleus and cytoplasm. Some classical pol III transcripts including tRNA, MRP RNA, 7SL RNA, 5S rRNA, Y RNA, vault RNA, and H1 RNA are shown in the picture. Detailed information about their unconventional roles is discussed in each section of the main text.

2.4. 7SL RNA

7SL RNA is a component of the signal recognition particle (SRP) in eukaryotes. SRP is a cytoplasmic ribonucleoprotein complex guiding nascent peptide chains and membrane proteins to the endoplasmic reticulum. Mammalian SRP is formed by 7SL RNA and six proteins (SRP9, SRP14, SRP19, SRP54, and the SRP68/72 heterodimer). 7SL RNA is composed of an Alu domain, an S domain, and a linker region. 7SL RNA is the structural center of SRP, and it offers binding sites for the six SRP proteins. Satoh et al. (2005) found that autoantibodies against 7SL RNA can be served as novel serological markers for a subset of polymyositis/dermatomyositis (PM/DM) cases on the basis that autoantibodies against SRP were detected in patients with PM/DM.

Recently, it is shown that 7SL RNA is an abundant component of infectious human immunodeficiency virus type 1 (HIV-1) (Onafuwa-Nuga et al., 2006). Zhang et al. (2010) demonstrated that the viral ribonucleoprotein (RNP) complex contained 7SL RNA, Gag, viral genomic RNA, and $tRNA^{Lys3}$. 7SL RNA is a key cofactor of the antiviral APOBEC3G, which is a cytidine deaminase enzyme upon its packaging into multiple retroviruses. APOBEC3G inhibits replication of HIV-1 in the absence of the viral protein Vif, which is an E3 ubiquitin ligase and can induce the degradation of APOBEC3G. Reduction of 7SL RNA packaging into HIV-1 impaired APOBEC3G antiviral function (Wang et al., 2007).

2.5. 5S rRNA

5S rRNA is a ~120 nt RNA existing in almost all eukaryotic ribosomes, except ribosomes in mitochondria of some species. 5S rRNA can form a complex with ribosomal protein L5, which keeps the stability of RNA-binding partners of L5 in eukaryotes (Ciganda and Williams, 2011). RNA-binding partners of L5 include pre-tRNAs, U6 RNAs, and 5S rRNA (Wolin and Cedervall, 2002). 5S rRNA-L5 complex can be transported to the nucleus and incorporated into the large ribosomal subunit for ribosomal assembly. Interestingly, Hammond et al. found a plant RNA P5SM, which is similar to 5S rRNA in both sequence and structure. P5SM bound to L5 and regulated alternative splicing of TFIIIA (transcription factor IIIA) pre-mRNA (Hammond et al., 2009). TFIIIA not only recognizes promoter sequence of the 5S rRNA gene but also binds to 5S rRNA for its stabilization in cytosol. Increased TFIIIA expression upregulated the synthesis of 5S rRNA. The interaction of P5SM, TFIIIA and the ribosomal protein L5 regulated the expression of 5S rRNA (Hammond et al., 2009). The discovery of P5SM offers a new insight into understanding the ribosomal protein–mRNA interaction.

The main role of 5S rRNA is linked with ribosomal proteins. However, it also interacts with various other protein complexes in cells. Li and Gu found that 5S rRNA interacted with Mdmx-associated complexes in human cells. 5S rRNA bound to the RING domain of Mdmx (aa 437–490) and blocked Mdmx degradation by Mdm2. This finding shows that 5S rRNA acts as a critical regulator for Mdmx stability besides its classic role in translation (Li and Gu, 2011). Both Mdmx and Mdm2 are crucial negative regulators in the activity of P53 (Wang, 2011). Knockdown of endogenous 5S rRNA induced Mdmx degradation and subsequently activated p53-dependent growth arrest (Li and Gu, 2011).

2.6. Y RNA

Y RNAs (about 100 nt) function with Ro60, La, and some other proteins to form Ro RNPs (Ro ribonucleoprotein particles) in human cells (Fabini et al., 2001). Y RNAs could regulate the subcellular distribution of Ro60 with binding to Ro60 also being modulated during cellular stress (Sim et al., 2009). Ro RNPs are associated with chromosomal DNA replication and are required for DNA replication in human cells, although the detailed mechanisms are still unclear (Christov et al., 2006). Ro RNPs proteins are not required for the role of Y RNA in chromosomal DNA replication in a human cell-free system, but Y RNA was involved in different cellular

regulatory pathways depending on the associated proteins (Langley et al., 2010).

Another study showed that human Y RNAs were significantly overexpressed in human tumors and were required for proliferation of cancer cell. It suggests that Y RNAs could serve as novel biomarkers for identification or treatments of cancer (Christov et al., 2008). miRNA-sized fragments derived from Y RNAs were recently identified (miY RNAs), indicating that Y RNAs may be microRNA precursors, and that the biogenesis of the miY RNAs may be modulated by Ro60 (Verhagen and Pruijn, 2011).

2.7. Vault RNA

Vault RNAs (v RNAs) are about 100 nt RNAs contained in the vault particles of eukaryotic cells. Vault particles are conserved organelles existing in many species. Vaults consist of proteins such as MVP, vPARP, TEP1, and vRNAs, and have been known to be related to multidrug resistance for many years (Scheffer et al., 1995).

Intriguing research from Persson et al. (2009) showed that human vRNAs may have structures resembling microRNA precursors, and vRNAs could indeed generate small regulatory RNAs (svRNAs). svRNAs are produced in a Drosha-independent and Dicer-dependent mechanism that is different from conventional miRNA pathway. Furthermore, svRNA can also guide sequence-specific cleavage to regulate gene expression through a complex similar to the RISC. svRNAs use a miRNA-like mechanism to down-regulate CYP3A4, a significant drug-metabolizing enzyme (Persson et al., 2009).

2.8. H1 RNA

H1 RNA is the RNA subunit of human RNase P, a tRNA processing ribonucleoprotein responsible for generating 5′ end of mature tRNA. H1 RNA is a ribozyme with the endonucleolytic activity in RNase P (Kikovska et al., 2007).

Some work has shown surprising functions of RNase P as transcription factor for RNA polymerase I and III (Reiner et al., 2006, 2008). Targeted cleavage of H1 RNA altered enzyme specificity of RNase P and caused a significant reduction in transcription of several noncoding RNA genes, including 7SL RNA, 5S rRNA, and other pol III transcripts (Reiner et al., 2006). Furthermore, targeted cleavage of H1 RNA abolished transcription of the rDNA gene by pol I (Reiner et al., 2008).

H1 RNA is imported into mitochondria in a polynucleotide phosphorylase dependent manner (Wang et al., 2010). Very recently, it was found that a 20 nt stem-loop sequence from the H1 RNA is essential for the transporting of H1 RNA into mitochondria and that this sequence could be utilized to deliver RNA molecules into mitochondria as a potential treatment for mitochondrial genetic disorders (Wang et al., 2012).

3. Therapeutic implications

As we noted in the discussion above, pol III transcripts are found to be associated with a wide range of diseases. For example, tRNAs and 5S rRNA are associated with carcinogenesis and both 7SL and 7SK RNAs have roles in HIV infection. MRP RNA gene is mutated in the inherited pleiotropic syndrome cartilage-hair hypoplasia. These findings create novel opportunities for disease diagnosis and treatment. It has already been proposed that autoantibodies against 7SL RNA could be utilized as diagnostic markers for a subset of polymyositis/dermatomyositis cases (Satoh et al., 2005). Many noncoding RNAs, including some of "conventional" pol III transcripts discussed above, are also related to human diseases such as tumors (Lin et al., 2012).

Strategies such as external guide sequence (EGS), based on discoveries in pol III transcripts with therapeutic potential, have already been invented (Yuan and Altman, 1994; Shan, 2010). In EGS technology, an artificial oligoribonucleotide known as an external guide sequence can be introduced into cells with various methods, and this EGS molecule with its sequence complementation to the specific mRNA target would form a complex resembling to a tRNA precursor. This complex could then be cleaved by RNase P, which is an enzyme for generating mature 5′ end for tRNAs. RNase P itself in eukaryotic cells has a core component of pol III transcript (H1 RNA in human). EGS molecules have been used successfully as antibacterial, anticancer, or antiviral agents in laboratories (Lundblad and Altman, 2010).

Novel diagnostic and therapeutic methods may also result from research surrounding pol III noncoding RNAs, as compared to those based on understanding protein–protein interaction networks, although a long road lies ahead of bringing these into reality. One major concern among other hurdles in front of the coming new treatments is targeting the unconventional roles of pol III transcripts while maintaining their house-keeping roles.

In summary, researchers have just started to recognize the existence of unconventional functions of many pol III transcripts. Now, these molecules could be viewed as regulatory elements in cells. As shown in Fig. 2, these noncoding RNAs, all transcribed by pol III, assemble a regulatory network with analogy to signaling pathways in eukaryotic cells. Such novel roles for pol III transcripts may also provide therapeutic implications and opportunities. We also need to rethink about how the expression of these pol III transcripts is regulated, as one would expect that the expression of any molecule with a regulatory or signaling role would be under careful control. Furthermore, genomic regions of some pol III transcripts such as 5S rRNA and sets of tRNAs are organized as repeats. Therefore, more studies are needed to investigate transcriptional regulation and genomic stability in these regions. Based on these novel mechanistic insights, with the assistance of new technologies in molecule biology such as RNA interference (Shan, 2010), it is sure that more unconventional roles of so-called "house keeping" pol III transcripts will be uncovered as part of the fast-moving research field of ncRNAs.

Signaling network facts

- Some "house-keeping" pol III transcripts have regulatory roles in cells.
- pol III transcripts could serve as "signals" in normal cells or cells in diseases.
- All these novel roles of pol III transcripts may also provide therapeutic implications or opportunities.

Acknowledgments

Thanks for Dr. Keith Szulwach at Emory University for proofreading. Due to the limitation in text and number of references, we are sorry for missing a lot of excellent publications in this field. Ge Shan is supported by the State Key Development Program for Basic Research of China (973, 2011CBA01103), National Natural Science Foundation of China (31071132 and 81171074), grant 1731112304041 from CAS, grant WK2070000010 from USTC.

References

Barrandon C, Spiluttini B, Bensaude O. Non-coding RNAs regulating transcriptional machinery. Biology of the Cell 2008;100:83–95.

Bayfield MA, Yang R, Maraia RJ. Conserved and divergent features of the structure and function of La and La-related proteins (LARPs). Biochimica et Biophysica Acta 2010;1799:365–78.

Christov CP, Gardiner TJ, Szüts D, Krude T. Functional requirement of noncoding Y RNAs for human chromosomal DNA replication. Molecular and Cellular Biology 2006;26:6993–7004.
Christov CP, Trivier E, Krude T. Noncoding human Y RNAs are overexpressed in tumors and required for cell proliferation. British Journal of Cancer 2008;98:981–8.
Ciganda M, Williams N. Eukaryotic 5S rRNA biogenesis. Wiley Interdisciplinary Review RNA 2011;2:523–33.
Fabini G, Raijmakers R, Hayer S, Fouraux MA, Pruijn GJ, Steiner G. The heterogeneous nuclear ribonucleoproteins I and K interact with a subset of the Ro ribonucleoprotein-associated Y RNAs in vitro and in vivo. Journal of Biological Chemistry 2001;276:20711–8.
Gill T, Cai T, Aulds J, Wierzbicki S, Schmitt ME. RNase MRP Cleaves the CLB2 mRNA to promote cell cycle progression: novel method of mRNA degradation. Molecular and Cellular Biology 2004;24:945–53.
Hammond MC, Wachter A, Breaker RR. A plant 5S ribosomal RNA mimic regulates alternative splicing of transcription factor IIIA pre-mRNAs. Nature Structural and Molecular Biology 2009;16:541–9.
He N, Jahchan NS, Hong E, Li Q, Bayfield MA, Maraia RJ, et al. A La-related protein modulates 7SK snRNP integrity to suppress P-TEFb-dependent transcriptional elongation and tumorigenesis. Molecular Cell 2008;29:588–99.
He N, Zhou Q. New insights into the control of HIV-1 transcription: when Tat meets the 7SK snRNP and super elongation complex (SEC). Journal of Neuroimmunology and Pharmacology 2011;6:260–8.
Kikovska E, Svärd SG, Kirsebom LA. Eukaryotic RNase P RNA mediates cleavage in the absence of protein. Proceedings of the National Academy of Sciences of the United States of America 2007;104:2062–7.
Langley AR, Chambers H, Christov CP, Krude T. Ribonucleoprotein particles containing non-coding Y RNAs, Ro60, La and nucleolin are not required for Y RNA function in DNA replication. PLoS One 2010;5:e13673.
Lebars I, Martinez-Zapien D, Durand A, Coutant J, Kieffer B, Dock-Bregeon AC. HEXIM1 targets a repeated GAUC motif in the riboregulator of transcription 7SK and promotes base pair rearrangements. Nucleic Acids Research 2010;38:7749–63.
Li M, Gu W. A critical role for noncoding 5S rRNA in regulating Mdmx stability. Molecular Cell 2011;43:1023–32.
Lin M, Wu J, Shan G. Noncoding RNAs: different roles in tumorigenesis. Chinese Science Bulletin 2012;57:959–65.
Lundblad EW, Altman S. Inhibition of gene expression by RNase P. Nature Biotechnology 2010;27:212–21.
Maida Y, Yasukawa M, Furuuchi M, Lassmann T, Possemato R, Okamoto N, et al. An RNA-dependent RNA polymerase formed by TERT and the RMRP RNA. Nature 2009;461:230–5.
Mak J, Kleiman L. Primer tRNAs for reverse transcription. Journal of Virology 1997;71:8087–95.
Marshall L, Kenneth NS, White RJ. Elevated $tRNAi^{Met}$ synthesis can drive cell proliferation and oncogenic transformation. Cell 2008;133(1):78–89.
Martin AN, Li Y. RNase MRP RNA and human genetic diseases. Cell Research 2007;17:219–26.
Mattijssen S, Welting TJ, Pruijn GJ. RNase MRP and disease. Wiley Interdisciplinary Review RNA 2010;1:102–16.
Mei Y, Yong J, Liu H, Shi Y, Meinkoth J, Dreyfuss G, et al. tRNA binds to cytochrome c and inhibits caspase activation. Molecular Cell 2010;37:668–78.
Nguyen VT, Kiss T, Michels AA, Bensaude O. 7SK small nuclear RNA binds to and inhibits the activity of Cdk9/cyclin T complexes. Nature 2001;414:322–5.
Onafuwa-Nuga AA, Telesnitsky A, King SR. 7SL RNA, but not the 54-kd signal recognition particle protein, is an abundant component of both infectious HIV-1 and minimal virus-like particles. RNA 2006;12:542–6.
Persson H, Kvist A, Vallon-Christersson J, Medstrand P, Borg A, Rovira C. The non-coding RNA of the multidrug resistance-linked vault particle encodes multiple regulatory small RNAs. Nature Cell Biology 2009;11:1268–71.
Satoh T, Okano T, Matsui T, Watabe H, Ogasawara T, Kubo K, et al. Novel autoantibodies against 7SL RNA in patients with polymyositis/dermatomyositis. Journal of Rheumatology 2005;32:1727–33.
Scheffer GL, Wijngaard PL, Flens MJ, Izquierdo MA, Slovak ML, Pinedo HM, et al. The drug resistance-related protein LRP is the human major vault protein. Nature Medicine 1995;1:578–82.
Shan G. RNA interference as a gene knockdown technique. International Journal of Biochemistry and Cellular Biology 2010;42:1243–51.
Sim S, Weinberg DE, Fuchs G, Choi K, Chung J, Wolin SL. The subcellular distribution of an RNA quality control protein, the Ro autoantigen, is regulated by noncoding Y RNA binding. Molecular Biology of the Cell 2009;20:1555–64.
Verhagen AP, Pruijn GJ. Are the Ro RNP-associated Y RNAs concealing microRNAs? Y RNA-derived miRNAs may be involved in autoimmunity. Bioessays 2011;33:674–82.
Wang G, Chen HW, Oktay Y, Zhang J, Allen EL, Smith GM, et al. PNPASE regulates RNA import into mitochondria. Cell 2010;142:456–67.
Wang G, Shimada E, Zhang J, Hong JS, Smith GM, Teitell MA, et al. Correcting human mitochondrial mutations with targeted RNA import. Proceedings of the National Academy of Sciences of the United States of America 2012;109:4840–5.
Wang T, Tian C, Zhang W, Luo K, Sarkis PT, Yu L, et al. 7SL RNA mediates virion packaging of the antiviral cytidine deaminase APOBEC3G. Journal of Virology 2007;81:13112–24.
Wang X. p53 regulation: teamwork between RING domains of Mdm2 and MdmX. Cell Cycle 2011;10(December (24)):4225–9, Epub 2011 December 15.
Winter AG, Sourvinos G, Allison SJ, Tosh K, Scott PH, Spandidos DA, et al. RNA polymerase III transcription factor TFIIIC2 is overexpressed in ovarian tumors. Proceedings of the National Academy of Sciences of the United States of America 2000;97:12619–24.
Wolin SL, Cedervall T. The La protein. Annual Review of Biochemistry 2002;71:375–403.
Yuan Y, Altman S. Selection of guide sequences that direct efficient cleavage of mRNA by human ribonuclease P. Science 1994;263:1269–73.
Zhang W, Du J, Yu K, Wang T, Yong X, Yu XF. Association of potent human antiviral cytidine deaminases with 7SL RNA and viral RNP in HIV-1 virions. Journal of Virology 2010;84:12903–13.
Zuker M. Mfold web server for nucleic acid folding and hybridization prediction. Nucleic Acids Research 2003;31(13):3406–15.