

## Review Article

# The Mitochondrial Thioredoxin System

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### ABSTRACT

Eukaryotic organisms from yeast to human possess a mitochondrial thioredoxin system composed of thioredoxin and thioredoxin reductase, similar to the cytosolic thioredoxin system that exists in the same cells. Yeast and mammalian mitochondrial thioredoxins are monomers of approximately 12 kDa and contain the typical conserved active site WCGPC. However, there are important differences between yeast and mammalian mitochondrial thioredoxin reductases that resemble the differences between their cytosolic counterparts. Mammalian mitochondrial thioredoxin reductase is a selenoprotein that forms a homodimer of 55 kDa/subunit; while yeast mitochondrial thioredoxin reductase is a homodimer of 37 kDa/subunit and does not contain selenocysteine. A function of the mitochondrial thioredoxin system is as electron donor for a mitochondrial peroxiredoxin, an enzyme that detoxifies the hydrogen peroxide generated by the mitochondrial metabolism. Experiments with yeast mutants lacking both the mitochondrial thioredoxin system as well as the mitochondrial peroxiredoxin system suggest an important role for mitochondrial thioredoxin, thioredoxin reductase, and peroxiredoxin in the protection against oxidative stress. *Antiox. Redox Signal.* 2, 801–810.

### INTRODUCTION

#### *The cytosolic thioredoxin system*

**T**HIOREDOXINS (Trx) are small, globular proteins of 12 kDa that participate in many different cellular functions that are dependent on thiol-disulfide interchange reactions catalyzed by their conserved active site WCGPC, the common characteristic of all thioredoxins (Holmgren, 1989). Thioredoxins are maintained in their active reduced form by the flavoenzyme thioredoxin reductase (TrxR) at the expense of NADPH, which constitutes the so-called thioredoxin system (Holmgren, 1989).

Before the identification of the mitochondrial thioredoxin system, all organisms studied so far, from lower prokaryotes to humans, were shown to contain at least one active thioredoxin system. For example, *Escherichia coli*, a bacterial

model, contained one thioredoxin (Trx1) and one thioredoxin reductase. Trx1 and TrxR from this organism constitute the first thioredoxin system characterized as electron donor for the essential enzyme ribonucleotide reductase that converts ribonucleotides to deoxyribonucleotides (Jordan and Reichard, 1998). Apart from being an electron donor for ribonucleotide reductase, Trx1 can also function as electron donor for adenosine 3'-phosphate 5'-phosphosulfate (PAPS) reductase and methionine-sulfoxide reductase and is necessary for the life cycles of some bacteriophages such as T7, M13, and f1 (Chamberlin, 1974; Tsang and Schiff, 1976; Ejiri *et al.*, 1989; Lim *et al.*, 1985; Russel and Model, 1985). Thirty three years later, a second *E. coli* thioredoxin (Trx2) with an extension at the amino terminus was discovered and demonstrated to be responsible

for the maintenance of the reduced environment of the cytoplasm (Miranda-Vizuite *et al.*, 1997a; Stewart *et al.*, 1998).

The lower eukaryote *Saccharomyces cerevisiae* also contains two thioredoxins (Trx1 and Trx2) and one thioredoxin reductase, all present in the cytoplasm. Trx1 and Trx2 have been implicated in vacuole inheritance, decreasing the rate of DNA synthesis, increasing cell size and generation time, and making the yeast cells auxotrophic for methionine/cysteine (Gan, 1991; Muller, 1991, 1994, 1995; Xu and Wickner, 1996). *E. coli* Trx1 and *S. cerevisiae* Trx1 and Trx2 are very similar in structure and have no additional cysteines other than those at the active site. However, *E. coli* Trx2 contains four cysteine residues at the amino terminus that might modulate its function as regulator of the cytosolic redox environment (Miranda-Vizuite *et al.*, 1997a). The picture becomes more complicated when we go higher in the evolutionary tree. In photosynthetic organisms three types of thioredoxins have been identified: two forms in chloroplasts (f and m) that are involved in regulatory systems in oxygenic photosynthesis and one form in cytosol and endoplasmic reticulum (h) (Besse and Buchanan, 1997). However, mammalian cells have only one thioredoxin and one thioredoxin reductase located in the cytosol (Holmgren and Björnstedt, 1995). Mammalian Trx1 differs from the yeast and bacteria thioredoxins by the presence of additional (structural) cysteine residues that can regulate its enzymatic activity by oxidation and dimer formation (Weichsel *et al.*, 1996).

Many functions have been ascribed to mammalian thioredoxin, including those already described for *E. coli* or yeast protein like electron donor for ribonucleotide reductase or methionine-sulfoxide reductase (Holmgren, 1989). Among the additional functions for mammalian thioredoxins are the modulation of transcription factors DNA binding activity, regulation of cell growth, and apoptosis and antioxidant properties (Schallreuter and Wood, 1986; Spector *et al.*, 1988; Abate *et al.*, 1990; Matthews *et al.*, 1992; Nakamura *et al.*, 1994; Baker *et al.*, 1997; Hirota *et al.*, 1997; Saitoh *et al.*, 1998; Ueno *et al.*, 1999). Mammalian thioredoxin reductases are homodimers (55 kDa/subunit) and contain selenocysteine as the

penultimate residue. (Gladyshev *et al.*, 1996; Gromer *et al.*, 1998). This residue, together with the immediate anterior cysteine, constitutes an additional active redox center that has been shown to be necessary for enzymatic activity (Gorlatov and Stadtman, 1998; Gromer *et al.*, 1998; Nordberg *et al.*, 1998; Zhong *et al.*, 1998). Selenocysteine is encoded by an UGA codon that normally works as stop codon. This alternative reading of the genetic code is driven by a palindromic sequence in the 3'-untranslated region (UTR) of the mRNA named SECIS and it is essential to obtain active enzyme (Stadtman, 1996). Indeed, inactivation of this residue by selective alkylation or peptidase treatment abolishes enzymatic activity (Gorlatov and Stadtman, 1998; Gromer *et al.*, 1998; Nordberg *et al.*, 1998; Zhong *et al.*, 1998). A hypothesis of the catalytic mechanism of thioredoxin reductase has been proposed in which the reducing power from NADPH is sequentially transferred to FAD, the active site, and the Cys-Secys pair. This hypothesis also proposes that this last redox center is located in a flexible carboxy-terminal arm of the protein, thus explaining the broad range of substrates of thioredoxin reductase (Gromer *et al.*, 1998). Furthermore, mammalian thioredoxin reductase can also reduce thioredoxin but it can reduce lipid hydroperoxides, the cytotoxic peptide NK-lysin, and other low-molecular-weight metabolites like selenite, selenocysteine, selenogluthathione, vitamin K<sub>3</sub>, and alloxan (Björnstedt *et al.*, 1995; Holmgren and Björnstedt, 1995; Andersson *et al.*, 1996).

## THE MITOCHONDRIAL THIOREDOXIN SYSTEM

### *Mammalian mitochondrial thioredoxin*

We used degenerate oligonucleotides based on the sequence of the human Trx1 active site for screening of a mammalian cDNA library in an attempt to isolate novel thioredoxins or thioredoxin-like proteins. This approach allowed us to isolate a rat cDNA that coded for a protein with the typical conserved active site of thioredoxins and an amino-terminal extension with high content of positively charged residues and a potential  $\alpha$ -helix followed by  $\beta$ -

sheets, both typical features of mitochondrial targeting sequences (MTS) (Spyrou *et al.*, 1997). The prediction that this cDNA codes for a mitochondrial thioredoxin was also supported by evidence reported in 1990 by Bodenstein and Follman. They described a slightly larger form of Trx present in pig heart mitochondria with different electrophoretic mobilities compared with cytosolic Trx1 (Bodenstein and Follman, 1990). We named this protein Trx2 to distinguish it from the cytosolic Trx1 and confirmed its mitochondrial localization by GFP (A.E. Damdimopoulos, in preparation) and Western blot analysis (Spyrou *et al.*, 1997).

So far, homologues of Trx2 have been cloned from human (A.E. Damdimopoulos, in preparation), mouse, and bovine cDNA libraries (Miranda-Vizuet *et al.*, 1997b; Watabe *et al.*, 1997). The mature proteins are very similar (only two amino acids are different); however, the MTS of the four homologues contains a higher number of nonconserved residues (~30%). A potentially important difference between the mitochondrial and the cytosolic thioredoxin is the absence of structural cysteines in Trx2 (Trx1 has two or three depending on the organism). Thus, preincubation with dithiothreitol (DTT) is required to obtain fully active Trx1 by reduction of these structural cysteines, whereas Trx2 activity is independent of DTT treatment (Spyrou *et al.*, 1997). Trx2 mRNA is ubiquitously expressed with higher expression in tissues with a high metabolic rate like testis, skeletal muscle, cerebellum, or heart (Spyrou *et al.*, 1997).

#### *Mammalian mitochondrial thioredoxin reductase*

The discovery of a mitochondrial thioredoxin predicted the existence of a thioredoxin reductase in mitochondria to maintain Trx2 in its reduced active form. Several groups identified almost simultaneously human, mouse, rat, and bovine mitochondrial thioredoxin reductase, which we named TrxR2 to distinguish it from the previously characterized TrxR1 (Gasdaska *et al.*, 1999; Lee *et al.*, 1999; Miranda-Vizuet *et al.*, 1999a,b; Sun *et al.*, 1999; Watabe *et al.*, 1999). Similar to Trx2, mitochondrial thioredoxin reductase has an amino-terminal extension with all the above commented features of a MTS. The cleavage of this pre-

sequence would result in a 55-kDa mature protein containing the conserved FAD, NADPH, and interface domains. Furthermore, rat and bovine TrxR2 were shown to be homodimers, which is probably also true for the other homologues (Lee *et al.*, 1999; Watabe *et al.*, 1999). A SECIS element found in all TrxR2 homologues identified suggests that all TrxR2 are selenoproteins. So far only the bovine TrxR2 amino acid sequence has shown the presence of selenocysteine (Watabe *et al.*, 1999). TrxR2 mRNA is expressed in all human, mouse, and rat tissues tested with TrxR2 highly expressed in tissues with an intense metabolism like testis or skeletal muscle and thus is similar to mitochondrial thioredoxin (Lee *et al.*, 1999; Miranda-Vizuet *et al.*, 1999a,b).

#### *Genomic organization and chromosomal localization of human mitochondrial Trx2 and TrxR2*

The logarithmic increase of entries in the sequence databases as a consequence of large-scale projects to sequence different genomes including the human, has greatly facilitated the determination of the genomic organization of many genes. When we first attempted to identify the genomic organization and the chromosomal localization of human Trx2, this information was not available. Using specific primers for human Trx2 cDNA we amplified the Trx2 gene by PCR from human genomic DNA. The gene spans approximately 13 kb and consists of three exons separated by two introns of 4.2 and 9 kb, respectively. By fluorescence *in situ* hybridization (FISH) analysis, we identified the human Trx2 gene at chromosome 22q12.1-q13 (A.E. Damdimopoulos, in preparation). More recently, genomic clones (accession number HS1119A7) that contained the human Trx2 gene have become available in public databases and they confirm our data.

The genomic organization of the human TrxR2 gene was solved with the help of public sequence databases. Using the full-length human TrxR2 cDNA as template, we identified two overlapping cosmid clones (accession numbers AC000090 and AC000078) with high homology to TrxR2. Computer-assisted analysis confirmed that the whole genomic sequence of

human TrxR2 was contained in these two clones. The human TrxR2 gene consists of 18 exons spanning about 67 kb and, similarly to Trx2, also maps at chromosome 22 but at position 22q11.2 (Miranda-Vizuite *et al.*, 1999a). This syntenic group is maintained also in mouse and rat, thus allowing us to map the mouse TrxR2 gene to chromosome 16 at 11.2 centimorgans from the top linkage group and the rat TrxR2 gene at chromosome 11q23 (Miranda-Vizuite *et al.*, 1999b). Chromosome 22 is the second smallest among the human chromosomes, with the exception of the sex chromosome Y, and is the only one fully sequenced to this date (Dunham *et al.*, 1999). Many genes responsible for different diseases have been mapped at chromosome 22, including several types of tumors, leukemias, neurological and behavioral disorders, *etc.* (Dunham *et al.*, 1999). In particular, the velocardiofacial/DiGeorge syndrome locus is located at position 22q11 and is characterized by cardiovascular malformations, thymic hypoplasia, hypocalcemia due to hypoparathyroidism, and craniofacial and palatal abnormalities (Lindsay and Baldini, 1998). Human TrxR2 maps in the DiGeorge syndrome region and partially overlaps with the catechol-O-methyltransferase (*comt*) (Grossman *et al.*, 1992) gene, although in opposite orientation (Miranda-Vizuite *et al.*, 1999b). A *comt* gene knockout mouse lacking exons 2–4 displays a severe behavioral and neurological disorder phenotype (Gogos *et al.*, 1998). It is likely that this construct might also remove part of the putative promoter region of TrxR2 gene. Therefore, it is plausible to think that any of the phenotypes ascribed to the lack of *comt* gene could be in part due to a dysregulation of TrxR2, although this hypothesis requires further investigation.

#### *Saccharomyces cerevisiae* mitochondrial thioredoxin system

Yeast, in particular *Saccharomyces cerevisiae*, is one of the most used living models for the study of cellular processes. In addition to the advantage of simple bacteria-like laboratory protocols, it offers all the advantages of a complete eukaryotic system with all its particular subcellular organelles and metabolism. Furthermore, its genomic sequence has been determined,

making the identification of novel genes straightforward. We decided to investigate whether *S. cerevisiae* contained a mitochondrial thioredoxin system similar to the one found in mammals, with the main objective of finding other functions of the system. We identified two open reading frames (ORF) in *S. cerevisiae* (YCR083W and YHR106W) that displayed high homology with the two yeast cytosolic thioredoxins and thioredoxin reductase (Gan, 1991); they were named Trx3 and Trr2, respectively (Pedrajas *et al.*, 1999). The presence of a MTS at their amino terminus suggested that both proteins are located in the mitochondria, which was later confirmed by Western blot analysis. The yeast mitochondrial Trx3 contained two structural cysteines whereas the yeast cytosolic homologues had none, opposite to the mammalian where mitochondrial Trx2 lacks structural cysteines. Surprisingly, yeast Trx3 activity was not dependent on DTT preincubation and therefore not regulated by redox (Pedrajas *et al.*, 1999). Yeast mitochondrial thioredoxin reductase, Trr2, is closer to yeast Trr1 and prokaryotic homologues than to mammalian ones. It is also a FAD-containing homodimer, but each monomer is smaller than the mammalian, 37 kDa versus 55 kDa, because mammalian thioredoxin reductases have a longer interface domain. More importantly, it does not contain any selenocysteine residue, indicating a different catalytic mechanism compared to mammalian TrxR (Pedrajas *et al.*, 1999).

Yeast mutants lacking both mitochondrial proteins have been studied for their resistance to oxidative stress and, surprisingly, only the mitochondrial thioredoxin reductase mutant was more sensitive to hydrogen peroxide treatment whereas the Trx3 mutant remained unaffected. Furthermore, treatment with CDNB (2,4-dinitrobenzene, reduces glutathione levels) was more toxic in the Trr2 mutant than the wild type or Trx3 mutant (Pedrajas *et al.*, 1999). This scenario resembles the one that predicted the existence of Trx2 in *E. coli* (Derman *et al.*, 1993). A screening of *E. coli* mutants that had a more oxidized cytoplasm than the wild type identified only thioredoxin reductase as the gene responsible for this phenotype, whereas the Trx1 mutant had no effect on the cytoplasmic redox status. Considering that *E. coli* thioredoxin

reductase only reduces thioredoxins, the presence of a novel thioredoxin responsible for the maintenance of a reduced cytosol was proposed. We discovered this new thioredoxin (Trx2) when searching *E. coli* genome for the mitochondrial thioredoxin ancestor (Miranda-Vizuete *et al.*, 1997a) and J. Beckwith's laboratory finally demonstrated its *in vivo* function (Stewart *et al.*, 1998). It is tempting to speculate that, in a similar way to what happens in bacteria, yeast and perhaps higher eukaryotes might contain a second mitochondrial thioredoxin-like protein, which could explain the sensitivity of the Trx2 mutant. Alternatively, mammalian cytosolic thioredoxin reductase can act as antioxidant in a thioredoxin-independent way, *e.g.*, as electron donor for plasma glutathione peroxidase, and is able to reduce lipid hydroperoxides (Björnstedt *et al.*, 1994, 1995). This could also be the case for the mitochondrial thioredoxin reductase.

#### *Functions of the mitochondrial thioredoxin system*

The majority of ROS (hydrogen peroxide, superoxide anion, hydroxyl radical, and singlet oxygen) are produced in mitochondria because the mitochondrial electron-transport system consumes 85–90% of the oxygen used by the cell (Shigenaga *et al.*, 1994). An abnormal increase of these metabolites promotes cellular damage in several molecular components such as DNA, proteins, and lipids. However, ROS are also regarded as signaling molecules that can modulate the activity of several transcription factors, thus regulating gene expression (Schulze-Osthoff *et al.*, 1993). Therefore, an exquisite regulatory mechanism is present in this organelle to avoid production of ROS in an uncontrolled fashion. The mitochondrial antioxidant defense is comprised of enzymatic systems like glutathione peroxidase, glutathione reductase, manganese-superoxide dismutase (Mn-SOD) (Fridovich 1997; Roveri *et al.*, 1994), and low-molecular weight antioxidants (tocopherols, ascorbate, lipoates, uric acid, and glutathione). SOD dismutates the superoxide radical and produces hydrogen peroxide ( $H_2O_2$ ), which is removed by catalase. Although catalases remove  $H_2O_2$  in the cytosolic compart-

ment, there has been no report of the presence of catalase in mitochondria, except in heart mitochondria (Radi *et al.*, 1991). Recently, a peroxidase named SP-22, which can reduce  $H_2O_2$  and alkylhydroperoxides, has been identified in bovine mitochondria. SP-22 is a Trx-dependent peroxidase that uses electrons from Trx to remove  $H_2O_2$  and plays an important role in the antioxidant defense in the cardiovascular system (Araki *et al.*, 1999). A mitochondrial thioredoxin-dependent peroxidase (Prx1p) has also been identified and characterized in *S. cerevisiae*, and its function in antioxidant defenses has been studied using yeast PRX1 null strains (Pedrajas *et al.*, 2000; Sung *et al.*, 2000). In experiments using sudden heat shock, which in yeast generates ROS and induces cell death (Davidson *et al.*, 1996), wild-type yeast cells showed a higher survival compared to the isogenic Prx1p null strain. In addition, this strain was more sensitive to  $H_2O_2$  compared to the isogenic wild-type control. Furthermore, the PRX1 null strain, expressing Prx1p from an episomal plasmid, was considerably more resistant to sudden heat shock as well as  $H_2O_2$ . The presence of a mitochondrial thioredoxin-dependent peroxidase/mitochondrial thioredoxin system in both yeast and mammalian cells suggests an important role in the removal of  $H_2O_2$  and a protective role in defense against oxidative stress and cell death and, thus, adds these enzymes to the list of mitochondrial antioxidant enzymatic defenses.

Mitochondria play a pivotal role in the apoptotic process, a form of controlled cell suicide that regulates the number of cells in an organism as well as removal of aged or damaged cells (Kroemer *et al.*, 1998). Although the pathways leading to apoptosis are not fully understood, it is well established that ROS generated in mitochondria participate in this process (Tan, 1998). One mechanism by which ROS induces apoptosis is by opening the mitochondrial permeability transition pore (PT), a dynamic multiprotein complex formed at the contact site between the inner and the outer mitochondrial membranes and implicated in the  $Ca^{2+}$  efflux from mitochondria (Zoratti and Szabo, 1995; Crompton, 1999). The opening of this complex has been shown to be modulated by a redox-sensitive dithiol group as well as the redox state

of pyridine nucleotides (Petronilli *et al.*, 1994; Costantini *et al.*, 1996) and mitochondrial thioredoxin reductase seems to play a key role in its regulation (Kim *et al.*, 1996; Rigobello *et al.*, 1998).

However, the idea that the mitochondrial thioredoxin system might have other functions in this organelle is enticing. This speculation can be based on the particular mitochondrial metabolism and several parallels with the different functions of the cytosolic thioredoxin system. For example, formation/reduction of disulfide bonds is a major regulatory mechanism for the function of several proteins and, despite the presence of several antioxidative defense systems in mitochondria, Trx2 is the only known protein that can reduce protein disulfides. Another function of the mitochondrial thioredoxin system could be the regulation of the F<sub>0</sub>-F<sub>1</sub> ATP synthase, a member of the respiratory chain. F<sub>0</sub>-F<sub>1</sub> ATP synthase is organized in two components: the F<sub>0</sub> membrane factor, integrated in the inner mitochondrial membrane, and the F<sub>1</sub> ATPase, facing the mitochondrial matrix (Hatefi, 1985). A similar enzymatic complex has been described in the inner membrane of plant chloroplasts, and its activity is regulated by thioredoxin (Mills *et al.*, 1995). Several lines of evidence indicate that the mitochondrial ATPase F<sub>0</sub>-F<sub>1</sub> complex is also redox regulated, so, it might be possible that mitochondrial thioredoxin is involved in this mechanism (Falson *et al.*, 1986; Yagi and Hatefi, 1987).

In an attempt to identify more functions of the mitochondrial thioredoxin system, we performed yeast two-hybrid screening using rat Trx2 as bait (A.E. Damdimopoulos, unpublished results) to identify Trx2 interacting proteins. Among the isolated interacting clones, we found two coding for known mitochondrial proteins—serinehydroxy-methyltransferase (SHMT) and cytochrome *c*-oxidase. SHMT is a mitochondrial matrix enzyme that participates in the metabolism of one-carbon units and its activity requires DTT *in vitro* (Garrow *et al.*, 1993). Therefore, it seems plausible that mitochondrial thioredoxin could replace DTT activation *in vivo*. Cytochrome-*c*-oxidase is a member of the respiratory chain, and its activity has also been reported to be regulated by a redox mechanism (Hatefi, 1985). Nitric oxide (NO) and its toxic metabolites can nitrosylate com-

ponents of the mitochondrial respiratory chain, leading to a cellular energy deficiency state (Ghafourifar and Richter, 1997; Heales *et al.*, 1999). Nanomolar concentrations of NO bind to and inactivate reversibly the reduced form of cytochrome *c*-oxidase. Trx2 is likely to revert this nitrosylation as well as nitrosylation of other mitochondrial proteins since such a function *in vitro* for Trx1 was demonstrated (Nikotovic *et al.*, 1998). Immunoelectron microscopy analysis identifies Trx2 as a mitochondrial matrix protein attached to the inner membrane (M. Peltto-Hiukko *et al.*, in preparation). This location strengthens the idea of Trx2 being a regulator of cytochrome *c*-oxidase and thus involved in the respiratory process.

Neurodegenerative diseases have widely disparate genetic aetiologies but share mitochondrial dysfunction as a final common pathway (Flint Beal *et al.*, 1997). Indirect evidence for an important role of the mitochondrial thioredoxin system in the pathophysiology of these diseases is provided from studies of Trx2 distribution in the rat brain using *in situ* hybridization and immunohistochemistry (Rybnikova *et al.*, 2000). Trx2 mRNA and protein were highly expressed in the neurons in several brain regions, including the olfactory bulb, the frontal cortex, the hippocampus, some hypothalamic and thalamic nuclei, the cerebellum, and numerous brainstem nuclei. Thus, the most prominent Trx2 expression in the brain was seen in areas with most intensive free radical production. The susceptibility of cells to NO toxicity is dependent on their antioxidant capacity, including the intracellular GSH concentration (Walker *et al.*, 1995). Therefore, it has been assumed that neurons are essentially more vulnerable to the toxic effects of NO because GSH is mostly found in glia, but not in neurons (Raps *et al.*, 1989; Philbert *et al.*, 1991). The presence of Trx2 in neurons, suggests that it might provide the major neuronal defense against NO toxicity.

Expression of Trx2 is high in the substantia nigra (Rybnikova *et al.*, 2000), a region with elevated concentrations of monoamine oxidase and transition metals (iron and copper), that also contribute to the production of free radicals (Riederer *et al.*, 1989; Jellinger, 1999). There are several reports that Parkinson's disease

(PD), which involves loss of dopaminergic neurons in the substantia nigra, is caused by an increase in oxidative stress and subsequent impairment of mitochondrial respiration (Shapira, 1994; Tritschler *et al.*, 1994; Zeevalk *et al.*, 1998). Thus, it is tempting to speculate that Trx2 plays a role in PD. Redox control provides the cell with a mechanism by which it can respond to changes in its environment through the modulation of the activity of certain genes, ultimately leading to an alteration in cell proliferation or cell death. The thioredoxin system plays a central role in this control and in protection against oxidative stress.

A new thioredoxin system has been identified in mitochondria of lower eukaryotes and in mammalian cells. Understanding its mechanism of action will provide insights for protection against oxidative stress induced cytotoxicity and tissue damage.

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## ABBREVIATIONS

FISH, Fluorescence *in situ* hybridization; MTS, mitochondrial targeting sequence; ORF, open reading frame; PAPS, adenosine 3'-phosphate 5'-phosphosulfate; ROS, reactive oxygen species; SECIS, selenocysteine insertion sequence; SHMT, serine-hydroxymethyltransferase; TPA, 12-O-tetradecanoyl-1,2-phorbol 13 acetate; Trx, thioredoxin; TrxR, thioredoxin reductase; UTR, untranslated region.

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