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Gene Section
Short Communication

SRXN1 (sulfiredoxin 1)

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Identity

Other names: C20orf139, Npn3, SRX1, YKL086W, dJ850E9.2

HGNC (Hugo): SRXN1

Location: 20p13

DNA/RNA

Note
Human Srx is located on chromosome 20 in the region of p13.

Description

Human Srx gene is 6632 bp in length, composed of 2 exons and located at chromosome 20p13.

Transcription

The size of Srx mRNA is 2580 bp. Srx transcript contains two exons. Exon 1 is 271 bp and exon 2 is 2300 bp. The catalytic domain of Srx reducing enzyme activity is localized in exon 2.

Protein

Note
Human Srx protein has a total of 137 amino acids and a 14 kDa molecular weight.

Description

Srx is a member of antioxidant protein family containing a ParB-like nuclease domain. It forms 5 beta strands and 6 helix secondary structures. Srxn1 binds to peroxiredoxins (Prxs) and reduces overoxidized Prxs in the presence of cofactors including magnesium and ATP.

Expression

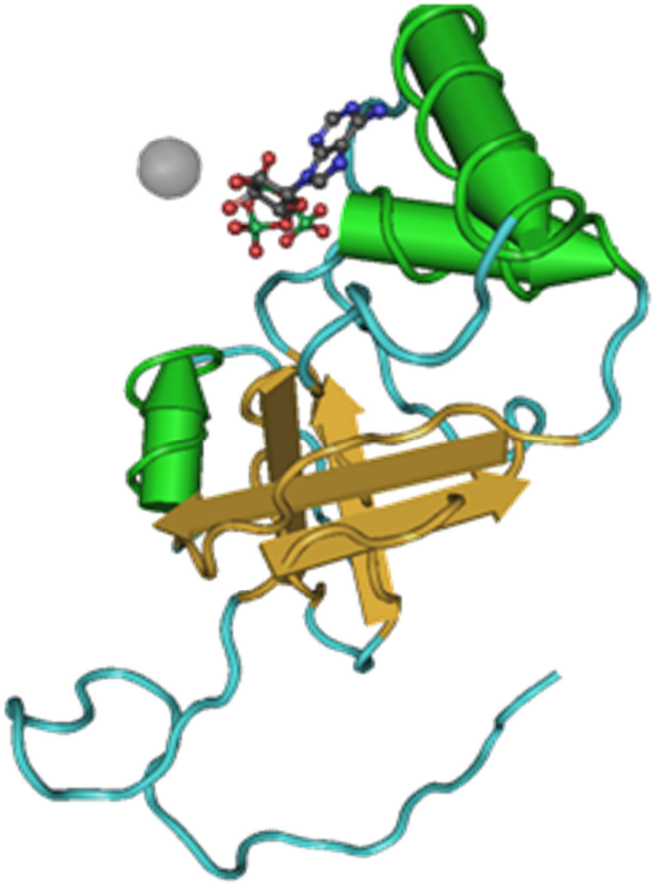
In adult, Srx protein was found in internal organs such as mouse liver and kidney. Expression pattern of Srx in embryonic development is not clear. Transcriptional regulation of Srx expression is mainly mediated through AP-1 and/or Nrf-2 activation (Jeong et al., 2012). In yeast, it may also be negatively regulated at the translational level through Ras-PKA pathway (Molin et al., 2011).

Localisation

Srx is mainly localized in the cytosol. In the presence of severe oxidative stress, it may also translocate to mitochondria (Noh et al., 2009).

Function

Srx was first identified as a gene preferentially expressed in transformed JB6 cells (Sun et al., 1994).
The primary biochemical function of Srx is to reduce the overoxidized cysteine residues of Prx I, Prx II, Prx III and Prx IV under severe oxidative stress (Biteau et al., 2003; Chang et al., 2004). The spectrum and specificity of its enzymatic function remains elusive. Srx may also cause the deglutathionylation of Prx II and others (Park et al., 2009; Findlay et al., 2006). The biological function of Srx may involve in the regulation of various cell signaling pathways to promote tumorigenesis and cancer progression. Abnormally high expression of Srx has been demonstrated in many malignant tumors including those of skin, lung, and colon (Wei et al., 2008). Srx may not be essential for development since Srx null mice are viable and normal (Planson et al., 2011).



Structure of Human Srx bound to an ATP molecule and Mg^{2+} in solution (NCBI).

Homology

Srx gene is conserved among species, from metazoan to human.

Implicated in

Various cancers

Note

Elevated expression of Srx has been associated with different types of human malignant tumors, such as skin squamous cell carcinoma, sweat gland carcinoma, basal cell carcinoma, melanoma, rectal carcinoma, lung adenocarcinoma and breast cancer (Wei et al., 2008; Hartikainen, et al., 2012). Increased Srx expression in lung cancer patients is positively associated with the deterioration of the clinic stages, and knockdown of Srx reduces cancer cell migration, invasion and their ability to form distal metastasis (Bowers et al., 2012; Wei et al., 2011). Srx genetic polymorphism of four SNPs (rs6116929, rs2008022, rs7269823, and rs9085283) is associated with breast cancer risk and patient survival (Hartikainen et al., 2011).

Tissue injury

Note

Srx, together with Prxs, are required for the protection of tissues from oxidative stress induced damages by alcohol and Pyrazole (Bae et al., 2012; Bae et al., 2011).

Lung fibrosis

Note

Srx is found to be expressed in alveolar macrophages in non-specific interstitial pneumonia and may contribute to the process of idiopathic pulmonary fibrosis (Mazur et al., 2010).

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