

ENOX2 (ecto-NOX disulfide-thiol exchanger 2)

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Identity

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| Other names | APK1 COVA1 tNOX |
| HGNC (Hugo) | ENOX2 |
| LocusID (NCBI) | 10495 |
| Location | Xq26.1 |
| Location_base_pair | Starts at 129757357 and ends at 130037291 bp from pter (according to hg19-Feb_2009) [Mapping] |
| Note | Also termed APK1 antigen, or cytosolic ovarian carcinoma antigen 1, or tumor-associated hydroquinone oxidase (tNOX). ECTO-NOX2 = Ecto-Nicotinamide Dinucleotide Oxidase Disulfide Thiol Exchange 2. |

DNA/RNA

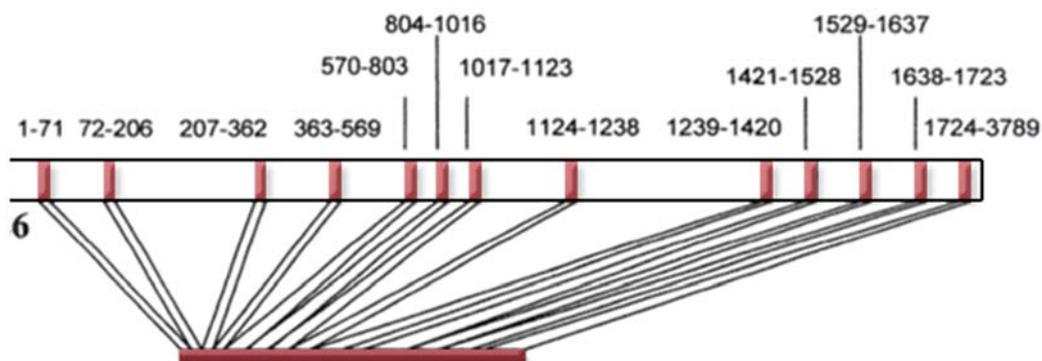


Figure 1. ENOX2 mRNA.

Description The human ENOX2 gene is located on the reverse strand of chromosome X (bases 4918 to 284856); according to NCBI Refseq Gene Database (gene ID: 10495, RefSeq ID: NG_012562.1), and is comprised of 279939 bp. ENOX2 is composed of 13 protein-coding exons between 71 bp and 2066 bp in length and 14 introns which vary greatly in length (1781 bp to 117994 bp). It has a 501 bp 5' untranslated region and a long 3' UTR (approximately 1935 bp).

Transcription According to NCBI the human ENOX2 gene encodes a 4036 bp mRNA transcript, the coding sequence (CDS) located from base pairs 356 to 2101 (NM_001281736.1). The CDS from the Ensembl genome browser database (ENST00000370927, transcript length 3788 bp) and NCBI (NM_001281736.1) are identical. Transcripts NM_001281736.1 and ENST 00000370927 are also included in the human CCDS set (CCDS14626) and encode a 610 aa long protein.

Pseudogene None known.

Protein

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Functional motifs: Quinone binding site (EEMTE)
                  Potential PDI motifs (CXXXXC)AND (CXXXXXC)
                  Copper binding sites (HVH)and YLH
                  Adenine binding site (TGVGASL)

(220) 1  M L A R E E R H R R R M E E E R L R P P S P P P V V H Y S D
(250) 31 H E C S I V A E K L K D D S K F S E A V Q T L L T W I E R G
(280) 61 E V N R R S A N N F Y S M I Q S A N S H V R R L V N E K A A
(310) 91 H E K D M E E A K E K F K Q A L S G I L I Q F E Q I V A V Y
(340) 121 H S A S K Q K A W D H F T K A Q R K N I S V W C K Q A E E I
(370) 151 R N I H N D E L M G I R R E E E M E M S D D E I E E M T E T
                                               Quinone binding site
(400) 181 K E T E E S A L V S Q A E A L K E E N D S L R W Q L D A Y R
(430) 211 N E V E L L K Q E Q G K V H R E D D P N K E Q Q L K L L Q Q
(460) 241 A L Q G M Q Q H L L K V Q E E Y K K K E A E L E K L K D D K
(490) 271 L Q V E K M L E N L K E K E S C A S R L C A S N Q D S E Y P
                                               Potential PDI motif
(500) 301 L E K T M N S S P I K S E R E A L L V G I I S T F L H V H P
                                               Copper binding site
(530) 331 F G A S I E Y I C S Y L H R L D N K I C T S D V E C L M G R
                                               Copper binding site Potential PDI motif
(560) 361 L Q H T F K Q E M T G V G A S L E K R W K F C G F E G L K L
(590) 391 T                               Adenine (NADH) binding site

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Figure 2. Deduced amino acid sequence and functional motifs of the bacterially expressed 46 kDa enzymatically active C-terminus of ENOX2.

Description

ENOX2 transcription variants all appear to be variations that include an exon 4 minus splicing event that allows for down-stream initiation and expression of the ENOX2 protein at the cell surface of malignant cells (Tang et al., 2007a; Tang et al., 2007b). Without the exon 4 deletion, mRNA derived from the gene does not appear to be translated into protein. Thus, the exon 4 deletion is the basis for the cancer specificity of the ENOX2 transcription variants. An hnRNP splicing factor directs formation of the Exon 4 minus variants of ENOX2 (Tang et al., 2011). The fully processed 34 kDa generic ENOX2 protein found on the cell surface of HeLa cells and in sera of about 23% of early cancer patients retains full-functional activity.

The deduced amino acid sequence of a bacterially expressed 46 kDa functional C-terminus of ENOX2 exhibits the same characteristics of alternation of the two activities and drug response as the cell surface and generic serums forms. Identified functional motifs include a quinone binding site, an adenine nucleotide binding site, a CXXXXC cysteine motif as a potential disulfide-thiol interchange site and two copper binding sites, one of which is conserved with superoxide dismutase. ENOX2 proteins lack flavin and only one of the two C-X-X-X-X-C motifs characteristic of flavoproteins are present in ENOX2. Yet the protein effectively carries out protein disulfide interchange. The motif C569-X-X-X-X-X-C575, alone or together with a downstream histidine (H582) provides an additional potential active site for protein disulfide-thiol interchange (Morré and Morr , 2013). The signature ENOX2 motif is that of the potential drug/antibody binding site E394EMTE. Antisera directed to this portion of the protein act as competitive inhibitors to drug binding. The sequence provides a putative quinone or sulfonylurea-binding site with four of the five amino acids in at least one other putative quinone site in the same relative positions. The correctness of the various assignments has, for the most part, been confirmed by site-directed mutagenesis (Chueh et al., 2002). While amino acid replacements that block oxidation of reduced pyridine nucleotide by ENOX2 also eliminated protein disulfide-thiol interchange and vice versa (Chueh et al., 2002), the two activities appear to occur independently. One can be measured in the absence of the other. The ENOX2 proteins have properties of prions and are protease resistant (Kelker et al., 2001) and N-terminal sequencing. Concentrated solutions aggregate and form amyloid-like filaments.

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|--------------|--|
| Expression | Widely expressed in malignant cells but only as exon 4 minus splicing variants (Tang et al., 2007b). |
| Localisation | External cell surface (Morr , 1995). |
| Function | <p>ENOX2 is a member of a family of cell surface metalocatalysts with binuclear copper centers that oscillate. They catalyze both NAD(P)H and hydroquinone oxidation in one configuration and carry out protein disulfide-thiol interchange in a second configuration (Figure 3). The two activities alternate creating a regular 22 min period to impart a time-keeping function (Morr  and Morr , 2003). The oscillations are highly synchronous and phased by low frequency electromagnetic fields.</p> <p>Functionally ENOX2 proteins of cancer cells act as terminal oxidases of plasma membrane electron transport (PMET) whereby electrons coming from cytosolic NAD(P)H are transferred to membrane-located coenzyme Q with eventual transfer of electrons and protons to oxygen to form water (Figure 4). The released energy is presumably utilized to drive cell enlargement. The protein disulfide-thiol interchange part of the cycle carries</p> |

out a function essential to the cell enlargement mechanism (Morré et al., 2006). The phenotype of unregulated accelerated growth is recapitulated in a transgenic mouse strain over expressing human ENOX2 (Yagiz et al., 2006).

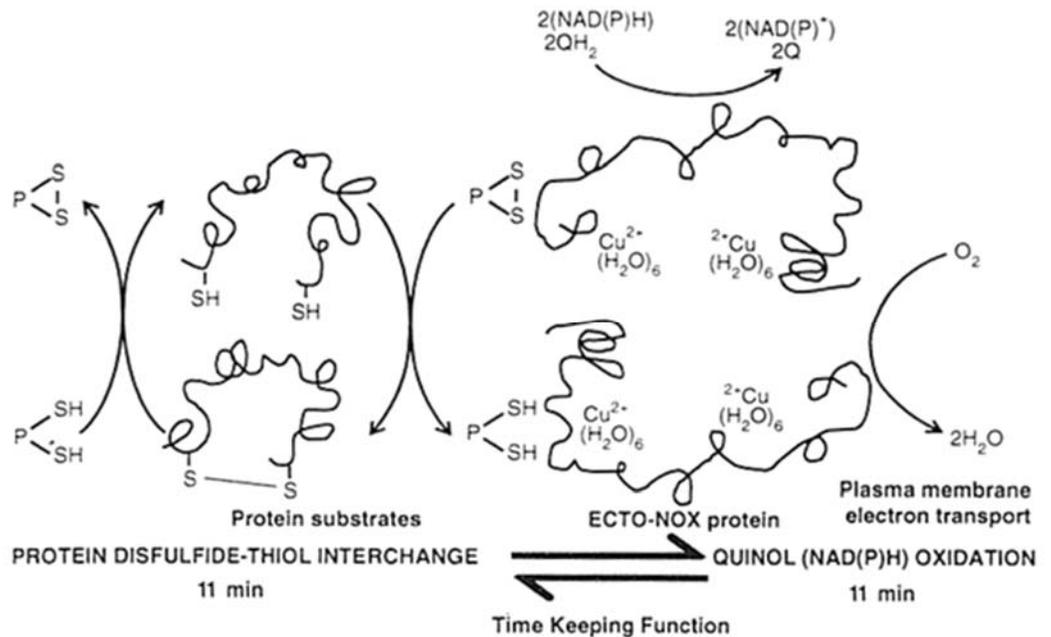


Figure 3. Diagrammatic representation of the functional unit of the ENOX2 proteins which is a dimer, each monomer of which contains two copper centers. During the oxidative portion of the ENOX cycle on the right, the net result is the transfer of 4 electrons plus 4 protons to molecular oxygen to form $2\text{H}_2\text{O}$. The left portion of the diagram illustrates the protein disulfide-thiol interchange activity portion of the cycle where the result is an interchange of protons and electrons that results in the breakage and formation of disulfide bonds important to cell enlargement.

Homology

RNA recognition motif (RRM) in the cell surface Ecto-NOX disulfide-thiol exchanger (ECTO-NOX or ENOX) proteins. This subgroup corresponds to the conserved RNA recognition motif (RRM) in ECTO-NOX proteins (also termed ENOX), comprising a family of plant and animal NAD(P)H oxidases exhibiting both oxidative and protein disulfide-like activities. The ENOX2 gene is present in the human genome as a single copy, with no obvious homologs and a single constitutive ENOX1 (CNOX) ortholog with 64% identity and 80% similarity (Jiang et al., 2008).

Mutations

Somatic No reports of mutations leading to inactivation of or inability to express ENOX2.

Implicated in

Entity Various cancers

Note The ENOX2 protein is universally associated with malignancies. It is not the result of an oncogenic mutation but appears to be similar if not identical to a form of ENOX protein with characteristics of an oncofetal protein important to maintenance of unregulated growth in very early development that may be re-expressed in malignancy (Cho and Morr , 2009). Re-expression as an oncofetal protein helps explain the role of ENOX2 of cancer cells in acquiring the well-known characteristic of uncontrolled growth. Consistent with this interpretation are observations that the malignant phenotypes of invasiveness and growth on soft agar of cancer cells in culture are lost when cells are transfected with ENOX2 antisense (Chueh et al., 2004; Tang et al., 2007a). ENOX2 is the first reported cell surface change absent from non-cancer cells and associated with most, if not all, forms of human cancer (Morr  and Morr , 2013). As such, ENOX2 emerges as a potential universal molecular cancer marker and, being an ecto-protein at the cell surface and shed into the circulation, a reliable cancer diagnostic marker both for cancer presence and tissue of cancer origin (Figure 4).

ENOX2 proteins are expressed differently by different tissues of cancer origin within the body with each type of cancer being characterized by one, two, three or more tissue specific transcript variants of characteristic molecular weights and isoelectric points (Morr  and Morr , 2012). ENOX2 proteins are absent or reduced to below the limits of detection from sera of healthy individuals or patients with diseases other than cancer. Circulating ENOX2 has been detected in sera of patients representing all major forms of human cancer including leukemias and lymphomas. All ENOX2 transcript variants appear to share the common antigenic determinant recognized both by an ENOX2-specific monoclonal antibody (Cho et al., 2002) and a corresponding scFv single chain variable region recombinant antibody expressed in bacteria and derived from the monoclonal antibody-producing hybridoma cells with analysis by 2-D-gel electrophoresis and western blot (Hostetler et al., 2009).

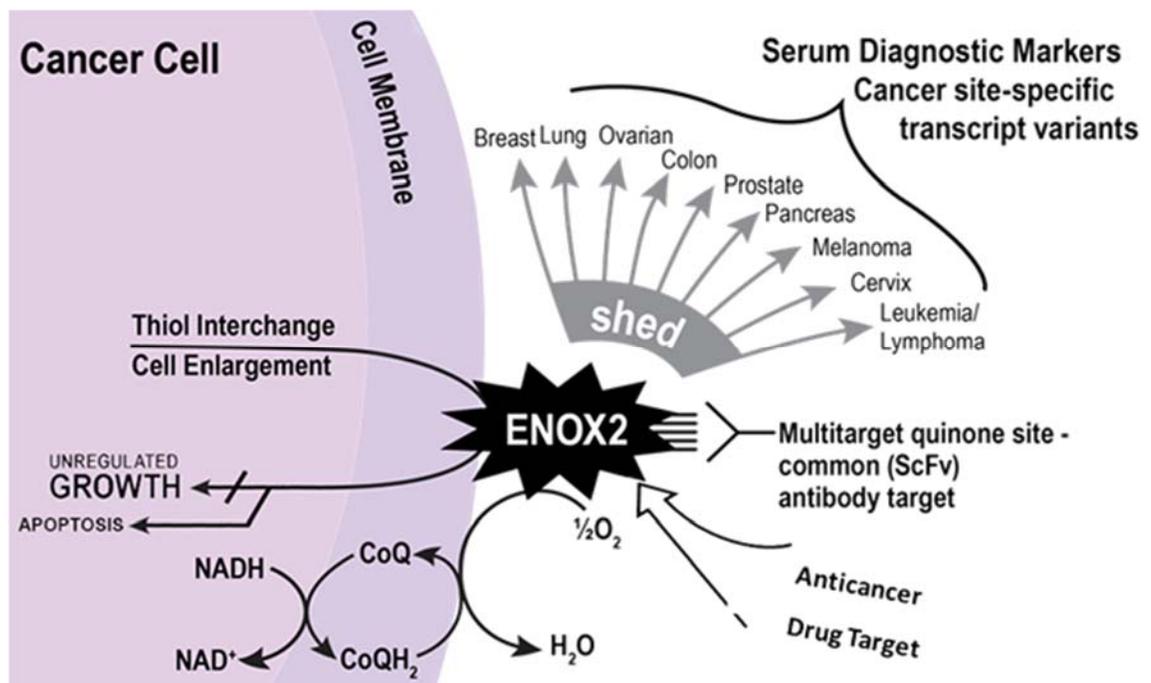


Figure 4. Schematic representation of the utility of the ENOX2 proteins as cancer-specific cell surface proteins for diagnosis and therapeutic intervention in cancer. Modified from Morr  and Morr  (2013).

For additional information such as notes, references and bibliography, please see the entire article:

<http://atlasgeneticsoncology.org/Genes/ENOX2ID40134chXq26.html>