

Gene Section Review

ESRRA (estrogen-related receptor alpha)

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Identity

Other names: ERR-alpha; ERR1; ERRa; ERRalpha; ESRL1; NR3B1

HGNC (Hugo): ESRRA

Location: 11q13.1

Note: Size: 11,172 bases; Orientation: plus strand.

DNA/RNA

Description

- Sequence length 11,172 bases;
- CDS: 2221;
- Exons: 7.

Transcription

Alternative splicing results in transcript variants, but these have not yet been well-characterized.

Pseudogene

A pseudogene has been reported, ESRRAP, located at 13q12.1. However, it is possible that this pseudogene is not transcribed (Sladek et al., 1997).

Protein

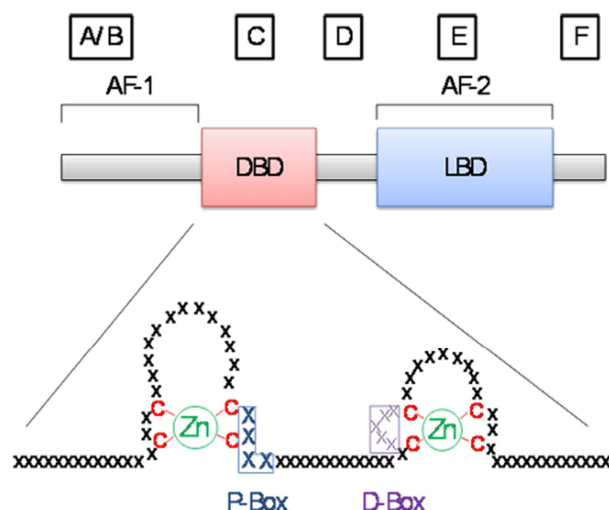
Description

ERRa is a 45.5 kDa, 423 amino acid orphan nuclear receptor. Although closely related to the estrogen receptors, its transcriptional activity is regulated to any significant degree by estrogens. ERRa binds to specific DNA sequences within target gene promoters as a monomer or homodimer and recruits coactivating proteins, the best known of which is PGC-1a.

Expression

ERRa is ubiquitously expressed throughout development with the highest levels of expression in

tissues that oxidize fatty acids such as kidney, heart, cerebellum, intestine and skeletal muscle (nursa).



Schematic of nuclear receptor structure and function.

ERRa is a member of the nuclear receptor (NR) superfamily of transcription factors and is most closely related to estrogen receptor alpha (ERa). The modular structure of NRs consists of seven (A-F) domains. The A/B region, which harbors activation function 1 (AF-1), is not well-conserved across NRs, but regions C and E are highly conserved and harbor, respectively, the DNA-binding domain (DBD) and ligand-binding domain (LBD). ERRa shares with ERa 68% sequence identity within the DBD and 33% within the LBD. The functional regions of the DBD have been finely mapped. In addition to two zinc finger motifs, this domain contains a Proximal-box (P-box) which determines DNA sequence specificity, and a Dimerization-box (D-box), which part of the dimerization interface.

Localisation

ERRa is thought to be predominately nuclear, although recently it has been reported to be perinuclear and cytoplasmic in breast cancer tissue (Jarzabek et al., 2009).

Function

The function of ERRa as a metabolic regulator is supported by the observation that erra-null mice demonstrate impaired fat metabolism and absorption (Luo et al., 2003). It has recently been demonstrated that erra-null mice also have a reduced capacity for adaptation to hemodynamic stressors. Due to this functional deficit, these mice often develop cardiac contractile dysfunction. The cardiac remodeling under stress in ERR-null mice is due to defects in ATP synthesis and reduced phosphocreatine stores, which are both characteristic of pathologic cardiac hypertrophy (Huss et al., 2007). That the expression of ERRa is elevated in exercising muscle and in fasting liver specifically implicates this receptor in beta-oxidation of fatty acids, a metabolic pathway that is highly active under these conditions. On a mechanistic level, several studies have revealed that ERRa is involved in the transcriptional regulation of genes required for mitochondrial biogenesis, oxidative phosphorylation and fatty acid oxidation (Huss et al., 2004; Mootha et al., 2004; Dufour et al., 2007).

Thus far, metabolic studies of ERRa function have mainly focused on its role as the downstream effector of PGC-1a. PGC-1a is a promiscuous nuclear receptor coactivator expressed at low basal levels but induced by fasting and other metabolic stresses (Puigserver and Spiegelman, 2003). PGC-1beta, a related cofactor, may have similar functions, although its expression level is not as acutely regulated by variations in energy demand (Yoon et al., 2001). Rather than being regulated by ligand, the magnitude of ERRa activity is thought to be largely dependent on the presence of transcriptional coactivators such as PGC-1a and beta. Interest in the ERR-PGC-1 regulatory axis was heightened by the observation that there is a decrease in both PGC-1a and PGC-1beta in the skeletal muscle of patients with diabetes and obesity (Mootha et al., 2003).

Homology

Sequence analysis reveals that the ERRs and the classical estrogen receptors share a high degree of homology within their DNA and ligand binding domains. In particular, ERRa shares with ERa approximately 68% sequence identity within the DNA binding domain and 33% within the ligand binding domains. This relationship provides a structural basis both for the conserved nature of DNA binding and the divergence in hormone binding between these two receptors.

Mutations

Note

Although over 80 SNPs have been reported, only one variant has been shown to carry clinical associations. Laflamme et al. reported a polymorphic hormone response element within the ESRRA promoter (Laflamme et al., 2005). The variant sequence, present

in 11% of the population tested (white, premenopausal women), included an ERRa responsive element within the additional 23-nucleotides. This longer variant was associated with higher bone mineral density measured in the lumbar spine.

Kamei et al. reported that the longer variant is associated with a significantly higher body mass index in their study population of 729 Japanese men and women (Kamei et al., 2005).

Implicated in

Breast cancer

Prognosis

Two independent clinical studies have implicated ERRa in breast cancer progression (Ariazi et al., 2002; Suzuki et al., 2004). In the first study to link ERRa to clinical and pathological characteristics of breast cancer, Ariazi et al. found that ERRa expression is significantly associated with ERa-negative and progesterone receptor-negative tumor status as well as Her2 status. Further exploring the relationship between ERRa and Her2, Barry et al. demonstrated that ERRa transcriptional activity can be enhanced by phosphorylation events downstream of Her2 (Barry and Giguere, 2005). Building on the association between ERRa and negative prognostic biomarkers, Suzuki et al. demonstrated a direct correlation between ERRa expression and unfavorable breast cancer patient outcomes including increased tumor recurrence and decreased survival (Suzuki et al., 2004). Importantly, the predictive value of ERRa expression was shown to be independent of ERa status, confirming that targeting the ERRa pathway may be of therapeutic benefit in patients with either ERa-positive or ERa-negative breast cancer.

Recently, the function of ERRa has been evaluated in xenograft models of breast cancer. Stein et al. demonstrated that ERRa is critical for the growth of ERa-negative breast cancer through use of RNAi (Stein et al., 2008). Furthermore, Chisamore and coworkers found that an ERRa antagonist inhibited the growth of ERa-positive and ERa-negative breast cancer cell lines in a xenograft model (Chisamore et al., 2009).

Ovarian cancer

Prognosis

Sun et al. demonstrated that the ovarian tumors had significantly higher ERRa mRNA levels than normal ovaries and that high ERRa expression correlated with clinically advanced and histologically aggressive disease. Furthermore, ERRa expression was shown to be an independent prognostic factor for poor overall patient survival (Sun et al., 2005).

Colorectal cancer

Prognosis

Analysis of 80 colorectal tumor samples demonstrated that higher levels of ERRa mRNA are expressed in

tumor tissue versus in the surrounding normal mucosa. Furthermore, tumor tissue ERRa mRNA levels are positively correlated with increased tumor stage and histological grade (Cavallini et al., 2005).

Prostate cancer

Prognosis

Cheung et al. investigated the expression patterns of the three ERR family members in normal and malignant human prostate epithelial cells and cell lines (Cheung et al., 2005). The authors also characterized ERR protein expression and localization in normal, dysplastic, and malignant prostate tissue (Cheung et al., 2005). They concluded that ERRbeta and ERRgamma protein expression is reduced in neoplastic prostatic cells versus their non-malignant counterparts and suggested that each is down-regulated in the progression of prostate cancer. The authors went on to measure the effect of overexpressing the ERRs on proliferation of an immortalized prostate cell line and a prostate cancer cell line in vitro and on prostate cancer xenograft growth in vivo (Yu et al., 2007; Yu et al., 2008). They found that ERRbeta and ERRgamma can inhibit proliferation in cells derived from normal and malignant prostate epithelium by inducing a G1-S cell cycle arrest. Furthermore, activation of either ERRbeta or ERRgamma using the agonist DY131 resulted in a decreased rate of prostate tumor growth in a xenograft model.

Endometrial cancer

Prognosis

Gao et al. explored the extent to which the ERRs are involved in ERa-positive endometrial adenocarcinoma (Gao et al., 2006). They measured the expression of each ERR family member in malignant versus normal endometrium and compared the expression levels to clinical and pathologic features. They concluded that the expression of ERRa mRNA was lower in ERa-positive endometrial adenocarcinoma versus normal endometrium. However, they also found that ERRa mRNA expression was positively correlated with tumor stage and myometrial invasion. Additionally Gao et al. found that the expression of ERRgamma mRNA was increased in endometrial adenocarcinoma compared to normal endometrium.

Breakpoints

None.

To be noted

Note

In the absence of known endogenous ligand, considerable effort has been made toward identifying small molecules to modulate ERRa activity. Several ERRa antagonists have been developed and recently a novel antagonist was described that inhibited the

growth of breast cancer xenografts (Chisamore et al., 2009).

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