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Award Number: DAMD17-98-1-8282

TITLE: Activation of Estrogen Receptor-Beta-Dependent
Transcription by Estrogen-Independent Pathways

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REPORT DATE: September 2000

TYPE OF REPORT: Annual

PREPARED FOR: U.S. Army Medical Research and Materiel Command
Fort Detrick, Maryland 21702-5012

DISTRIBUTION STATEMENT: Approved for Public Release;
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20010509 074

REPORT DOCUMENTATION PAGE

Form Approved
OMB No. 074-0188

Public reporting burden for this collection of information is estimated to average 1 hour per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing this collection of information. Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions for reducing this burden to Washington Headquarters Services, Directorate for Information Operations and Reports, 1215 Jefferson Davis Highway, Suite 1204, Arlington, VA 22202-4302, and to the Office of Management and Budget, Paperwork Reduction Project (0704-0188), Washington, DC 20503

1. AGENCY USE ONLY (Leave blank)		2. REPORT DATE September 2000	3. REPORT TYPE AND DATES COVERED Annual (1 Sep 99 - 31 Aug 00)	
4. TITLE AND SUBTITLE Activation of Estrogen Receptor-Beta-Dependent Transcription by Estrogen-Independent Pathways			5. FUNDING NUMBERS DAMD17-98-1-8282	
6. AUTHOR(S) Carolyn L. Smith, Ph.D.				
7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES) Baylor College of Medicine Houston, Texas 77030 E-MAIL: carolyns@bcm.tmc.edu			8. PERFORMING ORGANIZATION REPORT NUMBER	
9. SPONSORING / MONITORING AGENCY NAME(S) AND ADDRESS(ES) U.S. Army Medical Research and Materiel Command Fort Detrick, Maryland 21702-5012			10. SPONSORING / MONITORING AGENCY REPORT NUMBER	
11. SUPPLEMENTARY NOTES				
12a. DISTRIBUTION / AVAILABILITY STATEMENT Approved for public release; distribution unlimited			12b. DISTRIBUTION CODE	
13. ABSTRACT (Maximum 200 Words) There are two known receptors for estrogens, ER α and ER β . The existence of ER β was only recently appreciated, and little is understood about its ability to be activated by intracellular signaling pathways in the absence of estrogens. The purpose of this research program is to characterize the ability of ER β to be activated by various ligand-independent signaling pathways, and to characterize the structural regions of ER β , in comparison to ER α , that regulate how this receptor isotype responds to intracellular cross-talk. We have found that stimulation of HeLa cells with forskolin and IBMX results in the activation of ER α and ER β dependent expression in a receptor-dependent and promoter context-dependent manner, and that protein kinase A mediates this response. Factors that interact with an AP-1 binding site contribute to forskolin/IBMX activation of estrogen receptor-dependent gene expression, and do so in a manner that does not require the A/B domain of either receptor. ER α and ER β differ in their requirement for interaction with the putative AP-1 binding site factor. ER β -mediated transcription is dependent on this site suggesting that forskolin activation reflects the synergistic action between ER β and other transcription factor, while ER α can activate gene expression in a AP-1-independent manner.				
14. SUBJECT TERMS Breast Cancer			15. NUMBER OF PAGES 51	
			16. PRICE CODE	
17. SECURITY CLASSIFICATION OF REPORT Unclassified	18. SECURITY CLASSIFICATION OF THIS PAGE Unclassified	19. SECURITY CLASSIFICATION OF ABSTRACT Unclassified	20. LIMITATION OF ABSTRACT Unlimited	

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Introduction

Breast cancer remains the major cancer (excluding skin cancer) among women in the United States with more than 180,000 new cases anticipated in 2000. The requirement of estrogens for normal breast development is well documented (1). However, estrogens also have been linked to breast cancer, presumably through their ability to stimulate cell proliferation (2) and inhibition of estrogen action therefore has been a primary objective in the treatment, and more recently the prevention of, breast cancer. For many years, estrogen effects were thought to be mediated by a unique, high affinity intracellular receptor protein, the estrogen receptor (ER), that is a member of a superfamily of transcription factors (3,4). The basic mechanisms of ER activity have been ascertained. Hormone binding to ER results in receptor homodimerization and binding to specific enhancer DNA elements located in the promoter regions of target genes (5,6). This process, which is accompanied by increases in ER phosphorylation (7-12), enables "activated" receptors to regulate the transcription of hormone-responsive target genes and the resulting changes in mRNA and protein synthesis are ultimately responsible for alterations in cellular function. The structural features of the estrogen receptor (ER α) responsible for hormone binding, dimerization, DNA binding and transcriptional activation have been identified (3,13-16) and these studies have provided the basis of our understanding of the molecular mechanisms by which estrogens regulate the growth and differentiation of mammary tissues.

Clearly, the transcriptional activity of the ER can be regulated by estrogens, such as 17 β -estradiol (E2). However, the ER α also can be activated in the absence of exogenous ligand by agents that stimulate intracellular signal transduction cascades (EGF, IGF-1, heregulin, dopamine, TPA and cAMP) (7,17-23) or inhibit protein phosphatases (okadaic acid) (19). Furthermore, cyclin D1, independent of cyclin-dependent kinases, also can activate the ER in the absence of estrogen (24). The ER α knock-out mouse model confirms that ER α is required for some but not all *in vivo* EGF effects and established the importance of ligand-independent activation of ER to physiological events (25). Most of these ligand-independent activation pathways (with the exception of cyclin D1) increase receptor phosphorylation (7,12,23,26,27) and mutation of the only known ligand-independent (EGF) phosphorylation site (serine¹¹⁸) to an alanine residue abolishes EGF activation of the ER (28), suggesting that phosphorylation may play an important role in these activation pathways. However, this point mutant does not block cAMP-mediated gene expression and different domains are required to respond to EGF and cAMP signaling pathways (29), suggesting that multiple mechanisms must exist to enable ER to activate target gene expression in response to diverse regulatory events.

In 1996, a new member of the nuclear receptor superfamily was cloned from a prostate cDNA library (30). When the resulting cDNA was sequenced and expressed, it became apparent that a novel estrogen receptor had been identified. This new member of the nuclear receptor superfamily was named ER β , and the original estrogen receptor was renamed ER α . The ER β binds to estradiol with an affinity (K_d 0.4 nM) similar to ER α and binds to the same DNA response element as ER α (30-32). Thus, it is reasonable to predict that ER β regulates the expression of at least a subset of ER α target genes. However, the relatively undeveloped mammary glands in the ER α knock-out mouse indicate that ER β is not equivalent to ER α (33). The reasons for this are unclear, but could be related to differential expression and/or differences in the ability of α and β estrogen receptors to activate target gene expression. Mouse, rat and human ER β s are approximately 65 amino acids smaller than their corresponding α -receptors,

and the A/B, D and F domains (**Figure 1**) are poorly conserved (30,32,34). Furthermore, the ligand binding domains (domain E) of ER α and ER β are only ~55% identical and rat ER α and ER β receptors do not bind equally well to all ligands (31). The expression patterns of ER α and ER β mRNAs are different but overlapping (31) suggesting that the genes for ER α and ER β are independently regulated. However, both ER α and ER β mRNA have been detected in human mammary gland, breast tumors and several human breast cancer cell lines (35,36). Taken together, these data suggest that ER β is likely to play a role in mediating estrogen action in mammary gland, but that this receptor is unlikely to be functionally equivalent to ER α .

The identification of a second estrogen receptor raised a number of important biological questions such as, what is the expression of ER β , relative to ER α , in normal and malignant mammary tissue? However, knowledge regarding the expression of ER β in mammary gland will be of limited value without detailed information on the transcriptional activity of ER β . Do ER α and ER β respond similarly to ligand-independent pathways? Are currently used antiestrogens equally effective antagonists of ER α and ER β ? Do ER α and ER β activate the same target genes to a comparable extent? Studies of this nature will provide the information necessary to determine whether resources are required to develop new strategies to more effectively and/or selectively block ER α - and ER β -mediated estrogen effects. Indeed, increasing evidence demonstrates that ER α and ER β are not functionally equivalent, and our experiments reported below contribute to the foundation upon which new strategies to regulate ER α and ER β biological activity can be developed. Moreover, comparing and contrasting the structure/function relationships of ER α and ER β with respect to activation by ligand-independent pathways represents a novel approach to study mechanistic questions relating to activation of gene expression in the absence of estrogens.

Body

A new member of the nuclear receptor superfamily, ER β , has been identified that binds to estrogens with high affinity, and binds to the same DNA response elements as the classical estrogen receptor, ER α . Both of these ligand-regulatable transcription factors possess a well-defined, centrally located, DNA binding domain and carboxy-terminal domain, which contains a ligand-dependent activation function (AF-2); however the amino terminus which possesses a second activation function (AF-1) is poorly conserved. Thus, it is highly likely that the biological activity of ER β will differ from that of ER α . This hypothesis is being tested in the following two technical objectives:

1. To determine if estrogen-independent signaling pathways can stimulate ER β transcriptional activity.
2. To determine what regions of ER β contribute to its estrogen-independent transcriptional activity and to compare these regions to known ER α activation functions to characterize the structural features of these receptors that contribute to their respective biological properties.

The originally reported form of ER β represented a truncated version of the subsequently identified full length form of the receptor. In the first year of this award, we conducted experiments directed towards resolving differences in activity and expression of the full-length

and truncated forms of ER β . All of our studies in year 2 utilized the full-length form of ER β , (unless deletion mutations were being analyzed).

We have continued our analyses of the ability of ER β to be activated by ligand-independent, cAMP stimulated, signaling pathways. As reported last year, both ER α and ER β are activated in cells treated with forskolin and isobutylmethylxanthine (IBMX). Forskolin is an activator of adenylyl cyclase and IBMX is a phosphodiesterase inhibitor, and treatment of cells with these compounds therefore results in an increase in intracellular cAMP levels. In transient transfection assays, 10 μ M forskolin and 100 μ M IBMX stimulated the ER β activation of ERE-E1b-CAT target gene by ~6-fold while ER α -dependent gene expression was stimulated by ~3-fold (**Figure 2**). Minimal change in target gene expression was observed in cells transfected with the reporter gene and an empty expression vector indicating that the increased CAT activity is receptor-dependent (**Figure 2**). Furthermore, an ER α mutant possessing point mutations in its DNA binding domain (C201H/C205H) was unable to mediate forskolin/IBMX-induced CAT gene expression indicating that receptor binding to DNA was required (**Figure 2**). Further analysis demonstrates that a target gene lacking the ERE cannot be stimulated by the forskolin/IBMX-induced signaling pathway in cells expressing ER α or ER β (**Figure 3**). Thus, intracellular cAMP signaling pathways have the potential to activate the transcriptional activity of both ER α and ER β , and this activation is dependent on the expression of an estrogen receptor, the receptor's ability to bind to DNA and the presence of an estrogen response element within the target gene. To ensure that target gene expression resulted from forskolin/IBMX activation of the cAMP-dependent/protein kinase A (PKA) signaling pathway and not a non-specific event, we assessed whether the specific protein kinase inhibitor, H89, could block activation of ER α - and ER β -dependent transcription. As shown in **Figure 4**, H89 blocked forskolin activation of both receptor isotypes, but not transcriptional activity stimulated by E2, supporting that activation occurs via a cAMP/PKA dependent signaling pathway.

The preceding experiments were performed with the ERE-E1b-CAT or ERE-tk-CAT target genes which consist of an estrogen response element linked to a TATA box or thymidine kinase promoter, and the CAT reporter gene. To investigate whether the target gene influenced the ability of forskolin/IBMX to activate receptor-dependent gene expression, the same experiment was repeated, but using other target genes. As can be seen in **Figure 5** (and data not shown), the expression of the pS2-CAT, pATC0, pATC1, pATC2, ERE-E1b-Luc and pC3-Luc target genes was not stimulated by forskolin/IBMX, although E2 increased gene expression in every target gene that possessed an ERE. In contrast, the activity of the ERE-tk-CAT, ERE-E1b-CAT (**Figures 2 & 3**) and pC3110-tk-Luc (data not shown) target genes was increased. This indicates that the ability of the cAMP-dependent PKA pathway to activate target gene expression was dependent on the nature of the reporter gene examined. The majority of these target genes contain consensus EREs, so we therefore turned our attention to other potential transcription factor binding sites that are present within the synthetic target gene vectors, in order to determine what role, if any, they play in forskolin/IBMX activation of ER-dependent gene expression.

Many vectors have an imperfect AP-1 binding site (also known as a TPA responsive element or TRE) located several hundred base pairs upstream of their minimal promoters. Both the ERE-E1b-CAT and ERE-tk-CAT vectors have such a site. In order to determine if this binding site contributed to the overall activation of gene expression following forskolin/IBMX stimulation of cells, we made a four nucleotide insertion within the putative AP-1-binding site of ERE-E1b-

CAT that prevents AP-1 from binding to DNA (37). Interestingly, forskolin/IBMX was unable to activate ER β -dependent expression of the resulting mutated target gene even though E2 could still stimulate ER β activity (**Figure 6**). In contrast, mutation of the putative AP-1 site (mTRE) did not block forskolin/IBMX activation of target gene activity by ER α , although it decreased the relative magnitude of the response. Similar results were obtained when the AP-1 site was removed (Δ NdeI-Eco0109) through a more extensive deletion of 195 bp surrounding the AP-1 binding site (**Figure 6**). These experiments suggested that AP-1 sites were contributing to the ability of ER α and ER β to stimulate ERE-dependent gene expression, and that factors that bound to the AP-1 binding and ERE sites were cooperating to bring about activation of transcription. In support of this, we (**Figure 7**) and others (38,39) have shown that forskolin/IBMX activates AP-1-dependent gene expression of target genes that lack estrogen response elements. Although the reporter genes that we have used in our studies are by their very nature, synthetic in origin, it is interesting to note that AP-1 binding sites are widely distributed in the promoter region of many endogenous genes, including the progesterone receptor which has been shown to be stimulated in an ER-dependent manner by treatment of cells with cholera toxin and IBMX (40), an agent that like forskolin/IBMX will stimulate intracellular cAMP production/accumulation and activation of a PKA signaling pathway, or forskolin (41).

It has been reported previously that ER α can interact with c-jun, one component of the AP-1 transcription factor directly through the receptor's A/B domain (42). However, both ER α and c-jun are also able to bind to coactivators, such as CBP/p300 (43-45), and it is possible that the cooperative functional interactions between these two transcription factors are direct (e.g. they bind to one another) or indirect (e.g. they interact via association with a common coactivator). To begin to distinguish between these two possibilities, we analyzed the ability of ER α and ER β deletion mutants lacking their A/B domains to be activated by the forskolin/IBMX-stimulated signal transduction pathway. In our first experiment, the A/B domains of ER α and ER β were deleted to generate expression vectors for ER α -179C and ER β -143C, respectively. These deletion mutants were tested for their ability to activate the expression of the ERE-E1b-CAT target gene in response to the forskolin/IBMX-induced signaling pathway. Forskolin/IBMX activated the transcriptional activity of ER α -179C and ER β -143C, the former to an extent reduced in comparison to its respective wild type receptor (**Figure 8, top**). However, when assays were performed with the mutated target gene, ERE-E1b-CAT (mTRE) in which the AP-1 site has been disrupted by a four nucleotide insertion within the putative AP-1 site, neither receptor deletion mutant was able to stimulate transcription of the target gene (**Figure 8, bottom**). Taken together, this indicates that activation of target gene transcription by the cAMP-dependent/PKA signal transduction pathway requires an estrogen receptor as well as another transcription factor activity, in this case AP-1, and that these interactions do not require the A/B domain of either ER α or ER β . Ongoing experiments are further assessing whether the interaction between either ER and the putative AP-1 transcription factor is direct (e.g. jun interaction with ER) or indirect (e.g. jun interaction with ER via a bridging coactivator such as SRC-1 or CBP). It should also be noted that these experiments highlight a functional difference between ER α and ER β . While both of these receptors, when lacking their A/B/ domains can stimulate gene expression of the ERE-E1b-CAT target gene, only full-length ER α retains the ability to activate transcription of the mutated TRE-containing target gene [ERE-E1b-CAT (mTRE)], while full-length ER β is unable to do so. This suggests that ER α has an enhanced

ability to interact with cellular proteins that increase its transcriptional potency. We have evidence of this from other experiments we have conducted (see below).

Work performed in the first year of this project resulted in the construction of vectors that will enable us to examine the structural features that enable ER α and ER β to respond in equal or dissimilar ways to various estrogen-independent signals. Expression vectors for chimeric proteins consisting of the amino-terminal domains of ER α and ER β (individually), have been fused C-terminal to the heterologous Gal4 DNA binding domain (DBD). These constructs isolate the A/B region that encompasses the AF-1 domain from the remainder of the respective receptor and will facilitate an examination of their transcriptional activity in response to ligand-independent signaling pathways. When assessed in HeLa cells, the A/B domain of ER α has significantly more transcriptional activity than the Gal4 DBD alone, while the A/B domain of ER β has weak activity in comparison to ER α , but is distinguishable from that observed for the GAL4 DBD alone. We have examined these chimeric proteins for their ability to be activated by forskolin/IBMX-stimulated signal transduction pathways and found that the activity of neither Gal-A/B α nor Gal-A/B β was affected (data not shown). However, it should be noted that these experiments were performed on the pG5-Luc reporter construct that does not possess an AP-1 binding site in a position comparable to that found in the ERE-E1b-CAT expression vector. These experiments will therefore be repeated using a target gene, 4x17mer-tk-CAT which does so. Expression vectors for chimeric ER α and ER β proteins in which the respective ligand binding domains have been fused C-terminal to the Gal4 DBD have also been generated in the last year. These constructs have been tested for their ability to be stimulated by estradiol, and are appropriately regulated (data not shown). They will now be used to assess the ability of forskolin and other signaling pathways to stimulate estrogen receptor-dependent transcription. Collectively, these constructs will enable us to compare and contrast the ability of various estrogen-independent signaling pathways to activate a) the full-length receptor, b) the A/B region (AF1), c) the DNA and ligand binding domain and d) the ligand binding domain alone (AF2).

Last year we reported that the intrinsic transcriptional activities of the A/B domains of ER α and ER β were distinct, with the activity of ER β being approximately 33% of the corresponding ER α domain. Since coactivator proteins are thought to be major determinants of the transcriptional activity of transcription factor activation domains, we wanted to examine whether the A/B domain of ER α and ER β differed in their ability to be coactivated by SRC-1, a member of the p160 family of steroid receptor coactivators (46), or SRA, a recently identified novel coactivator of the steroid receptor family that appears to exert its biological effects as a RNA molecule (47). While SRC-1 exerts its effects via the AF-1 and AF-2 domains of steroid receptors, SRA appears to mediate its biological effects via the AF-1 domain of steroid receptors. In HeLa cells transiently transfected with an expression vector for SRC-1, both Gal-A/B α and Gal-A/B β chimeras were coactivated by SRC-1, in agreement with other investigators. In contrast, SRA was able to coactivate the transcriptional activity of only the A/B domain of ER α , but not ER β (**Figure 9**). Thus these two AF-1 domains have a differential ability to functionally interact with coactivator proteins, and this may explain, in part, the relative differences in the ability of these two domains to stimulate target gene expression. Furthermore, differences such as these may also contribute to the differential ability of steroid receptors to respond to intracellular signaling pathways as we have observed in our studies of forskolin activation of ER α and ER β . These differences will be further investigated in the coming year in order to determine whether differences in the ability of these coactivators to bind to the A/B domains of

ER α and ER β play a significant role relative to their ability to activate transcription in response to ligand-independent signaling pathways.

Key Research Accomplishments

1. Stimulation of HeLa cells with forskolin and IBMX results in the activation of ER α and ER β dependent expression of the ERE-E1b-CAT and ERE-tk-CAT synthetic target genes.
2. Activation of target gene expression is receptor-dependent and requires the receptor to bind to its DNA response element.
3. Forskolin/IBMX stimulated estrogen receptor activation is mediated by a protein kinase A signaling pathway.
4. Forskolin/IBMX stimulation of estrogen receptor-dependent gene expression is promoter-dependent.
5. Factors that interact with an AP-1 binding site contribute to forskolin/IBMX activation of estrogen receptor-dependent gene expression.
6. The A/B domain is not required for forskolin/IBMX activation of estrogen receptor-dependent gene expression.
7. ER α and ER β differ in their requirement of the putative AP-1 binding site factor for their ability to be activated by a forskolin/IBMX activated signaling pathway.
8. Forskolin/IBMX signal pathways do not alter the transcriptional activity of the ER α or ER β A/B domains.
9. The A/B domains of ER α and ER β differ in their ability to be stimulated by the SRA coactivator.

Reportable Outcomes

A portion of the work outlined in this progress report was presented at the Keystone Symposia – Nuclear Receptor 2000, Steamboat Springs, CO. (March 25-31, 2000) in poster form. The abstract (see Appendix) was entitled “Stimulation of estrogen receptor α and β transcriptional activity by the RNA coactivator, SRA”. This work has been submitted for publication as a portion of a manuscript entitled “SRA coactivates the AF-1 domain of ER α but not ER β , and stimulates the agonist activity of the partial antiestrogen, 4-hydroxytamoxifen” (see Appendix).

Conclusions

The originally published amino acid sequence of ER β represents an amino-terminally truncated form, which lacks the first 45 amino acids of this receptor isotype. In transient transfection assays, ER α is clearly more active than the long and short forms of ER β . The

potentially large differences in ER β_S and ER β_L expression levels indicate that their relative expression levels must be taken into account when considering transactivation activity. Furthermore, the AF-1 activity of ER α exceeds that of ER β and this likely contributes to the relative differences in transcriptional activity observed for these two receptor isoforms.

Both isoforms of estrogen receptor (α and β) can be activated in the absence of exogenous estrogens. In cells treated with forskolin and IBMX, ER α and ER β were activated by a cAMP signaling pathway. This indicates that there is sufficient homology between these two receptor isoforms to mediate activation of gene expression by this signaling pathway. This activation pathway required the expression of estrogen receptors within the target cell, the presence of an estrogen response element in the target gene, and that the receptor can bind to DNA. However, the stimulation of receptor-dependent transcription can be significantly enhanced by the presence of the binding site for another transcription factor, in these studies a putative AP-1 binding site. Furthermore, the ability of ER α and ER β to participate in this combinatorial response differs, supporting our original hypothesis that the ability of both estrogen receptor isoforms needs to be examined in order to determine the potential of each of these receptors to respond to ligand-independent signaling pathways

As anticipated, the experiments performed to date have provided information on the transcriptional activity of ER β relative to ER α , as well as the ability of ER β to respond to an alternative signaling pathway, induced by elevated intracellular cAMP, in the absence of estrogens. Taken together, this information will increase our understanding of the molecular mechanisms by which ER α and ER β respond to cross-talk within a cell. It also will provide a framework for critical evaluation of whether it is possible to selectively regulate ER α and ER β transcriptional activity.

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Appendices

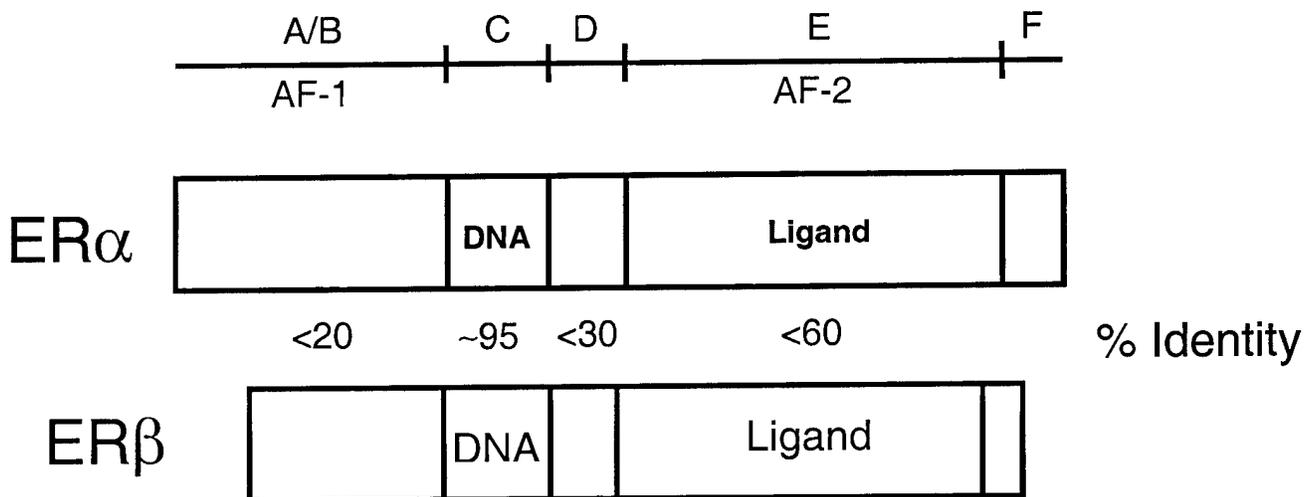


Figure 1: Structure of ER α and ER β . The *top panel* represents the location of various regions of estrogen receptor (A to F) and its activation functions (AF-1 and AF-2). The *bottom panel* represents the comparative structure of ER α and ER β . Values given between the two receptor forms represent approximately homologies in their respective amino acid sequences.

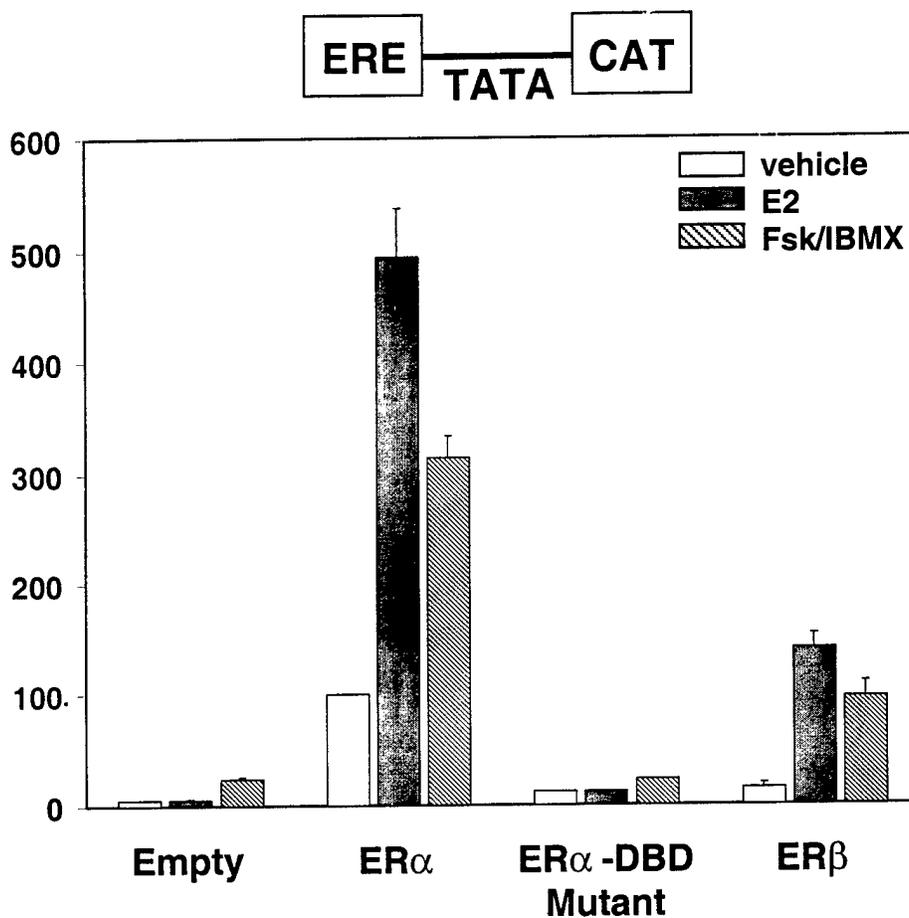


Figure 2: ER α is More Active than ER β in Response to Stimulation with Forskolin and IBMX. HeLa cells were cotransfected with 1 μ g ERE-E1b-CAT reporter plasmid and 10 ng pCMV₅, pCMV₅-hER α (ER α), pCR3.1-hER α -C201/205H (ER α -DBD Mutant) or pCXN₂-hER β (ER β) and stimulated with 1nM E2 or 10 μ M forskolin + 100 μ M IBMX. CAT measurements were corrected for protein values and standardized to ER α activity in the presence of ethanol. Transfections were performed in duplicate and values represent the mean \pm SEM of at least three experiments.

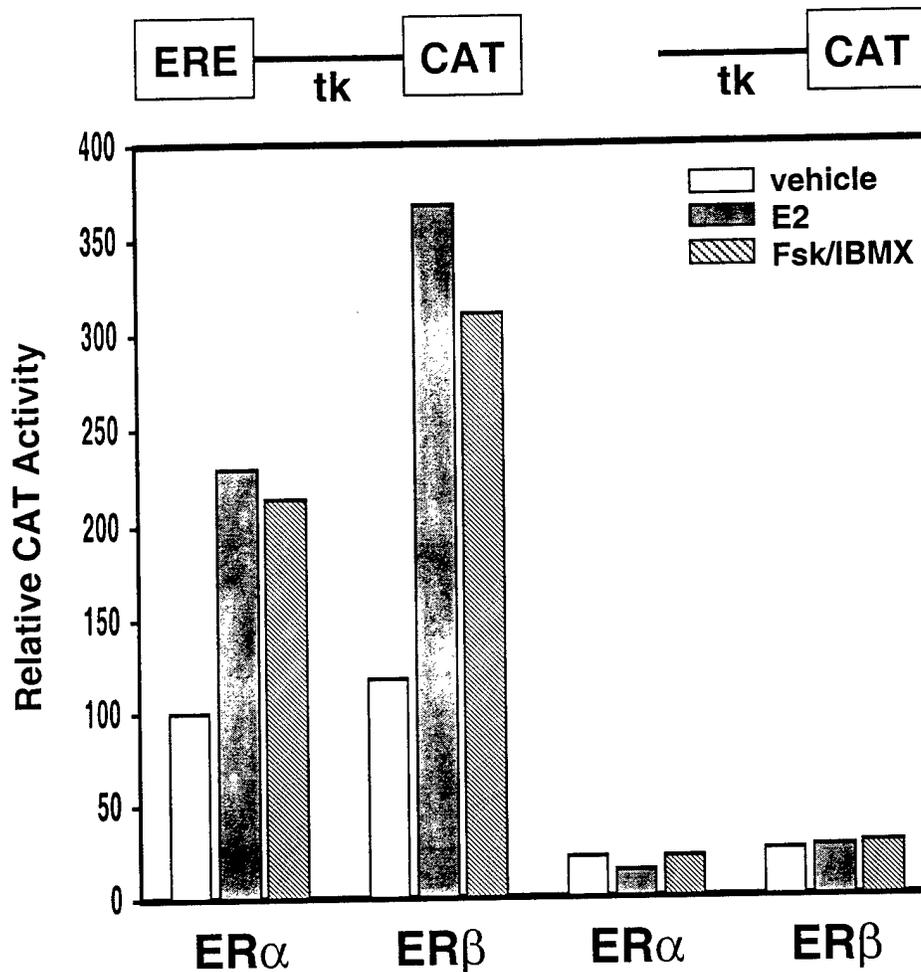


Figure 3: Estrogen Response Element is Needed for ER α and ER β activation by Forskolin. HeLa cells were cotransfected with either 1 μ g ERE-tk-CAT or tk-CAT reporter plasmid along with 10 ng pCMV₅-hER α (ER α) or pCXN₂-hER β (ER β) and stimulated with 1nM E2 or 10 μ M forskolin + 100 μ M IBMX. CAT measurements were corrected for protein values and standardized to ER α activity on the ERE-tk-CAT reporter in the presence of ethanol. Transfections were performed in duplicate and values represent the mean of two experiments.

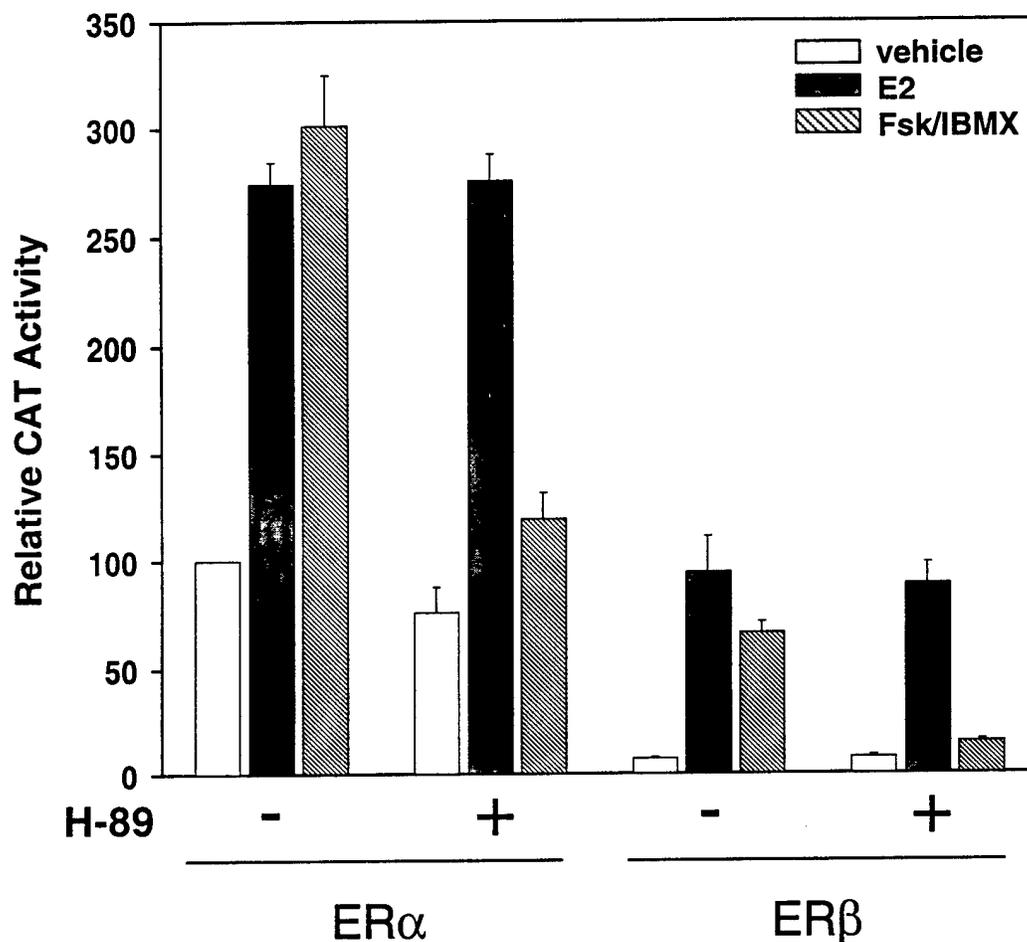


Figure 4: Forskolin Activation of ER α and ER β is Mediated by Protein Kinase A. HeLa cells were cotransfected with 1 μ g ERE-E1b-CAT reporter plasmid and 10 ng pCMV₅-hER α (ER α) or pCXN₂-hER β (ER β). Cells were stimulated with either 1nM E2 or 10 μ M forskolin + 100 μ M IBMX in the presence or absence of 10 μ M H89 inhibitor. CAT measurements were corrected for protein values and standardized to ER α activity on the ERE-E1b-CAT reporter in the presence of ethanol. Transfections were performed in duplicate and values represent the mean \pm SEM of at least three experiments.

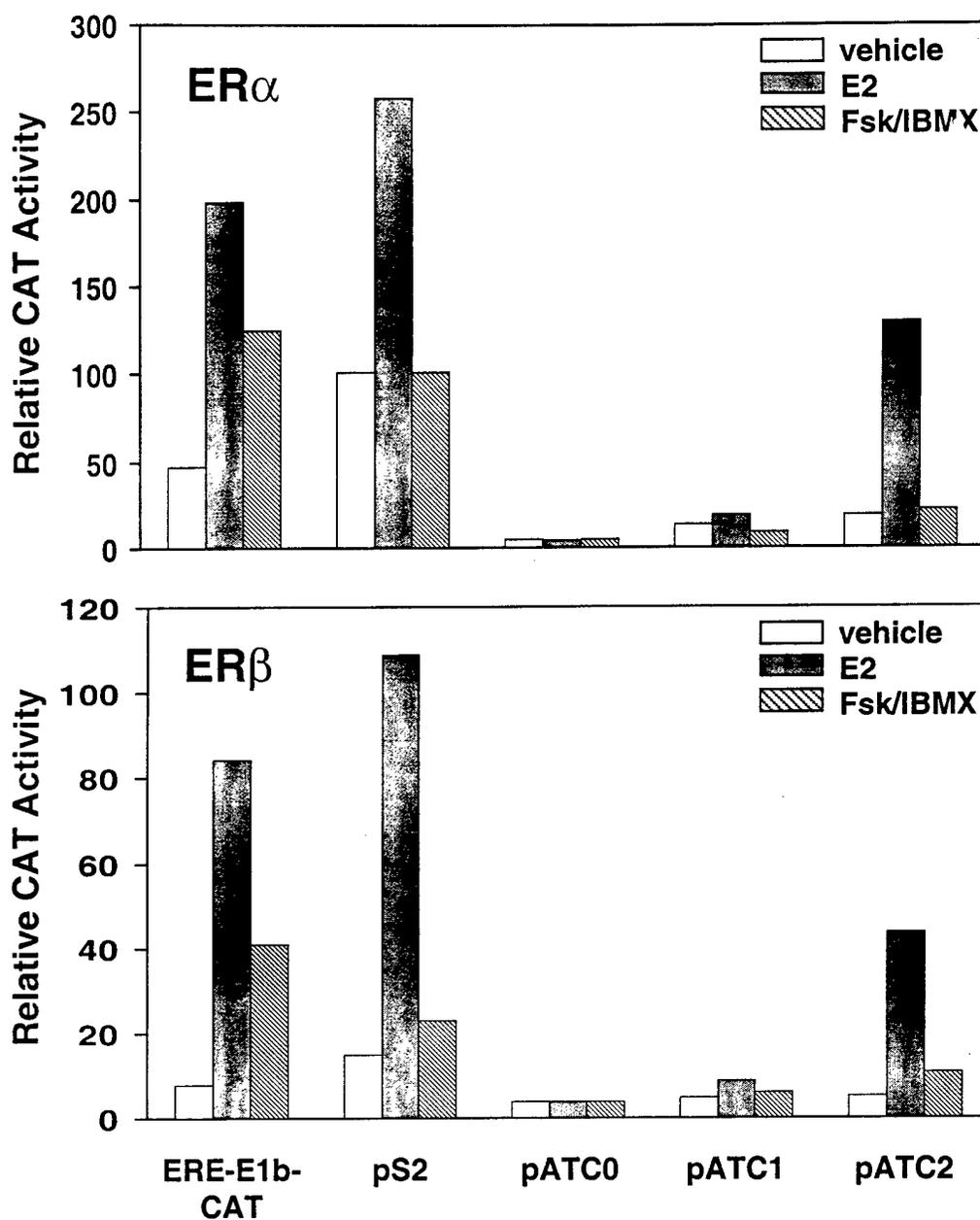


Figure 5: PKA-induced Activation of ER α and ER β is Promoter Context Dependent. HeLa cells were cotransfected with either 1 μ g ERE-E1b-CAT, pS2-CAT, pATC0, pATC1, or pATC2 reporter plasmid and 10 ng pCMV₅-hER α (ER α) or pCXN₂-hER β (ER β). Cells were stimulated 1nM E2, or 10 μ M forskolin + 100 μ M IBMX. CAT measurements were corrected for protein values and standardized to ER α activity on the ERE-E1b-CAT reporter in the presence of ethanol. Transfections were performed in duplicate and values represent the mean of two experiments.

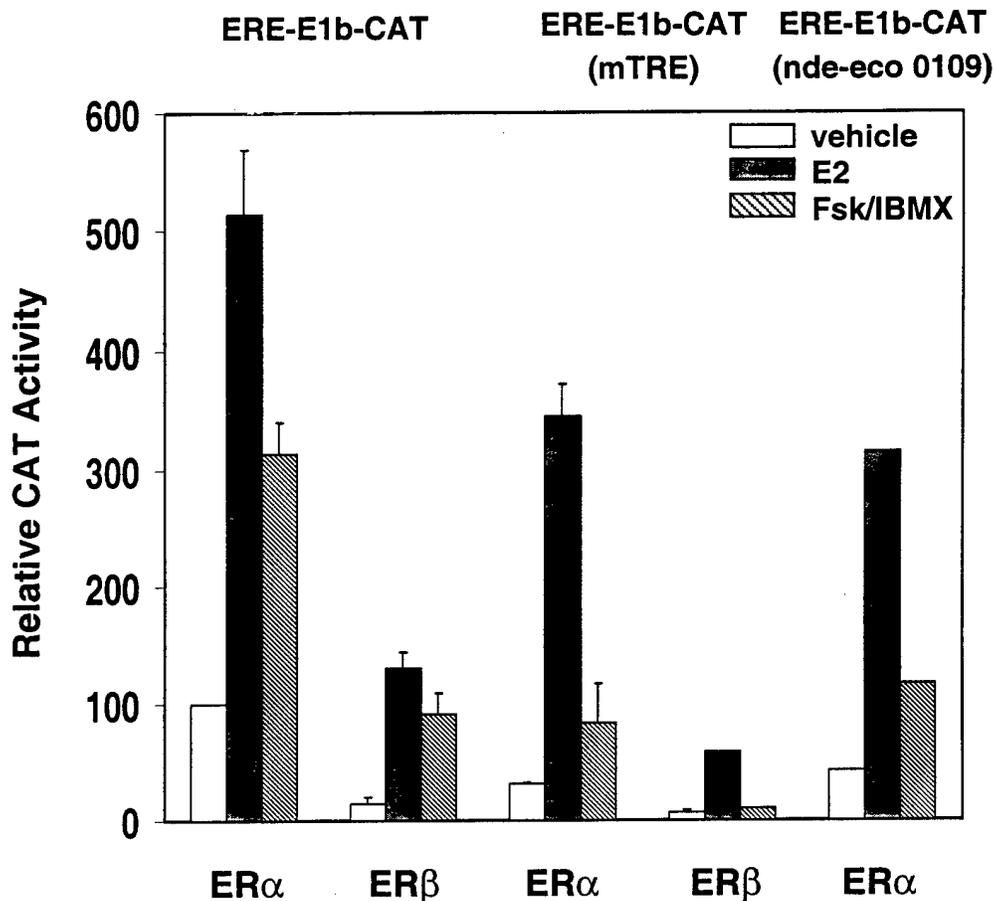


Figure 6: Putative AP-1 Response Element Contributes to PKA stimulation of ER α - and ER β -dependent Gene Expression. HeLa cells were cotransfected with either 1 μ g ERE-E1b-CAT or ERE-E1b-CAT (mTRE) reporter plasmid and 10 ng pCMV₅-hER α (ER α) or pCXN₂-hER β (ER β). Cells were stimulated with 1nM E2 or 10 μ M forskolin + 100 μ M IBMX. CAT measurements were corrected for protein values and standardized to ER α activity on the ERE-E1b-CAT reporter in the presence of ethanol. Transfections were performed in duplicate and values represent the mean \pm SEM of at least three experiments for the ERE-E1b-CAT and ERE-E1b-CAT(mTRE) and results from one experiment for ERE-E1b-CAT(NdeI-Eco0109).

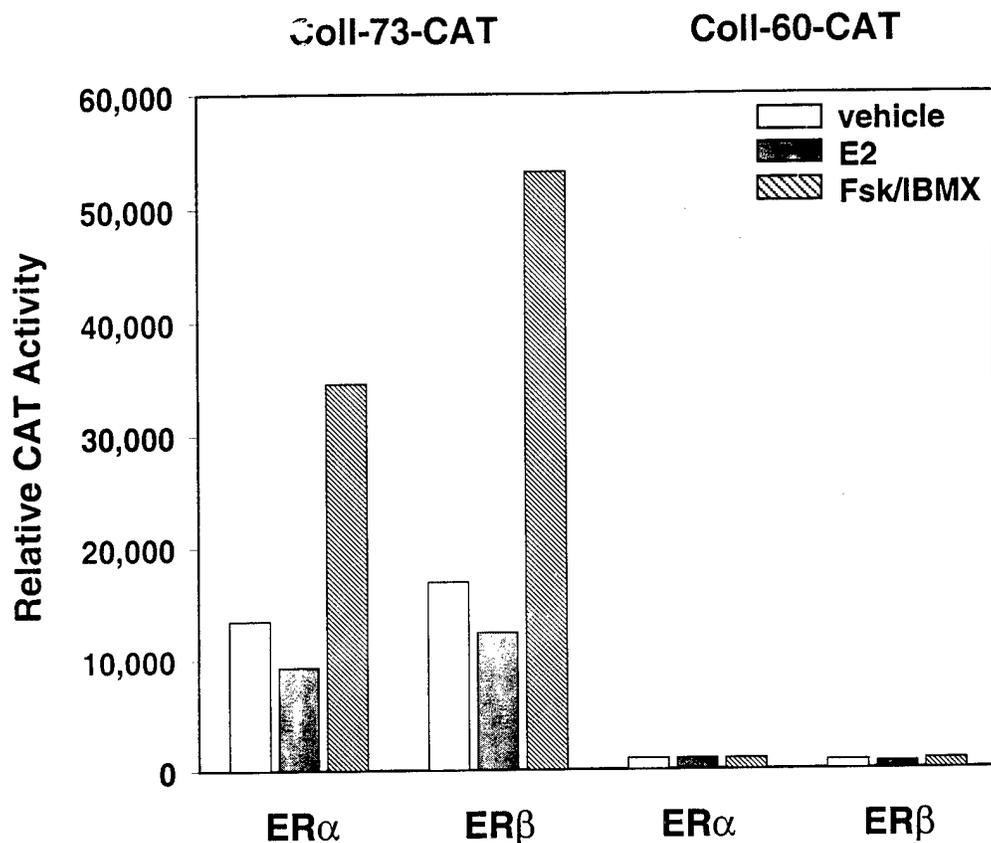


Figure 7: Forskolin and IBMX Stimulate AP-1 Activity. HeLa cells were cotransfected with either 1 μ g Coll-73-CAT or Coll-60-CAT reporter plasmid along with 10 ng pCR3.1-hER α (ER α) or pCXN₂-hER β (ER β). Cells were treated with ethanol, 1nM E2, or 10 μ M forskolin + 100 μ M IBMX and CAT measurements corrected for protein values. Transfections were performed in duplicate and values represent an individual experiment.

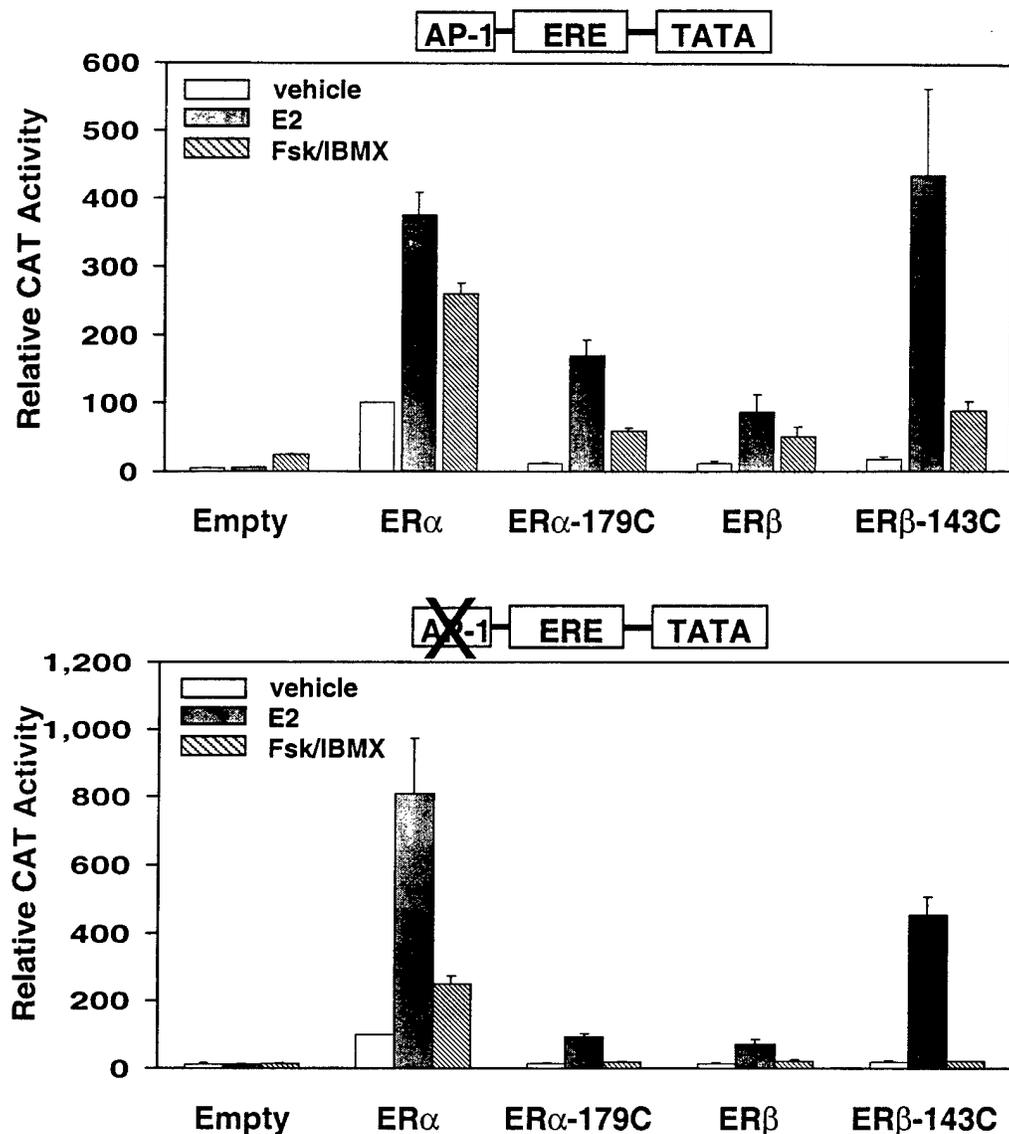


Figure 8: Amino Terminal A/B domains of ER α and ER β are not Required for Functional Interaction with AP-1 Transcription Factors. HeLa cells were cotransfected with (A) 1 μ g ERE-E1b-CAT or (B) 1 μ g ERE-E1b-CAT (mTRE) reporter plasmid and either 10 ng pCR3.1, pCR3.1-hER α (ER α), pCXN₂-hER β (ER β), pCR3.1-hER α -179C (ER α -179C), or pCR3.1-hER β -143C (ER β -143C). Cells were stimulated with 1nM E2 or 10 μ M forskolin + 100 μ M IBMX. CAT measurements were corrected for protein values and standardized to ER α activity on the ERE-E1b-CAT reporter in the presence of ethanol. Transfections were performed in duplicate and values represent the mean \pm SEM of at least three experiments.

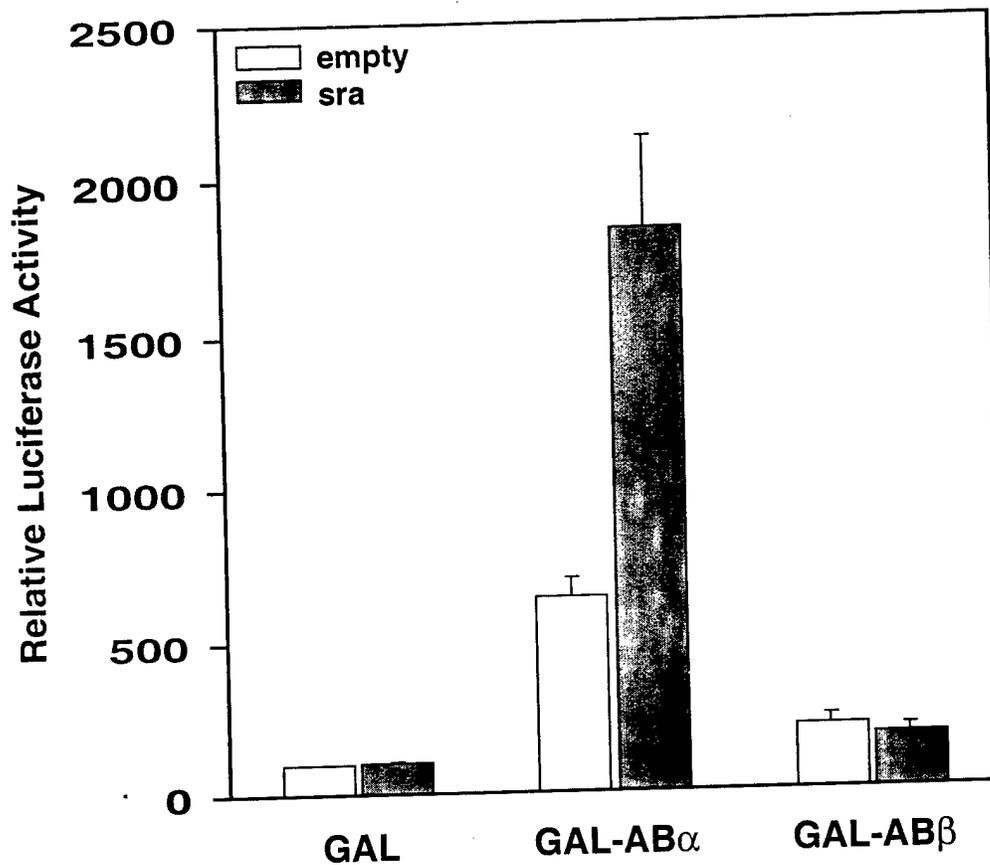


Figure 9: SRA Coactivates Amino Terminal A/B Domain of ER α but not ER β . HeLa cells were cotransfected with 1 μ g pG5-Luc reporter plasmid and either 1 μ g pSCT-SRA (sra) or pSCT parent vector (empty) along with 100 ng pBind (GAL), pBind-ER α -A/B (GAL-AB α), or pBind-ER β -A/B (GAL-AB β). Luciferase measurements were corrected for protein values and standardized to AB α activity in the absence of transfected coactivator. Transfections were performed in duplicate and values represent the mean \pm SEM of at least three experiments.

**Stimulation of Estrogen Receptor α and β
Transcriptional Activity by the RNA Coactivator, SRA.**

Kevin M. Coleman, Vinh D. Lam, Rainer B. Lanz, Bert W. O'Malley, and Carolyn L. Smith. Dept. of Molecular and Cellular Biology, Baylor College of Medicine, Houston, TX 77030

The biological effects of estrogens are mediated via the estrogen receptors α and β (ER α and ER β). Recently, a novel coactivator which functions as an RNA transcript, termed Steroid receptor RNA Activator (SRA), was identified and shown to increase the ability of type I nuclear receptors to activate target gene expression, presumably through their activation function-1 (AF-1) domains. Because the transcriptional activity of the ER β AF-1 has been shown to be very weak, we compared the ability of SRA to coactivate ER α and ER β in transiently transfected HeLa cells. Transactivation assays demonstrated that exogenous SRA coactivated both ER α and ER β by ~3-fold. Expression vectors encoding the A/B domain of each ER isotype fused to the Gal4 DNA binding domain were employed to study the effect of SRA on AF-1 transcriptional activity independent of other receptor domains. The ER α A/B domain activity was increased ~3-fold by SRA whereas the activity of the ER β A/B domain was unchanged, indicating that the amino terminus of ER α , but not that of ER β , can functionally interact with SRA. Successive deletions in the ER α amino terminus, which were used to map regions of the ER α A/B domain required for functional interaction with SRA, reduced overall receptor activity but did not substantially decrease the ability of SRA to coactivate ER α transcriptional activity. Moreover, ER α and ER β deletion mutants lacking the entire A/B domain were coactivated by SRA, indicating that the amino termini are not required for SRA coactivation and that ER deletion mutants containing only activation function-2 (AF-2) can be stimulated by SRA. Previously, SRA was shown to exist in a complex with Steroid Receptor Coactivator-1 (SRC-1), primarily an AF-2 coactivator. We therefore assessed the combined effects of overexpression of SRA and SRC-1 on ER-dependent gene expression. Together, SRA and SRC-1 increased ER α and ER β transcriptional activity to a greater extent than either coactivator alone, suggesting that these two molecules do not fulfill the same role in amplifying ER transcriptional responses. These data indicate that SRA, potentially as a complex with SRC-1, positively modulates the activity of the AF-1 and AF-2 domains of ER α but does not coactivate the AF-1 domain of ER β . Thus, the lack of SRA effect on the A/B domain of the latter receptor may contribute to its relatively low activity in comparison to the corresponding domain of ER α . This work is supported by a grant from the Department of Defense to CLS (DAMD 17-98-1-8282).

Presented at The Keystone Symposia—Nuclear Receptor 2000,
Steamboat Springs, CO. Abstract #315, March 25-31, 2000.

**SRA Coactivates the AF-1 Domain of ER α but not ER β , and
Stimulates the Agonist Activity of the Partial Antiestrogen, 4-
Hydroxytamoxifen**

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Running title: Selective Coactivation of the A/B Domain of ER α

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ABSTRACT

Estrogenic responses are mediated by two estrogen receptors (ERs), ER α and ER β , which possess poor sequence homology in their amino terminal (A/B) domains. This region encompasses the hormone-independent activation function-1 (AF-1), and functional differences in this domain are thought to contribute to the relatively weak transcriptional activity of ER β in comparison to ER α , presumably through differences in coactivator interaction. Steroid receptor RNA activator (SRA) was identified as an AF-1-specific coactivator, and we therefore examined its ability to contribute to differences in ER α and ER β transcriptional activity. In transient transfections, exogenous SRA expression increased ER α - and ER β -dependent gene expression. However, when the A/B regions of ER α and ER β were examined as GAL4 DNA binding domain fusions, SRA enhanced the transcriptional activity of GAL-AB α but not GAL-AB β . In cells, SRA and SRC-1 are found in a steroid receptor coregulator complex, but cotransfection of expression plasmids for these coactivators yielded GAL-AB β activity comparable to that obtained by SRC-1 alone. In contrast, SRA and SRC-1 synergistically coactivated the ER α A/B domain. The mixed antiestrogen, 4-hydroxytamoxifen (4HT) is an ER α AF-1 agonist. While SRA enhanced 4HT-stimulated ER α activity it was unable to convert 4HT to an ER β agonist. However, deletion of the A/B region of both receptors demonstrated that AF-1 is not required for SRA-mediated coactivation and that SRA effects can be mediated by the carboxy-terminus of either ER. Thus, SRA is an ER α AF-1-specific coactivator that may account, at least in part, for differences in AF-1 transcriptional activity between ER α and ER β , as well as the ability of tamoxifen to exert partial agonist activity on ER α .

INTRODUCTION

Estrogen receptors (ERs) are members of a superfamily of ligand-regulated transcription factors that stimulate gene expression in response to 17β -estradiol and other estrogenic compounds. There are two nuclear receptors for estrogens, ER α and ER β , that are encoded by separate genes [[4266,5210]]. Sequence analysis and molecular studies reveal that these receptors can be divided into structural/functional regions, designated A through F (see Figure 1 [[469,1073]]). While the vast majority of work has been performed with ER α , it is clear that both receptors encompass a centrally located DNA binding domain, and two activation functions; the one located in the amino-terminal domain is referred to as activation function-1 (AF-1), while a second located in the carboxy-terminal ligand binding domain is named AF-2. The AF-1 domain is constitutively active, but functions in a cell- and promoter-dependent manner [[15,36]]. In contrast, the AF-2 domain contributes to the transcriptional activity of both ER α and ER β in a ligand-dependent fashion. In many cellular contexts, both AF-1 and AF-2 of ER α are required for full receptor activity with the two activation domains exerting their effects on gene expression in a synergistic manner [[15,4000,363]]. In contrast, the AF-1 of ER β appears to repress the activity of its corresponding AF-2 domain [[5366]].

The ability of nuclear receptors, including the estrogen receptors, to activate target gene expression is intimately linked to their ability to interact with coactivators. These proteins serve as bridging factors between estrogen receptors and components of the general transcriptional machinery, thus facilitating interactions between site-specific and general transcription factors [[5227]]. Several estrogen receptor coactivators have been identified and characterized [[5369]], including members of the p160 steroid receptor coactivator-1 (SRC-1) family (*e.g.* SRC-1, TIF2/GRIP1 and RAC3). These proteins, in addition to their intrinsic activation domains also

encompass and/or interact with other proteins that possess histone acetyltransferase activity [[5044,5138,3989,5285]]. Thus, estrogen receptors recruit coactivator proteins with the ability to modify the local chromatin structure of target gene promoters and in so doing enhance gene expression [[5358]]. In addition, another ER coactivator, E5-AP, possesses ubiquitin ligase activity [[5061,5371]]. Although it is not clear what role if any, this enzymatic activity may play in regulating gene expression, it is becoming increasingly apparent that coactivators fulfill multiple functional roles in stimulating receptor-dependent gene expression. Interaction of protein coactivators with the ligand binding domain of estrogen receptors has been extensively studied and depends on the presence of agonists; antagonists do not promote coactivator binding to the ER [[5038,3993,3979]]. Crystallographic analyses indicate that an agonist-dependent shift in the orientation of helix 12 of the ER α ligand binding domain relative to the rest of this region facilitates binding of a GRIP1 coactivator peptide to the receptor [[5075]]. Furthermore, ligand-dependent alterations in the position of helix 12 have been noted for with the ligand binding domain of ER β suggesting that these two receptor subtypes may interact with coactivators via common structural motifs [[5364]].

In an effort to identify and characterize potential AF-1 coactivator(s), interest has turned to the identification of molecules that interact with the amino-termini of nuclear receptors. Unlike the AF-2 domain, this region is poorly conserved in type I receptors (*e.g.* receptors for progestins, glucocorticoids, estrogens and androgens), and is absent in the type II receptors for thyroid hormone, retinoic acid and vitamin D. Recently, by a yeast two-hybrid approach that employed the A/B domain of progesterone receptor-A (PR_A) as bait, a novel coactivator was identified that stimulated the transcriptional activity of type I, but not type II receptors [[5060]]. Interestingly, this molecule enhanced PR_B transcriptional activity in the presence of

cycloheximide, regardless of the presence of termination codons in the RNA. It was therefore suggested to act as an RNA molecule [[5060]] and was termed steroid receptor RNA activator (SRA). In T47D cells, this molecule is found in a large multiprotein, ribonucleoprotein complex that also contains SRC-1, and it appears to activate PR_B- and glucocorticoid receptor (GR)-dependent transcription via their AF-1 domains [[5060]].

Differences in the ability of ER α and ER β to activate estrogen-dependent target gene expression in transient transfection assays have been attributed to functional inequalities of their poorly conserved A/B domains, presumably due to distinct AF-1 activity [[5366,5264,5263]]. Tamoxifen stimulation of classical ER-mediated gene expression is dependent on the receptor's AF-1 domain, and it has been demonstrated that this antiestrogen blocks AF-2, but not AF-1, function [[3939,4000,3266,16]]. The ability of tamoxifen to act as a partial agonist of ER α , but not ER β on ERE-containing target genes is therefore also likely a reflection of the distinct activities of the ER α and ER β AF-1 domains [[5366,5264,5370,5024]]. Several protein coactivators (*e.g.* SRC-1 family members) interact with the A/B domains of both ER α and ER β and therefore are not likely to be responsible for the differences in the activities of these two ER subtypes [[5023,5033,5120]]. However, a p68 RNA helicase with coactivator activity was recently shown to act in an ER α -specific manner [[5363]], suggesting that functional differences between ER α and ER β may result from distinct receptor-coactivator interactions. In order to determine whether SRA functional interactions with ER α and ER β were comparable, we have examined the ability of SRA to stimulate the transcriptional activity of each receptor subtype in the presence of ER agonists and antagonists, as well as their isolated A/B domains. In addition, we examined the ability of SRA and SRC-1 to functionally interact with respect to stimulating

ER α and ER β transcriptional activity. Our results indicate that SRA acts as a coactivator of the A/B domain of ER α but not ER β , and that SRA and SRC-1 can cooperate with one another in certain contexts to activate transcription, suggesting that SRA can enhance AF-1 and/or AF-2 function in a receptor-dependent manner. Thus, SRA is a selective ER α AF-1 coactivator, and this may explain, in part, the differences in transcriptional activity observed for ER α and ER β .

MATERIALS AND METHODS

Chemicals

17 β -Estradiol (E₂) was obtained from Sigma Chemical Company (St. Louis, MO). The antiestrogens, ICI 182,780 and 4HT were gifts from Alan Wakeling (Zeneca Pharmaceuticals, Macclesfield, UK) and D. Salin-Drouin (Laboratoires Besins Iscovesco, Paris, France), respectively.

Plasmid DNAs

The mammalian expression plasmids for human ER α [pCMV₅-hER α [[2208]]; pCR3.1-hER α , ref. [[5061]]; or pRST₇-hER α , ref. [[4000]], the full-length [pCXN₂-hER β , ref. [[5216]]] and a short form of human ER β composed of amino acids 46-530 (pCMV₅-hER β , ref. [[5210]]), and the AF-2 mutants of hER α (pRST₇-hER-3x and pRST₇-hER-TAF2-3x, ref. [[4000]]) were described previously as were the synthetic target genes, pERE-E1b-Luc [[5061]] and pC3-Luc [[4000]]. The pG5-Luc target gene, which contains five binding sites for the GAL4 DNA binding domain (DBD) fused to the luciferase gene, was obtained from Promega Corporation. The mammalian expression vector for SRA (pSCT-SRA) and its corresponding parent vector (pSCT) have been used in a previous study [[5060]].

The mammalian expression vector for SRC-1e (pCR3.1-SRC-1e) was constructed as follows: Oligo(dT)₁₂₋₁₈ primers (Life Technologies) were used to reverse transcribe total RNA isolated from HeLa cells and the resulting material was PCR amplified with 5' (5'-TGTGTTCAAGCTGTCC-3') and 3' (5'-GATGTCTGATCACCTTACGAG-3') primers (the latter containing an *SpeI* site, underlined) to produce a 327 base pair (bp) portion of the SRC-1e cDNA. This fragment was digested with *BstZ17I* and *SpeI* and substituted for a 556 bp *BstZ17I-XbaI* region of the expression plasmid for SRC-1a (pCR3.1-SRC 1a, ref. [[5065]]) to yield pCR3.1-SRC-1e. In order to make the pCMV₅-hER α -87C expression plasmid, PCR was employed to amplify the portion of pCMV₅-hER α encoding amino acids 87-315 using the 5' primer 5'-GCCCGCGGACCATGGCGGCGTTCGGCTCCAACGGC-3' [containing a *SstII* (underlined) and start codon (bold) followed by the codons for amino acids 87-93] and the 3' primer 5'-TCCCTGACGGCCGACCAGATG-3' containing an *XmaIII* site (underlined). This PCR product (698 bp) was cloned into the pCR3.1 expression vector using the TA cloning kit (Invitrogen). The *SstII-XmaIII* fragment from this vector was excised, and substituted for a 974 bp *SstII-XmaIII* fragment of wild type pCMV₅-hER α . An expression vector encoding an ER α mutant lacking the first 108 amino acids (pCR3.1-hER α -109C) was constructed by digesting the wild type ER α expression vector (pCR3.1-hER α) with *SacII* to remove the first 324 nucleotides of the coding region and religated. The constructs for hER α -179C (pCR3.1-hER α -179C) and hER β -143C (pCR3.1-hER β -143C) were made by PCR using the primers 5'-ACCATGGCCAAGGAGACTCGCTACTGT-3' and 5'-CTCTCAGACTGTGGCAGGGAAACC-3' to amplify the segment of pCMV₅-hER α encoding amino acids 179 to 595 and the primers 5'-ACCATGAAGAGGGATGCTCACTTCTGC-3' and

5'-GCGTCACTGAGACTGTGGGTTCTG -3' to PCR amplify the segment of pCXN₂-hER β cDNA encoding residues 143 to 530, respectively. Each of the resulting PCR fragments was cloned into the pCR3.1 expression plasmid using the TA cloning kit. All PCR products were verified by sequence analysis to ensure that errors did not occur during their synthesis.

The mammalian expression plasmids for the A/B domain of ER α and ER β fused to the GAL4 DNA binding domain were constructed as follows. First, PCR amplification was performed using the primers 5'-TAAACGGGCGGGATCCCGATGACCATGACCCTCCACACCAAA-3' and 5'-CCCCGGGATCCTTAAGTCTCCTTGGCAGATTCCATAGC-3' to amplify a portion of the human ER α cDNA (pCMV₃-hER α) encoding amino acids 1-182, while the primers 5'-GGGCCGGGATCCCGATGGATATAAAAAACTCACCATCT-3' and 5'-CCCCGGGATCCTTAAGCATCCCTCTTTGAACCTGG-3' were used to amplify the region of the human ER β (pCXN₂-hER β) cDNA encoding amino acids 1-146. Each of these primers possesses a *Bam*H1 restriction site (underlined). The resulting cDNA fragments were subcloned into the pCR3.1 TA cloning vector to produce pCR3.1-hER-AB α and pCR3.1-hER-AB β , respectively. Plasmids were digested with *Bam*H1 and each of the resulting cDNA fragments was subcloned into the *Bam*H1 restriction site of the pBind vector (Promega), such that the coding sequences for each ER A/B domain is in-frame with and downstream of the coding sequence for amino acids 1-147 of the GAL4 DNA binding domain. The resulting vectors were sequenced to ensure that no errors were introduced during plasmid construction.

Cell Culture and Transfections

HeLa (human cervical carcinoma) cells were routinely maintained in Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% fetal bovine serum (FBS). Twenty four hours prior to transfections, cells were plated in six-well culture dishes at a density of 3×10^5 cells per well in phenol red-free DMEM with 5% charcoal-stripped fetal bovine serum (sFBS). DNA was introduced into cells in the indicated amounts using Lipofectin (Life Technologies), according to the manufacturer's guidelines. Eight hours later, serum-free media was replaced with phenol red-free DMEM supplemented with 5% sFBS. Twelve hours thereafter, cells were treated with the indicated amounts of various hormones. After 7 hours of hormone treatment, cells were harvested and extracts were assayed for luciferase activity using the Luciferase Assay Systems kit (Promega) and a Monolight 2010 Luminometer (Analytical Luminescence Laboratory). Relative luciferase units were normalized to total cellular protein, as determined by Bio-Rad Protein Assay. Experiments were done in duplicate and values represent the mean \pm SEM of at least three individual experiments.

HepG2 (hepatocellular carcinoma) cells were maintained in similar growth conditions as those for HeLa cells. Twenty four hours prior to transfection, cells were plated at a density of 8×10^5 cells per well in six-well culture plates in phenol red-free DMEM with 5% sFBS. DNA was introduced into cells using Lipofectamine (Life Technologies), according to the manufacturer's recommendation. Following 8 hours of transfection, media was changed to phenol red-free DMEM with 5% sFBS. Twenty hours later cells were treated with the indicated amounts of hormone for 20-24 hours. Cells were harvested and cell lysates prepared and assayed for luciferase activity as described above. Experiments were done in triplicate and values are reported as the mean \pm SEM from at least three individual experiments.

RESULTS

It has been previously demonstrated that the RNA coactivator, SRA, stimulates the transcriptional activity of several type I nuclear receptors including the PR_B, GR, androgen receptor (AR) and ER α , and experiments with deletion mutants of both PR_B and GR indicated that their AF-1 domains were required for SRA to enhance transcriptional activity [[5060]]. The two subtypes of estrogen receptors, ER α and ER β , are poorly conserved in their A/B domains which share ~26% identity, while the DNA binding and ligand binding domains (84% and 58%, respectively) are relatively well conserved. In order to assess whether SRA could coactivate ER α and ER β transcriptional activity in a similar fashion, SRA was overexpressed in cells transfected with expression vectors for the full-length form of human ER α or ER β (**Figure 1**) and the estrogen receptor-dependent synthetic target gene, ERE-E1b-Luc, which consists of a consensus estrogen response element linked upstream of a TATA box and luciferase reporter gene. When cells were treated with 1 nM estradiol, both ER α and ER β activated luciferase expression (**Figure 2**), and as expected, full-length ER β was ~50% less active in comparison to ER α (data not shown). However, the ability of SRA overexpression to enhance receptor-dependent target gene expression did not vary; both ER α and ER β activities were stimulated approximately 3-fold. Therefore, SRA is a coactivator for ER α and ER β which is consistent with SRA being selective for type I nuclear receptors.

The ability of the mixed antiestrogen, 4-hydroxytamoxifen (4HT) to stimulate ER α transcriptional activity is dependent upon the amino-terminal AF-1 function, and the cell and promoter context in which gene activation studies are performed [[16,4000]]. Furthermore,

overexpression of protein coactivators including SRC-1 and GRIP1 stimulates the transcriptional activity of ER α liganded with the mixed antiestrogen, 4HT [[5023,4225,5363]]. Therefore, because SRA is an AF-1-dependent coactivator of PR β and GR, its ability to enhance 4HT-stimulated transcriptional activity of ER α and ER β was assessed (Figure 3). As anticipated, in the absence of exogenous SRA, 4HT is a relatively poor agonist in HeLa cells. However, overexpression of SRA increased the ability of 4HT to activate gene expression in comparison to estradiol (~4-fold *versus* 3-fold, respectively), suggesting that ER α liganded with this partial agonist/antagonist was able to functionally interact with SRA. In contrast, other investigators have been unable to demonstrate activation of ER β -dependent transcription by 4HT even though ER β binds to 4HT with an affinity comparable to that of ER α [[4263,5024,4266,5255]]. In order to determine if SRA overexpression might partially overcome ER β resistance to 4HT agonist activity, luciferase gene expression was measured in HeLa cells transfected with expression plasmids for ER β and SRA, and treated with 4HT. As shown in figure 3, 4HT alone was unable to stimulate the transcriptional activity of ER β in this system and SRA overexpression was unable to rescue the inability of 4HT to stimulate ER β -dependent gene expression.

In order to determine if SRA overexpression could alter the transactivation induced by a second class of antiestrogens, the ability of the pure antiestrogen ICI 182,780 to activate transcription in the absence and presence of exogenous SRA was also assessed (Figure 3). This antiestrogen inhibits ER α and ER β transcriptional activity in most contexts in which it has been tested, and in HeLa cells it is unable to stimulate the activity of either ER α or ER β whether or not SRA was cotransfected. These data indicate that the ability of SRA to stimulate the transcriptional activity of ERs liganded with antiestrogens depends on the nature of the

antiestrogen [partial (4HT) *versus* pure (ICI 182,780)] and the subtype of estrogen receptor (α *versus* β).

The observation that SRA overexpression resulted in enhanced transcription stimulated by 4HT was confirmed and extended in HepG2 cells using the pC3-Luc target gene. The mixed antiestrogen, 4HT, is a relatively good agonist in Hep G2 cells [[4000]], and ER α activity is highly dependent upon AF-1 activity, whereas in HeLa cells both AF-1 and AF-2 are usually required for robust transcriptional activity [[16]]. The pC3-Luc target gene consists of the -1807 to +58 region of the human complement-3 (C3) gene fused to a luciferase reporter and contains three imperfect estrogen response elements [[3987]]. As expected [[4225]], 100 nM 4HT was able to stimulate the transcriptional activity of ER α in HepG2 cells as well as 10 nM estradiol (Figure 4). Furthermore, SRA overexpression stimulated the transcriptional activity of ER α in the presence of 4HT to the same extent as when the receptor was liganded by 17 β -estradiol. When the experiment was performed with an expression vector for ER β , the luciferase activity induced by E2 was only ~ 40% as great as that stimulated by ER α (data not shown), and consistent with its refractoriness to mixed antiestrogens, no activation of target gene expression was detected in 4HT-treated cells. Exogenous SRA, introduced via transient transfection, resulted in coactivation of luciferase gene expression only when cells were treated with estrogen; 4HT-liganded ER β was still unable to stimulate target gene activity. Consistent with the results obtained in HeLa cells, the pure antiestrogen ICI 182,780 was unable to activate transcriptional activity of either ER α or ER β , and SRA overexpression had no effect on the ability of these receptor-ligand complexes to activate transcription.

Taken together, the above data indicated that SRA can coactivate estrogen-stimulated ER α - and ER β -dependent gene expression even though the amino-termini of these receptors share little identity. However, differences between the two receptors are observed when cells are treated with 4HT in the presence or absence of exogenous SRA, suggesting that their respective AF-1 domains are not functionally homologous. Therefore, in order to determine if SRA could coactivate the transcriptional activity of the AF-1 domains of each receptor subtype isolated from the context of the remainder of the receptor molecule, expression vectors encoding fusions of the GAL4 DBD to either the A/B domain of ER α (GAL-AB α) or ER β (GAL-AB β) were made. These were cotransfected into HeLa cells with a target gene containing five GAL4 DNA binding sites (pG5-Luc) in the presence or absence of an expression vector for SRA. As shown in **Figure 5A**, the A/B α domain in the absence of exogenous coactivator has considerable transcriptional activity in comparison to the GAL4 DBD alone. However, the transcriptional activity of GAL-AB β is very weak in comparison to the GAL-AB α chimeric protein, indicating that the two A/B regions are distinct in their ability to activate target gene expression, and that the AF-1 activity of ER α is significantly stronger than that of ER β in this cellular context. The ability of SRA to coactivate these regions independently of AF-2 was tested in parallel by SRA overexpression in transient transfection assays. As expected, SRA had no effect on the minimal activity seen in cells transfected with the GAL4 DBD alone. In contrast, exogenous SRA stimulated the ability of the GAL-AB α chimera to activate target gene expression nearly 3-fold, but did not enhance the transcriptional activity of the GAL-AB β chimera. This suggests that SRA is an ER α -specific coactivator of the AF-1, and that SRA must coactivate ER β through a region other than the A/B domain.

To confirm that ER α could be activated via its AF-1 domain in the context of a full length receptor, the ability of a mutant ER α (ER α -3x) in which three amino acids in the core AF-2 domain are mutated (D538A/E542A/D545A), was assessed for its ability to be coactivated by exogenous SRA. These mutations severely inhibit ER α interaction with the nuclear receptor interaction domains of SRC-1 and GRIP1 [[5380]]. As shown in **Figure 5B**, the gene expression stimulated by this receptor was increased by SRA, although to a lesser extent than wild type receptor (2.6-fold *versus* 3.4-fold, respectively). However, when the AF-1 domain was deleted in addition to the AF-2 point mutations to yield the ER α -TAF2-3x mutant, no hormone-induced transcriptional activity was observed and SRA overexpression was unable to substantially increase luciferase gene expression. As a further control, the effect of exogenous SRA in cells transfected with the target gene and the parent expression vector lacking any ER α cDNA was assessed, and no change in luciferase activity was noted. Taken together, these data demonstrate that in the context of the holoreceptor an intact AF-2 domain is not required for SRA to coactivate ER α transcriptional activity.

To date, it is unclear whether SRA binds directly to type I receptors or via an intermediary protein. It has been shown previously by coimmunoprecipitation experiments that SRA and SRC-1 can physically associate with one another in *Xenopus* oocytes and that SRC-1 could facilitate detection of SRA in a complex containing an AF-1 deletion mutant of the androgen receptor [[5060]]. Thus, it is possible that SRA may interact with steroid receptors via SRC-1. Although SRC-1 was identified as an AF-2-binding coactivator protein [[3096]], evidence has been obtained demonstrating that it also can interact with the amino-terminus of ER α and ER β [[5023,5033,5120]]. Therefore, expression vectors for SRC-1e, the SRC isoform with greatest ER enhancing activity [[5038]], and SRA were transfected into HeLa cells to determine if

coexpression of these coactivators would facilitate coactivation of the ER α or ER β AF-1 activity in a cooperative manner. As shown in **Figure 6**, coexpression of SRA and SRC-1 increased the transcriptional activity of the ER α A/B domain to an extent greater than either coactivator alone indicating that these two proteins may be part of a functionally interactive pathway able to modulate ER α AF-1 activity. In contrast, only SRC-1 was able to stimulate the transcriptional activity of the ER β A/B domain, and the addition of exogenous SRA did not modulate the magnitude of this response. This finding is consistent with the inability of SRA alone to stimulate the transcriptional activity of the GAL-AB β chimera, and suggests that SRA functional and/or physical interactions with A/B domains of type I receptors are not simply the results of SRA interactions with SRC-1. Thus, these data further emphasize that SRA has the potential to act via the AF-1 domain of ER α but not ER β , and that the molecular nature of this cooperative response requires appropriate interactions of SRA and SRC-1 within the context of the A/B domain, and not simply interaction of SRC-1 and subsequent recruitment of SRA.

The results obtained above suggested that SRA coactivates ER α via its AF-1 domain, but that this region of ER β was insufficient for a functional interaction with this RNA coactivator. Therefore, in order to determine whether the AF-1 domain of ER α was required for SRA coactivation, and whether SRA could coactivate ER β via its ligand binding domain, a series of A/B deletion mutants of ER α and ER β were tested for their ability to activate target gene expression in the absence and presence of exogenous SRA. Expression vectors for the truncated forms of ER α were cotransfected into HeLa cells along with the ERE-E1b-Luc synthetic target gene and the transcriptional activity in the presence of vehicle or 1 nM E2 was assessed. Deletion of the first 86 amino acids of ER α reduced its transcriptional activity, in the presence of

estradiol, to ~60% of wild type receptor activity (**Figure 7A**). Deletion of amino acids 1-108 also reduced activity to approximately the same extent (**Figure 7B**) which is consistent with the concept that these amino acids contribute to ER α AF-1 activity stimulated by estradiol [[5256]]. However, this region was not required for SRA coactivation, since deletion of these residues did not block the enhancement of the transcriptional activity of the resulting receptor mutants. In order to determine if any portion of the A/B domain was required for this receptor to be coactivated by SRA, a more extensive deletion mutant of ER α lacking the entire A/B domain (ER α -179C) was generated and examined for its ability to support SRA coactivation of target gene expression (**Figure 7B**). Surprisingly, the coactivator retained its ability to enhance luciferase activity indicating that while SRA could activate transcription via the A/B domain, this region was not necessary for SRA coactivation of ER α -dependent target gene expression.

The first human ER β cDNAs cloned did not encode the full-length receptor [[5210,4268]], and the ability of a truncated form of ER β , lacking the first 45 amino acids also was tested for its ability to be coactivated by exogenous SRA expression. As shown in **Figure 7C**, the transcriptional activity of this short form of ER β was stimulated as well as wild type receptor by SRA, suggesting that the extreme amino-terminus of ER β is not required for coactivation by SRA. The ability of an ER β mutant lacking all A/B domain sequences (ER β -143C) was next examined and as shown in **Figure 7D**, SRA was able to stimulate the transcriptional activity of this mutant receptor to an extent comparable to wild type ER β , suggesting that coactivation of ER β is mediated by the remaining carboxy-terminal portion of the receptor. Taken together, these data suggest that SRA, while an ER α -specific coactivator of the AF-1 domain, also

possesses the ability to coactivate transcription via the ligand and/or DNA binding domains of both estrogen receptor subtypes.

Since the carboxy-terminal portion of both ER subtypes was able to be coactivated by SRA and SRC-1, the ability of these two coactivators to functionally interact with ER α and ER β was assessed in the context of the respective full length receptors. As shown in **Figure 8A**, under conditions where SRA and SRC-1 individually are weak activators of ER α -dependent target gene expression, transient transfection of the expression plasmids for the RNA and protein coactivators resulted in gene expression, as measured by luciferase activity, greater than either coactivator alone. When similar experiments were performed with ER β , coexpression of SRA and SRC-1 resulted in luciferase activity that also was greater than additive (**Figure 8B**). Taken together, this suggests that SRA and SRC-1 can functionally interact in the context of the full-length receptor, and that the carboxy-terminal portion of ER β , but not ER α , is required to support this transcriptional response.

DISCUSSION

The identification of a second receptor for estrogens, ER β , has substantially increased the potential complexity of estrogen action *in vivo*, and much effort is currently underway to resolve both mechanistic and physiological consequences of this second estrogen receptor subtype. Although both receptors bind estradiol with nearly equivalent affinity [[5255,4263]], their abilities to stimulate target gene transcription are distinct. In general, ER α is a superior activator with respect to the magnitude of ERE-containing target gene expression in transient transfections [[5263,4268,5264,5265,5370]], although it is possible that target genes remain to be identified

where ER β will be a more robust activator of transcription. Alternatively, ER β may be considered as a negative regulator of estrogen action since it inhibits ER α transcriptional activity in some contexts, presumably through a heterodimerization mechanism [[5366,5265]]. In view of the divergent amino-terminal sequences of ER α and ER β , and the reported ability of SRA to activate the AF-1 domain of steroid receptors [[5216,5367,5060]], as well as to better understand the mechanistic basis for differences in the ability of ER α and ER β to stimulate gene expression, we have conducted a series of experiments to characterize the ability of these receptors to functionally interact with the novel RNA coactivator, SRA.

Exogenous SRA increased levels of both ER α - and ER β -dependent gene expression suggesting that the relative differences in these two receptor subtypes to activate target gene transcription was not due to an absolute inability of SRA to functionally interact with ER β . Furthermore, the ability of SRA to enhance the transcriptional activity of either receptor was not restricted to a specific cell or promoter type since SRA coactivated ER α and ER β transcriptional activity in HeLa and HepG2 cells on the ERE-E1b-Luc and pC3-Luc promoters, respectively. Thus, SRA coactivates ER α and ER β transcriptional activity. In addition, SRA and SRC-1 appear to work together, since activation of target gene expression is greater following transfection of expression vectors for both coactivators than would be anticipated from either coactivator alone, and this is consistent with the presence of SRA in SRC-1, but not p300 containing complexes isolated from T47D cells [[5060]]. At present the mechanism(s) by which SRA alters ER-dependent target gene expression is unclear. In general, there is an increasing appreciation of the potential roles that RNA plays in regulating transcription, including even functions more generally associated with proteins. For example, RNA may regulate gene expression in *trans* by assuming a structural role and recruiting proteins to promoters [[5379]],

altering mRNA translation or stability by antisense RNA-RNA interactions [[5378,5376]], or by regulating the enzymatic activity of associated proteins that affect transcription factor activity [[5377]].

The ability of SRA to affect the transcriptional activity of A/B domains isolated from the remaining portion of their respective receptors was assessed to determine the ability of SRA to specifically serve as an AF-1 coactivator. We first characterized the activity of each A/B domain in the absence of exogenous coactivators. Interestingly, when tethered to the GAL4 DBD, the A/B domain of ER α was significantly more active than the corresponding region of ER β . This work confirms and extends earlier observations in which it was shown that a GAL4 DBD fusion with 95 amino acids of the N-terminal region of ER β (corresponding to amino acids 54 - 148 of the human ER β full length sequence) was less active than a chimeric protein comprised of the full length A/B domain of ER α (amino acids 1-182) linked to the GAL4 DBD [[5366]], and indicates that even the full length ER β A/B domain (amino acids 1-143) is less active than the corresponding region of ER α . Similar results have also been shown in HepG2 cells [[5263]]. This also supports the hypothesis that functional differences in ER subtypes arise, at least in part, from differences in the activity of the amino-terminal domains.

The basis for the differences in ER α and ER β A/B domain activities are presumably related to the relative ability of these regions to physically and/or functionally interact with coactivators. It had been shown previously that this region of both receptors could interact with SRC-1, suggesting that the relative inactivity of the ER β A/B domain is not due to a failure of this region to bind p160 coactivators [[5023,5120]]. Although it is not clear whether SRA binds directly to the A/B domain of nuclear receptors, there is a distinct difference in the ability of

SRA to functionally interact with this region of ER α and ER β when they are isolated from their respective DNA and ligand binding domains, and this likely contributes to the relatively poor transcriptional activity of the ER β A/B domain. This is even more striking because previous studies had demonstrated that SRA is found in a complex in cells with SRC-1 [[5060]], and we hypothesized that it might be possible for SRA to interact with the A/B domain of either receptor subtype via this p160 coactivator. However, a synergistic response was observed only when SRA and SRC-1 were co-expressed in the GAL-AB α , but not GAL-AB β transfected cells, further emphasizing the inability of SRA to functionally interact with the A/B domain of ER β . This result also argues that the functional interaction of SRA with the ER α AF-1 is not simply the result of its recruitment to that region via SRC-1, and suggests that SRA either interacts directly with the A/B domain of ER α but not ER β , or that it interacts with and/or requires other factors that selectively associate with the A/B domain of ER α .

Recently, the identification of another AF-1 coactivator for ER α was reported [[5363]]. The p68 RNA helicase was isolated as an ER α AF-1 domain interacting protein that selectively enhanced the activity of the A/B domain of ER α , but not ER β in COS-1 cells [[5363]]. Although it is tempting to speculate that p68 and SRA function together, p68 does not coactivate the AF-1 domain of ER α in HeLa cells [[5363]]. Furthermore, p68 RNA helicase does not activate the AF-1 domains of other receptors, such as the androgen receptor, that are targets for SRA effects [[5363,5060]]. In addition, the ATP-dependent RNA helicase activity of p68 can be abolished by point mutation and the resulting protein still retains its transcription enhancing activity [[5363]]. Taken together, the p68 RNA helicase and SRA appear to be functionally distinct, but their existence argues that there are AF-1-specific coactivators which act in a cell-

type- and/or receptor-specific manner, and are likely to contribute to the distinct transcriptional activity of ER β in comparison to ER α .

The ability of SRA to coactivate the transcriptional activity of the ER β holoreceptor, but not its AF-1 suggested that SRA could modulate receptor function through a region other than the A/B domain. Sequential deletion of the A/B domain of ER α demonstrated that the AF-1 region required for tamoxifen (amino acids 1-88) or estradiol (89-108) agonist activity [[5256]] was not required for SRA functional interactions. Furthermore, the ability of SRA to coactivate mutant forms of ER α and ER β lacking their entire A/B domains (ER α -179C and ER β -143C, respectively) also indicates that SRA, like the p160 SRC-1 family of coactivators [[5033,5023]] can stimulate transcriptional activity through the amino- and carboxy-terminal portions of the receptor. The ER α mutant in which the AF-1 deletion was combined with point mutations of AF-2 (ER α -179C-3x) further confirms that this coactivator modifies ER transcriptional activity through the receptor's activation domains. Although SRA interactions with the ligand binding domain of nuclear receptors are not defined, SRA could be detected in complexes immunoprecipitated with an androgen receptor antibody from *Xenopus* oocytes expressing an AF-1 deletion mutant of androgen receptor only when SRC-1 was coexpressed [[5060]]. Thus, SRA is able to physically interact with the carboxy-terminal portion of a nuclear receptor through an interaction with SRC-1, suggesting that SRA can enhance the transcriptional activity of the AF-2 domains of ER α and ER β through a similar mechanism. This result also highlights the differences between the amino- and carboxy-terminal regions with respect to SRA coactivation, since coexpression of SRC-1 was insufficient to enable SRA coactivation of the ER β AF-1 domain.

Tamoxifen is a member of a class of drugs referred to as selective estrogen receptor modulators (SERMs), that can manifest agonist or antagonist activity depending on the cell, promoter and estrogen receptor subtype [[5356]]. The crystal structure of the ER α ligand binding domain has been solved [[5075,5076,5045]], and the surface of the receptor to which p160 coactivators bind has been defined [[5372]]. In the presence of tamoxifen the LBD adopts a conformation that produces an intramolecular interaction of helix 12 (amino acids 536 to 544) with the receptor's coactivator interaction surface that occludes binding of a GRIP-derived coactivator peptide [[5075]]. Thus, the position of helix 12 induced by tamoxifen is likely to block coactivator interaction with the ligand binding domain, and in so doing antagonize AF-2 activity. Tamoxifen does not inhibit the AF-1 of ER α , and deletion experiments indicate that the A/B region is required for tamoxifen-stimulated gene expression [[16,3266,5256]]. Thus, this SERM's agonistic properties are believed to be dependent on cell-specific coactivator interactions with ER α [[5356]]. The inability of tamoxifen to stimulate ER β transcriptional activity on ERE-containing target genes implies an AF-1 deficiency relative to ER α , and highlights the importance of defining AF-1-coactivator interactions [[5366,5264,5370,5024]]. Since tamoxifen-stimulated ER α activation is enhanced by SRC-1, GRIP1 and RAC3 [[4225,5023,5363]], and at least SRC-1 can interact with the A/B domain of ER β [[5120]], the p160 coactivators are unlikely to be the primary basis for differences in ER α and ER β transcriptional activity in the presence of tamoxifen. The identity of SRA as an ER α -specific AF-1 coactivator suggests that this positive coregulator may contribute to the tissue-specific activity of SERMs. Furthermore, this suggests that alterations in SRA expression may have a significant impact on a tissue's responsiveness to tamoxifen. Interestingly, elevated expression of an SRA variant has been strongly correlated with breast tumors of high grade [[5373]], raising

the intriguing possibility that changes in SRA expression may have implications for the sensitivity of breast tumors to tamoxifen therapy.

ACKNOWLEDGEMENTS

The authors acknowledge the generous gifts of Drs. Donald McDonnell for pC3-Luc, pRST7-hER plasmids, Jan-Åke Gustafsson for ER β -46C and Masami Muramatsu for wild type ER β . The SRC-1e and ER α -109C expression vectors were made by Martin Dutertre and David Lonard, respectively. We also thank Judy Roscoe and Cheryl Parker for technical assistance. Kevin Coleman and Vinh Lam made equal contributions to this research. This work was supported by funds obtained from the Public Health Service grant DK53002, the Department of Army and the American Heart Association (to C.L.S.) and an UNCF-Merck Dissertation fellowship (K.M.C.).

REFERENCES

FIGURE LEGENDS

Figure 1: Schematic representation of wild type and mutant forms of ER α and ER β used in this study. A schematic of the structural regions (A-F) and functional domains [DNA binding and activation functions (AF-1 and AF-2)] are shown on top. The A/B domains of ER α (fine diagonal) and ER β (speckled), and the ligand binding domains of ER α (solid) and ER β (coarse diagonal) are indicated below.

Figure 2: Coactivation of human ER α and ER β by SRA overexpression. HeLa cells were cotransfected with 40 ng of the indicated ER expression vector (pCMV₅-hER α or pCXN₂-hER β) and 1500 ng of ERE-E1b-Luc in the presence or absence of 1000 ng of SCT-SRA and treated with ethanol (NH) or 1 nM 17 β -estradiol (E2). Values are the average \pm SEM of three independent experiments standardized to the luciferase data obtained in the presence of estrogen and absence of transfected SRA expression vectors.

Figure 3: SRA enhances the agonist activity of 4-hydroxytamoxifen on ER α , but not ER β . HeLa cells were cotransfected with 40 ng of the indicated ER expression vector (pCMV₅-hER α or pCXN₂-hER β) and 1500 ng of ERE-E1b-Luc in the presence or absence of 1000 ng of SCT-SRA and treated with ethanol (NH), 1 nM 17 β -estradiol (E2), 100 nM 4-hydroxytamoxifen (4HT) or 100 nM ICI 182,780 (ICI). Values are the average \pm SEM of 4-7 independent experiments standardized to the luciferase data obtained in the presence of estrogen and absence of transfected SRA expression vectors.

Figure 4: SRA coactivates ER α transcriptional activity in the presence of mixed, but not pure antiestrogens in HepG2 cells. Cells were cotransfected with 50 ng of the indicated ER expression vector (pCMV₅-hER α or pCXN₂-hER β) and 1000 ng of pC3-Luc in the presence or absence of 1000 ng of SCT-SRA and treated with ethanol (NH), 10 nM 17 β -estradiol (E2), 100 nM 4-hydroxytamoxifen (4HT) or 100 nM ICI 182,780 (ICI). Values are the average \pm SEM of three independent experiments standardized to the luciferase data obtained in the presence of estrogen and absence of transfected SRA expression vectors.

Figure 5: Coactivation of the ER α AF-1 domain by SRA. **A)** SRA coactivation of GAL-AB α and GAL-AB β chimeric proteins by SRA. HeLa cells were cotransfected with 100 ng of pBIND (GAL), pBIND-AB α (GAL-AB α) or pBIND-AB β (GAL-AB β) and 1000 ng pG5-Luc in the presence or absence of 1000 ng pSCT-SRA. Values are the average \pm SEM of four independent experiments standardized to the luciferase data obtained for the GAL4 DNA binding domain in the absence of transfected SRA expression vectors. **B)** SRA coactivation of an AF-2 mutant of ER α . HeLa cells were cotransfected with 250 ng of the pRST₇ expression vector for wild type, 3x or TAF2-3x forms of ER α or parent vector alone along with 1500 ng of ERE-E1b-Luc in the presence or absence of 1000 ng of SCT-SRA and treated with ethanol (NH) or 1 nM 17 β -estradiol (E2). Values are the average \pm SEM of five independent experiments standardized to the luciferase data obtained for wild type ER α in the presence of estrogen and absence of transfected SRA expression vectors.

Figure 6: Coactivation of the ER α AF-1 domain by simultaneous coexpression of SRA and SRC-1e. HeLa cells were cotransfected with 40 ng of pBIND (GAL), pBIND-AB α (GAL-AB α) or pBIND-AB β (GAL-AB β) and 1500 ng pG5-Luc in the presence or absence of 1000 ng pSCT-SRA and 1000 ng pCR3.1-SRC-1e. Values are the average \pm SEM of five independent experiments standardized to the luciferase data obtained for the GAL4 DNA binding domain in the absence of transfected expression vectors for coactivators.

Figure 7: Activation of amino-terminal deletion mutants of ER α and ER β by SRA in HeLa cells. (A) Forty ng of the pCMV₅ expression vectors for ER α and ER α -87C (n=3), or (B) pCR3.1 expression vectors for ER α , ER α -109C and ER α -179C (n=3), or (C) pCXN2-ER β and pCMV5-ER β -46C (n=3) or (D) pCR3.1 expression vectors for wild type ER β and ER β -143C (n=4) were cotransfected with 1500 ng of ERE-E1b-Luc in the presence or absence of 1000 ng of SCT-SRA and treated with ethanol (NH) or 1 nM 17 β -estradiol (E2). Values are the average \pm SEM of the indicated number of independent experiments standardized to the luciferase data obtained for wild type receptor in the presence of estrogen and absence of transfected SRA expression vectors.

Figure 8: Simultaneous coactivation of ER α and ER β by SRA and SRC-1e. HeLa cells were cotransfected with 40 ng of pCR3.1-hER α (A) or pCXN2-ER β (B) and 1500 ng of ERE-E1b-Luc in the presence or absence of 1000 ng pSCT-SRA and 1000 ng pCR3.1-SRC-1e and treated

with ethanol (NH) or 1 nM 17 β -estradiol (E2). Values are the average \pm SEM of five independent experiments standardized to the luciferase data obtained for either receptor in the absence of exogenous coactivator expression.