The AF-1 Activation Function of Estrogen Receptor α Is Necessary and Sufficient for Uterine Epithelial Cell Proliferation In Vivo

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Estrogen receptor-α (ERα) regulates gene transcription through the 2 activation functions (AFs) AF-1 and AF-2. The crucial role of ERαAF-2 was previously demonstrated for endometrial proliferative action of 17β-estradiol (E2). Here, we investigated the role of ERαAF-1 in the regulation of gene transcription and cell proliferation in the uterus. We show that acute treatment with E2 or tamoxifen, which selectively activates ERαAF-1, similarly regulate the expression of a uterine set of estrogen-dependent genes as well as epithelial cell proliferation in the uterus of wild-type mice. These effects were abrogated in mice lacking ERαAF-1 (ERαAF-10). Four weeks of E2 treatment led to uterine hypertrophy and sustained luminal epithelial and stromal cell proliferation in wild-type mice, but not in ERαAF-10 mice. However, ERαAF-10 mice still presented a moderate uterine hypertrophy essentially due to a stromal edema, potentially due to the persistence of Vegf-a induction. Epithelial apoptosis is largely decreased in these ERαAF-10 uteri, and response to progesterone is also altered. Finally, E2-induced proliferation of an ERα-positive epithelial cancer cell line was also inhibited by overexpression of an inducible ERα isoform lacking AF-1. Altogether, these data highlight the crucial role of ERαAF-1 in the E2-induced proliferative response in vitro and in vivo. Because ERαAF-1 was previously reported to be dispensable for several E2 extrareproductive protective effects, an optimal ERα modulation could be obtained using molecules activating ERα with a minimal ERαAF-1 action. (Endocrinology 154: 2222–2233, 2013)

Estrogens, particularly 17β-estradiol (E2), play a pivotal role in sexual development and reproduction but are also implicated in other physiologic processes in mammals. The uterus is a major estrogen target, and waves of steroid hormone-induced cell proliferation and differentiation dictate the cyclical changes that occur in the uterine epithelium during the reproductive cycle (1). In addition, estrogens induce a rapid increase in endometrial microvascular permeability, leading to stromal edema and marked uterine weight increase. Stromal edema is believed to create an optimal environment for the growth and remodeling of the endometrium in preparation for embryo implantation and pregnancy (2). Estrogens and progesterone (P4) actions, mediated by their respective receptors, cause molecular and cellular events during uterine receptivity, and the balance between them is important for the
endometrium functions (3). At menopause, after cessation of ovarian function, estrogen replacement is used to relieve climacteric symptoms, in order to prevent osteoporosis but also coronary disease when given early after menopause (4, 5). To minimize the proliferative effects of estrogens on the uterus and reduce the risk of endometrial cancer, progestins are routinely administered together with estrogens in hormone replacement therapy. However, the Women’s Health Initiative trial highlighted that the estrogen-medroxyprogesterone acetate association might increase the risk of breast cancer and cardiovascular diseases, whereas administration of estrogens alone in hysterectomized women have protective (breast cancer) and neutral (coronary heart disease) effects (6, 7).

The different physiologic responses to estrogens are initiated by their binding to the estrogen receptors (ERs) ERα and ERβ, which belong to the nuclear receptor superfamily and are structurally organized into 6 functional domains (A to F). The E domain allows hormone binding, an event that induces specific conformational changes that are required for ER transcriptional activity through the modulation of 2 activation functions (AFs), AF-1 and AF-2, located in the A/B and E domains, respectively (8). ER-mediated transcriptional regulation involves either direct interaction of ER with specific estrogen-responsive elements (EREs) in or near the promoter region of target genes, or an indirect mechanism via protein/protein interactions with other transcriptional factors (9). ER-mediated transactivation is then achieved via an ordered sequence of interactions between the AFs and various coactivators, such as members of the p160 subfamily or the CAMP response element binding protein/p300 (10–12).

In the rodent uterus, E2 generates a robust and rapid transcriptional response with a biphasic temporal effect. Early response includes RNA transcription, hyperemia, and water imbibition, whereas later responses comprise cycles of DNA synthesis and mitosis in epithelial cells (13–15). The strong expression of ERα in the uterus is powerful evidence for its importance in the response to E2. In fact, ERα ligand-induced signaling is critical for the normal development of uterine tissue (13, 16, 17). Recently, an ERαAF-2 mutant mouse line allowed us to show that this AF-2 is required for regulating some uterine gene expression and epithelial cell proliferation in response to E2 (18). Although weak E2 action on uterine weight in ERαAF-1−/− mice has been previously reported (19), the precise role of ERαAF-1 in uterine function has not been precisely studied. Therefore, to explore the role of AF-1 in the molecular mechanisms of uterine growth, we used a combination of pharmacologic and genetic approaches to compare the effects of acute and chronic administration of E2 on uterine gene expression and epithelial cell proliferation in wild-type mice and in mice lacking ERαAF-1 (ERαAF1−/−) (19). We proved that ERαAF-1 is required for E2-induced uterine epithelial cell proliferation, whereas it is partially dispensable for the induction of edema after chronic E2 stimulation.

Materials and Methods

Mice

All procedures involving experimental animals were performed in accordance with the principles and guidelines established by the National Institute of Medical Research (INSERM) and were approved by the local Animal Care and Use Committee. ERα+/− and ERαAF-1−/− mice were generated as previously described (19, 20). C57Bl/6 as well as ERα−/−, ERαAF-1−/−, and their corresponding wild-type littermates (all backcrossed at least 10 times on a C57Bl/6J genetic background) were ovariectomized at 4 weeks of age, and 3 weeks after were sc injected with vehicle (castor oil), 17β-estradiol (E2, 8 μg/kg), the ERα agonist 16α-LE2 (also termed cpd1471) (28.8 μg/kg), tamoxifen (4 mg/kg) or P4 (1 mg). Mice were humanely destroyed 2, 6, 12, and 24 hours after unique or daily repeated treatment (during 3 d). For chronic E2 treatment, ovariectomized mice were implanted with sc pellets that release either placebo or E2 (0.01 mg 17β-estradiol, 60-d release, ie, 8 μg/kg/d; Innovative Research of America, Sarasota, Florida). Because no significant statistical difference was observed in the parameters of ERα+/− and ERαAF-1+/+ mice, these two control groups were pooled and indicated as WT in Figures 4 and 6 and Supplemental Figure 10.

Analysis of mRNA levels by quantitative RT-PCR

Dissected uteri were homogenized using a Precellys tissue homogenizer (Bertin Technology, Cedex, France) and total RNA from tissues was prepared using TRIzol (Invitrogen, Carlsbad, California). One microgram of RNA was reverse transcribed at 25°C for 10 minutes and then at 37°C for 2h in 20 μL final volume using the High Capacity cDNA reverse transcriptase kit (Applied Biosystems, Foster City, California). The 96.96 Dynamic Arrays for the microfluidic BioMark system (Fluidigm Corp., South San Francisco, California) were used to study by high throughput quantitative PCR the gene expression profile in 6.5 ng cDNA from each mouse uterus, as described previously (21, 22). Primers (Supplemental Figure 1 published on The Endocrine Society’s Journal Online web site at http://endo.endojournals.org) were validated by testing the PCR efficiency using standard curves (95% ≤ efficiency ≤ 105%). Gene expression was quantified using the comparative Ct (threshold cycle) method, and HPRT1 expression is used as reference. Each probe was indeed normalized to each respective genotype placebo in order to better visualize the impact of E2 or tamoxifen on gene expression changes because no significant difference was detected between wild-type and ERαAF-1−/− untreated ovariectomized mice.

Immunohistochemistry

Paraffin-embedded transverse sections (4-μm) from formalin-fixed uterine specimens were dewaxed in toluene and rehydrated through acetone bath to deionized water. Antigen re-
Acute administration of E2 in ovariectomized C57Bl/6J mice (Supplemental Figure 2, B and C). Nuclear expression of Ki-67 (a proliferation marker) was observed in 87% (E2) and 93% (16α-LE2) of uterine luminal epithelial cells, whereas no Ki-67-positive cells were detected in placebo-treated animals and ERα−/− mice (Supplemental Figure 2, B and C).

Then, to determine the role of ERαAF-1 in the uterine response to E2, we compared uterine gene transcription and cell proliferation in ovariectomized wild-type mice given either 8 μg/kg E2 or 4 mg/kg tamoxifen, a selective ERαAF-1 agonist and ERαAF-2 antagonist (28–30) (Figure 1 and Supplemental Figure 4). The set of genes regulated by E2 was very similarly regulated by tamoxifen after 12 or 24 hours, although the earlier response (at 2 and 6 h) to tamoxifen was somewhat delayed compared with E2 (Figure 1A and Supplemental Figure 4), in agreement with a previous report (31). The effects of E2 and tamoxifen on uterine weight, LEH, and Ki-67 expression were also quite similar in wild-type mice, and abrogated in ERα−/− mice (Figure 1, B and C). These findings suggest that ERαAF-1 activation is sufficient to mediate the ERα-dependent uterine response.

Uterine gene expression in response to acute E2 or tamoxifen administration requires ERαAF-1

To further evaluate the role of ERαAF-1 in the E2 or tamoxifen-induced uterine transcriptional response in vivo, we used transgenic mice, in which the sequence coding for the main part of the A/B domain of ERα including AF-1 was deleted (ERαAF-10 mice) (19). Regulation of most of the genes regulated by acute E2 treatment in ERαAF-1−/− mice was lost in ERαAF-10 mice (Figure 2A and Supplemental Figure 5). Only 2 genes, encoding the family with sequence similarity 65 member B (Fam65b) and the progesterone receptor (Pr) were still significantly up-regulated by E2, although in a lesser extent than in wild-type mice (Figure 2B and Supplemental Figure 5).

The transcriptional regulation of the classical ERE-responsive genes by E2, such as insulin-like growth factor (Igf1) and cyclin-dependent kinase inhibitor 1A (P21), was strictly ERαAF-1 dependent. Interestingly, Vegf-a, which is implicated in vascular permeability and water imbibition (32), was up-regulated in response to an acute treatment with E2 in wild-type but not in ERαAF-10 mice (Figure 2B). In the same way, E2 strongly induced the activity of the C3 (ERE) promoter and of the AP-1 site in human endometrial adenocarcinoma Ishikawa cells transfected with the wild-type ERα, but not with the ERαAF-10 in luciferase reporter assays (Supplemental Figure 6). The transcriptional effect of tamoxifen was totally abrogated using the ERαAF-10 mice (Figure 2 and Supplemental Figure 5).
ERαAF-1 is required for cell proliferation in response to acute E2 or tamoxifen treatment

Next we investigated the role of ERαAF-1 in the induction of uterine epithelial cell proliferation after acute administration of E2 or tamoxifen. First, we verified that ERα was similarly expressed in the epithelium and in the stroma of both wild-type and ERαAF-1<sup>−</sup> mice using immunohistochemistry (Figure 3A). Uterine weight, LEH, and stromal height were significantly increased in wild-type mice, but not in ERαAF-1<sup>−</sup> mice 24 hours after acute ad-
To assess the role of the other AF of ERα, ie, AF-2, we used ERαAF-2\(^0\) mice in which the sequence encoding 7 amino acids in helix 12 that are crucial for AF-2 activity has been deleted (33). No increase in uterine weight, LEH, and epithelial proliferation were observed in these ERαAF-2\(^0\) mice after acute E2 or tamoxifen (Supplemental Figure 8). Thus, we confirmed the crucial role of ERαAF-2 for uterine response to E2 previously demonstrated with another mouse model of invalidation of this AF (18).

Interestingly, overexpression of an AF-1-deficient ERα isoform inhibited the cell proliferation in response to E2 of the MCF7 ERα-positive breast cancer cell line (Supplemental Figure 9). Altogether, these results show the crucial role of ERαAF-1 in the proliferative response to acute E2 treatment both in vitro and in vivo.

**Luminal epithelial cell proliferation is inhibited in ERαAF-1\(^{-/} \)** mice after chronic exposure to E2

We then evaluated the role of ERαAF-1 in uterus-mediated E2 signaling after chronic exposure to E2 (8 \(\mu\)g/kg/d for 4 wk) (Figure 4). In wild-type animals, chronic E2 treatment strongly increased uterine weight in comparison to placebo (Figure 4A). The luminal epithelium from wild-type E2-treated mice was characterized by the presence of large columnar cells with eosinophilic cytoplasm, apoptotic bodies, and neutrophilic infiltration; 19% of luminal epithelial cells were Ki-67 positive (Figure 4B). The uterine stroma presented significant decrease of cell density and presented loosely arranged oval fibroblasts, glands with cystic dilatation and neutrophilic infiltration. In parallel, stromal cell proliferation was increased by E2 in comparison with placebo-treated controls (Figure 4B). Conversely, chronic E2 treatment did not have any effect in ERα\(^{-/-} \) animals. Indeed, in these mice, uterine stroma was compact and dense without mitotic activity, and the luminal epithelium was composed of

**Figure 2.** ERαAF-1 is Necessary for the Uterine Transcriptional Response to E2 or Tamoxifen (TMX) Acute Exposure in Vivo. Ovariectomized ERαAF-1\(^{+/+} \) and ERαAF-1\(^{0} \) mice (7 wk of age) were injected sc with placebo (PLB, castor oil), 17\(\beta\)-estradiol (E2, 8 \(\mu\)g/kg), or TMX (4 mg/kg) and euthanized 6 hours later. A and B, Data obtained from 96.96 Dynamic Arrays were used to generate a cluster diagram of the significant changes in the expression of the E2-regulated genes. Each horizontal line represents a single gene, and each vertical line an individual sample. Genes that were up-regulated at least 2-fold after E2 administration relative to placebo are in red, whereas down-regulated genes are in green. The color intensity indicates the degree of variation in expression. C, Quantification of the relative mRNA level of PR and Vegf-a by quantitative PCR. Data were normalized to HPRT1 expression. Results are expressed as mean ± SEM. To test the respective roles of treatment and genotype, a 2-way ANOVA was performed. When an interaction was observed between the two factors, the effect of treatment was studied in each genotype using Bonferroni post test (***, \(P < .001; n = 6\) to 9 mice per group).

administration of E2 (8 \(\mu\)g/kg) or tamoxifen (4 mg/kg) (Figure 3B). A strong induction of epithelial proliferation, as indicated by Ki-67 nuclear expression, was observed in wild-type, but not in ERαAF-1\(^{0} \) mice after E2 or tamoxifen exposure (Figure 3, C and D). The absence of uterine hypertrophy after E2 or tamoxifen treatment in ERαAF-1\(^{0} \) mice was associated with the absence of regulation at 24 hours of most of the studied genes (Supplemental Figure 7).
cuboidal, nonproliferating cells with a high nuclear-cytoplasmic ratio (Figure 4B). On the other hand, in ERαAF-1° mice, chronic E2 administration had a moderated, but significant, effect on uterine weight, luminal epithelial height (LEH), stromal height, and stromal cell density (Figure 4A). The uterine stroma cell density of ERαAF-1° mice was modest, but significantly reduced in response to chronic E2 treatment in comparison with wild-type mice, highlighting the persistent induction of stromal edema. Moreover, in ERαAF-1° mice, glandular epithelial cells showed mitotic activity, whereas no proliferation was observed in the luminal epithelium and in the stromal compartment. No apoptotic events were observed in the epithelium from all 3 genotypes in ovariectomized untreated mice. The increase in active caspase-3 in wild-type mice (11%), which indicates a normal regulation between growth and apoptosis after E2-induced epithelial proliferation, was abrogated in ERαAF-1° mice and largely attenuated in ERαAF-1° mice (~2%) (Figure 4C). Detection of ERα by immunohistochemistry showed same protein expression levels in epithelium and stroma of wild-type and mutant mice (Figure 4D). Whereas acute E2 treatment did not up-regulate the expression of vascular endothelial growth factor (VEGF) A (Vegf-a) in ERαAF-1° mice (Figure 2B), this gene became quite similarly regulated after chronic E2 treatment in wild-type and ERαAF-1° mice (Figure 4E), probably explaining the delayed decrease in uterine stroma cell density and revealing another impact on edema.

PR protein is expressed exclusively in the epithelium from ovariectomized untreated mice independent of the genotype, including ERα−/− mice (Figure 4F). In wild-type mice, E2 caused a redistribution in which the expression of epithelial PR was repressed whereas its expression in the stromal compartment was induced (34–36) (Figure 4F). In ERαAF-1° mice, the PR labeling was still observed on the epithelium whereas a significant labeling
Figure 4. ERαAF1 is Necessary to Induce Uterine Endometrial Proliferation in Response to Chronic and Physiologic E2 treatment but Is Partially Dispensable for Water Imbibition. Ovariectomized wild-type (WT), ERα−/− and ERαAF1-10 mice (7 wk of age) were given placebo (PLB) or 17β-estradiol (E2, 8 µg/kg/d) for 4 weeks. A, Uterine weight, LEH, stromal height (SH), and stromal cell density (number of cells/2.5 mm²) were calculated. B, Ki-67 immunodetection in transverse uterus sections. Percentage of Ki-67-positive cells in uterine stroma (strom) and epithelium (epith). Results are expressed as mean ± SEM. To test the respective roles of treatment and genotype, a 2-way ANOVA was performed. When an interaction was observed between the two factors, the effect of treatment was studied in each genotype using Bonferroni post test (*, P < .05; **, P < .01; ***, P < .001; n = 4 to 6 mice per group). C, Active caspase-3 immunodetection in epithelial compartment of wild-type and ERαAF1-10 mice. D, ERα immunodetection in stromal and epithelial compartment. E, mRNA levels of Vegf-a in wild-type littermates, ERα−/− and ERαAF1-10 mice were measured by quantitative PCR and normalized to HPRT1 expression. Results are expressed as mean ± SEM. To test the respective roles of treatment and genotype, a 2-way ANOVA was performed. When an interaction was observed between the two factors, the effect of treatment was studied in each genotype using Bonferroni post test (***, P < .001). F, PR immunodetection in stromal and epithelial compartment.
Figure 5. ERαAF-1 Is Necessary for the Uterine Transcriptional Proliferative Response to E2 Chronic Exposure in Vivo but Is Dispensable for Water Imbibition. Ovariectomized ERαAF-1+/+ and ERαAF-10 mice (7 wk of age) were given placebo (PLB) or 17β-estradiol (E2, 8 µg/kg/d) for 4 weeks. mRNA levels of PR (A), CCNE (B), IGFBP3 (C), BIRC1A (D), LTF (E), MUC1 (F) in wild-type littermates and in ERαAF-10 mice were measured by quantitative PCR and normalized to HPRT1 expression. Results are expressed as mean ± SEM. To test the respective roles of treatment and genotype, a 2-way ANOVA was performed. When an interaction was observed between the two factors, effect of treatment was studied in each genotype using Bonferroni post test (*, P < .05; **, P < .01; ***, P < 0.001; n = 4 to 6 mice per group).

Discussion

In this work using pharmacologic and genetic approaches, we confirmed that ERα and its AF-2 function are absolutely required for the uterine response to E2 stimulation and demonstrated, for the first time, the crucial role of AF-1 in uterine luminal epithelial proliferation. However, a moderate uterine hypertrophy was still observed in ERαAF-10 mice after chronic administration of E2, essentially due to stromal edema in the absence of epithelial and stromal proliferation.
So far, the specific roles of ERα/H9251AF-1 and ERα/H9251AF-2 have been explored mainly in vitro in cultured overexpressed cell lines. These studies have shown that the relative involvement of ERα/H9251AF-1 and ERα/H9251AF-2 in ERα activity depends on the type and the differentiation stage of the cells and requires specific cofactors and posttranslational modifications (12, 39). ERα/H9251AF-1 and ERα/H9251AF-2 can synergize for the recruitment of different cofactors (40–43), and this functional synergism depends strongly on the promoter context (44). In addition, an interaction between the A and E domains has been identified (45), suggesting that “repositioning” of helix 12 in response to E2 binding to the ligand pocket not only unmasks ERαAF-2 activation, but also allows the activation of ERαAF-1 through the release of the A domain.

An important role of the nuclear, “genomic,” transcriptional action of ERα was previously demonstrated in vivo. Indeed, the EAAE mice, which harbor mutations in 4 amino acids crucial for ERα DNA binding activity are characterized by full abrogation of E2-dependent uterine gene expression and growth (46). Moreover, in the mouse model where 2-point mutations of leucine 543 and 544 to alanine (L543A, L544A) have been introduced in helix 12 (also named AF2ERKI mouse), Korach and coworkers (18) previously demonstrated that ERαAF-2 mutation results in an abrogation of the E2 action in the uterus. How-
ever, in this model, tamoxifen still induced endometrial proliferation and ER-mediated gene responses. In another model of ERαAF2 in which 7 amino acids, 543-549 in the helix 12, were deleted (33), we report here that the proliferative effect of both E2 and tamoxifen on the endometrial epithelium are abrogated. Thus, whereas 2-point mutations (L543A, L544A) in ERα allow to tamoxifen to act as an agonist, a more extensive alteration of helix 12 (deletion of 7 amino acids in the helix 12) abrogates the effect of tamoxifen. These discrepancies may be a consequence of an altered synergism between ERαAF-1 and ERαAF-2, at least on endometrial proliferation. On the other hand, E2 can also induce a rapid nongenomic response through the activation of a pool of ERs localized at the plasma membrane (47). However, the selective activation of this response using an estrogen-dendrimer conjugate has no effect on uterine growth (48), demonstrating that the "nongenomic"/membrane-initiated activation of ERα is not sufficient to elicit uterine growth or cell proliferation. Altogether, these findings demonstrate that endometrial proliferation induced by E2 is highly dependent on the ERα genomic actions and requires the recruitment of ERαAF-1. We demonstrate here that ERαAF-1 is required for the uterine transcriptional and proliferative responses to E2. Indeed, although the expression of 2 genes remained significantly regulated in early response to E2 in ERαAF-1<sup>0</sup> mice, the magnitude of their induction or repression was strongly attenuated compared with wild-type littermates. Similarly, we show that ERαAF-1 is required for E2 induction of C3 (ERE) and AP-1-dependent luciferase activity in a human endometrial adenocarcinoma cell line (Ishikawa cells), suggesting a crucial role of ERαAF-1 in this cell type. We then provide the first evidence that ERαAF-1 is necessary for luminal epithelial cell proliferation in response to both acute and chronic E2 treatment in vivo. Tamoxifen, known as a selective activator of AF-1, further emphasizes the crucial role of AF-1 because the specific induced endometrial proliferation by tamoxifen is lost in ERαAF-1<sup>0</sup> mice.

It was previously demonstrated that activation of ERα in the uterine stromal cells elicits the release of paracrine factors that are required to induce epithelial cells proliferation (49). However, ERα of the uterine epithelial cells is dispensable for their proliferative response (37). Similarly, tissue recombination studies (50) and genetic approach with epithelial ERα-deficient mice (37) indicated that down-regulation of epithelial PR by E2 requires stromal, but not epithelial, ERα. Here, we report that the complete redistribution of PR expression from epithelium to stroma under E2 treatment is lost in ERα<sup>−/−</sup> mice, but partially preserved in the ERαAF-1<sup>0</sup> mice. Whereas epithelial proliferation is completely abrogated in ERαAF-1<sup>0</sup> mice, these data suggest that stromal ERαAF-1 activation could play a crucial role for endometrial epithelial proliferation and a significant role in PR redistribution. During the female reproductive cycle, a balance between proliferation and subsequent elimination of proliferative cells by apoptosis is regulated, in particular, by E2. In wild-type mice, an increase in active caspase-3 is a key actor of this balance. Epithelial ERα contributes to prevent uterine epithelial apoptosis after E2 stimulation and, at its targeted deletion, doubles the level of apoptosis without directly altering the proliferative response (37). Here, we report that the level of epithelial apoptosis is strongly attenuated in ERαAF-1<sup>0</sup> mice compared with wild-type controls, and the precise role of ERαAF-1 in the proliferation-apoptosis balance should be delineated in future studies.

In contrast to the crucial role in endometrial proliferation, we found that ERαAF-1 was partially dispensable to the E2 effect on the uterine vascular permeability. Indeed, E2 was still able to increase uterine weight in ERαAF-1<sup>0</sup> mice, a response essentially due to an interstitial tissue infiltration. The persistence of the normal regulation of some E2-dependent gene at 4 weeks, in particular Vegf-a known vascular permeability factor, probably plays a significant role in this residual vascular action. Importantly, this dissociation between endometrial proliferation and uterine weight highlights the limitation of this later parameter as a marker of the pathophysiologic impact of E2 on the uterus.

We and others previously showed that the beneficial effects of estrogens on cortical bone (51) and atheroma (19, 33) are ERαAF-1 independent and ERαAF-2 dependent. We provide evidence here that ERαAF-1 plays a crucial role in uterine cell proliferation and could thereby contribute to the physiopathology of endometrial cancer, in line with the harmful action of tamoxifen on this target. Finally, we confirm here that full ERαAF-1 activity is required for E2-dependent proliferation of cultured MCF-7 breast cancer cells (52–54).

Prevention of breast cancer, type 2 diabetes, osteoporosis, and cardiovascular diseases by novel selective ER modulators (SERMs) represents the major challenge for the future treatment of menopause (55). We hypothesize that a SERM that preferentially stimulates ERαAF-2 and has a minimal effect on ERαAF-1 would retain many of the E2-protective responses, but would not elicit uterine and breast cell proliferation. This SERM would not require the addition of a progestin to prevent uterine proliferation, thereby offering an optimized therapeutic profile for menopausal women. Alternatively, strategies aiming at blocking ERαAF-1 in the presence of E2 would confer a similar benefit, as already reported for inhibitors of the androgen receptor AF-1 (56).
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