

Cracking the Estrogen Receptor's Posttranslational Code in Breast Tumors

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Estrogen signaling pathways, because of their central role in regulating the growth and survival of breast tumor cells, have been identified as suitable and efficient targets for cancer therapies. Agents blocking estrogen activity are already widely used clinically, and many new molecules have entered clinical trials, but intrinsic or acquired resistance to treatment limits their efficacy. The basic molecular studies underlying estrogen signaling have defined the critical role of estrogen receptors (ER) in many aspects of breast tumorigenesis. However, important knowledge gaps remain about the role of posttranslational modifications (PTM) of ER in initiation and progression of breast carcinogenesis. Whereas major attention has been focused on the phosphorylation of ER, many other PTM (such as acetylation, ubiquitination, sumoylation, methylation, and palmitoylation) have been identified as events modifying ER expression and stability, subcellular localization, and sensitivity to hormonal response. This article will provide an overview of the current and emerging knowledge on ER PTM, with a particular focus on their deregulation in breast cancer. We also discuss their clinical relevance and the functional relationship between PTM. A thorough understanding of the complete picture of these modifications in ER carcinogenesis might not only open new avenues for identifying new markers for prognosis or prediction of response to endocrine therapy but also could promote the development of novel therapeutic strategies. (*Endocrine Reviews* 32: 597–622, 2011)

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I. Introduction

The steroid hormone estrogens play a critical role in various target tissues, including the reproductive tract and the central nervous, vascular, and skeletal sys-

tems, as well as in normal mammary gland development (1). This effect is mediated by two receptors, estrogen receptor (ER) α and ER β , which function in the nucleus as ligand-dependent transcription factors. ER α is responsible for many of the effects of estrogens on normal and malignant breast tissues. Lifetime exposure to 17 β -estradiol (E₂) or estrogenic compounds constitutes a major risk factor for breast cancer development (2), through either transcriptional regulation (genomic action) (3) or involvement in membrane and cytoplasmic signaling cascades (nongenomic action) (4). In normal breast, only 10 to 20%

Abbreviations: AF-1, Activation function; AF-2, transactivation function; AI, aromatase inhibitor; AP-1, activator protein-1; CBP, CREB binding protein; Cdk, cyclin-dependent kinase; DBD, DNA-binding domain; E₂, 17 β -estradiol; E6-AP, E6-associated protein; EGF, epidermal growth factor; EGFR, EGF receptor; ER, estrogen receptor; ERE, estrogen response element; GSK3, glycogen synthase kinase-3; HAT, histone acetyltransferase; HDAC, histone deacetylase; hER, human ER; IKK, I κ B kinase; LBD, ligand-binding domain; LMP2, low molecular mass polypeptide 2; mER, mouse ER; PAK1, serine/threonine p21-activated kinase; PAT, palmitoyl acyltransferase; PI3K, phosphatidylinositol 3-kinase; PKA, protein kinase A; PRMT1, protein arginine methyltransferase 1; PTM, posttranslational modification; RSK, ribosomal S6 kinase; SDF-1, stromal cell-derived factor-1; SERD, selective ER down-regulator; SERM, selective ER modulator; SRC, steroid receptor coactivator; SUMO, small ubiquitin-related modifier.

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of epithelial cells express ER α (5), but ER α -null mice only develop a rudimentary mammary gland, indicating that ER α expression is essential to mammary development (1). By contrast, the mammary glands of ER β -null mice develop normally (1). Interestingly, in breast cells, ER β seems to act as an antagonist of ER α activity, impairing the ability of estrogen to stimulate proliferation (6–8). Thus, ER β may play a protective role in breast tumors by inhibiting proliferation and invasion (9–11).

There is compelling clinical and experimental evidence that sustained exposure to estrogens increases the breast cancer risk and promotes cancer progression by stimulating malignant cell proliferation (12). Although in the normal breast ER α and ER β are expressed at low levels (13), 70% of breast cancers are ER α positive, underpinning the use of agents that suppress receptor function (antiestrogens) or estrogen synthesis (aromatase inhibitors) in breast cancer treatment (14). ER α is a well-established predictive marker for hormone sensitivity and a good prognostic marker in breast cancer; it helps identify tumors that are likely to respond to endocrine treatment. Unfortunately, about 40 to 50% of the women receiving endocrine therapy fail to respond (*de novo* resistance) or become resistant (acquired resistance) to the treatment (15). A focus on estrogen signaling could help understand its deregulations in patients prone to develop resistance to endocrine therapy. Cellular responses to estrogens are complex and highly controlled. They involve the regulation of ER functions through coactivators that stabilize ER binding to DNA, thus promoting gene transcription (genomic action) and the direct activation of signaling cascades (nongenomic action).

Further levels of complexity are added by the fact that several isoforms have been identified for each receptor (16), as well as mutations (17, 18) and numerous posttranslational modifications (PTM) (19) that regulate their function by influencing a number of interactions with other proteins including cytoplasmic signaling molecules (20). In addition to the long-known phosphorylation of ER α , other covalent additions such as acetylation, ubiquitination, sumoylation, and methylation have been recently described. The complexity of ER regulation is a rapidly growing issue because new PTM are continuously being identified. Reviews focusing on ER phosphorylation (21, 22) or acetylation (23) have been published, but there is a real need for more recent updated information about other ER-targeting PTM. The aim of this article is to summarize current and emerging knowledge on ER PTM, particularly on those that are deregulated in breast tumors; this could help to identify new prognostic biomarkers or biomarkers predictive of response to endocrine therapy and/or to circumvent endocrine-resistant tumor growth.

II. Biology of Estrogen Receptors and Breast Cancer

A. ER α and ER β subtypes

ER belong to the superfamily of ligand-activated transcription factors (24). There are two known ER isoforms, ER α and ER β . They arise from separate genes located on different chromosomes, but they share a high degree of overall homology, especially in their DNA binding domain (25), whereas they display different physiological functions. Like other members of this class of transcription factors, ER proteins have a characteristic modular structure. They are organized into five main domains: an N-terminal A/B region bearing the ligand-independent activation function (AF-1), a DNA-binding domain (DBD) composed of two zinc fingers, a hinge region containing the nuclear localization signal, and a domain E harboring the ligand-binding domain (LBD) and the ligand-dependent transactivation function (AF-2). The adjacent region F, located at the C terminus of the receptors, is a variable domain whose specific function has not yet been fully clarified (Fig. 1) (26). The classical 66-kDa ER α (27) and the 60-kDa ER β (28, 29) have similar structures in their central DNA-binding region (98% identity), whereas they largely differ in their activation domains (less than 15% homology in their N termini), suggesting that they may recruit different coactivator proteins, thereby altering their specific transcriptional effects. Moreover, even if ER β , like ER α , binds to E₂, ER β has a markedly reduced transcriptional activation partially due to the lack of AF-1 activity (30). The two receptors share little homology (53%) in their LBD (31), which accounts for the differences in their affinity for various ligands. For example, both full-length ER bind to E₂ with high affinity, but they differ in their ability to bind other natural and synthetic ligands. In particular, ER β has higher affinity for phytoestrogens like genistein, quercetin, or coumestrol than ER α (32, 33). Two distinct classes of synthetic ER ligands have been developed; by binding to ER, they give rise to distinct tissue-selective pharmacological profiles. Selective ER modulators (SERM) are a class of ER ligands, exemplified by tamoxifen and raloxifene, that inhibit AF-2 (but not AF-1)-dependent activation of ER (34). Tamoxifen acts as an antagonist in breast cells, in which ER activity is mainly dependent on AF-2, and as an agonist mimicking the action of estrogens in tissues like the uterus, where AF-1 activity is more important (35). Selective ER down-regulators (SERD), including the pure ER antagonist ICI 162,780 or Faslodex (also called fulvestrant), are antiestrogenic in all tissues (36, 37). They bind to ER α with 100-fold greater affinity than tamoxifen, thus inhibiting receptor dimerization and abrogating estrogen signaling. The development of knockout or transgenic mice with

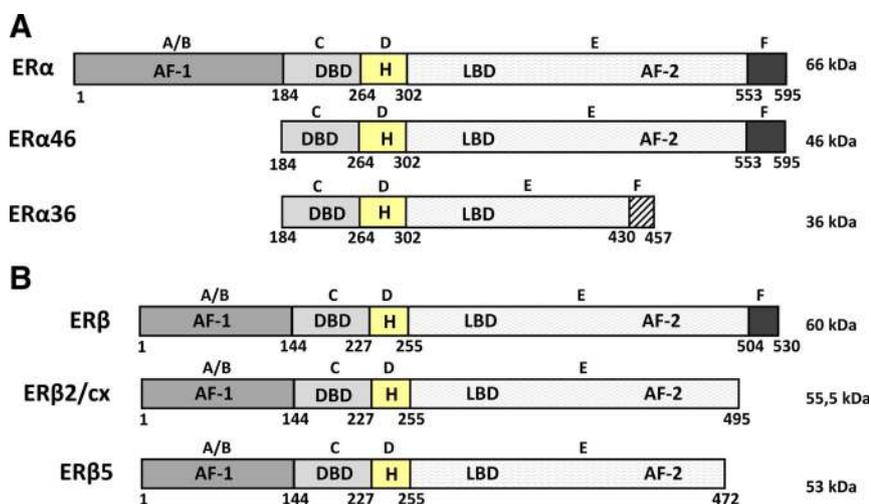


FIG. 1. Structure of ER isoforms for ER α (A) and ER β (B). ER, like other members of the nuclear receptor family, display conserved functional domains: A/B, encompassing AF-1; C, containing the DBD; D, called hinge domain contains nuclear localization signals; E, containing the LBD and AF-2; and F, the agonist/antagonist regulator. A, ER α 46, a truncated form of ER α lacking AF-1 is also shown. Another spliced variant lacking the AF-1 and AF-2 domains, ER α 36, has been cloned in breast cells. B, ER β 2/cx and ER β 5 are two spliced variants of ER β lacking the F domain.

disruptions, mutations, or overexpression of ER has increased our understanding of the relative roles and biological functions of ER α and ER β (38–41). ER α is essential for proliferation, and in contrast, ER β has an anti-proliferative role (40, 42–44). The two receptors regulate different genes in response to E₂ as well as antiestrogens (42, 43, 45). They can form heterodimers that may contribute to differences in ER-dependent gene expression (46, 47). Finally, ER β is known to inhibit both ER α -mediated transcription and E₂-induced proliferation in various cancer cells (6, 7, 48–51).

For both ER, the type of response elicited by ligand binding also depends on the cell type and on the promoters that “communicate” most of the mitogenic and survival stimuli of estrogens through direct or indirect effects on gene expression.

In addition to the classical transcripts of both receptors, numerous mRNA splice variants arising from alternative splicing or alternative promoters have been characterized. The full-length ER α 66 (named ER α in this review) is produced from an mRNA transcribed from the ER α gene that contains at least seven upstream promoters (52). The ER α 46 variant lacking the AF-1 domain (Fig. 1A) has been identified in MCF-7 breast cancer cells (53), osteoblasts (54), human macrophages (55), and endothelial cells (56). ER α 46 represses the AF-1 activity of ER α 66 (57) and inhibits the E₂-induced transcription of the *pS2* gene through recruitment of corepressors (58). In breast cell lines, this variant inhibits the action of wild-type ER in terms of both E₂ binding (59) and transcriptional response (60, 61), thus participating in endocrine resistance. The

transfection of ER α 46 in tamoxifen-resistant breast cancer cells inhibits ER α 66 responses and enhances endocrine treatment (62). However, the expression of this isoform has not been evaluated in breast tumor samples.

A 36-kDa variant (ER α 36) lacking both AF-1 and AF-2 domains has been found in breast cancer cell lines (Fig. 1A) (63). This isoform transduces membrane-initiated estrogen-dependent activation of the MAPK pathway in nongenomic E₂-mediated signaling (64, 65). Interestingly, patients who express ER α and high levels of ER α 36 are less likely to respond to tamoxifen treatment (65, 66).

In addition to ER β 1, the full-length or wild-type receptor of ER β , other variants resulting from differential splicing, namely ER β 2/cx (67, 68) and ER β 5 (25, 67, 69), have been identified in breast tumors (Fig. 1B). Their precise role in breast cancer is still poorly understood, but their implication in various forms of resistance is strongly suspected (70).

B. Genomic action of ER

The classical model of ER activation implies that, after ligand binding, a ligand-specific conformational change of the receptor occurs, allowing its dissociation from inhibitory heat shock protein complexes and subsequent phosphorylation (71–73). These modifications trigger homo- or heterodimerization of ER and binding to specific estrogen response elements (ERE) in target genes (Fig. 2, path A). The ligand-induced conformational change of the receptor facilitates the association/dissociation of components of coregulator complexes associated with enzymatic activities that regulate chromatin function, including nucleosome remodeling, histone acetyltransferase (HAT), or methyltransferase, as well as communication with the transcriptional machinery (reviewed in Refs. 74–76) (Fig. 2, path A).

In contrast to estrogens, the binding of estrogen antagonists from the SERM group induces a distinct conformation of ER that triggers their association with corepressors like NCoR and SMRT, thereby shutting off gene transcription (77). Tamoxifen, which aims to block ER α action, has been the mainstay of hormonal therapy in both early and advanced breast cancer patients for approximately three decades (78, 79). Interestingly, tamoxifen has mixed agonist/antagonist activity and may either stimulate or antagonize ER function in tissues and genes (35). As

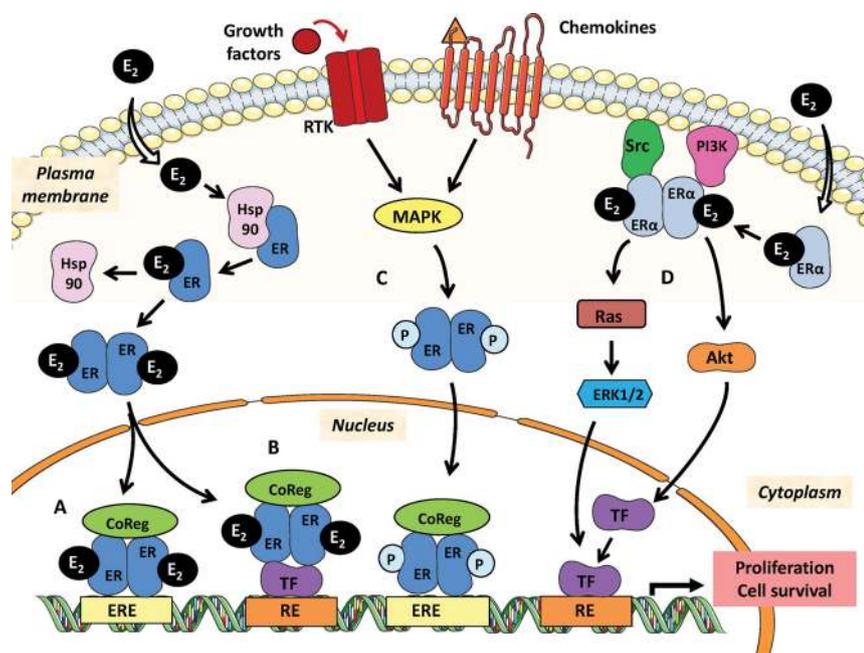


FIG. 2. ER signaling pathways. When pathways are common for ER α and ER β , we designated ER; otherwise, ER subtype is specified. Four distinct pathways of estrogen signaling through ER are shown. Pathway A is called the classical genomic pathway; E₂-bound ER dimerize and, after a change of conformation, go to the nucleus and bind ERE and recruit coactivators that will activate the transcription of target genes. Pathway B, the nonclassical genomic pathway, involves ER interactions with other transcription factors like AP-1. Pathway C is E₂-independent and activates ER through phosphorylation induced by growth factors. Pathway D, the nongenomic pathway, involves a small pool of ER located close to the membrane that, through recruitment of protein kinases (Src and PI3K), activate signaling cascades (Akt, MAPK). All of these pathways converge to cell proliferation and survival. RE, Response elements to other transcription factors; P, phosphorylation; RTK, tyrosine kinase receptor; CoReg, coregulators; TF, transcription factor; Hsp90, heat shock protein 90.

previously demonstrated, the level of expression and/or activity of coregulatory proteins can lead to alterations in ER signaling. Several studies have reported that high expression of the ER coactivator steroid receptor coactivator (SRC)-3/AIB1 (for review, see Ref. 80) in patients receiving tamoxifen adjuvant therapy is associated with poor clinical outcome, which is indicative of tamoxifen resistance (81, 82).

ER can also regulate the activity of other transcription factors through protein-protein interactions with coactivator proteins (83). Via this so-called “nonclassical” action, nuclear ER interact with specificity protein 1 (84, 85) or activator protein-1 (AP-1) (84, 86) or nuclear factor- κ B (87) through a process referred to as transcription factor cross talk (84, 86) (Fig. 2, path B). However, there is an interesting difference between ER α and ER β at AP-1 sites. In the presence of estrogens, ER α induces AP-1 driven reporter activity, whereas ER β has no effect (88). Of interest, increased AP-1 and nuclear factor- κ B transcriptional activities have been shown to be involved in endocrine resistance (89–91).

Finally, ER activities are also regulated by estrogen-independent pathways involving kinases that are activated

through growth factor receptors like epidermal growth factor receptor (EGFR) (92, 93) (Fig. 2, path C). ER β is also known to be phosphorylated by the chemokine receptor CXCR4 after its activation by binding to CXCL12/stromal cell-derived factor-1 (SDF-1) through Erk activation (94) (Fig. 2, path C). Very recently, this pathway has also been involved in acquired tamoxifen resistance (95).

C. Nongenomic action of ER

Estrogens also exert rapid stimulatory effects on a variety of signal transduction proteins. This pathway, largely studied for ER α , begins outside the nucleus and is independent of gene transcription. The identity of the receptors mediating this rapid signaling is still a matter of controversy (96–98). However, there is clear evidence that this activity is mediated, at least in part, by a small fraction of ER α that is localized near or at the plasma membrane (99). Dimers of ER α (100) activate multiple signal transduction cascades through direct interactions of ER with various proteins, including the tyrosine kinase Src, the phosphatidylinositol 3-kinase (PI3K), and adaptor proteins (101–105) (Fig. 2, path D). ER α localization to the membrane can also be mediated by interactions with the membrane adaptor protein Shc (106) and with a variety of proximal signaling molecules such as G proteins (107). ER α interactions with Src and PI3K are also activated by other accessory proteins such as the adaptor protein p130Cas, which regulates the activation of Src kinase in T47D human breast carcinoma cells (108). Other partners may be involved, like the caveolin-binding protein striatin, which targets ER α to the plasma membrane (109). Estradiol-dependent complex formation of ER α with Src and the PI3K subunit p85 activates two major pathways: the Src/ras/MAPK and the PI3K/Akt pathways.

The activation of kinases triggers biological responses that are either dependent or independent of transcription. For example, the activation of Src and PI3K leads to increased cell proliferation (103) and abrogation of apoptosis through inactivation of the proapoptotic protein BAD via phosphorylation (110). More recently, nongenomic signaling has been shown to be associated with other cel-

lular processes. E₂ activation of PI3K/Akt signaling, for instance, inhibits the Ataxia Telangiectasia-mutated and Rad3-related kinase pathway controlling cell cycle checkpoints and DNA repair (111) and the interaction of histone deacetylase (HDAC) 6 with membrane-localized ER α , causing rapid deacetylation of tubulin that potentially contributes to cell migration and to aggressiveness of ER α -positive breast cancer cells (112). Catalano *et al.* (113) have identified another role of nongenomic estrogen signaling, namely that E₂-stimulated Src increases aromatase activity, revealing the existence of an autocrine loop between E₂ and aromatase possibly involved in breast tumorigenesis. Even if little is known on ER β nongenomic signaling, the presence of ER β at the plasma membrane suggests that it must also be involved in extra nuclear actions (114) and particularly through its association with Src (115).

For convenience, we present the genomic and nongenomic pathways separately. However, these signaling pathways are not mutually exclusive but rather complementary, with many interactions between them. The idea is that nongenomic and genomic effects may integrate a unique mode of action of estrogens in which the nongenomic signaling pathways converge for transcriptional regulation (116).

D. Endocrine therapies in breast cancer

Approximately 70% of all breast cancers are dependent on estrogen and on a functional ER α for growth. Hence, ER α -positive breast cancer is usually treated with hormone reduction or antiestrogens (15). Treatment approaches include the blockade of ER α activity by SERM like tamoxifen (117) or the destabilization and degradation of ER by SERD like fulvestrant (118–121). The antineoplastic effects of endocrine drugs are largely mediated by the inhibition of ER transcriptional effects on gene expression. Tamoxifen, which binds to and antagonizes ER, only blocks the transcriptional activating function AF-2 and thus only partially inactivates ER-regulated transcription (122, 123). Fulvestrant, which blocks both AF-1 and AF-2 functions, induces complete abrogation of the transcription of ER-regulated genes (36, 37). In the past two decades, tamoxifen has been the mainstay of endocrine therapy for both early and advanced breast cancers and has significantly contributed to the decrease in breast mortality (124). However, approximately 50% of patients with advanced disease do not respond to first-line treatment with tamoxifen, and almost all patients with metastases relapse and die from the disease (15). A second endocrine therapy strategy has recently emerged. It consists of reducing the production of estrogen in peripheral tissues and within the tumor using aromatase inhibitors (AI) like anastrozole, letrozole, or exemestane (125, 126). AI

inhibit tumor growth and have proven superior to tamoxifen in certain patient subsets (127).

However, whatever the endocrine treatment used, intrinsic or acquired resistance may occur. The molecular causes of endocrine resistance are multiple and not completely understood. Several mechanisms have been described, including the deregulation of ER expression and maturation, as well as the deregulation of PTM for both receptors and their cofactors. Moreover, increased Her2/NEU (Erb-B2) receptor tyrosine kinase signaling and deregulation of the cell cycle and apoptosis machineries have also largely been associated with resistance (for review, see Ref. 128).

Because only 1% of primary breast cancers carry ER α mutations (129), it seems more relevant to focus on ER signaling to elucidate the mechanisms responsible for resistance, to develop more specific biomarkers predictive of response to endocrine therapy, and to identify new therapeutic targets for endocrine-resistant disease.

III. Posttranslational Modifications of Estrogen Receptors

Because PTM are crucial to the physiological function of proteins, understanding the coding of these modifications is particularly important to elucidate the activity of a given protein.

ER and their coregulators are targets for multiple PTM (130). The synergic coupling between extranuclear and genomic actions of hormones is accompanied by highly specific PTM that serve not only as triggers but also as mediators and promoters of the signaling cascades. Deregulating both the phosphorylation cascades and the acetylation process, for example, can dramatically affect the fate of a number of factors involved in ER signaling (121, 131, 132) and impact cell survival. The development of site-specific antibodies recognizing only modified forms of ER α has greatly simplified the analysis of PTM and has led to rapid advances in mechanistic studies. More recently, mass spectrometry has facilitated the identification of additional PTM, and the catalog of ER α PTM now comprises modifications of approximately 22 sites throughout the molecule, including phosphorylation, methylation, acetylation, sumoylation, and ubiquitination. Much less information is available for ER β . Most of our understanding of ER β PTM is derived from the pioneering work of A. Tremblay and relates to phosphorylation (133). However, it seems that the phosphorylation of ER β by protein kinases varies with the type of cell, the type of promoter, and the identity of the effector.

In this section, we will focus on well-documented PTM targeting ER (less well-documented PTM are de-

scribed only in Table 1). These modifications influence ER functions, integrating genomic and rapid action, as they act on protein stability, subcellular localization, dimerization, DNA binding, and interaction with coregulators. We will also describe the known interplay between modifications as well as their deregulation in breast cancer.

All modified residues and their functional data are listed in Table 1 for ER α and in Table 2, for ER β . PTM are

also presented on ER sequences to permit visualization of the domain where the modification occurs (Fig. 3).

A. PTM involved in ER genomic signaling

1. Phosphorylation of ER α on serine

It has been known since the early 1980s that ER α is a phosphoprotein whose ligand-binding activity is enhanced by phosphorylation (134) through the activation

TABLE 1. Modified sites of human ER α and their function

Amino acid	Modification	Activator	Enzyme involved	Function	Ref.
Y52	Phosphorylation	Ligand independent	c-Abl	Activates stability, transcription	262
S102	Phosphorylation	Constitutive, E ₂	GSK3	Activates transcription	137
S104/106	Phosphorylation	Constitutive, E ₂	GSK3	Activates transcription	137
		Constitutive, E ₂ , Tam	Cyclin A-Cdk2	Activates transcription	138
		E ₂ , Tam, ICI, PMA	MAPK	Activates transcription	136
		E ₂	MAPK	Dimerization	140
		E ₂ , Tam, ICI	ND	Activates transcription	145
S118	Phosphorylation	EGF, IGF-I	MAPK	Activates transcription	92, 146
		E ₂	Cdk7	Activates transcription	146, 263
		ND	MAPK	Activates RNA splicing	139
		E ₂	GSK3	Activates transcription	137
		E ₂	IKK α	Activates transcription	147, 148
		Prolactin	ND	Activates transcription	149
		ROS	MAPK	Down-regulation	264
		E ₂	MAPK	Dimerization	140
S154	Phosphorylation	Constitutive, E ₂ , EGF	ND	ND	265
S167	Phosphorylation	Constitutive	Akt	Activates transcription	152
		ROS	Akt	Down-regulation	264
		EGF	p90 RSK	Activates transcription	151
		Insulin, PMA	S6K1	Activates transcription	153, 154
		ND	Akt	Activates stability	266
S236	Phosphorylation	Constitutive	PKA	Inhibits dimerization	155
Y219	Phosphorylation	ND	c-Abl	Activates: dimerization, DNA binding, stability, and transcription	262
R260	Methylation	E ₂	PRMT1	Nongenomic signalling	227
K266	Acetylation	E ₂	p300	Activates transcription	181
	Sumoylation	E ₂ , Tam	SUMO-1	Activates transcription, DNA binding,	206
K268	Acetylation	E ₂	p300	Activates transcription	181
	Sumoylation	E ₂ , Tam	SUMO-1	Activates transcription, DNA binding	206
S282	Phosphorylation	E ₂	CK2	Inhibits transcription	267
S294	Phosphorylation	E ₂	ND	Activates transcription	267
K299	Acetylation	Constitutive	p300	Inhibits transcription	182
	Sumoylation	E ₂ , Tam	SUMO-1	Activates transcription, DNA binding	206
K302	Acetylation	Constitutive	p300	Inhibits transcription	182
	Sumoylation	E ₂ , Tam	SUMO-1	Activates transcription, DNA binding	206
K303	Ubiquitination	Constitutive, E ₂ , ICI	Ubiquitin	Proteasomal degradation	201
	Methylation	Constitutive	SET7	Activates stability	208
	Acetylation	Constitutive	p300	Inhibits transcription	182
S305	Sumoylation	E ₂ , Tam	SUMO-1	Activates transcription, DNA binding	206
	Ubiquitination	Constitutive, E ₂ , ICI	ubiquitin	Proteasomal degradation	201
	Phosphorylation	ND	PAK1	Activates transcription	158, 160
T311	Phosphorylation	ND	PKA	Activates transcription	157
		ND	Akt	Resistance to AI	163
		E ₂	p38-MAPK	Nuclear localization	268
C447	Palmitoylation	Constitutive	PAT	Plasma membrane localization	215
Y537	Phosphorylation	E ₂	Calf uterine kinase	E ₂ binding	269
		Constitutive	Src	Dimerization, DNA binding	223, 270
		Constitutive	Src	E ₂ binding	271
		EGF	EGFR	Proliferation	272
		Constitutive	CK2	Inhibits transcription	267

ND, Not determined; ICI, ICI 172 780; PAK1, p21-activated kinase-1; PMA, phorbol myristate acetate; ROS, reactive oxygen species; Tam, tamoxifen; CK2, casein kinase 2.

TABLE 2. Modified sites of mouse ER β and their function

Amino acid	Modification	Activator	Enzymes involved	Functions	Ref.
S80 (S60)	Glycosylation	ND	ND	Inhibits ER β degradation	169
	Phosphorylation	ND	ND	Stimulates ER β degradation	169
S94 (S75)	Phosphorylation	Constitutive	MAPK	Stimulates ER β degradation	170
S106 (S87)	Phosphorylation	EGF, Ras	MAPK	Enhances the recruitment of SRC-1	93
		Constitutive	MAPK	Stimulates ER β degradation	170
		CXCR4/SDF-1	MAPK	Activates transcription	94
S124 (S105)	Phosphorylation	EGF, Ras	MAPK	Enhances the recruitment of SRC-1	93
		E ₂ , DPN, genistein	ND	ND	261
		Erb-B2, Erb-B3	Akt	Inhibits transcription	173
S255 (C399)	Phosphorylation	ND	PAT	Plasma membrane localization & activation of proapoptotic cascades	219
	Palmitoylation	ND	PAT	Plasma membrane localization & activation of proapoptotic cascades	219
Y507	Phosphorylation	Constitutive	Src	Activates transcription	174

Most studies have been performed using mouse transfected HA-tagged ER β ; residues in *parentheses* correspond to residues in human ER β . ND, Not determined; CXCR4, (CXC motif) receptor 4; DPN, diarylpropionitrile.

of a Ca⁺⁺-dependent calmodulin kinase (135) possibly involved in ER nuclear translocation. Although pioneer experiments were carried out with partially purified calf uterine ER α and although they caused some controversy at the time they were published, the concept of the relationship between a nuclear hormone receptor activity and its phosphorylation-dependent activation was launched.

The target residues include serine, threonine, and tyrosine; phosphorylated serines are more concentrated within the AF-1 domain, resulting in ligand-independent regulation of receptor transactivation (21). There are so many targets for phosphorylation that we have chosen to focus on the most widely analyzed residues; for the others, information can be found in Table 1.

a. S104/106. These two sites, when phosphorylated, are involved in ER α activity because acidic amino acid substitution stimulates ER α activity as strongly as S118 substitution (136). The particularity of S104/106 phosphorylation is that it is induced exclusively by estrogen and not by growth factor pathways. So far, both glycogen synthase kinase-3 (GSK3) and cyclin-dependent kinase 2 (Cdk2) kinases were involved in this modification (137, 138). More recently, MAPK has also been shown to phosphorylate these residues (136). Of note, the two residues are required for the agonist activity of tamoxifen, in conjunction with S118, suggesting that these sites might contribute to tamoxifen resistance in breast cancer (136).

b. S118. S118 has been the most widely studied target site and is a good example of the complexity of ER α phosphorylation. S118 has been reported to be important for the dimerization of ER α and ER α -mediated RNA splicing (139, 140). In addition, phosphorylation at this site is also important for direct binding to and activation/repression of several ER α target genes (141). S118 phosphorylation facilitates ER α interactions with coactivators such as

CREB binding protein (CBP)/p300 (142) and SRC-1 (143) and then mediates ligand-dependent as well as ligand-independent activation of the receptor (144, 145). In support of this statement, it has been documented that both estrogens and growth factors such as epidermal growth factor (EGF) and IGF-I can result in S118 phosphorylation on ER α (146). Growth factors trigger S118 phosphorylation through Ras-MAPK cascades (92). The S118A mutant is not activated by EGF because no enhancement of E₂-induced ERE reporter activity has been observed in transfected cells (144), demonstrating the independence from ligand and the phosphorylation requirement for ER α transcriptional activity. Several different kinases are responsible for the estrogen-dependent phosphorylation of S118. Cdk7 (146), I κ B kinase (IKK) α (147), and GSK3 (137) have been identified as good candidates. However, a recent study performed in MCF-7 cells using specific inhibitors has shown that IKK α , but not Cdk7, is involved in estrogen-mediated phosphorylation at S118 (148). More recently, this residue has also been shown to be phosphorylated upon prolactin treatment, but the kinase responsible remains unidentified (149). This phosphorylation is also involved in ER α -mediated RNA splicing. This effect is mediated by the binding of ER α with a component of the spliceosome complex, the splicing factor SF3a, which is dependent on the MAPK-mediated phosphorylation of ER α at S118 (139).

c. S167. S167 is a major multiregulated phosphorylated residue in ER α (150). Mutation analysis of this site has demonstrated its involvement in the transcriptional activity of the receptor (151). Its phosphorylation was previously attributed to Akt and p90RSK (p90 ribosomal S6 kinase) (151, 152), but recent convincing data have shown that S6K1 is a physiological kinase for S167 that regulates ER α transcriptional activity, thus contributing to the pro-

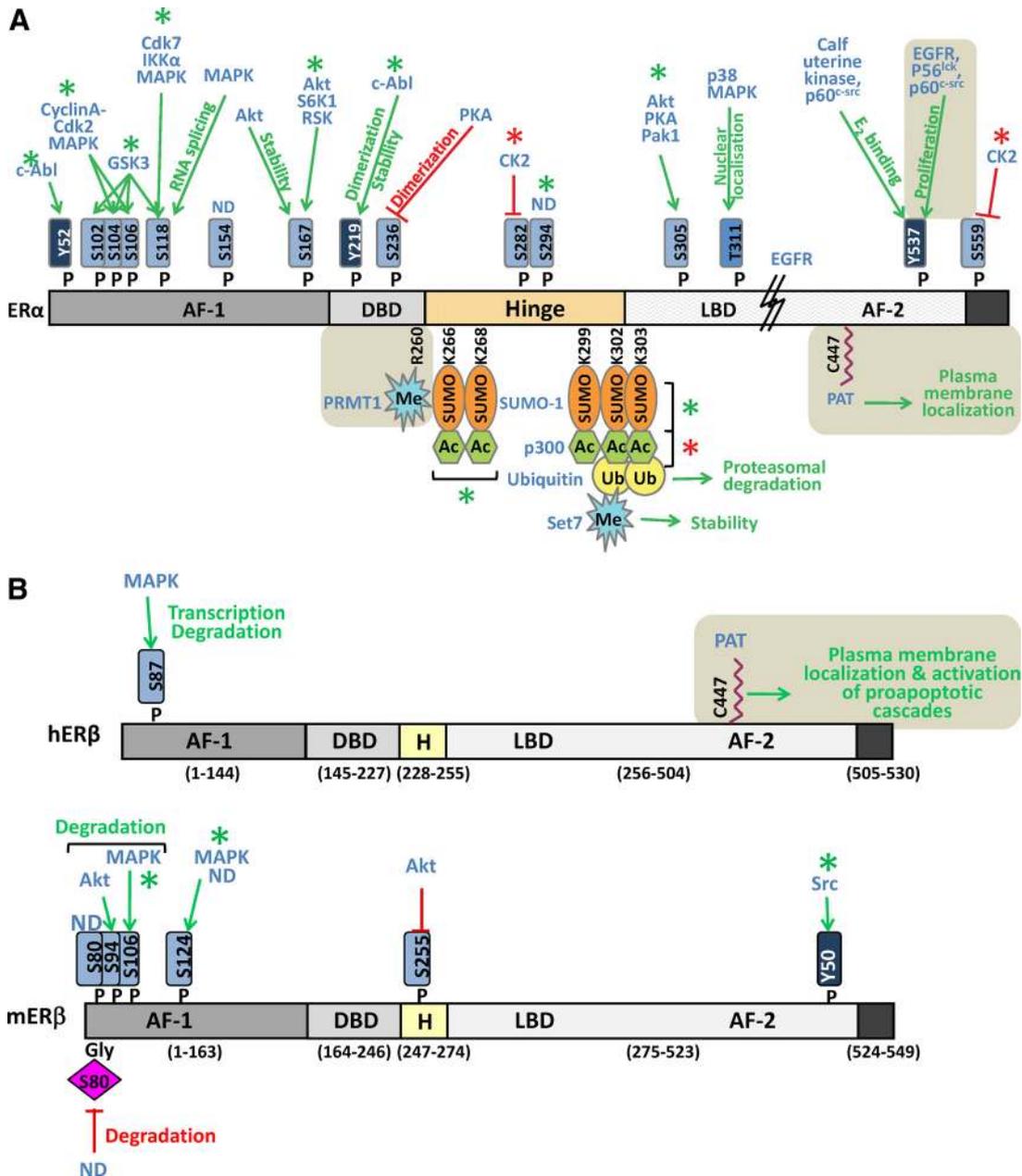


FIG. 3. Amino acids modified in ER are presented in panel A for ER α and in panel B for ER β . All modified residues and kinases implied are represented on ER sequences. A, For ER α , the hinge domain was highly modified by PTM. B, For ER β , because most of the sites have been described on the mouse receptor, we present both the human (hER β) and the mouse (mER β) isoforms. Modifications are designated as follows: Me, methylation; P, phosphorylation; Ac, acetylation; Ub, ubiquitination; Sumo, sumoylation; Gly, glycosylation. Palmitoylated sites are represented as wavy lines. Functions of modifications are presented in green for activation and red for inhibition. *, Transcription activity. PTM involved in nongenomic pathways are shaded in gray. ND, Not determined.

liferation of ER-positive breast cancer cells (153). In fact, this phosphorylation is regulated by a temporal combination of two pathways: the MAPK/RSK and the mammalian target of rapamycin 1/S6K1 pathways (154). Interestingly, pS167 is associated with tamoxifen resistance and agonist activity in endometrium cancer cells (143).

d. S236. *In vitro*, in the absence of estrogen, protein kinase A (PKA) can phosphorylate S236, located in the DNA binding domain. S236 phosphorylation participates in ER α dimerization as a mutation of serine to glutamic acid

prevents DNA binding by inhibiting dimerization. In addition, this mutation reduces E₂ and 4-hydroxy-tamoxifen activity in both the presence and absence of PKA (155). Other works have shown that S236 phosphorylation protects ER α from ligand-mediated proteasome degradation (156). This is in agreement with previous data showing that inhibition of PKA decreases ER α stability in both the presence and absence of ligands (121).

e. S305. A large body of information on S305 phosphorylation in ER α has been gathered by Michalides *et al.* (157),

who have shown that this site is phosphorylated by PKA *in vitro* and thus participates in ER α transcriptional activity. An ER α S305E mutant, mimicking constitutive phosphorylation, has been shown to increase receptor dimerization and fixation to promoters of target genes in the presence of estrogen (158). Interestingly, ER α activation at S305 is sufficient to up-regulate the expression of several ER-regulated genes like cyclin D1, a major ER-regulated gene involved in the E₂-induced progression of breast cancer (159). S305 phosphorylation and activation of ER α transcriptional activity have also been evidenced in a murine model expressing a constitutively activated serine/threonine p21-activated kinase (PAK1) (160). These mice have developed mammary gland hyperplasia, revealing a role for the PAK1-ER α pathway in promoting tumorigenesis in mammary epithelium (160). Michalides' team has shown that the down-regulation of PKA-R1 α , a negative regulator of PKA, triggers PKA hyperactivation leading to S305 phosphorylation, converting tamoxifen from an ER α inhibitor into a growth stimulator (157). These authors have also pointed out the prime importance of phosphorylation at S305 for interactions of ER α with coactivators like SRC-1 and activation of gene transcription upon tamoxifen treatment (161). Interestingly, despite its ability to induce tamoxifen resistance, pS305 ER α alone does not modify the response to another endocrine molecule like the SERD fulvestrant, and the additional overexpression of cofactors like cyclin D1 and SRC-1 is required (157).

However, recent data obtained using an antibody specific for pS305 ER α have demonstrated that in a cellular context, PKA (and not PAK1) can induce this phosphorylation (162).

Recently, Fuqua's team (163) has shown that this residue is also phosphorylated by Akt through a cross talk between the IGF-I and ER α pathways. They have also demonstrated that when the K303R ER α mutant is overexpressed in breast cancer cells, S305 is constitutively phosphorylated, leading to resistance to tamoxifen (164) but also to the AI anastrozole (163, 165).

2. Phosphorylation of ER β

Much less is known about the phosphorylation of ER β . Although the intracellular kinases involved have not yet been precisely identified, residues, mostly localized in the AF-1 domain, have been observed, whether in the presence or in the absence of ligand binding to the receptor. The modulation of several kinase activities could activate unliganded ER β -mediated transcription (166).

Contrary to the situation for ER α , for ER β most of the modified residues have been identified in the mouse re-

ceptor; the corresponding amino acids in human will be given in *parentheses*. It appears that there is a discrepancy in ER β amino acid nomenclature due to the discovery of a longer transcript at the 5' end of the molecule (166, 167).

a. S80 (S60). The phosphorylation of mouse S80 has been identified by mass spectrometry (168). The same study has reported that this site could also be modified through O-GlcNAcylation (Table 2). S80 is located in a PEST region enriched with proline, glutamine, serine and threonine, responsible for the rapid degradation of proteins, suggesting that modification of this residue could be involved in ER β stability (169). Studies using mutants of mouse ER β (mER β) S80E mimicking phosphorylation have clearly demonstrated that phosphorylation of S80 results in rapid degradation of the receptor (169).

b. S94 (S75). In mouse, phosphorylated S94 regulates the nuclear mobility of ER β through a proteasome-dependent pathway implicating the E6-associated protein (E6-AP) ubiquitin ligase (170). This observation suggests that the AF-1 domain of ER β is involved not only in E6-AP-dependent transactivation but also in ER β stability through phosphorylations via MAPK pathways.

c. S106 (S87) and S124 (S105). Both EGF and the oncogene Ras are also able to activate ER β through MAPK-directed phosphorylation of mouse S106 and S124 (corresponding to human S87 and S105), favoring the recruitment of SRC-1 and HAT CBP to the AF-1 domain (93, 171). Additionally, these two phosphorylated sites are partially responsible for the Erb-B2/Erb-B3-mediated inhibition of liganded ER signaling (172).

Finally, mouse ER β S106 has been shown to be phosphorylated by MAPK in response to CXCL12/SDF-1, the ligand of the chemokine receptor CXCR4. S106 phosphorylation leads to enhanced ER transcriptional activity and expression of ER target genes involved in cancer cell growth, including SDF-1 (94). This phosphorylation enables ER β responsiveness at AP-1 sites in an autocrine/paracrine feedback loop, even when the receptor is complexed with a SERM like tamoxifen.

Other sites have been shown to be phosphorylated (Table 2). S255 (equivalent to human S234), for instance, is phosphorylated via the PI3K/Akt pathway through the phosphorylation-dependent release of CBP (173), whereas Y507 in mouse (corresponding to human Y488) is involved in the ligand-independent activation of ER β (174), which is suppressed by antiestrogens. Mutation of this Y488 [which corresponds to Y537 for human ER α (hER α)] in arginine is involved in the ligand-independent activation of ER β (174).

Although it has been shown that inhibitors of protein phosphatases regulate ER α signaling (175, 176), little information is available regarding the identities of the ER phosphatases involved. There is only one paper describing that the serine/threonine phosphatase PP5 targets the dephosphorylation of S118 in ER α , mediating an inhibition of its transcriptional activity (177). Efforts should be made to identify more of these phosphatases and to modulate the level of phosphorylation of ER α .

3. Acetylation of ER α

Acetylation of proteins plays an important role in the regulation of their activity. In addition to histones, a broad range of other proteins, including transcription factors, are acetylated, resulting in enhanced or reduced activity (23, 178). The HAT p300/CBP has been described as a coactivator for ER α through interaction with proteins to form “enhanceosomes” or acetylation of specific lysines in the N terminus of histones (179, 180). ER α is acetylated at multiple sites because five lysines have been reported to be acetylated by p300: K266, K268, K299, K302, and K303 (181, 182) (Table 1). Interestingly, the effect of acetylation on ER α activity varies with the target lysine; acetylation of K299, K302, and K303 inhibits the transcriptional activity of the receptor (182), whereas acetylation of K266 and K268 triggers a stimulatory effect (181). Acetylation of K299, K302, and K303 is constitutive, whereas acetylation of K266 and K268 is estrogen-dependent. However, antibodies specific for acetylated lysines are not available to address the relevance of this modification *in vivo*. Little is known about the mechanisms regulating ER α acetylation, but recent data show that BRCA1 could be a potent inhibitor of ER α activity, partly through impairment of p300-mediated ER α acetylation (183). The enzyme responsible for the reversal of this modification remains to be identified, even if deacetylase sirtuin 1 has emerged as a good candidate in *in vitro* experiments (181). For ER β , no acetylation has been described so far.

Interestingly, the degradation of native ER α after HDAC inhibitor exposure of ER-positive breast cancer cells has been shown to occur through the proteasome pathway, an important tool to reduce estradiol-mediated cell growth (132, 184). On the contrary, the stability of ER β seems to be unaffected by HDAC inhibitors (185).

4. Ubiquitination of ER α

All steroid receptors are subjected to ubiquitination, and several of the enzymes involved in this PTM have been identified (19). In most cases, however, the exact site of modification is uncertain, possibly due to the instability of polyubiquitinated proteins.

It has long been known that the regulation of ER α cellular level and transcriptional activity involves the ubiquitin-26S proteasome system (118–120). Although both basal (*e.g.*, ligand-independent) and ligand-induced ER α degradations are mediated by this proteolysis pathway (121, 186), the regulation of receptor degradation at the molecular level is highly dependent upon the physiological state and nature of the cellular stimuli. Ubiquitin-dependent degradation of E₂-bound receptor is thought to be critical for promoter clearance and additional rounds of transcription (187). Distinct mechanisms are involved in the down-regulation of ER α and the promotion of lysine polyubiquitination and subsequent proteasome-mediated receptor degradation. ER α is degraded via three distinct pathways in breast cancer cells.

First, unliganded ER α is very stable, with a half-life of up to 5 d (188), and it is targeted for degradation by dynamic interactions with heat-shock proteins, cochaperones, and the ubiquitin E3 ligase carboxy terminus of Hsp70-interacting protein (189). This degradation pathway is important for the quality control of ER α because it maintains appropriate steady-state receptor levels in the cytoplasm and is responsible for the clearance of misfolded ER α . Recent data demonstrate that the oncogene E3 ubiquitin ligase MDM2 (mouse double minute-2) could be involved in this ligand-independent turnover of ER α (190).

Second, in the presence of E₂, the ER α half-life drops dramatically to 3–5 h (188, 191), and the receptors are targeted for degradation through a transcription-coupled pathway requiring new protein synthesis. During each binding cycle, ER α recruits specific ubiquitin-proteasome components to the target gene promoter (118–120, 187, 192, 193). Evidence from several studies shows that the inhibition of ubiquitin-proteasome activity blocks both ER α cycling and the activation of target gene expression despite increased ER α abundance obtained by immobilizing ER α on the nuclear matrix, as determined by fluorescence recovery after photobleaching (186). Métivier *et al.* (194) report that the initial steps of transcription are linked to monoubiquitination of the liganded ER α , and this process may enhance receptor interaction with DNA or coactivators. As transcription progresses, ER α is degraded as a consequence of the recruitment of several proteins implicated in the proteasome system. The proteins putatively involved are: 1) ER α E3 ubiquitin ligases like E6-AP (118, 195), MDM2 (187, 190, 196), and EFP (estrogen-responsive finger protein) (197); 2) the low molecular mass polypeptide 2 (LMP2) subunit of the 26S proteasome (193) and the 26S protease regulatory subunit 8 (PRS8/SUG1) in the 19S regulatory cap of the proteasome (187); and 3) the coactivators SRC-1 and SRC-3. SRC-1

interacts directly with LMP2, and this recruitment of LMP2 by SRC coactivators is necessary for cyclic association of ER-regulated transcription complexes on ER targets (193). SRC-3 has been shown to be required for the E₂-dependent turnover of ER α through interaction with the ubiquitin-E3 ligase EFP (198).

And third, in the presence of fulvestrant or other SERD like RU58668, ER α is targeted to degradation independently of transcriptional activity and new protein synthesis (120, 121, 199). Fulvestrant induces ER α degradation by dissociating the Hsp90-ER α complex and immobilizing ER α to the nuclear matrix by inducing its association with CK8 and CK18, two members of the family of nuclear matrix intermediate filament structural proteins, for subsequent degradation (200).

Although ER α ubiquitination was well documented, the target K302 and K303 have only recently been identified. Both lysines protect ER α from basal degradation and are necessary for efficient E₂- and fulvestrant-induced turnover in breast cancer cells (201). As previously demonstrated by *in vitro* ubiquitination assays, in the presence of E₂, K302 and K303 are monoubiquitinated by the ubiquitin ligase BRCA1/BARD1 (183, 202). But the impact of K302 monoubiquitination on ER α stability is unknown, and the possible existence of other ubiquitination sites has not been ruled out.

A recent publication has shown that the protein OTU domain-containing ubiquitin aldehyde-binding protein 1 (OTUB1) deubiquitinates the receptor and represses its transcriptional activity. OTUB1 also regulates endogenous ER α level by stabilizing the protein on the chromatin (203).

5. Ubiquitination of ER β

The carboxy terminus of Hsp70-interacting protein binds to the N-terminal domain of the receptor, which is ubiquitinated to induce ER β degradation and the cessation of transcription (204). Suppressor of Gal 1, a regulatory subunit of the 26S proteasome, is also involved in ER β degradation in a ligand-dependent manner (205), but the target lysines have not been identified so far.

6. Sumoylation of ER α

Although other steroid receptors contain clearly identifiable ψ KXE small ubiquitin-related modifier (SUMO) acceptor sites, neither ER α nor ER β matches this consensus sequence (19). Nevertheless, ER α has been described to be sumoylated by SUMO-1 (206). This sumoylation, which occurs in overexpressed and endogenous ER α and is dependent on the presence of ER α ligands like E₂ or tamoxifen, targets five lysines located in the hinge region: K266, K268, K299, K302, and K303. In addition, ER α

sumoylation is stimulated in the presence of the SUMO E3 ligases PIAS1 and PIAS3 (protein inhibitor of activated signal transducer and activator of transcription). Because mutations that prevented SUMO modification impaired ER α -induced transcription through decreased receptor binding to DNA without affecting ER α nuclear localization, ER α sumoylation results in enhanced ER α transcriptional activity (206). The sumoylation of ER β has not yet been described, but it would be of interest to determine whether this modification could be involved in the regulation of ER β activity.

7. Lysine methylation of ER α

Although lysine methylation is commonly attributed to histones, methylation has recently been described in non-histone proteins such as p53 or DNA methyltransferase. Methylation on K residues is a complex process because a lysine can be mono-, di-, or trimethylated (207). Monomethylation of ER α at K302 is mediated by SET7 lysine methyltransferase; this modification acts on ER α stability and facilitates the recruitment of ER α to its target genes for their transactivation (208). However, the timing of this modification has not been studied in detail because the endogenous modified form of ER α has been undetectable.

8. Other modifications

Other modifications have been identified in ER α , although they have not been studied in details. These include S-nitrosylation, which occurs in nonidentified ER cysteine residues and results in inhibition of DNA binding at specific ERE (209). ER α glycosylation has also been reported, but the targeted residues have been identified only for murine receptors (210, 211). Recently, a systematic study of ER α PTM by tandem mass spectrometry has identified new sites, but their function has not been clarified (212).

B. PTM involved in ER nongenomic signaling

Although E₂ rapid effects are well documented, the molecular mechanisms involved remain elusive. It is not clear how the signals are initiated. Recently, some ER α PTM have been shown to be involved in nongenomic signaling, which gives new insight into this pathway.

1. Palmitoylation of ER α and ER β

Palmitoylation is the attachment of a long chain of fatty acids that targets proteins to membrane microdomains (lipid rafts and caveolae). ER α was long ago reported to be located at the plasma membrane (213). Cycles of palmitoylation and depalmitoylation affect protein activation and allow protein movements within membrane subdomains. The small population of ER α localized at the plasma membrane is known to be palmitoylated on Cys447 by palmitoyl acyltransferase (PAT) (214). Upon

E₂ binding, ER α undergoes depalmitoylation and dissociates from caveolin-1, which facilitates ER α association with signaling molecules like Src and PI3K. S-Palmitoylation is a critical step for E₂-induced rapid events because the unpalmitoylable ER α mutant does not induce E₂ proliferative effects (106, 215). The plant-derived flavonoid naringenin is known to inhibit estrogen nongenomic signaling through a rapid depalmitoylation of the receptor (216). Targeting this modification could be a good strategy for antagonizing estrogen proliferative effects.

ER β has also been shown to localize at the plasma membrane through palmitoylation (217). The site of palmitoylation has not been clearly identified, but C399 is a good candidate because it is conserved with ER α binding (218). In ER β , contrary to observation in ER α , E₂-decreased palmitoylation increases receptor association with caveolin-1. The outcome effect is also totally different because ER β palmitoylation is necessary for the p38-dependent activation of proapoptotic cascades (219).

2. Phosphorylation of ER α on tyrosine

The phosphorylation of Y537 was first reported to regulate E₂ binding in MCF-7 cells and the ability of ER α to interact with kinases containing SH2 domains (220–222). *In vitro* data suggest that Src tyrosine kinases (p56^{lck} and p60^{c-src}) could be responsible for this phosphorylation (223). Auricchio *et al.* (224) recently obtained interesting results using peptides containing phosphoY537. They have shown that the phosphorylated peptide inhibits G₁/S transition by preventing ER α /Src interactions induced by E₂ in MCF-7 cells. This peptide also inhibits the growth of mammary cancer cell xenografts, supporting its potential therapeutic interest (224, 225).

Finally, *in vitro* results from Katzenellenbogen's lab (226) strongly indicate that Src phosphorylates ER α on other tyrosine residues.

3. Arginine methylation of ER α

Recently, our team reported a novel paradigm of ER α regulation through arginine methylation by protein arginine methyltransferase 1 (PRMT1), which transiently methylates R260 within the ER α DBD (227). The methylated ER α is localized exclusively in the cytoplasm of breast epithelial cells. This methylation event is required for mediating the extranuclear function of the receptor by triggering its interaction with the p85 subunit of PI3K, Src, and the focal adhesion kinase, and thereby propagating the signal to downstream transduction cascades via Akt activation (228). The transient methylation of the receptor suggests that a putative arginine demethylase could be involved in the regulation of this process.

Rapid down-regulation of ER α methylation and/or Src activity may serve to control rapid physiological responses to estrogen, inducing the dissociation of the complex and ultimately the repression of downstream kinase activation.

In conclusion, for ER α , although phosphorylation sites are scattered throughout the protein, the other modifications are highly concentrated around the hinge region (Fig. 3) and sometimes even on the same residue (K302, for instance, is targeted for multiple modifications), which facilitates cross talks between modifications. It is important to decipher the interplay between ER PTM and to determine precisely which PTM will be impacted if a given enzyme is targeted.

C. Molecular events affecting ER PTM

1. ER mutations

Although the number of mutations affecting ER α in breast tumors is relatively low (129), the impact of PTM on ER signaling is indirectly supported by ER α mutations affecting PTM target sites of the receptor. For example, the Y537N mutant (phosphorylated site) identified in tumors of metastatic breast cancer patients has been shown to confer a constitutive transactivation function to the receptor (229).

It has also been shown that the K303R mutation (a multimodified residue) associated with breast cancer modifies K302 methylation both *in vitro* and *in vivo* (208). The K303R mutant leads to hyperphosphorylation of ER α by PKA (230) and by Akt-dependent pathways (165) at residue 305, suggesting a cross talk between ER α acetylation and phosphorylation. Moreover, the K303R mutation has been shown to result in altered recruitment of coactivators or corepressors like calmodulin or BRCA1 (183, 231). Interestingly, the K303R mutation of ER α has been found associated with predictors of unfavorable outcome and poor prognosis like lymph node positivity or enlarged tumor size (232). Altogether, these observations suggest that events affecting K303 (PTM or mutations) might seriously affect the functional role of ER α through a deregulation of ER α PTM.

2. Cross talk between ER PTM

A protein can be modified by more than one type of PTM or by the same PTM at different residues. The occurrence of several PTM, acting sequentially and/or in concert, seems to be a very efficient mechanism to initiate, terminate, or fine-tune the outcome of signaling pathways.

Although the implications of individual ER modifications such as phosphorylation, acetylation, and methylation have been relatively well documented, interactions between these modifications remain to be elucidated. It

appears that one modification may be coupled to the enhancement or suppression of another one at the same or a nearby residue.

In this context, we will try to discuss the known interplay between PTM and to investigate other potential ones.

3. Phosphorylation and phosphorylation

The first cross talk between two phosphorylation sites, S118 and S305, in ER α has been described by the group of Kumar (233). They have found that ER α phosphorylation by PAK1 on S305 influences the activation status of S118 and that the S305-associated ER α transactivation activity requires a functional S118 (233). This cross talk has not been analyzed in clinical studies, but it has been shown that transgenic mice expressing a kinase-active PAK1 exhibit both activated ER α -305 and ER α -S118.

Although less well-documented, a positive cross talk also exists between S104, S106, and S118 (136).

4. Phosphorylation and acetylation

K303 resides adjacent to a phosphorylation site, S305, and a negative cross talk has been found between S305 phosphorylation and K303 acetylation (230). Mutation of S305 to E305 mimicking constitutive phosphorylation blocks K303 acetylation and generates an enhanced transcriptional response. This cross talk could partially explain the link between the phosphorylation of S305 and tamoxifen resistance in breast tumors. On the contrary, the phosphorylation of S118 and S167 positively regulates ER acetylation (183).

5. Phosphorylation and ubiquitination

Multiple agents regulating phosphorylation also impact ER α proteolysis (183, 234). A direct link between ER α phosphorylation and ubiquitination has been established. S118 plays an important role in E₂-mediated ER α degradation by regulating differential recruitment of factors mediating proteolysis (183, 235, 236).

A recent study by the group of Tremblay has shown that ER β phosphorylation serves as a signal for receptor ubiquitination and degradation (170). The recruitment of the E3 ubiquitin ligase E6-AP to mouse ER β is induced by Erk phosphorylation at S94 (conserved at S75 in hER β) and S106 (equivalent to hS87), but the target lysines have not been identified.

6. Phosphorylation and glycosylation

It appears that reciprocal occupancy of S80 (conserved at S60 in hER β) by either O-phosphate or O-GlcNAc modulates the degradation and activity of mER β . In fact, the saccharide may act by blocking the addition of phosphate, which itself targets the protein for rapid degradation (169). This interplay is another good example of co-

ordinated modifications responsible for regulating ER β activity.

7. Acetylation and methylation

Because ER α K302 can be either acetylated or methylated, one could imagine a competition between the two modifications. *In vitro* experiments have shown that a previously acetylated ER α peptide is a poor substrate for SET7-induced methylation (208). Given the fact that lysine methylation stabilizes ER α , this negative cross talk may destabilize the receptor mediating the inhibitory effect of K303 acetylation on transcription.

8. Methylation and ubiquitination

Estrogen-stimulated ubiquitination and subsequent degradation by the proteasome play an important role in ER transcriptional activity (187). Given that K302 methylation can stabilize ER α , this modification could be antagonistic to ubiquitination because of direct competition for the same lysine residue. Because methylated lysine residues can serve as docking sites for binding proteins through bromo- or chromodomains, the formation of new complexes would thereby limit ER α ubiquitination and degradation. Calmodulin would be a good candidate because K302 falls within a calmodulin-binding motif, and its binding to ER α prevents ubiquitination by E6-AP and degradation of the receptor. Interestingly, K302 mutation has been shown to reduce interactions between the two proteins (237). As a consequence, targeting K302 methylation could help to increase the degradation of ER α . In addition, K302 methylation could recruit a methyl lysine-binding protein that would, in turn, modulate ER α degradation through regulating the recruitment of E3 ubiquitin ligases.

In conclusion, several interactions between PTM have been described *in vitro*, but one must be careful in interpreting these results because most studies have been performed with mutants. One cannot exclude that the observed effects are due to conformational changes of the receptors rather than to a change in the modification. To integrate these findings for a better understanding of their significance, the next step will be to study the correlations between PTM *in vivo* (knock-in mice and patient tumors).

Finally, it is reasonable to assume that ongoing studies should clarify the combinatorial relationships between the different PTM and help to unravel ER-dependent gene transcription and to improve response to endocrine therapy.

D. ER PTM deregulated in breast cancer

The presence or absence of ER α is a well-established prognostic marker in breast cancer (at least in the early years after diagnosis) and a predictive marker for endo-

crine therapy (238–240). Because ER PTM have been shown to affect hormone sensitivity and localization, receptor stability, and/or ER transcription activity, it is tempting to speculate that immunohistochemical detection and quantification of these PTM could be an important new prognostic or predictive biomarker for tumor evaluation. Studies with antibodies specific to PTM have shown that several ER α modifications are deregulated in breast tumors, although it is so far unclear whether these deregulations are a cause or a consequence of the disease. Three phosphorylation sites of ER α (S118, S167, and S305) have received particular attention, especially because they have been implicated in ligand-independent activation of ER α . This section will focus mainly on ER α because almost nothing is known yet about ER β PTM in breast tumors. A list of the PTM found to be deregulated in breast tumors and the corresponding survival outcome are given in Table 3.

1. S118 of ER α

Immunohistochemical studies of pS118-ER α expression have found a significant positive correlation with active p-MAPK (241–245), active p-Akt (244, 246), and p-p90-RSK (246), suggesting that these kinases may be involved, directly or indirectly, in the S118 phosphorylation of ER α *in vivo*. High pS118-ER α expression levels have been associated in breast tumors with more differentiated phenotype, lower grade, and other markers of good prognosis such as ER α or progesterone receptor (241–244, 247–249). Concerning its predictive value for response to tamoxifen, the clinical studies yielded conflicting results. In fact, four studies do not associate S118

phosphorylation with tamoxifen response (243, 244, 250, 251), although other groups found this phosphorylation associated with better disease outcome in women treated with tamoxifen (242, 248, 252), and higher levels are found in ER α -positive cancer patients who respond to tamoxifen than in those who progress. These discrepancies probably result from the use of different antibodies in small nonrandomized patient series. Recently, a randomized study of 239 patients has confirmed that pS118-ER α is associated with tamoxifen response (248), and Generali *et al.* (253) have described this modification as an independent factor for endocrine responsiveness in patients receiving AI (letrozole)-based treatment, confirming that when this residue is phosphorylated, patients are more likely to respond to endocrine therapy.

2. S167 of ER α

In ER-positive primary breast cancers, pS167-ER α has been shown to be positively correlated with p-MAPK (244, 246), p-p90-RSK (246), and p-Akt (244, 246). pS167-ER α is also associated with good prognostic factors (such as lower tumor grade or lymph node negativity) and with increased relapse-free and overall survival (246). pS167-ER α has been found to be predictive of response to endocrine therapy (250). These data strongly suggest that phosphorylation of ER α at S167 could be a useful marker for selecting the patients who are most likely to benefit from endocrine therapy.

3. S305 of ER α

A number of *in vitro* studies have indicated that phosphorylation of S305 by PKA and/or PAK1 in ER α resulted

TABLE 3. ER PTM deregulated in breast cancer

Amino acid	Status in breast tumors	Survival outcome	Marker	References
ER α S104/106	Hyperphosphorylation	Good	ND	249
ER α S118	Hyperphosphorylation	Good	Tam response	242
		Good	Tam response	248
		Poor	Not for Tam response	250
		Good	ND	241
		Good	Good prognosis	243
		Good	ND	249
ER α S167	Hypophosphorylation	Good	Tam response	244
	Hyperphosphorylation	Good	Good prognosis	246
		Good	Tam response	250
		Good	Good prognosis	244
		Good	ND	249
ER α R260	Hypermethylation	ND	ND	227
ER α S282	Hyperphosphorylation	Good	ND	249
ER α K303	Mutated to arginine	Poor	Poor prognosis	232
ER α S305	Hyperphosphorylation after PKA activation	Poor	Tam resistance	157
	Hyperphosphorylation	Poor	Tam resistance	162, 257
ER α T311	Hyperphosphorylation	Poor	ND	249
ER α S559	Hyperphosphorylation	Good	ND	249
ER β S105	Hyperphosphorylation	Good	ND	261

ND, Not determined; Tam, tamoxifen.

in enhanced transactivation of ER (158, 161) and was associated with tamoxifen resistance (157, 161).

A link between PKA expression, ER α phosphorylation on S305, and resistance to tamoxifen has been demonstrated in breast cancer patients (157), consistent with early data from clinical studies correlating deregulation of PKA with tamoxifen resistance (254). Other studies have associated tamoxifen resistance with nuclear expression or amplification of PAK1 (255, 256).

A recent clinical study of a large series of tumors from node-negative postmenopausal breast cancer patients has established that the concomitant expression of nuclear PAK1 and pS305ER α correlates with reduced response to tamoxifen, suggesting a putative importance of this signaling pathway for treatment prediction. Furthermore, lack of nuclear pS305ER α or of nuclear PAK1 expression results in tamoxifen-improved response in postmenopausal breast cancers (257).

Although validating the correlation between PAK1 expression and tumor progression after tamoxifen treatment, the work by Michalides and colleagues (162) shows no direct link between PAK1 expression and pS305ER α . This analysis concludes that both PAK1 and PKA/pS305ER α levels are associated with sensitivity to tamoxifen in breast tumors, and the combination of these variables is predictive of tamoxifen benefit (162). Furthermore, a gene expression analysis has shown an enrichment of the PKA pathway in pS305ER α -positive tumors, but not of the PAK1-related pathway.

The discrepancy between these studies can be explained by the use of distinct anti-phosphoantibodies and differences between patients: premenopausal breast cancer (257) *vs.* postmenopausal (162) patients.

In conclusion, phosphorylation of ER α at S305 could be a new predictive marker for tamoxifen response, and targeting PKA to block S305 ER α phosphorylation represents a promising new strategy to prevent or to reverse endocrine resistance.

4. S282 and T311 of ER α

Phosphorylation of S282 is associated with better disease outcome (longer relapse-free survival) and phosphorylation of T311 with poor clinical outcome (decreased relapse-free survival) in women treated with tamoxifen (249).

5. R260 of ER α

The use of an antibody specific for ER α methylated on R260 has shown that this modification is relatively rare in normal epithelial breast tissue and that its expression is deregulated in breast tumors. ER α methylation status varies between tumors. In fact, ER α is hypermethylated in about 55% of invasive breast tumors (227). This deregulation

could be due to an overexpression of the arginine methyltransferase PRMT1 because isoforms of the enzyme have been shown to be overexpressed in breast tumors (258). So far, no correlation with clinical outcome or clinical parameters has been evidenced, and whether this modification is a cause or a consequence of the disease is still under investigation.

6. K303 of ER α

K303, a hot spot for PTM, was first shown to be mutated to arginine in ductal hyperplasia (259) and more recently in invasive breast tumors (232, 260). This mutation has been significantly associated with aggressive biological behavior and has been shown to be a marker of poor prognosis associated with reduced relapse-free survival (232). K303 mutation triggers ER α hypersensitivity to estrogen and resistance to tamoxifen and aromatase inhibitors (163). This hyperactivity is partly due to the hyperphosphorylation of the adjacent S305. Given that K303 can be modified by sumoylation, acetylation, or ubiquitination, and that it regulates K302 lysine methylation (208), we can speculate that this mutation disrupts one or more of these modifications, thereby inducing ER α hypersensitivity. For example, the mutation impeding acetylation triggers S305 phosphorylation and ER α hyperactivation. This is a striking example of the importance of understanding the complex relationship between ER PTM for deciphering the mechanisms of endocrine resistance and circumventing this major problem in breast cancer treatment.

7. S105 of hER β (equivalent to S124 of mER β)

An antibody specific for ER β phosphorylated on the S105 residue has been used to analyze its expression in tamoxifen-treated breast tumors. S105 phosphorylation is associated with better survival, even in tamoxifen-resistant cases (261). However, these results need to be confirmed on other cohorts of patients before S105 can be considered as a potential new marker.

IV. Discussion

Over the last several years, numerous studies have reported that ER, particularly ER α , are subject to a plethora of PTM in response to different stimuli and that these PTM differentially regulate the functions of these receptors, adding another layer of complexity to the regulation of estrogen signaling.

Some of these PTM are deregulated in breast cancer, even if we ignore whether they are just a consequence of the disease or they actually play a role in breast tumorigenesis. However, literature data show that they could at

least constitute new prognosis and/or predictive markers for the disease.

ER α phosphorylation, the most extensively studied PTM to date, has been shown to play important roles in most, if not all, estrogen-regulated pathways. In particular, a number of *in vitro* studies have shown that some ER α phosphorylation sites are clearly involved in endocrine therapy responsiveness. To validate the significance of these observations, several groups have investigated the relevance of various ER α phosphorylation sites by immunohistochemical detection in breast tumors. Many studies have focused on the phosphorylation of S118, S167, and S305. The obtained results illustrate the complexity of identifying a specific marker of the emergence of endocrine resistance. Indeed, contrary to what had been expected from *in vitro* observations, pS118-ER α and pS167-ER α do not seem to be associated *in vivo* with *de novo* endocrine resistance. Indeed the presence of pS118-ER α or pS167-ER α has been associated with better outcome in patients on endocrine therapy (162, 242, 245, 246, 252, 253), suggesting that these two ER α PTM could rather indicate good prognosis and responsiveness to endocrine therapy. Conversely, *in vitro* and clinical studies have validated that pS305-ER α modification is strongly associated with endocrine resistance because high pS305-ER α expression level is a predictive biomarker for endocrine therapy responsiveness. However, contradictory *in vivo* data from other groups (243, 244, 250, 251) have highlighted the complexity of such evaluation. The controversial results published could reflect differences in the antibodies used, in the stability of the phosphoepitopes during tumor collection and storage, in the size of the study cohorts, in the pre- or postmenopausal status of the patients, in the type of molecule used (ER ligand or AI) for endocrine therapy, and/or in the type of treatment (short-term neoadjuvant *vs.* long-term adjuvant endocrine therapy).

The limitation of the clinical studies described above can arise from the analysis of a single biomarker to distinguish between responders and nonresponders to endocrine therapy. Indeed, each phosphorylation could alter the receptor function in a distinctive manner, individually or in combination. So, it would be important to develop new scores combining several PTM and allowing more accurate identification of the patients likely to benefit from endocrine therapy.

In this context, recent studies from the laboratory of L. C. Murphy (252) have demonstrated the presence of multiple phosphorylated isoforms of ER α (S104/106, S118, S167, S282, S294, T311, and S559) in breast tumors. Interestingly, they have shown that any individual phosphoepitope is positively correlated with at least two others, and pS559 is positively correlated with all other

epitopes (252). They have also investigated the relationship between these phosphorylated forms of ER α and clinical outcome after tamoxifen therapy in 300 patients with ER α -positive breast tumors (249). Interestingly, they have found that phosphoepitopes clustered in the N terminus of ER α (S104/106, S118, S167, S282, S294) are predictors of good outcome, whereas other epitopes clustered toward the C terminus (T311 and S559) are predictors of bad outcome. Accordingly, the authors propose a “phospho-score” that, by taking into account seven phospho-sites on ER α , integrates both “good” and “bad” sites. This score has been shown to be a statistically significant independent predictor of overall survival and relapse-free survival in tamoxifen-treated ER-positive patients (249). Along this line, the FRET analysis published by Zwart *et al.* (30) has illustrated that the combinations of ER α phosphomodifications lead to different conformational changes upon each antiestrogen treatment. In consequence, we can speculate on the existence of a specific code for each type of endocrine therapy.

Additional complexity has been introduced with a recent study describing that the hyperphosphorylation of ER β on the S105 residue is associated with improved disease-free and overall survivals in breast tumor samples (261), suggesting that ER β modification should be included in the “phospho-score.”

Investigations of the relationship between modifications of ER α and resistance to hormone therapy have mainly focused on phosphorylation. As discussed above, ER α also undergoes several other modifications affecting multiple sites. However, these modifications are less well characterized, and because of the unavailability of specific antibodies, their *in vivo* significance is poorly understood. Little or no *in vivo* studies have been published about other ER PTM, and the preliminary data obtained need to be validated on independent cohorts.

Given the complexity described above, assessing the expression of the different molecules involved in ER modifications might allow more accurate selection of patients with different responses to endocrine therapy. The enzymes triggering the PTM have not yet been clearly identified, and very little is known about the enzymes responsible for reversing these modifications. Actually, in breast tumor samples, a significant positive correlation has been found between the expression of p-MAPK or p-Akt and pS167- or pS118-ER α and between p-p90-RSK and pS118-ER α , indicating that these kinases participate directly or indirectly in these modifications (241–246). In addition, two recent studies have shown that combinations of pS305ER α and nuclear PAK1 (257) or PKA/pS305ER α and PAK1 are more powerful in predicting response to tamoxifen (162).

Altogether, these data suggest that assessing the PTM code of ER α , either individually or in association with the expression and/or activity of the enzymes responsible for these PTM, could provide an efficient personalized anti-estrogen therapy.

V. Future Directions

At present, ER α status is the only factor used routinely for prediction of response to endocrine therapy and patient selection in breast cancer. As we have largely discussed above, PTM play a pivotal role in the regulation of ER α functions, and their deregulation is clearly involved in phenomena of resistance to endocrine therapies in breast cancer patients.

Before we can elucidate the mechanisms by which breast cancers evade antiestrogen-mediated growth arrest, we need to understand how PTM regulate ER actions. Undoubtedly, our understanding of these dynamic modifications is still at an early stage due to the lack of appropriate tools to monitor modifications of endogenous proteins. Future studies should investigate how a specific modification regulates a subset of ER target genes to determine specificity and how these different modifications act, sequentially and/or in concert, under physiological and pathological conditions. Using proteomic approaches, including developing site- and modification-specific antibodies and employing mass spectrometry techniques, would allow a better understanding of the regulation of these dynamic modifications *in vivo*. Furthermore, genetic approaches, such as the generation of modification-deficient ER knock-in animals, would provide new insights into the possible physiological functions of these modifications. Important efforts should also be made to better define the actors involved in PTM regulation, notably the enzymes responsible for reversing ER PTM.

New treatments targeting the molecules responsible for modifying or reversing PTM could be used in combination with endocrine therapies or after treatment failure or acquired resistance. However, specifically targeting PTM in breast cancer cells is a prerequisite to any efficient therapy because most of the enzymes involved in such modifications are present in both the tumor and healthy tissues and treatment may cause a wide range of unwanted side effects. Important advances have been made in this direction with the development of nanocarriers loaded with cytotoxic drugs (stealth liposomes, for example) characterized by a prolonged blood circulation time when injected iv [for review, see Urbinati *et al.* (273)].

Many approaches and avenues remain unexplored in developing targeted drugs for effective blockade of ER α signaling. We can anticipate that in the future, thanks to the ER posttranslational code, a molecular subtyping of individual tumors will help to define the antihormonal treatment for each patient.

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