

# Delineation of a unique protein–protein interaction site on the surface of the estrogen receptor

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Recent studies have identified a series of estrogen receptor (ER)-interacting peptides that recognize sites that are distinct from the classic coregulator recruitment (AF2) region. Here, we report the structural and functional characterization of an ER $\alpha$ -specific peptide that binds to the liganded receptor in an AF2-independent manner. The 2-Å crystal structure of the ER/peptide complex reveals a binding site that is centered on a shallow depression on the  $\beta$ -hairpin face of the ligand-binding domain. The peptide binds in an unusual extended conformation and makes multiple contacts with the ligand-binding domain. The location and architecture of the binding site provides an insight into the peptide's ER subtype specificity and ligand interaction preferences. *In vivo*, an engineered coactivator containing the peptide motif is able to strongly enhance the transcriptional activity of liganded ER $\alpha$ , particularly in the presence of 4-hydroxytamoxifen. Furthermore, disruption of this binding surface alters ER's response to the coregulator TIF2. Together, these results indicate that this previously unknown interaction site represents a bona fide control surface involved in regulating receptor activity.

coregulator | phage display | structure

The estrogen receptor (ER) functions as a ligand-activated transcription factor and is responsible for mediating the physiological effects of the steroid hormone 17 $\beta$ -estradiol (E2). Transcriptional activation is facilitated by two distinct activation functions (AF), the constitutively active AF1 located at the N terminus of the receptor and a ligand-dependent AF2 that resides in the C-terminal ligand-binding domain (LBD) (1), which recruit a range of coregulatory protein complexes to the DNA-bound receptor (2). ER agonists promote association with coactivators, whereas antagonists favor recruitment of corepressors.

The LBD serves as the major interaction point between nuclear receptors (NRs) and coregulatory proteins. Coactivator recruitment is mediated by short  $\alpha$ -helical, leucine-rich LxxLL consensus motifs (NR-box) that bind to the AF2 region of the LBD (3–5). Structural analysis of NR LBDs has established that agonist binding stabilizes a receptor conformation in which elements of AF2 form a hydrophobic groove that can accommodate the LxxLL motifs found within coactivators (6–8). In contrast, ER antagonists affect the positioning of the AF2's mobile C-terminal helix (H12), thereby disrupting the LxxLL-binding site and preventing coactivator recruitment (7, 9). The resultant antagonist-induced conformation favors recruitment of corepressor complexes (10). Although the details of corepressor binding to ERLBD are not known, antagonist-induced displacement of H12 in other NRs promotes corepressor recruitment to an interaction surface that overlaps with the AF2 groove (11–13).

Although this conformational mechanism can be used to rationalize the differential recruitment of coactivators and corepressors to a common surface on ER, it is not immediately apparent how this alone can account for the diverse pharmacology of selective ER receptor modulators (SERMs). SERMs, such as raloxifene and 4-hydroxytamoxifen (OHT), are a class of synthetic ER ligands that exhibit tissue-dependent pharmacology, imitating the action of

estrogens in certain tissues while opposing their action in others (14). These compounds appear to elicit their effects by inducing distinct conformational changes in ER that favor interaction with specific subsets of coactivators (15). The mechanisms of such coactivator binding are unclear but are likely to involve recognition surfaces, which are unrelated to AF2, that are revealed in response to a particular modulator.

The screening of random peptide libraries is a powerful method for isolating motifs that mimic protein–protein interaction surfaces. Phage display techniques using both focused and random peptide libraries have been used to investigate the interaction of coregulators with liganded ER (13, 16–19). These studies have isolated a number of short peptides with characteristic sequence motifs that specifically recognize different liganded states of ER. Such peptides, in addition to acting as conformational probes (16), have been shown to interfere with receptor activity both *in vitro* and in cell-based assays (18, 19). These observations have led to the suggestion that such motifs represent biologically relevant interaction modules or, alternatively, that they mimic receptor–cofactor interactions. Although some of the isolated motifs are directed to the region around ER's AF2 binding groove, several possess previously undescribed consensus sequences and appear to interact with distinct regions of the receptor.

To address whether ERLBD harbors additional protein–protein interaction sites, we have studied an ER interaction motif that binds specifically to ER $\alpha$ . The 11-residue peptide antagonist, referred to as  $\alpha$ II, was initially isolated from a random peptide phage display library by using E2- or OHT-bound ER $\alpha$  and found to interact in the presence of a broad spectrum of receptor modulators (16). In this study, we have used a combination of techniques to both delineate the  $\alpha$ II binding site on ER $\alpha$ LBD and demonstrate that this surface is involved in ER's response to certain ligands.

## Materials and Methods

**Protein Expression and Purification.** The H12 truncated mutant (ER $\alpha$  $\Delta$ H12) used for structural analysis was generated by inserting a stop codon after Val-533 in a pET15b-ER $\alpha$ LBD construct (20). ER $\alpha$  $\Delta$ H12 was expressed in *Escherichia coli* strain C41 (DE3). ER $\alpha$  $\Delta$ H12 was extracted from inclusion bodies with a buffer (150 mM NaCl/1 mM EDTA/2 mM DTT/10% glycerol/1 mM PMSF/50 mM Tris, pH 8.0) containing 1% (wt/vol) Zwittergent 3-12. The detergent was removed by dialysis, and the extract was applied to an E2-Sepharose column. The E2-affinity matrix was prepared as described (21). Bound ER $\alpha$  $\Delta$ H12 was carboxymethylated overnight with 10 mM iodoacetic acid and eluted with 50  $\mu$ M

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Abbreviations: ER, estrogen receptor; E2 17 $\beta$ -estradiol; AF, activation function; LBD, ligand-binding domain; NR, nuclear receptor; OHT, 4-hydroxytamoxifen; SPR, surface plasmon resonance.

Data deposition: The atomic coordinates have been deposited in the Protein Data Bank, www.pdb.org (PDB ID code 2BJ4).

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OHT in a buffer containing 1 mM DTT, 1 mM EDTA, 250 mM NaSCN, and 25 mM Tris (pH 8.5). ER $\alpha$  $\Delta$ H12 was further purified by using ion exchange chromatography. Pooled fractions containing ER $\alpha$  $\Delta$ H12 were combined with a 1.5-fold molar excess of  $\alpha$ II peptide and concentrated to 10 mg/ml. Additional peptide was added to obtain a final peptide/LBD molar ratio of 3:1.

**Crystallization and Structure Determination.** Hanging drops composed of equal volumes of ER $\alpha$  $\Delta$ H12-OHT- $\alpha$ II complex and reservoir solution [20% (wt/vol) polyethylene glycol (PEG) 2000 monomethyl ether (Mme)/620 mM sodium formate/3% (wt/vol) glucose in 100 mM Tris, pH 8.0] were equilibrated against reservoir solution at 19°C. Crystals were cryoprotected in mother liquor containing 32.5% (wt/vol) PEG 2000 Mme and vitrified in liquid nitrogen. Crystals belong to space group  $P2_12_12_1$  and have a single LBD homodimer per asymmetric unit. Diffraction data, collected to a resolution of 2 Å on beamline ID29 at the European Synchrotron Radiation Facility (Grenoble, France), were indexed, reduced, and scaled by using the HKL suite of programs (22). The structure was solved by molecular replacement using AMORE (23). Initial electron density maps clearly indicated the position of OHT and the  $\alpha$ II peptide. The structure was refined with REFMAC5 (24) using all available data. All model building was carried out with QUANTA (Accelrys, San Diego). The final model has an  $R_{\text{cryst}}$  of 18.7% and a  $R_{\text{free}}$  of 21.9%. Data collection and refinement statistics are shown in Table 1, which is published as supporting information on the PNAS web site.

**Surface Plasmon Resonance (SPR).** Measurements were performed by using a BIAcore X instrument and streptavidin-coated sensor chips. Experiments were carried out as described (8). Biotinylated  $\alpha$ II peptide (SGSGLTSRDFGWSYA) was immobilized to variable responses (60–160 relative units). Qualitative binding experiments with liganded ER $\alpha$ / $\beta$ LBD and LBD mutants were performed by flowing each complex (1  $\mu$ M dimeric concentration) over the  $\alpha$ II chip for 2 min at 5  $\mu$ l·min<sup>-1</sup>. A sensor chip comprising an immobilized biotinylated SRC2-2 peptide (EKHKILHRLQDS) (8) was used as a control binding surface to assess the structural integrity of the LBD mutants. Methods used for construction of the LBD mutants, the kinetic analysis and preparation of protein used for SPR studies are described in *Supporting Text*, which is published as supporting information on the PNAS web site.

**Mammalian Two-Hybrid and Reporter Assays.** Details of the ER and TIF2 expression plasmids used are described in *Supporting Text*. Mammalian two-hybrid experiments were carried out as described (19). For the transcriptional assays with the engineered TIF2 coactivator, Cos-7 cells were cotransfected with expression vectors (pSG5) for wild-type ER $\alpha$  and either TIF2-NR12 or TIF2 $\alpha$ II together with the estrogen responsive 3 $\times$  ERE-TATA-luc reporter. Experiments were performed in triplicate and contained 30 ng of ER $\alpha$  construct, 30 ng of  $\beta$ -gal construct, 150 ng of reporter construct, and 150 ng of TIF2 expression plasmid. After transfection, cells were treated with 10 nM E2, 100 nM OHT, or dimethylsulphoxide for 16 h before analyzing luciferase and  $\beta$ -gal activity. For the transcriptional assays comparing wild-type and mutant (ER $\alpha$  G442H) receptor activity, Cos-7 cells were cotransfected with expression vectors (pSG5 or Gal4DBD) for wild-type ER $\alpha$ , ER $\alpha$  G442H, Gal4-tagged ER $\alpha$   $\Delta$ DEF $\Delta$ H12, or Gal4-tagged ER $\alpha$  DEF $\Delta$ G442H $\Delta$ H12 and either empty expression vector (pSG5) or TIF2wt expression vector together with either the estrogen responsive 3 $\times$  ERE-TATA-luc reporter or the Gal4 responsive reporter 5 $\times$  UAS-TATA-luc. Each triplicate contained 30 ng of ER $\alpha$  construct, 30 ng of  $\beta$ -gal construct, 150 ng of reporter construct, and 30 ng of TIF2 expression plasmid. After transfection, cells were treated with 100 nM OHT or dimethylsulphoxide for 16 h before analyzing luciferase and  $\beta$ -gal activity.

## Results

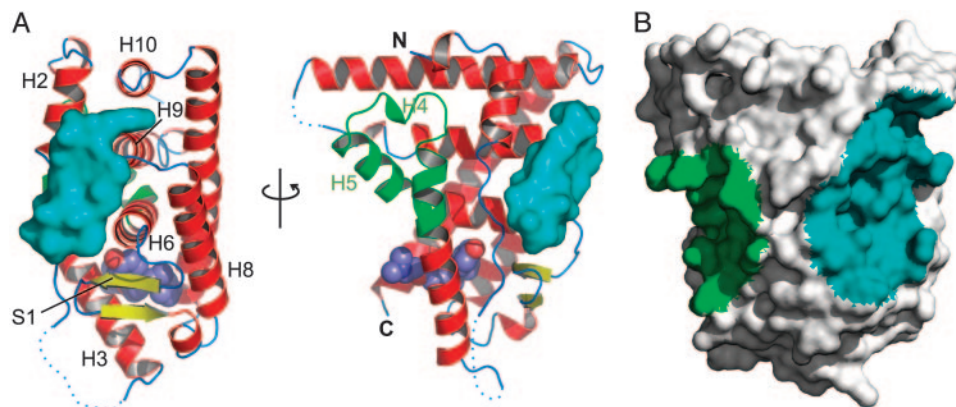
**$\alpha$ II Peptide Motif Interacts Specifically with Liganded ER $\alpha$ LBD.** Previous reports of  $\alpha$ II binding to ER $\alpha$  showed that the interaction occurs within the C-terminal LBD region between residues 282 and 535 (18). To confirm that  $\alpha$ II interacts with the alkylated LBD used for crystallization (9), we carried out real-time analysis of the binding between ERLBD and the  $\alpha$ II interaction motif by using SPR. A biotinylated  $\alpha$ II peptide immobilized onto a streptavidin-coated sensor chip can specifically recognise various liganded forms of ER $\alpha$ LBD (Fig. 5A, which is published as supporting information on the PNAS web site). The  $\alpha$ II peptide interacts with ER $\alpha$ LBD bound to both agonists (E2, diethylstilbestrol, genistein) and an AF2 antagonist (OHT). The ligand interaction preference is similar to that observed for full-length ER $\alpha$  (16). As previously reported (18),  $\alpha$ II binding is not dependent on AF2, because a LBD mutant lacking the C-terminal activation helix H12 (ER $\alpha$  $\Delta$ H12) retains its ability to bind to the  $\alpha$ II peptide (Fig. 5B). Kinetic analysis demonstrates that the  $\alpha$ II peptide binds to ER $\alpha$ LBD with moderate affinity and has an apparent dissociation constant ( $K_d$ ) of 34  $\mu$ M (Fig. 5C).

**Structure of the ER $\alpha$ LBD- $\alpha$ II Peptide Complex.** To get a better understanding of the nature and location of the  $\alpha$ II-binding site on ER $\alpha$ , we cocrystallized ER $\alpha$ LBD with an 11-residue peptide corresponding to the  $\alpha$ II interaction motif (LTSRDFGWSYA). Initial crystallization trials with various ER $\alpha$ LBD- $\alpha$ II complexes did not yield crystals suitable for structural analysis. Based on our observations that  $\alpha$ II binding was independent of H12, we also set up trials using the truncated ER $\alpha$  $\Delta$ H12 mutant. The resultant complex, liganded with OHT, produced well diffracting crystals. The overall ER $\alpha$  $\Delta$ 12 mutant structure is very similar to that seen previously for ER $\alpha$ LBD in complex with either E2 (9) or OHT (7) (rms deviation for  $\alpha$ -carbons of 0.51 and 0.69 Å, respectively). Removal of H12 and the preceding loop has no discernable effect on the integrity of the LBD fold.

**Peptide-Binding Site.** The ER $\alpha$  $\Delta$ H12-OHT- $\alpha$ II peptide complex crystallises with a single LBD homodimer in the asymmetric unit. Each monomer within the homodimer interacts with a peptide motif (Fig. 6A, which is published as supporting information on the PNAS web site). Difference Fourier maps revealed well defined electron density for the peptide, allowing us to model the entire 11-residue  $\alpha$ II sequence (Fig. 6B). The  $\alpha$ II motif binds across the  $\beta$ -hairpin face of the LBD (Fig. 1A). The interaction site is centered on a shallow depression between H2, H6, and H9 that surrounds the entrance of the solvent-filled channel that leads to the buried hormone-binding cavity. This surface lies diametrically opposite the receptor's AF2 coactivator recruitment site (Fig. 1B). Residues from H2, the H2-H3 loop, H6, the S1-S2  $\beta$ -hairpin, H8-H9 loop, H9, and H10 contribute to an extensive binding surface (10 Å by 24 Å long).

The  $\alpha$ II peptide adopts an extended conformation that closely matches the surface topology of the LBD (Fig. 2A). Residues Leu-1-Phe-6 run parallel to the S1 strand with residues Ser-3-Asp-5 adopting a  $3_{10}$  helical conformation. At Gly-7, the peptide backbone turns 90° and climbs toward H10. This bent conformation is stabilized by an intramolecular interaction between the backbone carbonyl of Phe-6 and the indole nitrogen of Trp-9. Gly-7 appears to fulfil a structural role because of the strained backbone dihedral angles required at this position.

LBD recognition is mediated by an extensive network of hydrogen-bonded and nonpolar interactions. No single interaction appears to dominate, and the observed peptide conformation is reliant on multiple intra- and intermolecular contacts. Binding of the  $\alpha$ II motif buries 650 Å<sup>2</sup> of predominantly hydrophobic surface area on the LBD. Residues from the peptide make a total of eight direct hydrogen bonds with the LBD (Fig. 2B). The N terminus of



**Fig. 1.** Overall structure of ER $\alpha$ LBD in complex with the  $\alpha$ II interaction motif. (A) Ribbon representation of the ER $\alpha$  $\Delta$ H12-OHT- $\alpha$ II structure. Two perpendicular views of the LBD monomer are shown. The  $\alpha$ II peptide is represented by a molecular surface (cyan). Dotted lines represent regions of the structure that are poorly defined in the experimental electron density. Secondary structure elements are labeled, and the AF2 region of the LBD (H3–H5) is colored green. (B) Composite surface representation of the ER $\alpha$ LBD monomer highlighting the location and extent of the known AF2 (green) and proposed  $\alpha$ II (cyan) coregulator sites. The molecule is viewed in an identical orientation to the right ribbon representation in A.

the peptide is anchored to the loop between H2 and H3. Ser-3 is completely buried and plugs the entrance to the solvent channel. Contacts between the central portion of the motif and the LBD are mainly hydrophobic in nature (Fig. 2C). Phe-6 lies at the periphery of the site and packs against the aliphatic side chain of Arg-394, a residue that plays a critical role in recognition of the phenolic hydroxyl of ER ligands. Trp-9 is thrust toward the body of the LBD and packs against Gly-442 (H9) and Trp-393 (H6). Residues at the N-terminal end of H9 (Gln-441, Gly-442, Glu-443, and Glu-444) make multiple hydrogen-bonded interactions with C-terminal half of the  $\alpha$ II motif (Fig. 2B). The C-terminal end of the motif is anchored by two separate interactions. The main chain amides of Tyr-11 and Ala-12 interact with carboxylate side chain of Glu-443. In addition, the side chain of Tyr-10 projects over the H8–H9 loop and binds in a narrow cleft between Gln-441 and Ala-493 (Fig. 2A–C).

Comparison with all other ER $\alpha$ LBD ligand complexes demonstrates that the  $\alpha$ II-binding site is structurally invariant. This observation underlies  $\alpha$ II's ability to bind to any agonist-, AF2 antagonist-, or pure antagonist-bound ER $\alpha$ . The motif's specificity for ER $\alpha$  appears to derive from the fact that parts of the site are poorly conserved in ER $\beta$  and other NRs (Fig. 2D). In particular, sequence changes at the N-terminal end of H9 are likely to affect  $\alpha$ II binding. In ER $\beta$ , Gly-442 and Glu-443 are replaced by a histidine and lysine, respectively.

**Mutagenesis Studies of LBD Binding to  $\alpha$ II.** To validate the location of the interaction site delineated in the crystal structure and to investigate the ER $\alpha$ -specific nature of the interaction, we made a series of single site LBD mutants and evaluated  $\alpha$ II-binding by using SPR. Choice of appropriate mutations was complicated by the fact that residues lining the binding site fulfill key roles in maintaining the structural integrity of the LBD. Consequently, only residues that anchored the termini of the  $\alpha$ II motif were targeted (I326, Q441, G442, E443). These residues were either replaced with alanine (Q441, E443) or with the corresponding ER $\beta$  residue type (I326H, G442H, E443K).

Fig. 2E shows the binding response of each mutant (liganded to E2) to the  $\alpha$ II sensor chip. Changes at all sites were poorly tolerated and severely impaired the interaction. In contrast, binding of the mutants to an immobilized LxxLL peptide, derived from the NRbox2 region of TIF2 (SRC2–2) (8), was similar to that observed for the wild-type LBD (Fig. 2E Inset). These control binding experiments suggest that none of the mutations impacted on the LBD's ability to bind E2 and adopt an activated conformation

capable of recruiting coactivator. The mutant binding data indicates that the inability of the  $\alpha$ II motif to interact with ER $\beta$  derives primarily from steric clashes with the bulkier residues found at positions 326 and 442 (279 and 394 in ER $\beta$ ) in this isoform (Fig. 2D).

**Binding of  $\alpha$ II Peptide in Mammalian Cells.** Previous studies have demonstrated  $\alpha$ II binding to ER in a cellular context (18, 25). To confirm that the  $\alpha$ II binding site observed in the crystal structure of the LBD complex is maintained in the full-length receptor *in vivo*, we investigated the interaction by using a well established mammalian two-hybrid (M2H) assay (19). As demonstrated in Fig. 3A, the  $\alpha$ II peptide interacted with full-length ER $\alpha$  in the presence of both E2 and OHT, but not in the absence of ligand. Furthermore, whereas this interaction was independent of ER's AF2 domain ( $\Delta$ H12), disruption of the  $\alpha$ II site by the introduction of the G442H mutation abolished receptor–peptide association (Fig. 3B and C). In contrast, an LxxLL peptide (19) bound equally well to both the wild-type and G442H-mutated full-length receptor in the presence of E2.

To elucidate which amino acid residues of the  $\alpha$ II motif are essential for functional peptide–receptor interactions, we performed limited alanine scanning mutagenesis on the  $\alpha$ II sequence and tested variants for ER interaction in the M2H system (Fig. 3D and E). Replacement of Phe-6, Gly-7, Ser-8, Trp-9, or Tyr-10 completely abolished receptor interaction (Fig. 3E). In contrast, substitution of Ser-3 had a moderate effect on  $\alpha$ II binding. In the crystal structure, the O $\gamma$  of Ser-3 is buried and makes a single hydrogen bond with the carboxylate of Glu-323. Although this interaction appears to be dispensable for binding, the motif is otherwise highly sensitive to sequence changes. Such a high degree of sequence dependence reflects the nature of  $\alpha$ II binding, which relies on multiple interactions with the LBD.

**Enhancement of OHT-Dependent Transcriptional Activity by an Engineered Coactivator.** To investigate whether the  $\alpha$ II interaction surface can be used as a functional docking site for coregulators, we attempted to modify the behavior of the p160 coregulator TIF2 (GRIP1, SRC2, NcoA-2). TIF2 enhances ER-mediated transcriptional activity in an AF2- and hormone-dependent manner (26). TIF2's receptor-interacting domain contains three NR boxes that are involved in ligand-dependent NR interaction. Of these, NR box 1 and 2 have been implicated in high-affinity binding to ER (8, 27). We inactivated NR box3 (TIF2–NR12) and replaced NR box 1 and 2 with the  $\alpha$ II sequence by mutagenesis to create TIF2 $\alpha$ II (Fig. 4A).





that its interaction with ER is highly sequence-dependent. Database searches with either the  $\alpha$ II sequence or a redundant motif based on the binding mode observed in the crystal structure do not yield any obvious homologies. Based on the apparent lack of key hotspots within the sequence, we currently favor a model in which the  $\alpha$ II peptide acts as a structural, rather than sequence mimic of the true interaction partner. Consequently, the possibility that elements of the  $\alpha$ II motif are incorporated into a nonlinear recognition module, formed by discontinuous regions of primary sequence, cannot be ruled out.

**$\alpha$ II Interaction Surface: A Possible Coregulator Recruitment Site?** The question remains as to whether the  $\alpha$ II motif acts as a fortuitous conformational probe or an actual mimic of a bona fide ER interaction partner? Norris *et al.* (18) demonstrated that  $\alpha$ II is able to inhibit the partial agonist activity of OHT while having a minimal effect on E2-mediated transcription. This observation strongly suggests that  $\alpha$ II's cognate binding surface on ER $\alpha$  represents an important control site that is involved in regulating receptor activity under certain conditions. Short peptides that act as antagonists of protein-protein interactions have been isolated from naive libraries for a number of systems. Subsequent structural analysis has shown that the peptide binding site overlaps with that of a known binding partner (29). In the case of  $\alpha$ II, the crystal structure of the complex indicates that peptide binding to the isolated LBD does not induce any significant conformational changes. This finding suggests that  $\alpha$ II's antagonistic properties are manifested by a direct steric effect in which the peptide occludes a key binding site. At this stage, it is unclear whether the  $\alpha$ II site is a docking surface for another region of ER (i.e., involved in intramolecular domain signaling) or for an as yet unidentified coregulator. The coactivator engineering experiments clearly demonstrate that the  $\alpha$ II binding surface can serve as a valid receptor-coregulator interaction site. By replacing the NR-box/LxxLL regions of TIF2 with the  $\alpha$ II sequence, we generated a coactivator (TIF2 $\alpha$ II) that could be recruited to the  $\alpha$ II surface by both agonist and antagonist-bound ER in an AF1/AF2-independent fashion.

Our preliminary functional analysis indicates that the  $\alpha$ II surface may play a role in ER's sensitivity to coregulators in the presence of selective ER receptor modulators such as OHT (Fig. 4C). No differences in behavior were observed between wild-type and

$\alpha$ II-mutated ER in the presence of E2. This ligand-dependency mirrors the previously reported antagonistic effects of the  $\alpha$ II peptide on E2- and OHT-dependent receptor activity (18). The surprising result that the TIF2-mediated enhancement of OHT activity seen for the G442H mutant requires a functional AF2 H12/F domain only in the context of the full-length ER, but not in the context of the ER DEF, reinforces the idea that the functional interplay between different ER domains and coregulators determines the transcriptional properties of the wild type receptor (30). Furthermore, our demonstration that disruption of the  $\alpha$ II binding site enhanced rather than decreased the response to TIF2 does not necessarily contradict the currently held view that TIF2 acts primarily as a coactivator. Although TIF2 coactivator function is usually associated with recruitment to a functional AF1/2 surface, targeting to other surfaces cannot be discounted. Recent studies by Yamamoto and coworkers (31, 32) discovered a context-dependent corepressor function in TIF2, which may indeed account for the effect seen in our study. Alternatively, TIF2's role could be indirect and mediated by either endogenous coregulators known to cooperate with TIF2 (e.g., CBP/p300, CARM-1) or unidentified corepressors that bind directly to the  $\alpha$ II surface. Indeed, although our coregulator engineering experiment targeted a coactivator to the  $\alpha$ II surface, similar experiments utilizing an engineered corepressor would probably have illustrated that the  $\alpha$ II site may alternatively be involved in corepressor binding.

In summary, the site identified in this study appears to be involved in maintaining a reduced level of receptor activation in the presence of TIF2. Further studies are required to establish whether other recognized or unrecognized ER coactivators and corepressors also display sensitivity to the disruption of this unique control surface.

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