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The Human Transcription Factor IID Subunit Human TATA-binding Protein-associated Factor 28 Interacts in a Ligand-reversible Manner with the Vitamin D₃ and Thyroid Hormone Receptors*

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Using coexpression in COS cells, we have identified novel interactions between the human TATA-binding protein-associated factor 28 (hTAF_{II}28) component of transcription factor IID and the ligand binding domains (LBDs) of the nuclear receptors for vitamin D₃ (VDR) and thyroid hormone (TR α). Interaction between hTAF_{II}28 and the VDR and TR LBDs was ligand-reversible, whereas no interactions between hTAF_{II}28 and the retinoid X receptors (RXRs) or other receptors were observed. TAF_{II}28 interacted with two regions of the VDR, a 40-amino acid region spanning α -helices H3–H5 and α -helix H8. Interactions were also observed with the H3–H5 region of the TR α but not with the equivalent highly related region of the RXR γ . Fine mapping using RXR derivatives in which single amino acids of the RXR γ LBD have been replaced with their VDR counterparts shows that the determinants for interaction with hTAF_{II}28 are located in α -helix H3 and are not identical to those previously identified for interactions with hTAF_{II}55. We also describe a mutation in the H3–H5 region of the VDR LBD, which abolishes transactivation, and we show that interaction of hTAF_{II}28 with this mutant is no longer ligand-reversible.

Transcription factor IID (TFIID)¹ is one of the general factors required for accurate and regulated initiation by RNA polymerase II. TFIID comprises the TATA-binding protein (TBP) and TBP-associated factors (TAF_{II}s; Refs. 1–5). A subset

of TAF_{II}s are present not only in TFIID but also in the complexes (Refs. 6–10; for review, see Refs. 11–14).

TAF_{II} function has been studied genetically in yeast and by transfection experiments in mammalian cells. In yeast, a variable requirement for TAF_{II}s has been found. Temperature sensitive mutations in yeast TAF_{II}145 (yTAF_{II}145) result in cell cycle arrest and lethality, but the expression of only a small number of genes is affected (15). In contrast, tight temperature-sensitive mutations in yTAF_{II}17, yTAF_{II}25, yTAF_{II}60, yTAF_{II}61/68, and the TFIID-specific yTAF_{II}40 strongly affect the transcription of the majority of yeast genes (16–21).

An increasing body of results also shows that human TAF_{II}28 (hTAF_{II}28), hTAF_{II}135, and hTAF_{II}105 can act as specific transcriptional coactivators in mammalian cells. For example, distinct domains of hTAF_{II}135 interact specifically with Sp1, cAMP response element-binding protein, and E1A, and coexpression of these hTAF_{II}135 derivatives has a dominant negative effect on the activity of these activators (22–25), whereas coexpression of hTAF_{II}135 strongly potentiates transcriptional activation by several nuclear receptors (26). Similarly, hTAF_{II}105 interacts specifically with the p65 subunit of nuclear factor- κ B, and TAF_{II}105 expression potentiates activation by nuclear factor- κ B in mammalian cells (27).

The viral protein Tax interacts directly with hTAF_{II}28, and coexpression of hTAF_{II}28 strongly potentiates activation by Tax (28). Expression of hTAF_{II}28 also potentiates activation by the ligand-dependent activation function-2 of the nuclear receptors (NRs) for vitamin D₃ (VDR), 9-cis retinoic acid (RXR), and estrogen (29, 30). Coexpression of TBP and hTAF_{II}28 shows that they act synergistically to potentiate activation by the VDR or estrogen receptor. This synergism requires specific amino acids of the hTAF_{II}28 histone fold domain located in the conserved C-terminal half of the protein and can also be abolished by a mutation in the H1' helix of TBP (31, 32).

Despite its ability to act as a transcriptional coactivator for several NRs, we previously reported that no ligand-dependent interactions with the RXR could be observed (29). In this study, we show that hTAF_{II}28 does selectively interact with the VDR and thyroid hormone receptor (TR α) but does so in a ligand-reversible manner. Analysis of hTAF_{II} interaction with VDR deletion mutants shows that hTAF_{II}28 interacts with a 40-amino acid region spanning α -helices H3–H5 and containing the NR signature and previously shown also to interact with hTAF_{II}55 (33). Interaction was also seen with the H3–H5 region of the TR α but not with the analogous highly related region of the RXR γ . Substituting single amino acids of the RXR γ H3–H5 region with their counterparts from the VDR induced interactions with hTAF_{II}28, but comparison with the results previously obtained with hTAF_{II}55 indicates that the determinants for the interaction of these TAF_{II}s with this re-

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¹ The abbreviations used are: TFIID, transcription factor IID; TBP, TATA-binding protein; TAF_{II}, TATA-binding protein-associated factor; yTAF_{II}, yeast TAF_{II}; hTAF_{II}, human TAF_{II}; NR, nuclear receptor; VDR, vitamin D₃ receptor; RXR, retinoid X receptor; TR α , thyroid hormone receptor; CAT, chloramphenicol acetyltransferase; mAb, monoclonal antibody; LBD, ligand binding domain; G4, GAL4.

gion are not identical. We also show that exchange of amino acids in the H3–H5 region between the VDR and RXR leads to a loss of activity in the case of the VDR and a gain of activity in the case of the RXR.

MATERIALS AND METHODS

Construction of Recombinant Plasmids—The hTAF_{II} expression vectors are as described previously (29, 33–35). The mouse RXR, mouse retinoic acid receptor, Sp1, and AP-2 expression vectors are also as described (26, 29, 33, 36, 37). All the G4-VDR, TR α , and RXR chimeras were constructed by PCR using the appropriately designed oligonucleotides with restriction sites and cloned into the vector pXJ440 encoding the DNA binding domain of the yeast activator GAL4 (38). All plasmids were verified by automated DNA sequencing. Further details of constructions are available on request.

Transfection of COS Cells and Immunoprecipitations—COS cells were transfected by the calcium phosphate coprecipitation technique, and immunoprecipitations were performed as described previously (33–35). 48 h after transfection the cells were harvested by three cycles of freeze-thaw in buffer A (50 mM Tris-HCl, pH 7.9, 20% glycerol, 1 mM dithiothreitol, and 0.1% Nonidet P-40) containing 0.5 M KCl. The expression of the transfected proteins was verified on Western blots. For immunoprecipitations cell extracts were incubated for 1 h at 4 °C with 1–2 μ g of the indicated monoclonal antibodies after which time 50 μ l of protein G-Sepharose was added, and incubation was continued for another 2 h. After extensive washing the precipitated proteins were detected by immunoblotting with the indicated antibodies using an ECL kit (Amersham Pharmacia Biotech). Where indicated, ligands were added (50 nM all-*trans*-retinoic acid, 9-*cis*-retinoic acid, and 3,5,3'-triiodo-L-thyronine and 100 nM 1,25-dihydroxyvitamin D₃) at the same time as the DNA-calcium phosphate coprecipitate. For chloramphenicol acetyltransferase (CAT) assays, 3 μ g of the 17 m5-TATA-CAT reporter plasmid was cotransfected with 2 μ g of a β -galactosidase reporter as an internal control, along with the indicated concentrations of the G4-RXR γ expression vectors. After correction for transfection efficiency using β -galactosidase assays, CAT assays were performed by standard protocols, and the percentage of acetylated chloramphenicol was determined by quantitative phosphorimager analysis on a Fujix BAS 2000 apparatus.

Antibody Preparation—Monoclonal antibodies (mAbs) against hTAF_{II}18 (16TA), hTAF_{II}20 (22TA), hTAF_{II}28 (15TA and 1C9) the B10 epitope, and the G4 DBD (3GV2) were as described previously (29, 34, 35, 39, 40).

RESULTS

Selective Ligand-reversible Interactions between hTAF_{II}28 and the Ligand Binding Domains of the VDR and TR—We have previously reported that although expression of hTAF_{II}28 strongly potentiates activation by several NR activation function-2s, no ligand-dependent interactions with NRs could be observed that would account for its coactivator activity (29). In the course of these experiments we did, however, observe two hTAF_{II}28-NR interactions. These interactions were seen when vectors expressing chimeras comprising the VDR or TR α ligand binding domains (LBDs) (or full-length VDR) fused to the DNA binding domain of the yeast activator GAL4 (GAL4 (1–147),

G4) were cotransfected into COS cells along with vectors expressing native or B10-tagged hTAF_{II}28 (the expression vectors are schematized in Fig. 1).

When coexpressed with the G4 DNA binding domain (G4 (1–147)), B10-hTAF_{II}28 was precipitated only by mAb B10, and G4 (1–147) was precipitated only by the anti-G4 antibody (Fig. 2A, lanes 1–3). However, when coexpressed with B10-hTAF_{II}28, G4-VDR was coimmunoprecipitated by mAb B10 (Fig. 2A, lanes 4 and 5, and B, lanes 1 and 2). Most strikingly, G4-VDR could be coprecipitated with B10-hTAF_{II}28 when the transfection was performed in the absence of ligand, whereas no detectable G4-VDR was coprecipitated in the presence of ligand (Fig. 2B, compare lanes 1 and 2 and 3 and 4). Thus, hTAF_{II}28 interacts in a ligand-reversible manner with the VDR in transfected COS cells.

A series of deletion mutants (34) was used to determine the region of hTAF_{II}28 required for interaction with the VDR. G4-VDR coprecipitated with wild-type hTAF_{II}28 (1–211) and

EXPRESSION VECTORS

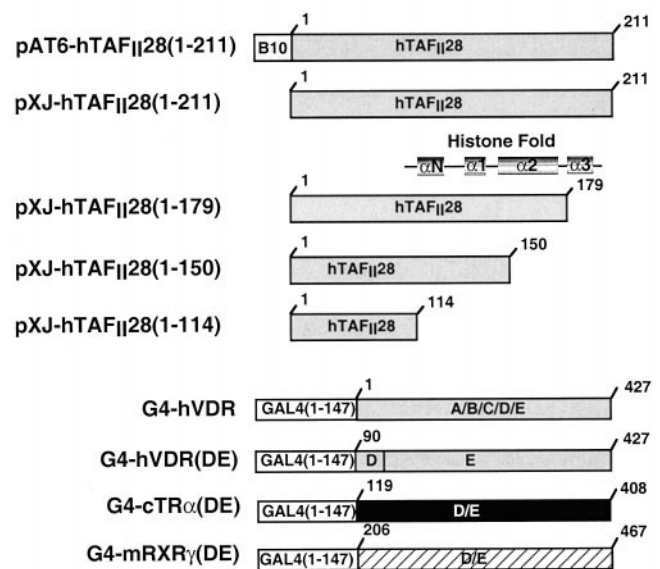


FIG. 1. Structure of the hTAF_{II}s and nuclear expression vectors. The pAT6 vectors contain the epitope for mAb B10 at the N terminus. The amino acid coordinates of the N- and C-terminal boundaries in each construct are shown. The locations of the α N– α 3 helices of the hTAF_{II}28 histone fold are indicated. All the NR expression vectors are cloned in the pXJ440 vector in which the NR sequences are fused to the GAL4 DNA binding domain (G4 (1–147)). *h*, human; *m*, mouse; *c*, chicken.

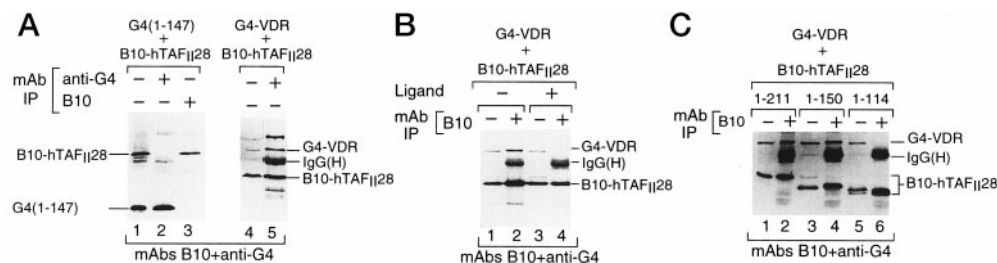


FIG. 2. Ligand-reversible interaction between hTAF_{II}28 and the VDR LBD. The transfected expression vectors are shown above each panel along with the antibodies used in the immunoprecipitations (IP) and in B the presence or absence of ligand. The antibodies used to reveal each blot are indicated at the bottom. Lanes where no antibody was used in the immunoprecipitation (e.g. A, lanes 1 and 4) show aliquots (10 μ l) of the transfected cell extracts used for the immunoprecipitations shown in the adjacent lanes. The locations of the relevant proteins are shown along with the location of the heavy chain of the immunoprecipitating antibody (IgG(H)) revealed upon incubation with the peroxidase-conjugated secondary antibody.

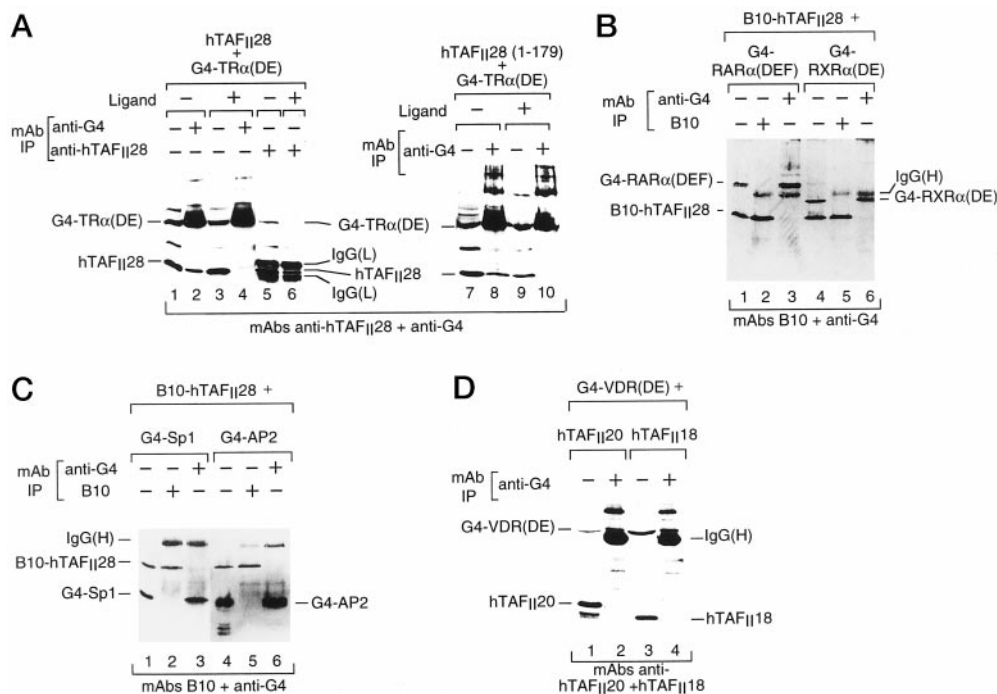


FIG. 3. *A*, ligand-reversible interactions of hTAF_{II}28 with the TR. The layout is as described in Fig. 2. Because the coprecipitated G4-TRα(DEF) is masked by the IgG(H), lanes 5 and 6 have been revealed with peroxidase-conjugated secondary antibody directed against the light chain (IgG(L)). TAF_{II}28 can be seen between the two signals generated in this region of the blot using this conjugated antibody. In subsequent figures either the light chain or the heavy chain of the immunoprecipitating antibody is indicated, depending on which peroxidase-conjugated secondary antibody was used. *B* and *C*, no interactions between hTAF_{II}28 and the retinoic acid receptor RXR Sp1 or AP-2 activation domains. *D*, no interactions between the VDR LBD and hTAF_{II}18 and hTAF_{II}20. The layout is as described for the other figures.

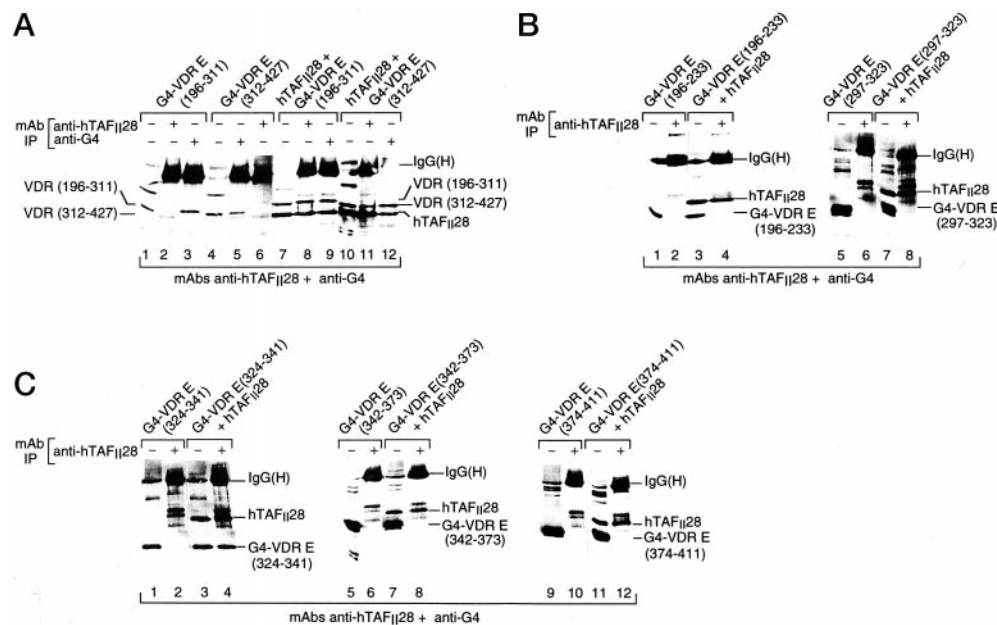


FIG. 4. Mapping of the hTAF_{II}28 interaction domains of the VDR LBD. The deletion constructs used are indicated above each lane. The lanes without cotransfected hTAF_{II}28 (e.g. *A*, lanes 1–6, and *B*, lanes 1 and 2) are control immunoprecipitations showing that the subsequent coprecipitation is hTAF_{II}28-dependent.

with the C-terminal deletion mutant (1–150) (Fig. 2*C*, lanes 1–4). In contrast, G4-VDR was not coprecipitated with hTAF_{II}28 (1–114) (Fig. 2*C*, lanes 5 and 6). Therefore, a region within or overlapping with amino acids 114–150, which encode the N-terminal portion of the hTAF_{II}28 histone fold, is required for interaction with the VDR.

The ability of hTAF_{II}28 to interact with other NRs was investigated. As observed with the VDR, hTAF_{II}28 could be

coprecipitated by the anti-G4 mAbs in the presence of coexpressed G4-TRα(DEF), and conversely G4-TRα(DEF) was coprecipitated by the anti-hTAF_{II}28 antibodies (Fig. 3*A*, lanes 1, 2, and 5). A similar result was observed with the C-terminal deletion mutant hTAF_{II}28 (1–179) (Fig. 3*A*, lanes 7 and 8). Strikingly, as observed with the VDR, this interaction is destabilized in the presence of ligand (Fig. 3*A*, compare lanes 2, 4, 5, 6, 8, and 10). Thus, the presence of ligand dramatically reduces

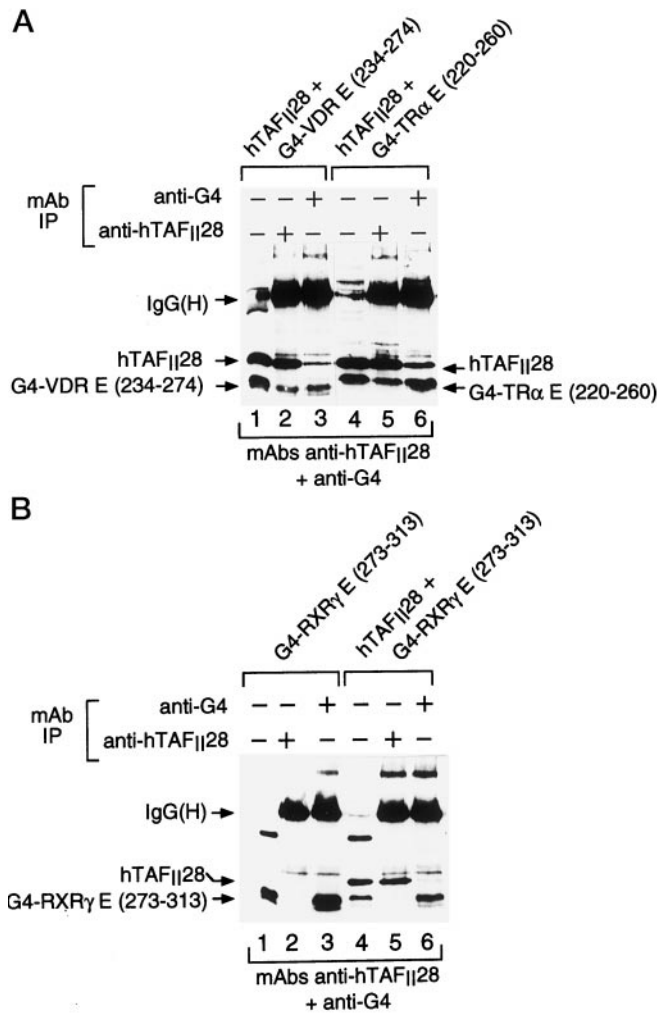


FIG. 5. Selective interaction of hTAF_{II}28 with the H3–H5 regions of the VDR and TR. The layout is as described in the previous figures.

the interactions between hTAF_{II}28 and the TR α and the VDR LBDs in transfected COS cells.

In contrast to the above, no interactions were observed with G4-RXR α (DE) or G4-retinoic acid receptor- α (DEF) in either the absence or presence of ligand (see Fig. 3B, lanes 1–6; Ref. 29; data not shown) or with several activators that do not belong to the NR superfamily (see Fig. 3C, G4-*Sp1* and G4-*AP2*).

As we have previously observed interactions of hTAF_{II}55 with the VDR and TR (33), we also verified the specificity of these interactions with respect to the TAF_{II}s. For this, the VDR was cotransfected with hTAF_{II}20 or hTAF_{II}18. In contrast to hTAF_{II}28 and hTAF_{II}55, no significant interactions were observed between the VDR and hTAF_{II}20 or hTAF_{II}18 (Fig. 3D).

The region of the VDR required for interaction with hTAF_{II}28 was next determined using the previously described series of G4-VDR LBD deletion mutants (33). G4-VDR DE (90–195) was not coprecipitated with B10-hTAF_{II}28 (data not shown). In contrast, both the N-terminal half of the E region present in G4-VDR E (196–311) (Fig. 4A, lanes 1–3 and 7–9) and the C-terminal half of the E region in G4-VDR E (312–427) (Fig. 4A, lanes 4–6 and 10–12) were coprecipitated with hTAF_{II}28. Therefore, hTAF_{II}28 interacts with two distinct sites in the VDR E domain but not with the VDR D domain.

The hTAF_{II}28 interaction regions in the N-, and C-terminal moieties of the VDR LBD were more precisely mapped. After cotransfection, no interaction was observed between hTAF_{II}28

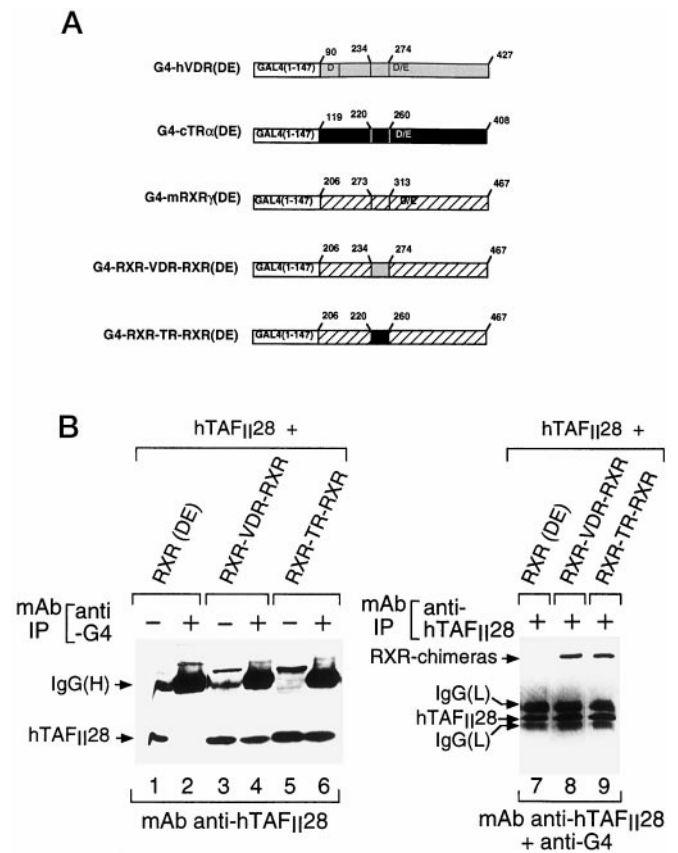


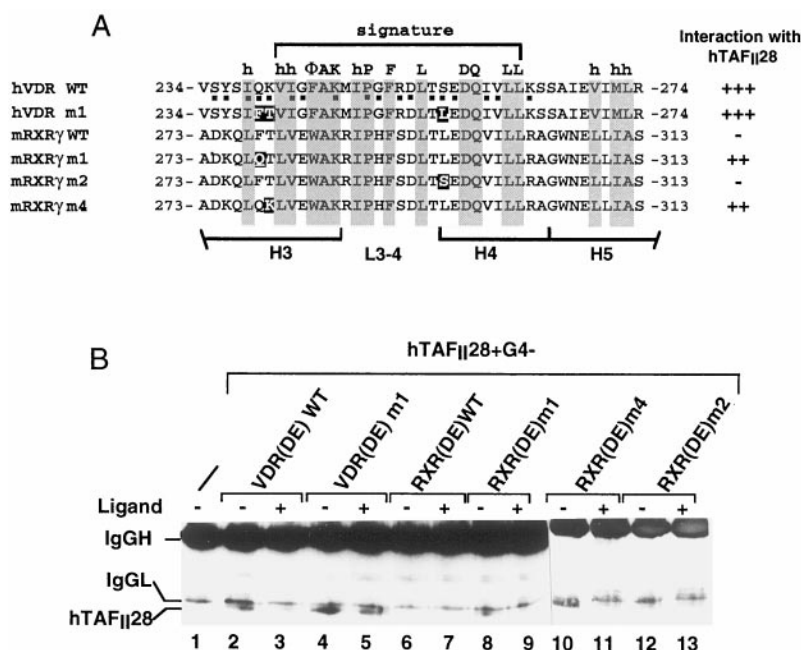
FIG. 6. A, schematic structure of the chimeric RXR γ LBDs. B, immunoprecipitations using the RXR LBD chimeras. The peroxidase-conjugated antibody against IgG(L) is used in lanes 7–9.

and G4-VDR E (196–233), (275–311), (297–323), (342–373), or (374–411) (Fig. 4, B, lanes 1–8, and C, lanes 5–8 and 9–12; data not shown). In contrast, hTAF_{II}28 interacted selectively with G4-VDR E (234–274) (Fig. 5A, lanes 1–3) and with G4-VDR E (324–341) (Fig. 4C, lanes 1–4). Thus, hTAF_{II}28 interacts with the helix H3–H5 NR signature-containing region and with the helix H8 region of the VDR.

Selective Interaction of hTAF_{II}28 with the H3–H5 NR Signature-containing Regions of the VDR and TR α —The H3–H5 region of the NRs contains the NR signature, which is a group of well conserved amino acids involved in intramolecular interactions required for stabilization of the LBD fold (41, 42). As a consequence the H3–H5 region is one the most highly conserved regions within the NR LBDs. Based on the above results, we next investigated hTAF_{II}28 interactions with the related H3–H5 regions of the chicken TR α and the mouse RXR γ . G4 chimeras containing these H3–H5 regions (G4-TR E (220–260) and G4-RXR γ E (273–313)) were coexpressed along with hTAF_{II}28. G4-TR α E (220–260) was specifically precipitated along with hTAF_{II}28 (Fig. 5A, lanes 4–6). In contrast, no coprecipitation of G4-RXR γ E (273–313) was observed (Fig. 5B). The selective interaction of hTAF_{II}28 with the H3–H5 region of the VDR and TR α , but not the RXR γ , therefore mimics the specificity seen using the complete LBDs of these NRs.

The above result was confirmed using chimeric RXR γ (DE)s in which amino acids 273–313 of RXR γ containing the H3–H5 region have been replaced by the equivalent amino acids of the VDR or TR α E domains (G4-RXR-VDR-RXR and G4-RXR-TR-RXR; see Fig. 6A). As seen above, no coprecipitation of hTAF_{II}28 with G4-RXR γ (DE) was observed (Fig. 6B, lanes 1, 2, and 7). In contrast, the RXR-VDR-RXR and RXR-TR-RXR chi-

Fig. 7. *A*, sequences of the H3–H5 regions in each G4-NR(DE) chimera. The amino acids mutated in G4-RXR(DE) m1, m2, and m4 and G4-VDR(DE) m1 are highlighted. *B*, immunoprecipitation of the RXR and VDR mutants with hTAF_{II}28. The presence of ligand in the transfections is shown above each lane. All immunoprecipitations were performed using the anti-G4 antibody. A weak signal for IgG(L) is seen in this series of experiments migrating just above the hTAF_{II}28 (see control lane 1).



meras were both coprecipitated with hTAF_{II}28 (Fig. 6*B*, lanes 3–6, 8, and 9). Thus, the VDR or TR H3–H5 regions can mediate interactions with hTAF_{II}28 in the context of the RXR_γ DE region.

Determinants in the α 3 Helix of the VDR Are Required for Interactions with hTAF_{II}28—The above results show that hTAF_{II}28 interacts with the H3–H5 regions of the VDR and TR α but not the RXR_γ. We have previously shown that hTAF_{II}28-RXR_γ LBD interactions can be induced by exchanging solvent-exposed amino acids of the RXR_γ H3–H5 region by their VDR equivalents. We next determined which if any of these mutations (Fig. 7*A*) could induce hTAF_{II}28-RXR interactions.

hTAF_{II}28 was precipitated with the wild-type VDR in a ligand-reversible manner, whereas no coprecipitation with the wild-type RXR_γ was observed (Fig. 7*B*, lanes 2, 3, 6, and 7). In contrast to wild-type RXR_γ, hTAF_{II}28 was coprecipitated in a ligand-reversible manner with G4-RXR_γ(DE) m1 (F278Q) and m4 (T279K) (Fig. 7*B*, lanes 8–11), whereas no significant coprecipitation with m2 (L295S) was observed (Fig. 7*B*, lanes 12 and 13). Therefore, exchange of single amino acids between the RXR_γ and VDR LBDs in the α 3-helix can induce interactions with hTAF_{II}28.

In a converse experiment we simultaneously introduced the above three RXR_γ amino acids into the equivalent positions of the VDR LBD to generate a triply mutated G4-VDR(DE) m1 (Q239F,K240T,S256L; Fig. 7*A*). This triple mutation did not abolish interaction with hTAF_{II}28, as expected from the fact that hTAF_{II}28 interacts also with the VDR H8 region. Interestingly, however, the interaction with the mutated VDR LBD was no longer ligand-reversible (Fig. 7*B*, lanes 4 and 5 compared with 2 and 3).

We next determined whether the triple mutation had affected the ability of the VDR to activate transcription. To do this, increasing quantities of vectors expressing the wild-type or mutated G4-VDR(DE) were cotransfected along with a G4-responsive CAT reporter (see “Materials and Methods” and Refs. 26, 29). The wild-type VDR LBD strongly activated transcription from this promoter (Fig. 8*A*, lanes 2–4), whereas the mutated VDR was unable to activate transcription (Fig. 8*A*, lanes 5–7). As described previously (29, 33, 43), little or no activation of transcription from this promoter is observed with

the wild-type G4-RXR_γ(DE), whereas the mutant bearing the three VDR amino acids strongly activates transcription (Fig. 8*A*, lanes 8–10 and 11–13, respectively). Equivalent expression of each of the chimeras was detected by immunoblotting (Fig. 8*B*). Consequently, replacing the three amino acids of the VDR with their RXR_γ equivalents leads to a loss of function, whereas in the converse experiment there is a gain of function. These three amino acids therefore play a critical role in transactivation.

DISCUSSION

Ligand-reversible hTAF_{II}28-NR Interactions—We describe here novel interactions between the LBDs of the VDR and the TR α and the hTAF_{II}28 component of transcription factor TFIID. After coexpression in COS cells, hTAF_{II}28 could be specifically coprecipitated with the LBDs of the VDR and TR α in the absence of the appropriate ligands, whereas coprecipitation is dramatically reduced in the presence of ligand. The selectivity of the interactions is shown by the observation that under the same conditions no interactions between hTAF_{II}28 and other NRs were observed, nor did hTAF_{II}20 or hTAF_{II}18 interact with the VDR or TR LBDs.

Interaction with the VDR requires the evolutionary conserved C-terminal domain of hTAF_{II}28, which contains the histone fold motif (31). Interaction is seen with a deletion mutant (1–150) in which the α 2- and α 3-helices of the histone fold are deleted, but not with (1–114), in which the α N- and α 1-helices are deleted. Therefore, interaction with the NRs does not require the integrity of the histone fold domain but does require determinants in the α N- α 1 region. In support of this, interaction with the VDR is abolished by mutation of exposed residues in the α 1-helix, further suggesting that this helix plays an important role in the interaction.²

hTAF_{II}28 interacts with two independent sites in the VDR LBD. We have characterized in detail the interaction of hTAF_{II}28 with one of these sites located between amino acids 234 and 274 spanning α -helices H3–H5 and containing the NR signature. The equivalent region of the chicken TR α also interacts with hTAF_{II}28, whereas no interaction is seen with the

² G. Mengus, Y. G. Gangloff, L. Carré, A.-C. Lavigne, and I. Davidson, unpublished observations.

A

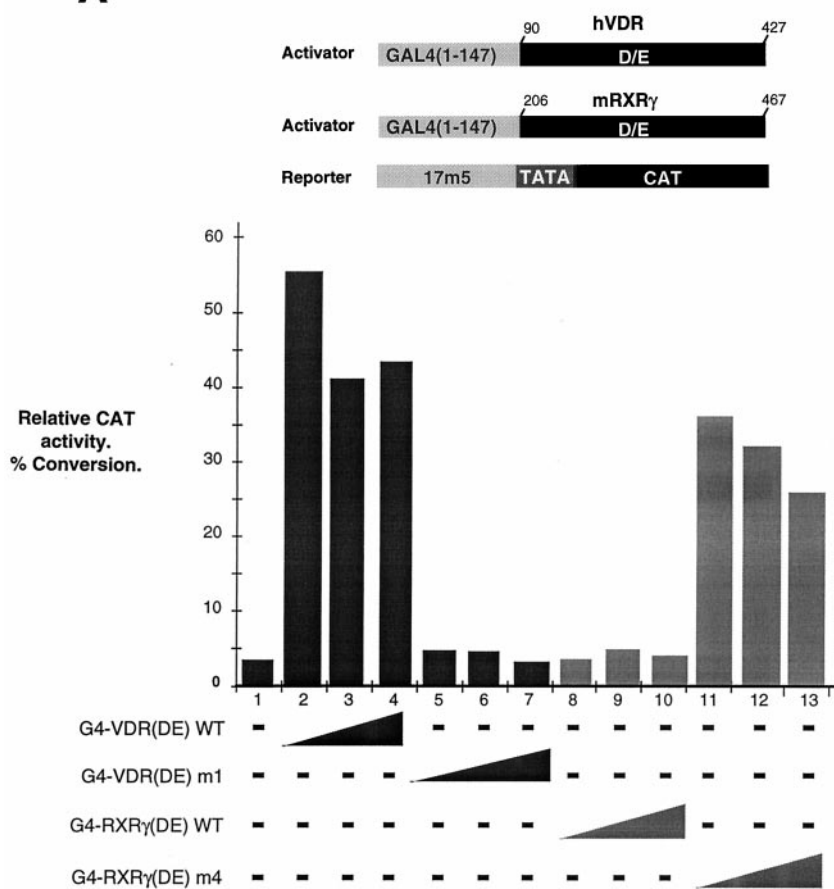
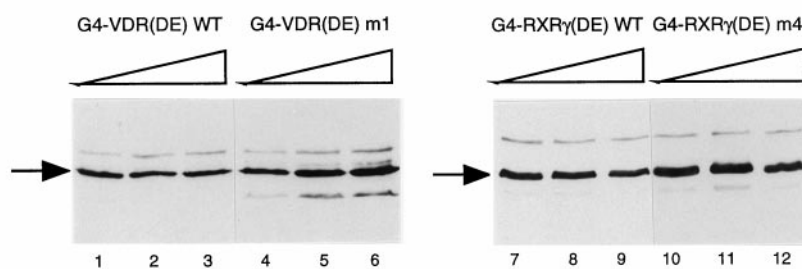


FIG. 8. A, graphic representation of CAT assays. The structures of the activator and reporter constructs used are shown schematically at the top. The transfected expression vectors used are shown below each lane. Transfections contained 0, 0.25, or 0.5 μ g of the expression vectors as indicated. All transfections were performed in the presence of ligand. B, expression of the wild-type and mutated RXR and VDR chimeras. Cells were transfected with 0.1, 0.25, or 0.5 μ g of the expression vectors indicated above each lane, and the expressed proteins were detected using the anti-G4 antibodies. The arrows indicate the expressed G4-NR chimeras.

B



equivalent region of the RXRs. Two amino acids in helix H3 are critically involved in the ability of hTAF_{II}28 to discriminate between the VDR and RXR γ LBDs. In the context of the full RXR γ DE region, replacement of Phe²⁷⁸ or Thr²⁷⁹ with Gln or Lys, respectively, of the VDR induces a ligand-reversible interaction with hTAF_{II}28. No significant interaction, however, was seen with mutant L295S located in helix H4.

We have previously shown that position Leu²⁹⁵ is an important determinant for interaction with hTAF_{II}55, which also interacts with the H3–H5 region of the VDR and TR. The differential interaction of hTAF_{II}55 and hTAF_{II}28 with the L295S mutation indicates that, although both TAF_{II}s interact with the H3–H5 region, the determinants for their respective interactions are not identical. TAF_{II}28 may interact only with the H3 helix, whereas hTAF_{II}55 requires determinants in both the H3 and H4 helices.

As discussed previously (33), the hTAF_{II}28 and hTAF_{II}55 interaction sites are close to, but not identical to, with those required for interaction with the LXXLL motif in several transcriptional intermediary factors (44–46). The close proximity of these two interaction sites may nevertheless explain the ligand reversibility observed with the hTAF_{II}28 interaction, because there may be steric hindrance between hTAF_{II}28 and the TIF(s) whose association with the LBD is ligand-induced (see below). It is not clear, however, how the ligand-induced conformational change in the LBD, which brings helix H12 in proximity to H3 and H4 to create the hydrophobic TIF interaction surface, would affect the interaction of hTAF_{II}28 with its second interaction site in helix H8.

Possible Roles of the VDR/TR-hTAF_{II}28 Interaction—Our previous results indicated that there is a correlation between

transcriptional activation potential and interaction with hTAF_{II}55. The wild-type RXR LBD, which has negligible transactivation potential on a minimal promoter, does not interact with hTAF_{II}55. In contrast, the single amino acid changes in the RXR γ LBD induce weak interactions with hTAF_{II}55 and an increase in transactivation, whereas the F278Q,L295S double mutation induces a strong interaction with hTAF_{II}55, and this derivative activates transcription to a level equivalent to that seen with the VDR itself (33).

On the other hand, the NR interaction with hTAF_{II}28 does not correlate with activation, since it is ligand-reversible. We therefore do not suggest any obvious role for the NR-hTAF_{II}28 interaction in the transcriptional activation described here. Ligand-reversible interactions with NRs are not observed with transcriptional coactivators but are characteristic of those seen with the corepressors N-CoR and SMRT (47, 48). At present we have no direct evidence that NR-hTAF_{II}28 interactions are involved in the transcriptional repression seen with the unliganded TR or VDR, and the RXR mutants that interact with hTAF_{II}28 do not gain repressor properties, at least not on the promoters that we have tested.

Transcriptional activation is thought to involve both the recruitment of histone acetylase complexes and interactions with the basal transcription apparatus. It is therefore tempting to speculate that, in addition to recruitment of histone deacetylase complexes, interactions such as those described here between the VDR and TR and the basal transcription apparatus may contribute to transcriptional repression. Indeed, previous *in vitro* experiments have suggested that the unliganded TR may target TBP itself and block preinitiation complex formation leading to transcriptional repression (49, 50). It has also been shown that TBP/TFIID may be a target of other repressors such as the homeodomain protein even-skipped (51, 52). Furthermore, ligand-reversible interactions between the TR and TFIIB have also been suggested to contribute to transcriptional silencing (53).

Our results identify amino acids in helices H3 and H4 critical for transcriptional activation by the VDR. These amino acids, which all lie on the surface of the receptor and are not involved in ligand binding (54), cannot be replaced by their RXR homologues, whereas their incorporation into the RXR yields a potent transcriptional activator. Because the interaction of hTAF_{II}28 with the VDR m1 mutant, which does not activate transcription, is ligand-independent rather than ligand-reversible, this would suggest that the introduction of the RXR amino acids has abrogated the ability of the VDR to interact with coactivators (one of which may be TAF_{II}55), which normally displace hTAF_{II}28 in the presence of ligand. Indeed, a similar constitutive interaction is seen when the VDR activation function-2-AD core in helix H12 is deleted.³ In other receptors deletion of the activation function-2-AD core does not impair ligand binding but does abolish interaction with TIFs. TAF_{II}28 interacts with the mutated RXR LBDs in a ligand-reversible manner. Thus, in this context, which is the converse of that observed with VDR m1, it is likely that the introduction of the VDR amino acids allows interactions not only with hTAF_{II}28 but also with coactivators that displace hTAF_{II}28 in the presence of ligand. Together, these results show that the H3–H5 region contains receptor-specific determinants for transactivation.

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The Human Transcription Factor IID Subunit Human TATA-binding Protein-associated Factor 28 Interacts in a Ligand-reversible Manner with the Vitamin D₃ and Thyroid Hormone Receptors

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