Molecular Cloning and Characterization of CAPER, a Novel Coactivator of Activating Protein-1 and Estrogen Receptors*

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Transcriptional coactivators either bridge transcription factors and the components of the basal transcription apparatus and/or remodel the chromatin structures. We isolated a novel nuclear protein based on its interaction with the recently described general coactivator activating signal cointegrator-2 (ASC-2). This protein CAPER (for coactivator of activating protein-1 (AP-1) and estrogen receptors (ERs)) selectively bound, among the many transcription factors we tested, the AP-1 component c-Jun and the estradiol-bound ligand binding domains of ERα and ERβ. Interestingly, CAPER exhibited a cryptic autonomous transactivation function that becomes activated only in the presence of estradiol-bound ER. In cotransfections, CAPER stimulated transactivation by ERα, ERβ, and AP-1. Thus, CAPER may represent a more selective transcriptional coactivator molecule that plays a pivotal role for the function of AP-1 and ERs in vivo in conjunction with the general coactivator ASC-2.

The activation protein-1 (AP-1) transcription factors are immediate early response genes involved in a diverse set of transcriptional regulatory processes (for a review see Ref. 1). The AP-1 complex consists of a heterodimer of a Fos family member and a Jun family member. This complex binds the consensus DNA sequence (TGAGTCA) (termed AP-1 sites) found in a variety of promoters. The Fos family contains four proteins (c-Fos, Fos-B, Fra-1, and Fra-2), whereas the Jun family is composed of three proteins (c-Jun, Jun-B, and Jun-D). Fos and Jun are members of the basic region-leucine zipper (bZIP) family of sequence-specific dimeric DNA-binding proteins (1). The C-terminal half of the bZIP domain is amphipathic, containing a heptad repeat of leucines that is critical for the dimerization of bZIP proteins, whereas the N-terminal half of the long bipartite helix is the basic region that is responsible for the sequence-specific DNA binding.

The nuclear receptor superfamily is a group of ligand-dependent transcriptional regulatory proteins that function by binding to specific DNA sequences named hormone-response elements in the promoters of target genes (reviewed in Ref. 2). The superfamily includes receptors for a variety of small hydrophobic ligands such as steroids, triiodothyronine, and retinoids as well as a large number of related proteins that do not have known ligands, referred to as orphan nuclear receptors. The C terminus of the ligand binding domain of these proteins harbors an essential ligand-dependent transactivation function, activation function 2 (AF2), whereas the N terminus of many nuclear receptors often includes AF1.

Genetic studies implicated that transcription coregulators (or cofactors) with no specific DNA binding activity are essential components of transcriptional regulation, which ultimately led us to identify a series of coregulatory proteins (for reviews, see Refs. 3 and 4). They appear to function by either remodeling chromatin structures and/or acting as adapter molecules between transcription factors and the components of the basal transcriptional apparatus. These proteins include the steroid receptor coactivator-1 (SRC-1) family, CREB-binding protein (CBP)/p300, activating signal cointegrator-2 (ASC-2), and many others (3–4). SRC-1 and its homologue ACTR, along with CBP and p300, were recently shown to contain histone acetyltransferase activities and associate with yet another histone acetyltransferase protein P/CAP (3–4). Interestingly, unliganded retinoic acid receptor (RAR) and thyroid hormone receptor (TR) bind to their target genes and repress transcription. “The silencing mediators of RAR and TR” and “nuclear receptor corepressors” are known to mediate this repression (3–4). Interestingly, the silencing mediators of RAR and TR and nuclear receptor corepressors appear to interact with the estrogen receptor (ER) and the progesterone receptor only in the presence of their respective antagonists (5–8). These proteins harbor transferable repression domains that associate with various histone deacetylases. These results are consistent with the notion that acetylation of histones destabilizes nucleosomes and relieves transcriptional repression by allowing transcription factors access to recognition elements, whereas deacetylation of the histones stabilizes the repressed state (3–4). It is important to note that many of these coregulatory proteins have shown a very broad spectrum of action with many different nuclear receptors and transcription factors, including AP-1 (3–4). More recently, however, a series of more target-selective coactivators have been isolated. These include peroxisome proliferator-activated receptor γ (PPARγ) coactivator-1 (PGC-1) (9), the human homologue of the yeast DNA repair and TFIIH general coactivator; CAPER, coactivator of AP-1 and ERs; GST, glutathione S-transferase; RRM, RNA recognition motif; RNP, ribonucleoprotein; hnRNP, heterogeneous nuclear RNP; CoAA, coactivator activator; E2, estradiol.
regulator MMS19 (10) and p68 RNA helicase (11), both of which were shown to be AP1-specific coactivators of ERα, and prothrombin α, which selectively enhances ER activity by interfering with “the repressor of ER” activity (12, 13). In addition, ARA160 was recently reported as the first androgen receptor N-terminal-associated coactivator in human prostate cancer cells (14), and a neuronal-specific corepressor “neuronal interacting factor X 1” was shown to repress transactivation by a subset of nuclear receptors (15). Interestingly, Smad3 specifically represses transcriptional activation mediated by androgen receptor in prostate cancer cells (16) while acting as a coactivator specific for ligand-induced transactivation of vitamin D receptor by forming a complex with a member of the SRC-1 family in the nucleus (17). ARA70 has also been shown to stimulate selectively PPARγ and androgen receptor (18). Finally, JAB1, interacting with c-Jun and JunD but not with JunB or v-Jun, is known to selectively potentiate transactivation by c-Jun or JunD (19).

In this report, we describe the molecular cloning and characterization of a nuclear protein, which was originally isolated as a novel autoantigen from a patient with liver cirrhosis who progressed to hepatocarcinoma (20). Our results show that this protein functions as a specific transcriptional coactivator of AP-1, ERα and ERβ.

**EXPERIMENTAL PROCEDURES**

*Plasmodium*—HCC1.4 and HCC1.3 (20) were kind gifts from Dr. Eng M. Tan at University of California, San Diego. Polymerase chain reaction fragments encoding CAPER (for coactivator of AP-1 and ERs), CAPER-N, -MI, -MI-C, -ΔC1, -ΔC2, -ΔN1, -ΔN2, -MI-1, -MI-2, -ASC2-4Δ1, -ASC2-4Δ2, and -ASC2-4Δ3 were constructed into EcoRI and XhoI restriction sites of the LexA fusion vector pEG202PL. The B42 fusion vector pG4-5, the mammalian two-hybrid vector pCMXGal4 and pCMXVP16, the mammalian expression vector p425-Gal1 (23). The yeast ASC-2-interacting proteins, and the screening was executed essentially as described previously (25). The yeast expression vector p425-Gal1 (23) carried restriction sites of the LexA fusion vector pEG202PL, the B42 fusion vector pG4-5, the mammalian two-hybrid vector pCMXGal4 and pCMXVP16, the mammalian expression/in vitro translation vector pDNA3, and the glutathione S-transferase (GST) fusion vector pGEX4T-1. Similarly, PCR fragments encoding ERα-ABC, -ABCD, -EF, -D, and -DE were cloned into EcoRI and XhoI restriction sites of pG4-5. Gal4 fusions to ERα and ERβ, LexA fusions to ERαΔAP2, ASC2-4A, ASC2-4A, ASC2-4B, and ASC2-4LR, B42 fusions to ERα, ERγ, c-Jun, c-Fos, JunD1, JunD2, JunD3, FosL1, FosL2, and Fos3, GST fusions to ERα and ERβ, mammalian expression/in vitro translation vector for ERα, ASC2-2, ASC2-4, c-Jun, and c-Fos, the reporter constructs ERE-Luc, AP1-Luc, Gal4-Luc, and LexA-β-gal, and the translation indicator construct pRSV-β-gal were as described (21, 22). Finally, PCR fragment encoding the full-length ERα was subcloned into the HindIII and XhoI restriction sites of the yeast expression vector p425-Gal1 (23).

**Yeast Two-hybrid Screenings and Tests**—The LexA-ASC2-4 (24) was used as a bait to screen a mouse liver cDNA library in pG4-5 to identify ASC-2-interacting proteins, and the screening was executed essentially as described previously (25). The yeast β-galactosidase assay was done as described (25). For each experiment, at least three independently derived colonies expressing chimeric proteins were tested.

**GST Pull-down Assays**—The GST fusions or GST alone was expressed in *Escherichia coli*, bound to glutathione-Sepharose 4B beads (Amersham Biosciences), and incubated with labeled proteins expressed by in vitro translation by using the TNT-coupled transcription-translation system, with conditions as described by the manufacturer (Promega, Madison, WI). Specifically bound proteins were eluted from beads with 40 mM reduced glutathione in 50 mM Tris (pH 8.0) and analyzed by SDS-PAGE and autoradiography as described (26).

**Cell Culture and Transfection**—CV-1 cells were grown in 24-well plates with medium supplemented with 10% charcoal-stripped serum. After 24 h of incubation, cells were transfected with 100 ng of β-galactosidase expression vector pRSV-β-gal and 100 ng of an indicated reporter gene, along with c-Fos, ASC-2, ERα, CAPER, CAPER-MI-2, and Gal4 fusions to ERα and ERβ as well as various CAPER fragments. Total amounts of expression vectors were kept constant by adding additional amount of the CDMS expression vector to transfections. Twelve hours later, cells were washed and refed with Dulbecco's modified Eagle's medium containing 10% charcoal-stripped fetal bovine serum. After 12 h, cells were left unstimulated or stimulated with 0.1 μM ligand. Cells were harvested 24 h later, and luciferase activity was assayed as described (26), and the results were normalized to the β-galactosidase expression.

Molecular Cloning of ASC-2 Interacting Protein, CAPER—To search for interacting proteins with the recently described transcriptional coactivator ASC-2 (24, 27, 28), we screened a yeast two-hybrid-based mouse liver cDNA library using ASC2-4 (i.e. the ASC-2 residues 1172–1729) (24) as a bait. A few independent cDNAs encoded a protein similar to human proteins HCC1.3 and HCC1.4 (20). These proteins were described previously as novel nuclear autoantigens identified with antibodies from human hepatocarcinoma. These proteins are identical except the presence of additional six amino acids in HCC1.4. The isolated mouse clones retained the internal six amino acids, like HCC1.4, and had only two amino acid changes from the human proteins (results not shown). HCC1.3 and HCC1.4 were indistinguishable in their binding and transcriptional coactivation properties (results not shown), and thus we focused only on HCC1.3 for the rest of the studies presented here. Based on their functional properties (this paper) and ubiquitous expression pattern (20), we renamed these proteins CAPER (for coactivator of AP-1 and ERs). Despite the lack of direct sequence homology, it is interesting to note that CAPER and PGC-1, the recently defined transcription coactivator of PPARγ (9), has a few conserved features in common (Fig. 1A). These include a cryptic autonomous transactivation domain (Fig. 5B), a region rich in Ser-Arg pairs (so called SR domains) (reviewed in Ref. 29), and an RNA recognition motif (RRM) (30) with homology to corresponding domains found in hnRNP proteins and SR factors (Fig. 1B). The RRM, consisting of two highly conserved peptide motifs, ribonucleoprotein (RNP)-1 and RNP-2, confers both RNA and single-stranded DNA binding activity (30). The hnRNP family of proteins includes members that are involved in all aspects of RNA metabolism (reviewed in Ref. 31), and some of them have been shown to have transcriptional activity through association with single-stranded DNA enhancer sequences in the promoter region of the genes they regulate (32–34). The association of SR domains and RMRs is typical of the classical SR splicing factors that play a key role in both constitutive splicing and in the regulation of alternative splicing in vivo (29). Interestingly, PGC-1 was recently shown to mediate mRNA splicing (35), suggesting the presence of a novel class of proteins that may coordinate the coupled events of transcription and mRNA processing in vivo (reviewed in Ref. 36). Thus, it will be interesting to examine whether CAPER and the recently defined “PGC-1-related coactivator,” a serum-inducible coactivator of nuclear respiratory factor 1-dependent transcription in mammalian cells (37), are also involved with mRNA processing. When LexA fusion to ASC2-4 was coexpressed in yeast with the amphotropic acidic transactivation domain B42 (25) fused to various CAPER constructs (Fig. 2A), only the full-length CAPER and CAPER-C enhanced the LexA-ASC2-4-directed transactivation (Fig. 2B). These results suggest that the interaction interface with ASC-2 may involve the C-terminal region of CAPER (i.e. CAPER-C in Fig. 2A). Consistent with these yeast results, GST fusions to the full-length CAPER and CAPER-C but not GST alone interacted with in vitro translated ASC2-4 (Fig. 2C). The CAPER-interacting domain was further mapped to the N-terminal region of ASC2-4 (i.e. ASC2-433 consisting of the ASC-2 residues 1172–1273) in yeast, as shown in Fig. 2D.

**Specific Binding of AP-1 and ERs by CAPER**—To explore the possibility of CAPER as a transcriptional coregulator, we examined bindings of CAPER with a series of different transcription factors in yeast. These included p53, the NFκB component p50, the activating protein-1 components c-Jun and c-Fos, serum response factor, retinoid X receptor α, RARα, TRα and -β, PPARα, liver X receptor α and β, farnesoid X receptor, glucocor-
ticoid receptor, and ERα and -β. Among these factors, only c-Jun, ERα, and ERβ appeared to interact significantly with CAPER (see below). Transactivation mediated by LexA fusion to CAPER was stimulated by B42 fusions to the full-length c-Jun and JunΔ3 but not JunΔ1, JunΔ2, c-Fos, FosΔ1, FosΔ2, and FosΔ3 in yeast (Fig. 3, A and B). In addition, B42-JunΔ3 stimulated transactivation by LexA fusion to CAPER-MII fragment but not -N, -MI, and -C fragments (Fig. 3C). It is noteworthy that the transcriptionally inert full-length CAPER contains a cryptic autonomous transactivation function ascribed to the MII region (i.e. compare the basal activities of LexA fusions to the full-length CAPER and CAPER-MII in Fig. 3C). Corroborating these yeast results, GST fusion to CAPER-MII interacted with in vitro translated c-Jun but not c-Fos (Fig. 3D). Thus, the MII subregion of CAPER appears to interact specifically with the C-terminal region of c-Jun (i.e. JunΔ3). Transactivation directed by LexA fusions to the full-length CAPER and CAPE-MII but not CAPER-N, -MI, and -C was stimulated by B42 fusion to ERα and ERβ in an E2-dependent manner (Fig. 4A). Interestingly, these E2-dependent interactions were retained with a mutant ERα that lacks the AF2 core region (i.e. ERαΔAF2). This AF2-independent interaction of CAPER with ERα is consistent with the lack of LXXLL motif in CAPER, which was recently shown to be a binding interface for many AF2-dependent coactivators (38, 39). In contrast to the wild type ERα, however, ERαΔAF2 also bound CAPER in the presence of partial antagonist tamoxifen. The yeast results further suggested that the interaction interfaces involve the EF domains of ERα (Fig. 4B) and the MI-2 fragment of CAPER (i.e. the CAPER residues 356–400) (Fig. 4C). This prediction was also confirmed in the in vitro pull-down assays, in which radiolabeled CAPER or CAPER-MII specifically interacted with GST fusion to ERα only in the presence of E2 (Fig. 4D). Similarly, CAPER-MII also interacted with GST fusion to the full-length ERβ only in the presence of E2 but not tamoxifen.

Overall, these results clearly indicated that CAPER binds the AP-1 component c-Jun and both ERα and β.

Inducible Autonomous Transactivation Function of CAPER—Many transcription coactivators are known to exhibit transcriptional activities when forced to bind DNA (2–4). Interestingly, Gal4 fusions to the full-length CAPER or CAPERΔC1, -AC2, -N, -AN1, -AN2, and -C fragments directed transcriptional activities lower than that mediated by Gal4 alone in CV-1 cells (Fig. 5A). However, a cryptic activation function was unraveled with the MII fragment (i.e. the CAPER residues 291–355). These results also suggested the presence of independent transcriptional repression function, both at the N- and C-terminal regions of CAPER. However, it is not currently clear whether these regions have intrinsic repressive activities or simply mask the activation function within the MII-1 region. Surprisingly, the transcriptionally inert full-length CAPER fused to the DNA-binding protein LexA, upon coexpression of ERα in the presence of E2, became fully active in yeast (Fig. 5B). Consistent with the direct involvement of the activation function within the MII region in this E2/ERα-dependent activation of CAPER, transactivation mediated by LexA-CAPER-MII was further stimulated by E2/ERα. Similar results were also obtained with Gal4 fusions to CAPER and CAPER-MII in CV-1 cells (results not shown). These results are analogous to the recent report (40), in which transcriptionally inactive PGC-1 was stimulated upon coexpression of activated PPARγ. They further demonstrated that the docking of PGC-1 to PPARγ stimulates an apparent conformational change in PGC-1 that permits binding of SRC-1 and CBP/p300, resulting in a large increase in transcriptional activity (40). Because CAPER was isolated based on its interaction with ASC-2, which also serves as an excellent coactivator of ERα (27), activated-ERα may also cause a conformational change with CAPER, resulting in better bindings with ASC-2 or other coactivator molecules. This pos-
sibility is currently under investigation.

**CAPER as a Transcriptional Coactivator of AP-1 and ERs**

The functional significance of the interactions of CAPER with c-Jun and ERs was tested in cotransfections. CAPER potentiated transactivation by AP-1 when tested with AP1-luciferase reporter construct (Fig. 6A). Interestingly, ASC-2 showed a relatively weak synergy with CAPER only in the presence of 200 ng of ASC-2 expression vector (compare the transactivation levels of 50 ng of CAPER, 200 ng of ASC-2, and both in Fig. 6A). Similar results were also obtained with Gal4 fusions to c-Jun and c-Fos (results not shown). With the ERE-luciferase and Gal4-luciferase reporter constructs, coexpression of CAPER in CV-1 cells stimulated the E2-dependent level of transactivation without significantly affecting the basal activities (Fig. 6B). In contrast, CAPER had no coactivating function with other transcription factors that did not show significant interactions with CAPER. These included TR, RAR, p53, and serum response factor (results not shown). Interestingly, CAPER-MII-2, which contains the ERα-interacting region (Fig. 4C), exhibited a dominant negative phenotype with the ERα transactivation (Fig. 6C), suggesting the possible importance of the direct ERα-CAPER interactions in E2-mediated transactivation. Overall, these results strongly suggest that CAPER is a bona fide transcriptional coactivator molecule of AP-1 and ERs.

**DISCUSSION**

In this report, we have shown that CAPER is a transcriptional coactivator molecule whose function, in contrast to multifunctional integrator molecules like CBP/p300, SRC-1, and ASC-2 (3, 4), is rather selective to AP-1, ERα, and ERβ. As summarized in Fig. 6D, CAPER contains distinct binding sites for c-Jun (Fig. 3) and ERs (Fig. 4) and significantly enhances their transactivation potential in cotransfections (Fig. 6D). In particular, a fragment of CAPER that contains a binding site for ERα (i.e., CAPER-MII-2) acted as a potent dominant negative mutant for E2-dependent transactivation by ERα (Fig. 6C), suggesting the possible importance of the direct ERα-CAPER interactions in E2-mediated transactivation. Overall, these results strongly suggest that CAPER is a bona fide transcriptional coactivator molecule of AP-1 and ERs.
transcriptionally inactive, unless coexpressed with E2-bound PER-MII-1) (Fig. 5A). Strikingly, the full-length CAPER was localized to the CAPER residues 291–311 (Fig. 5A), (Fig. 5B). Similar results were recently reported with PGC-1 (9), in which luciferase expressions from triplicate samples were calculated relative to the result with Gal4 alone, with the error bars as indicated. B, expression vectors for LexA/CAPER, LexA/CAPER-MII, and ERα were transformed into a yeast strain containing an appropriate lacZ reporter gene, as described (24). Open, hatched, and solid boxes indicate the absence of ERα, the presence of ERα, and ERα plus 100 nM of E2, respectively. Normalized lacZ expressions from triplicate samples were calculated relative to the result with LexA alone. The data are representative of at least two similar experiments, and the error bars are as indicated.

Fig. 4. CAPER as ER interactant. A and C, the indicated B42 and LexA plasmids were transformed into a yeast strain containing an appropriate lacZ reporter gene, as described (24). 100 nM E2 or tamoxifen was used where indicated. F indicates the full-length CAPER, whereas N, MI, MII, and C are as shown in Fig. 2A. All the ER fragments used were fusions to B42 (C). Normalized lacZ expressions from triplicate samples were calculated relative to the result with B42 alone. The data are representative of at least two similar experiments. B, the full-length ERα as well as five ERα fragments are as indicated, in which A–F denotes functional modules of nuclear receptors (2). C and E represent the DNA- and ligand-binding domains, respectively. D, the full-length CAPER and CAPER-MII were labeled with [35S]methionine by in vitro translation and incubated with glutathione beads containing GST alone and GST-ERα and ERβ, as indicated. Beads were washed, and specifically bound material was eluted with reduced glutathione and resolved by SDS-polyacrylamide gel electrophoresis. 100 nM ligand was used where indicated. Approximately 20% of the total reaction mixture were loaded as input.

Fig. 5. The autonomous transactivation domain of CAPER. A, CV-1 cells were transfected with lacZ expression vector (100 ng), the increasing amount of expression vectors for Gal4 alone or Gal4 fusions to the full-length CAPER and various CAPER fragments, and a reporter gene Gal4-Luc (100 ng), as indicated. Open and solid boxes indicate 50 and 100 ng of each Gal4 construct, respectively. Normalized luciferase expressions from triplicate samples were calculated relative to the full-length CAPER expressions (n-fold) over the value obtained with Gal4 alone, with the error bars as indicated. B, expression vectors for LexA/CAPER, LexA/CAPER-MII, and ERα were transformed into a yeast strain containing an appropriate lacZ reporter gene, as described (24). Open, hatched, and solid boxes indicate the absence of ERα, the presence of ERα, and ERα plus 100 nM of E2, respectively. Normalized lacZ expressions from triplicate samples were calculated relative to the result with LexA alone. The data are representative of at least two similar experiments, and the error bars are as indicated.

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tion function of CAPER and ASC-2, although some synergy was observed with the AP-1 transactivation in the presence of a higher dose of ASC-2 expression vector (Fig. 6A). Further work is warranted to fully resolve this issue.

CAPER contains an autonomous transactivation domain that was localized to the CAPER residues 291–355 (i.e. CAPER-MII-1) (Fig. 5A). Strikingly, the full-length CAPER was transcriptionally inactive, unless coexpressed with E2-bound ERα (Fig. 5A). The CAPER residues 291–400 (i.e. CAPER-MII) that also contains the neighboring ERα-binding site behaved similarly. These results strongly suggest that CAPER undergoes a conformational change upon binding activated ERs. Similar results were recently reported with PGC-1 (9), in which the docking of PGC-1 to PPARγ stimulates an apparent conformational change in PGC-1 that permits binding of SRC-1 and CBP/p900, resulting in a large increase in transcriptional activity (40). The similarity between CAPER and PGC-1 also includes the presence of SR domains and RRMs (Fig. 1). The association of SR domains and RRMs is typical of the classical SR splicing factors that play a key role in both constitutive splicing and in the regulation of alternative splicing in vivo (29). Indeed, PGC-1 was shown recently to mediate mRNA splicing (35). PGC-1-related coactivator, a serum-inducible coactivator of nuclear respiratory factor 1-dependent transcription in mammalian cells, was also isolated as an RRM-containing coactivator molecule (37). While this manuscript was in preparation, Iwasaki et al. (41) reported another RRM-containing coactivator activator (CoAA) as a novel ASC-2-interacting protein. Interestingly, CoAA, in contrast to CAPER, showed rather broad target specificity, stimulating transactivation mediated by multiple hormone-response elements (41). These results suggest an interesting possibility that ASC-2 may act as a platform to recruit various RRM-containing coactivator molecules such as CoAA and CAPER. Notably, p68 RNA helicase was recently isolated as a transcriptional coactivator specific for the AP1 of ERα (11), whereas RNA helicase A was found to mediate association of CREB-binding protein with RNA polymerase II (42). In addition, a novel transcriptional coactivator p52 interacted not only with transcriptional activators and general transcription factors to enhance activated transcription but also with the essential splicing factor ASF/SF2 both in vitro and in vivo to modulate ASF/SF2-mediated pre-mRNA splicing (43). It is important to note that post-transcriptional mRNA processings such as 5′-capping, splicing, and poly-
adenylation can take place cotranscriptionally in vivo (36). Thus, these proteins and CAPER may also act as adapter molecules to coordinate various pre-mRNA processing and transcriptional initiation of class II genes, in addition to functioning as transcriptional coactivators. Consistent with this idea, CAPER was originally found colocalized with splicing factors in nuclear speckles (20) like PGC-1 (35).

In conclusion, we have shown that CAPER is a novel transcriptional coactivator specific to ERs and AP-1. Studies of CAPER, along with PGC-1 and other related molecules, may provide an important insight into the coupling mechanisms of different mRNA processing in vivo.

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Molecular Cloning and Characterization of CAPER, a Novel Coactivator of Activating Protein-1 and Estrogen Receptors
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