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# Compilation of vertebrate-encoded transcription factors

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## INTRODUCTION

Since the discovery of DNA elements controlling the initiation of transcription by RNA polymerase II some ten years ago, it has become evident that the frequency of transcription initiation depends on proteins interacting with specific DNA elements of gene regulatory regions. Especially during the last three years an enormous number of such proteins, called transcription factors, have been isolated and characterized.

In the following table, we present a listing of transcription factors. It may serve as a dictionary of transcription factors, and should help to identify putative regulatory DNA elements of not yet analysed promoter regions. To keep the listing manageable, it was limited to vertebrate-encoded factors regulating the expression of genes transcribed into mRNA, i.e. by RNA polymerase II. An alphabetical order of the listing was chosen, since otherwise most of the well characterized factors had to be placed into more than one of the listed categories, such as protein families (e.g. zinc finger proteins) or factor families (e.g. steroid hormone receptor superfamily). Names of synonyms or of homologues derived from other species are listed in the second column. In the third column, the specific regulatory DNA element (if possible, the consensus sequence) that is recognized by the respective factor, is given (please note, that also the complementary sequence represents a specific binding site, since most transcription factors act in an orientation-independent manner).

In the following columns, structural features, tissue specificity and some general informations of each factor are noted. Unfortunately, the broad range of this listing left little space to describe all important features of well characterized factors such as AP1, NF$\kappa$B or Sp1. Also, we are sure to have missed some important elements. Hence, the following table, and especially the 'features' column, represents a rather personal and selective view, which might restrict its usefulness for some purposes. Hence, in order to avoid misinterpretations, readers are encouraged to refer to the original publications cited in the table, and to references therein.

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**Legend to the table:**

1) The species in which a factor has been identified is given in superscript letters (b: bovine; c: calf; ch: chicken; f: frog; h: human; ha: hamster, m: murine; r: rat; s: simian).
2) The names of factors listed here are synonyms of the names listed in the first column, or homologous factors found in other species, or both. The species in which the factors have been identified are given in superscript letters (cf. 1))
3) If possible, consensus sequences derived from several binding sites are given. Since most transcription factors act in an orientation-independent manner, also the complementary sequence represents a specific binding site (R: purine; P: pyrimidine; N: any nucleotide).
4) The molecular weight of the factors was determined by different methods as indicated by superscript letters (a: SDS–PAGE; b: gel filtration; c: estimated from the corrsponding cDNA). If a factor exists in two distinct forms, the $M_r$ of the two forms is shown with a slash (e.g. 45/50); if a factor exists in several forms, or if the size was not exactly determined, the range of the $M_r$ is shown (e.g. 45 – 50); if a factor consists of two or more polypeptides, the $M_r$ of the polypeptides is shown (e.g. 45 + 50).
5) bHLH: helix-loop-helix protein containing a basic domain; bZIP: leucine zipper protein containing a basic domain; FHD: fork head domain; HD: homeodomain; HSH: helix-span-helix protein; POU: POU specific domain; zinc f.: zinc finger.
6) Posttranslational modifications are given in brackets (Ph: phosphoprotein; O-gly: O-glycosylated).
7) Compounds inhibiting the action of the respective factor are given in brackets.

| Factor [1] | Synonyms, Homologs[2] | Binding sequence[3] | $M_r$ (kDa);[4] domains[5,6] | Tissue specificity | Inducers (repressors)[7] | Features | References |
|---|---|---|---|---|---|---|---|
| αA-CRYBP1[m] | | GGGAAATCCC | zinc f. | | | Implicated in lens-specific expression of the αA-cristallin gene. Lens-specific transactivation requires a single binding site. Related to MBP-1 and AGIE-BP1. | 1, 2 |
| AAF[h] | | TTTCATATTACTCT | | | INF-α, INF-γ | Has characteristics very similar to those of GAF. Induction of AAF by INF-γ does not depend on ongoing protein synthesis. | 3 |
| AhR[m,r] | | TGCGTGAGAAGA | 280[a] | | ß-naphtoflavone, tetrachlorodibenzo-p-dioxin, 3-methyl-cholanthrene | Binds to Xenobiotic response element (XRE). Soluble protein complex containing the ligand-binding subunit (95kDa[a]) and the 90 kDa heat shock protein. Translocates to the nucleus after ligand binding. Member of the steroid hormone receptor superfamily. | 4, 5 |
| AGIE-BP1[r] | | GGTTGGGAAATCCC | >250[a] zinc f. | | | Binding specificity is indistinguishable from NFkB. Related to αA-CRYBP1 and MBP1. | 6 |
| ANF[h,m] | | CTTTATCTGG | | ubiquitous | | Negative regulating factor of albumin gene expression. | 7 |
| AP1[h,m,r,ch] | PEA1[m] | TGA$^{G}/_{C}$T$^{C}/_{A}$A | v-Jun: 65[a]<br>c-Jun: 39[a]<br>v-Fos: 55[a]/75[a]<br>c-Fos:55[a]-65[a]<br>bZIP<br>(Ph) | ubiquitous | TPA, EGF, Ha-ras, raf, v-mos, IL-2, NGF, TGFß, ConA, picrotoxin, Py-mt, metrazole, serum, cAMP, retinoic acid, cell. transformation, brain seizure activity, membrane depolarization | Homodimer of Jun or heterodimer between members of the Jun and Fos or Jun and ATF families. Positive or negative regulating factor of various cellular and viral promoters. Fos down-regulates immediate-early gene expression via CArG boxes. DNA-binding is inhibited by IP1 (30-40kDa) which may interact with the Jun/Fos bZIP. | 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 |

| Factor [1] | Synonyms, Homologs[2] | Binding sequence[3] | $M_r$ (kDa);[4] domains[5,6] | Tissue specificity | Inducers (repressors)[7] | Features | References |
|---|---|---|---|---|---|---|---|
| AP2[h,r,f] | | CCC[A]/[C]N[G]/[C]C[G]/[C] | 50[a] HSH | most abundant in the neural crest lineage | TPA, cAMP, retinoic acid, forskalin (SV40 TAg, DNA methylation) | Also binds to Sp1, NF-1, and SV40 T antigen binding sites. Developmentally regulated. Binds as a dimer to a palindromic binding site. | 18, 19, 20, 21, 22 |
| AP3[h] | | TGTGG[A]/[T]A/[T]A/[T] | 48[a]/57[a] | | (Cyclosporin A) | Relatedness of the two proteins described as AP3 is not clear. is not clear. Both proteins bind to the GTIC motif of the SV40 promoter. May be related to TEF-2. | 23, 24, 25 |
| AP4[h] | | C/TCAGCTG[C]/TGG | 48[a] bHLH, bZIP | | | Contains multiple protein-protein interfaces to promote homodimer formation. Interacts with AP1 in regulation of SV40 gene expression | 26, 27 |
| AR[h,m,r] | | AGAACAN$_3$TGTTCT | 98.9[c] | | androgen | Androgen receptor, member of the steroid hormone receptor superfamily. | 28, 29 |
| ARP-1[h] | | TGANCCCTTGACCCCT | 47[a] zinc f. | ubiquitous | | Member of the steroid hormone receptor superfamily. Heterodimerizes with COUP. May participate in regulation of lipid metabolism and cholesterol homeostasis. | 30 |
| ATF[h,m,r] | CREB[h,m], NF21[h], E4TF3[h], CRE-BP1[h], CRE-BP2[m], PCRE[m], TREB[h], EivF[h], Tα1[h], ECRE[m] | TGACG[C]/[T]C/[A]G/[A] | 43[a] - 72[a], bZIP, (Ph) | ubiquitous (CRE-BP1 and HB16 are most abundant in brain) | cAMP, Ca++ | Binds to the cAMP response element (CRE). Family of at least ten different transcription factors encoded either by different genes or generated by differential splicing. Forms homo- or hetero-dimers with members of the ATF- or Jun families. Different dimers have different DNA-binding specificities. ATF-8 binds more efficiently to an AP1- than to an ATF site. | 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 316 |
| BGP1[ch] | | GGGGGGGGGGGGGGG | zinc f. | erythrocytes | | Different from Sp1. | 44 |

| Factor [1] | Synonyms, Homologs[2] | Binding sequence[3] | $M_r$ (kDa);[4] domains[5,6] | Tissue specificity | Inducers (repressors)[7] | Features | References |
|---|---|---|---|---|---|---|---|
| BSAP[h,m] | | GACGCAN$^{C}/_{T}$G$^{G}/_{A}$T$^{T}/_{A}$N$_3$C$^{C}/_{A}$G | 50[a] | B cells | | Binds to the promoter of tissue-specific late histone genes, no binding sites in Ig or MHC class II promoters. Present at early but not at late stages of differentiation. | 45 |
| CBF[h] | MAPF2[ch] | ACACCCAAATATGGCGAC | 35[a] (Ph) | | | Binds to muscle regulatory element. May be closely related to SRF. Binds also to serum response element, but does not activate it. | 46, 47 |
| CBP-1[h,m] | CBF-1<br>CP1[h] | TCAC$^{G}/_{A}$TGATA | 39[a]-49[a]<br>bHLH | | | Heat stable, centromere (CDE I) binding protein, implicated in chromosome segregation and transcriptional activation. Similar or identical to USF. | 48, 49, 50, 51 |
| CD28RC[h] | | AAAGAAATTCC | | | CD28 | Activates IL-2 promoter. | 52 |
| C/EBP[h,m,r,ch] | EBP20[h,m,r] | GTGG$^{T}/_{A}$T$^{T}/_{A}$T$^{T}/_{A}$G<br>ATTGC | 42[a]<br>bZIP | most abundant in liver, but also in brain, fat, intestine, lung, and skin | | Heat resistant, is presumed to be involved in energy metabolism and may have a role in regulating the balance between cell growth and differentiation. Reveals a rather loose binding specificity that includes CCAAT boxes, the enhancer core motif, and cAMP response elements. | 53, 54, 55, 56, 57, 313 |
| CF1 [m] | | ANATGG | | ubiquitous | | Acts on c-myc-, IgH-, and α-actin promoters. Interacts with PCF. | 58 |
| COUP[h,r,ch] | Ear-3[m] | GTGTCAAAGGTCA | 45-50[a] | | | Member of the steroid hormone receptor superfamily, interacts with the non DNA-binding factor S300II. Reveals similar binding properties as v-ErbA. | 29, 59, 60 |
| CP1[h] | NF-Y[m] | C$^{C}/_{T}$N$_6$A$^{A}/_{G}$A$^{A}/_{G}$CCAATCAN$^{C}/_{T}$G$^{G}/_{T}$T | A: 40[a]; 34[c]<br>B: 32[a]; 23[c] | | v-src, serum | Consists of two subunits (A and B). Binds to CCAAT boxes found in Y boxes. | 61, 62, 63, 64, 65 |
| CP2[h] | NF-Y*[m] | C$^{C}/_{T}$AG$^{C}/_{T}$N$_3$A$^{A}/_{G}$RCCAATCN$_3$G$^{G}/_{A}$ | | | v-src, serum | CCAAT box binding factor | 61, 62, 64, 65 |

| Factor [1] | Synonyms, Homologs[2] | Binding sequence[3] | $M_r$ (kDa);[4] domains[5,6] | Tissue specificity | Inducers (repressors)[7] | Features | References |
|---|---|---|---|---|---|---|---|
| CTCF$^{ch}$ | | CCCTC | 130[a] | erythrocyte, muscle, fibroblast | | Binds to three repeats of this motif spaced at five to six basepairs intervals. Adjacent sequences are required for tight binding. | 66 |
| DBP$^{r}$ | | TGATTTTGT | 43[a] basic domain | ubiquitous in adults (except testis), liver-enriched | (chemically induced liver regeneration) | Highest DBP levels are found at 8 p.m., not detectable during the night or in the morning. Member of the C/EBP family, but lacks a leucine zipper domain. Related to VBP. | 67, 68 |
| E2A$^{h}$ | E12$^{h}$=pan1$^{m}$ E47$^{h}$=pan2$^{m}$ | $G/_{A}CAGNTG$ | E12: 67,4[c] E47: 67,7[c] bHLH | ubiquitous (related E2 box binding factors may be myocyte or B cell-specific) | | E12 and E47 are generated by differential splicing of the E2A gene. Binds as a dimer to the κE2 motif , but also to the AP4 and USF binding sites. The E2A gene is rearranged in 95% of the t(1;19) chromosomal translocations found in acute lymphatic lymphomas. The rearrangement results in the replacement of the bHLH by a HD. E2A activates IgD-to-J rearrangement. Forms heterodimers with other bHLH proteins (such as MyoD or Id). | 69, 70, 71, 72, 73, 74, 75 |
| E2BP$^{ch}$ | | TGCAA$^{C}/_{T}A^{C}/_{T}$ | | | | Heat-labile, acts on U3 region of the RSV-LTR | 76 |
| E2F$^{h,s,m}$ | | TTTT$^{G}/_{C}{}^{G}/_{C}CG^{G}/_{C}$ | 54[a] | | E1a, serum (cAMP, retinoic acid) | Activity most abundant during S-Phase. Factor in a proliferation-dependent signal transduction pathway. Forms complexes with the retinoblastoma gene product, cyclin A and adenovirus E4 protein. Complexes are dissociated by adenovirus E1a protein. DNA-binding is inhibited by DNA methylation. | 77, 78, 79, 80, 81, 82, 83 |
| E4F$^{h}$ | ETF-A$^{h}$ | TGACGTAAC | 50[a] (Ph) | | E1a | Binds to a site containing the cAMP response element (CRE). Does not confer cAMP- but E1a inducibility. (cf. ATF) | 84, 35 |

| Factor [1] | Synonyms, Homologs[2] | Binding sequence[3] | $M_r$ (kDa);[4] domains[5,6] | Tissue specificity | Inducers (repressors)[7] | Features | References |
|---|---|---|---|---|---|---|---|
| E4TF1[h] | | CGGAAGTG | 60[a]+ 53[a] | | ras, raf | Consists of two subunits: A DNA-binding one of 60 kDa and a transactivating one of 53 kDa. Not induced by SV40, myc and fos. May be related or identical to EF-1A. | 85 |
| EBP1[h] | | GGGACTTTCC | 57[a]-60[a] | | | Binds to the κB motif and to the SV40 enhancer core. Different from NFκB, but may be related to LBP. | 86, 87 |
| EF-1A[h,m,r] | | CGGAAGTG | | ubiquitous | | Binds cooperatively to two binding sites. May be related or identical to E4TF1. | 88 |
| EF-C[ch,m] | EP[h] | GTTGC$^{T}/_{C}$NG$^{G}/_{A}$CAAC | | present in various human cell lines | | Binds as a dimer to the Py and HBV enhancer. Alteration of the spacing between the inverted repeats of the binding site decreases binding affinity. | 89 |
| EGR-1[m,r] | NGFI-A[m] Krox-24[m] Tis8, zif268[m] | CGCCC$^{C}/_{G}$CGC | 82+88[a] zinc f. (Ph) | ubiquitous, most abundant in brain | TPA, growth factors, metrazole, picrotoxin, retinoic acid, brain seizure activity | Consists of two polypeptides, short-lived, encoded by an immediate early response gene. Has a broad role in signal transduction pathways. (cf. WT-ZFP). | 90, 91, 92, 93 |
| EGR-2[h] | Krox-20[m] | CCGCCCCCGC | 43[a] zinc f. | | PMA, mitogen | May be involved in the regulation of the expression of homeobox-containing genes. | 94, 95 |
| ELP[m] | | CAAGGTCA | | undiff. embr. carcinoma cells | | Implicated in negative regulation of Mo-MuLV LTR. | 96 |
| ER[h,m,r,ch,f] | | AGGTCAN$_3$TGACCT | h:65[c] zinc f. | | estrogen | Estrogen receptor (steroid hormone receptor superfamily). The three spacing nucleotides are essential for the binding affinity. ER and GR binding sites are similar. May cooperate with AP. | 29, 60, 97, 98, 314 |

| Factor [1] | Synonyms, Homologs[2] | Binding sequence[3] | $M_r$ (kDa);[4] domains[5,6] | Tissue specificity | Inducers (repressors)[7] | Features | References |
|---|---|---|---|---|---|---|---|
| v-ErbA$^{h,m,ch}$ | | GTGTCAAAGGTCA | 75[a] zinc f. (Ph) | | | Member of the steroid hormone receptor superfamily. Consists of the thyroid receptor fused to the viral gag protein. Acts as antagonist to the thyroid receptor. Its oncogenic potential correlates with its ability to repress RAR action. | 60, 29, 99 |
| ETF$^{h}$ | | CAGCCCCCGCGCAGC | 120[a]; 270[b] | | phorbol esters | Has a rather loose binding affinity, binds to GC-rich sequences not recognized by SP1. Acts on EGF receptor gene promoter. | 100, 101 |
| Ets-1$^{h,m,ch}$ | | $G/_CA/_CGGAA/_TG T/_C$ | 54[a] (68[a]) (Ph) | B cells resting T cells | c-Ha-ras, v-src, v-mos (ConA, T cell stimulation) | In chickens also a 68 kDa-form exists. Short-lived protein with high turn-over rate. DNA-binding activity is phosphorylation-dependent. Binds in vitro to the PEA3 motif. May be a component of the signalling network. | 102, 103, 104, 105, 106, 107 |
| F-ACT1$^{ch}$ | | TGGCGA | | ubiquitous | | Binds to the serum response element (SRE). Its binding is mutually exclusive with that of SRF. May be a negative regulator of α-actin gene expression. | 108 |
| GAF$^{h}$ | | TTTCATATTACTCT | | | INF-α , INF-γ | Has characteristics very similar to AAF. Induction of GAF by INF-γ depends on ongoing protein synthesis. | 109, 3 |
| GATA-1$^{h,m,ch}$ | Eryf1$^{ch}$, GF-1$^{h,m}$, EF-1$^{m}$, NF-E1a$^{m,ch}$ | $T/_AGATAR$ | GF-1: 51[a] NF-E1a: 40[a] (18[a] + 19[a]) zinc f. | erythroid cells megacaryocytes mast cells | | May consist of two polypeptides, required for erythroid differentiation. Activates globin genes. Erythroid cell-specific transactivation requires multiple binding sites. Plays auto-regulatory role in its own expression. | 110, 111, 112, 113, 114, 115 |
| GATA-2$^{ch}$ | NF-E1b$^{ch}$ | $T/_AGATAR$ | 56[a] zinc f. | erythroid cells (limited in other tissues) | | Reveals tissue-specific RNA splicing. Early factor in differentiation, whereas GATA-1 and -3 are late factors. | 113, 111 |

| Factor [1] | Synonyms, Homologs[2] | Binding sequence[3] | $M_r$ (kDa);[4] domains[5,6] | Tissue specificity | Inducers (repressors)[7] | Features | References |
|---|---|---|---|---|---|---|---|
| GATA-3[h,m,ch,f] | NF-E1c[ch] | T/AGATAR | h: 49[a]; 48[c]<br>ch: 55[a]<br>zinc f. | T cells, brain, definitive erythrocytes | | May play a regulatory role in developing chicken brain and T cell-specific gene expression. The human GATA3 is only expressed in T cells. | 113, 111, 116, 117, 118 |
| GCF[h] | | C/GCGC/GC/GC/GC | 100[a]; 91[c] | | | Negative regulator of EGF receptor gene. | 100 |
| GHF-1[h,r] | Pit-1[m,r], PUF-1 | A/TTATC/TCAT | 34[a]<br>POU | adult anterior pituary (somato-, thyro-, and lacto-trophs) | | Activates the growth hormone gene and the prolactin gene, which has several binding sites. | 119, 120, 121 |
| GHF-5[r] | | A/TTATC/TCAT | | variety of cells | | Activates the growth hormone gene, binds to two sites. | 121 |
| GHF-7[r] | | A/TTATC/TCAT | | adult anterior pituary (somato-trophs) | | Activates the growth hormone gene, binds to two sites. | 121 |
| GR[h] | | AGAACAN$_3$TGTTCT | 88[a]-94[a]<br>zinc f. | | glucocorticoid | Glucocorticoid receptor, member of the steroid hormone receptor superfamily. May be negatively regulated by AP1. The same binding site is recognized by AR, MR, and PR. | 29, 122 |
| H1TF1[h] | | AACAAACACAAA | 90[a]? | | | Binds to AC box of the H1 histone gene. Most probably not identical to HiNF-A. | 123 |
| H1TF2[h] | | GCACCAATCACAGCGCGC | 47[a] | | | CCAAT box binding factor of H1 histone genes. Distinct from NF1. | 123 |
| H2RIIBP[h] | | TCAGGTCACAGTGACCTGA | 50[a,c]<br>zinc f. | | | Member of the steroid hormone receptor superfamily, binds to the cAMP response element and to the ER site. | 124 |
| H2TF1[h,m,r] | MBP-2[h] KB3[m] | TGGGGATTCCCCA | 48[a], 58[a]<br>zinc f. | ubiquitous | (N-myc) | Exists in two forms. Constitutively expressed. Binds to the κB motif. Implicated in MHC class II expression. | 125, 126, 127, 128 |

| Factor [1] | Synonyms, Homologs[2] | Binding sequence[3] | $M_r$ (kDa);[4] domains[5,6] | Tissue specificity | Inducers (repressors)[7] | Features | References |
|---|---|---|---|---|---|---|---|
| H4TF1[h] | | GGGGGAGGG | 105[a]+110[a] zinc f. | | | Acts specifically on H4 histone gene promoter, different from SP1. | 129 |
| H4TF2[h] | | GGTTCTCN$_4$CGGTCCG | 65[a] | | | Acts specifically on H4 histone gene promoter. | 129 |
| H-APF-1[h] | | CTGGRAA | | | IL-6 | Cooperates with NF-IL6, is quali tatively and quantitatively changed by IL-6. | 130 |
| HiNF-A[h] | | ATTTN$_4$ATTT | | | | Acts on human H1, H3, and H4 histone gene promoters. | 131 |
| HIP1[h] | | ATTCN$_{(1-30)}$GCCA | | | | Acts on TATA-less promoters of housekeeping genes to specify the site of transcription initiation. Was suggested to be E2F. | 132, 133 |
| HIVEN86A[h] | | TGGGGATTCCCCA | 86[a] | activated T cells, B lymphocytes | | Binds to κB site of the IL2Rα and HIV promoters. May be closely related to NFκB. | 134, 135 |
| HNF-1[h,r,m] | LF-B1[h,r], HP1, APF, HNF-1α | GTTAATNATTAAC | 92[a] POU | differentiated liver, kidney, stomach, intestine, spleen | | May be implicated in endodermic differentiation. Dimerizes in the absence of its DNA recognition sequence. | 136, 137, 138, 139 |
| vHNF-1[h,r,m] | LF-B3[r] + LF-Bu[r], HNF-1ß | GTTAATNATTAAC | 72[a] POU | liver, lung | retinoic acid | Replaces HNF-1 in dedifferentiated cells. Exclusive expression of vHNF-1 is associated with repression of liver-specific genes. HNF-1 and vHNF-1 have the potential to interact to produce an embryologically complex pattern of gene expression. | 136, 140, 141, 142, 143 |
| HNF-3A[r] | HNF-3α[r] | TATTGA$^{C}/_{T}$TTA$^{A}/_{T}$G | 50[a], 48.7[c] FHD | liver,intestine, lung | | May contribute to the differentiation of cells in internal organs. | 144, 145 |
| HNF-3B[r] | HNF-3β[r] | TATTGA$^{C}/_{T}$TTA$^{A}/_{T}$G | 47[a], 46[c] FHD | liver, intestine, lung | | May contribute to the differentiation of cells in internal organs. | 144, 145 |

| Factor [1] | Synonyms, Homologs[2] | Binding sequence[3] | $M_r$ (kDa);[4] domains[5,6] | Tissue specificity | Inducers (repressors)[7] | Features | References |
|---|---|---|---|---|---|---|---|
| HNF-3C[r] | HNF-3γ[r] | TATTGA$^{C}/_{T}$TTT$^{A}/_{T}$G | 42[a], 43[c] FHD | liver, intestine, testis | | May contribute to the differentiation of cells in internal organs. | 144, 145 |
| HNF-4[h,r] | | $^{G}/_{T}$GC$^{A}/_{T}$A$^{A}/_{G}$G$^{T}/_{G}$C$^{C}/_{T}$CA$^{C}/_{T}$ | 54[a] zinc f. | liver, kidney, intestine | | Member of the steroid hormone receptor superfamily, does not bind to the almost identical TR site. May be identical to LF-A1. | 5, 146, 147 |
| HNF-5[r] | | T$^{G}/_{A}$TTTG$^{C}/_{T}$ | | liver | | Binding sites are located close to those of other liver-specific factors. | 148 |
| HSF[h,m] | | $(NGAAN)_3$ | h: 83[a] | ubiquitous | heat shock | Does not bind prior to or after recovery from heat shock. Does not disturb binding of other factors to the same promoter. May trimerize. Each subunit thought to bind a GAA trinucleotide. | 149, 150, 151, 152 |
| IAF[r] | IEF1[r,ha] | GCCATCTGCT | | pancreatic-ß-cells | | Binds to insulin control element of the insulin II gene. Binds also to the USF site, where it is inactive. | 153, 154 |
| Ig/EBP1[m] | μEBP-E[m] | $^{A}/_{T}$GNATTNTG$^{C}/_{T}$AAT--$^{A}/_{G}$NTN$^{A}/_{T}$ | 45[a,b] bZIP | ubiquitous (highest levels in early B cells) | | Member of the C/EBP family. Binds to E sites in IgH gene promoter and to the RSV LTR. | 155, 156 |
| IREBF-1[m] | | CGGGAAATGGAAACTG | 35,5[c] bZIP | | interferon α, ß | Binds to interferon response element, unrelated to ISGF-1, -2, and -3. | 157 |
| IRBP[m] | | AGTGCACT | 110[a] | | TPA, PKA | Acts on Jun family gene promoters. | 158 |
| ISGF1[h] | IRF-2[m], ICSBP | CTTTCAGTTT | | differentiated cells | interferon ß | Constitutively expressed repressor of INF genes. | 159, 160 |
| ISGF2[h,r] (M+G) | IRF-1[m], IBP-1 | CTTTCTCTTT | M: 56[a]; G: 37[a] (Ph) | differentiated cells | interferon α (M;G), interferon γ (G), prolactin (rat), virus infection, dsRNA | M- and G-forms of ISGF2 are generated by posttranscriptional modifications. Slow interferon response factor, depends on protein synthesis. The rat homolog is an immediate-early gene in prolactin-stimulated T cells and may play a role in cell proliferation. | 159, 160, 161, 162 |

| Factor [1] | Synonyms, Homologs[2] | Binding sequence[3] | $M_r$ (kDa);[4] domains[5,6] | Tissue specificity | Inducers (repressors)[7] | Features | References |
|---|---|---|---|---|---|---|---|
| ISGF3[h] | | GCTTCAGTTT | 48[a] +84[a] +91[a] + 113[a] | | interferon α and γ (N-ethyl malcimide) | Multimeric complex, rapid interferon response factor. Translocates to the nucleus after interferon treatment. | 160, 163 |
| KBF-1[h] | Rel[h] | TGGGGATTCCCCA | 50[a] | ubiquitous | | p50 subunit of NFκB, but also acts independently. Member of the Rel family. | 165 |
| Ker1[h] | | GCCTGCAGGC | | keratinocytes | | Controls keratinocyte-specific gene expression. | 166 |
| LBP[m] | | TAACGCCATTT | | | | Binds to Mo-MuLV LTR, may be related to EBP1. | 96 |
| LF-A1[h,c,r] | | TGGAC$^{T}/_{C}$T/$_{C}$N$_{X}$TGGCCC | c: 40[a,b] | liver | | Binding site is bipartite, insertion or deletion of 1 to 4 nucleotides in the spacer region does not abolish DNA-binding. | 167 |
| LFB3[m] | | GTTAATNATTAAC | POU | epithel of endo- and mesodermal origin | retinoic acid | Is related to and forms heterodimers with HNF-1 (cf. vHNF-1). | 140, 141 |
| LIT-1[h] | | GCGCCCTTTGGACCT | 200[b] | | | Acts on apolipoprotein B gene promoter. | 168 |
| LSF[h] | | GGGCGGN$_4$GGGCGG GGTTCTTTCCGCC | 63[a] | | | Binds to two different sites on the SV40 promoter with the same affinity. Unrelated to Sp1 and MTF-1. Binds to SV40 GC boxes 2 and 3 and regulates SV40 late expression. | 169 |
| LyF-1[m] | | PPTGGGAGR | 50[a] | most abundant in B and T cells | | May be a member of the Ets family. | 170 |
| MBF-1[m] | | C$_{/T}$TAAAAATAAC$_{/T}$C$_{/T}$C$_{/T}$ | | myocytes | FGF, TGFß | Is regulated in a reciprocal manner to MEF-2. | 164 |
| MBF-I[m] | | TGCRCRC | 74[a] | | zinc | Binds to metal response element, may be related to MTF-1. | 171 |

| Factor [1] | Synonyms, Homologs[2] | Binding sequence[3] | $M_r$ (kDa);[4] domains[5,6] | Tissue specificity | Inducers (repressors)[7] | Features | References |
|---|---|---|---|---|---|---|---|
| MBP-1[h] | PRDII-BF1[h] HIV-EP1[h] | TGGGGATTCCCCA | 298[c] zinc f. | ubiquitous (low levels in B cells) | TPA, serum, mitogen, virus infection | Acts on MHC class II promoter, distinct from NFκB. May be regulator of cell proliferation. May be related to PRDII-BF1, HIV-EP1, αA-CRYBP1 and AGIE-BP1. | 172, 173, 174 |
| MCBF[ch] | | CATTCCT | | embryonic muscle tissue | | Factor regulating muscle-specific expression of the cTNT and α-actin promoters. | 175 |
| MEF-2[m] | | $C/_TTA^A/_TAAATA^A/_G$ | | myocytes | myogenin (mitogens, FGF, TGFß) | May participate in the coordinate regulation of genes during myogenesis. Regulated in a reciprocal manner to MBF-1. | 164, 176 |
| MEP-1[h,m] | | TGCRCNC | 115[a] | | | Binds to metal response elements (MREd ≥ MREa = MREc > MREb > MREe >MREf). | 177 |
| MR[h,r] | | $AGAACAN_3TGTTCT$ | 107[c] zinc f. | | mineralocorticoids glucocorticoids | Mineralocorticoid receptor, member of the steroid hormone receptor superfamily. | 178, 29 |
| MTF-1[m] | | TGCRCNC | | | zinc | Binds to the metal response elements, related to Sp1. | 179, 180 |
| mtTF1[h] | | TTAACAGTCACCCCCAAC | 24.4[c] HMG | | | Mitochondrial transcription factor. Activates mtDNA promoters. | 181 |
| Myb[h,m,r,ch] | | $T/_CAAC^G/_TG$ | v-Myb: 48[a] c-Myb: 75[a] | haematopoietic system, tumor cell lines | | Short-lived protein with higher affinity to tandem motifs, although it binds as a monomer. Plays a critical role in cell proliferation and differentiation. | 182, 183, 184, 185 |
| Myc[h,m,r,ch] | | CACGTG TCTCTTA | c-Myc: 64[a]/67[a] b/HLH/ZIP | | | Binds to random DNA sequences and to at least two specific DNA sequences. Functions both in transcriptional regulation and DNA replication. Binds to DNA as a homodimer, or, with altered activity, as a heterodimer with Max. | 186, 187, 188, 189, 190 |

| Factor [1] | Synonyms, Homologs[2] | Binding sequence[3] | $M_r$ (kDa);[4] domains[5,6] | Tissue specificity | Inducers (repressors)[7] | Features | References |
|---|---|---|---|---|---|---|---|
| MyoD[h,s,m] | MEF-1[m,ch] | CAACTGAC | 45[a] bHLH (Ph) | proliferating myoblasts and differentiated myotubes | (FGF, TGFß) | Implicated in myocyte differentiation, needs thirteen amino acids of its basic region for myocyte-specific activation. Forms heterodimers with other bHLH proteins (e. g. E2A or Id) | 69, 191, 192, 193 |
| NF1[h,m,r] | CTF[h,m] | $T/_{C}GGA/_{C}N_{5-6}GCCAA$ | 52[a]-66[a] basic domain (O-glycol.) | ubiquitous | TGFß | Family of at least six proteins. The quantity of the differenrt forms of NF1 varies with the growth conditions of the cells, but overall binding activity remains stable. Binds as a dimer both to palindromic and to half-side sequences. Flanking sequences, length and composition of the spacer region can greatly influence the binding affinity. Interacts also with DNA polymerase to enhance DNA replication. | 20, 213, 214, 211, 215, 216 |
| NF-AT[h,m] | NF-IL2-E[h] | GGAGGAAAAACTGTTTCAT | | activated T cells | PHA (CsA, FK506) | The concentration of NF-AT must exceed a critical threshold before transcription is initiated. Consists of a cytoplasmic and a nuclear subunit. Translocation of the cytoplasmic subunit to the nucleus is inhibited by Cyclosporin A (CsA) and FK506. Could account for the immunosuppressive effect of CsA. | 25, 217, 218, 219 |
| NF-E2[m] | | TGACTCAG | | foetal liver, myeloid cells | | Binds to AP1 site, but different from AP1. | 220, 221 |
| NF-D[m] | | GATGGCGG | | ubiquitous | | Trancription and replication factor. Acts on Py enhancer domain D. | 222 |
| NFe[h,m] | | GTGTCAGTCA | | | | Activates embryonic myosin heavy chain promoter, different from AP1 and ATF. | 223 |
| NF-GMa[h] | | $G^{A}/_{G}G^{A}/_{G}TT^{T}/_{G}CA^{T}/_{C}$ | | | PMA, ConA | Acts on cytokine gene promoter. | 224 |
| NF-GMb[h] | | $TCAG^{G}/_{A}TA$ | | | PMA, ConA | Acts on cytokine gene promoter. | 224 |

| Factor [1] | Synonyms, Homologs[2] | Binding sequence[3] | $M_r$ (kDa);[4] domains[5,6] | Tissue specificity | Inducers (repressors)[7] | Features | References |
|---|---|---|---|---|---|---|---|
| NF-IL6$^{h}$ | LAP$^{r}$<br>IL-6DBP$^{h,r}$<br>H-APF-2$^{h,r}$<br>AGP/EBP$^{m}$ | $T^{T}/_{G}NNGNAA^{T}/_{G}$ | NF-IL6: 40$^{a}$<br>LAP: 32$^{a}$<br>bZIP<br>(Ph) | ubiquitous,<br>most abundant<br>in liver, heart,<br>and muscle | lipopolysaccharide,<br>IL-1, IL-6 | Member of the C/EBP family, binds with higher affinity as heterodimer with C/EBP than as homodimer. Is involved in acute phase reactions, inflammation, and haematopoiesis. AGP/EBP may play a role in the glucocorticoid induction of the α1-acid glycoprotein gene. | 130, 225, 226, 227, 228, 229, 310 |
| NFκB$^{h,r,m}$ | Rel$^{h}$ | $GGGA^{A}/_{C}TN^{T}/_{C}CC$ | 50$^{a}$ + 65$^{a}$<br>>200$^{b}$ | ubiquitous | PMA, cAMP, IL-1,<br>lipopolysaccharide,<br>TNF α, TNF γ | Heterodi- or tetramer. NFκB may be one factor out of a family of rel-related proteins (40 - 125 kDa). Released after stimulation from an inactive cytoplasmic complex formed with IκBα or IκBβ. Constitutive in mature B cells, inducible in immature B cells, T cells, and non-lymphoid cells. A role for NFκB in the $G_0$-to-$G_1$ transition was suggested. | 126, 194, 195, 196, 197, 198, 199, 312 |
| NF-μE3$^{h,m}$ | CD2BP$^{m}$ | GCCACATGACC | 42.5$^{a}$+44$^{a}$<br>+45$^{a}$ | | | Binds to IgH μE3 motif. Oligomer of two to four polypeptides. Probably different from TFE3. | 200, 201 |
| NF-S$^{h}$ | | PyGTCAGC | | | cAMP? | Binds to MHC class II α-chain gene promoters. | 202 |
| NF-W1$^{m}$ | | GTTGCATC | 64$^{a}$ | mature<br>B cells | | Acts on MHC class II gene promoter, different from Oct-1 and -2. | 203 |
| NF-W2$^{m}$ | | GTTGCATC | 64$^{a}$ + 20$^{a}$ | ubiquitous | | Acts on MHC class II gene promoter, different from Oct-1 and -2. | 203 |
| NGFI-B$^{r}$ | nur77$^{m}$<br>N10$^{r}$ | AGGTCATGACCT | 63$^{a}$-88$^{a}$<br>61$^{c}$<br>zinc f.<br>(Ph) | | growth hormones,<br>brain seizure<br>activity, TPA | Member of the steroid hormone receptor superfamily. | 204, 205 |

| Factor [1] | Synonyms, Homologs[2] | Binding sequence[3] | $M_r$ (kDa);[4] domains[5,6] | Tissue specificity | Inducers (repressors)[7] | Features | References |
|---|---|---|---|---|---|---|---|
| NRF-1[h,s] | | T/CGCGCAT/CGCGCA/G | | | | Nuclear factor acting on genes whose products function in mitochondria. May coordinate the expression of nuclear and mitochondrial genetic systems in response to cellular energy demands. | 206 |
| NTF[h] | | GGAACCTCCCCC | | ubiquitous | | Interacts on heavy chain VH gene promoter with Oct-2. | 207 |
| Oct-1[h,m,r] | NF-A1[h], NF-III[h,m], OTF-1[h], OBP100[h], TRF, NF-IL2[h] | ATGCAAAT (CTCATGA) | 90[a]-100[a] POU (Ph) | ubiquitous | TPA, PHA | Preferentially expressed in early S-phase, also stimulates DNA replication. Has no apparent activation domains. also binds to heptamer motif when dimerized with Oct-2. Differential phosphorylation during the cell cycle. | 104, 208, 209, 210, 211, 212 |
| Oct-2[h,m,r,f] | NF-A2[h,m], OTF-2[h] | ATGCAAAT (CTCATGA) | Oct-2A: 60[a] Oct-2B: 75[a] POU, bZIP | lymphoid cells, intestine, testis, kidney, nervous system | TPA, PHA, IL-1 lipopolysaccharides (TGFβ) | Trimer, acts on IgH and MHC class II gene promoters. Also binds to the heptamer motif when dimerized with Oct-1. Multiple isoforms are generated by alternative splicing. Stimulates DNA replication. | 209, 210, 230, 231, 232 |
| Oct-4[h,m] | Oct-3[h,m], Oct-5[m], NF-A3[h,m] | ATGCT/AAAT (TTAAAATTCA) | 42[a] (35[a]) POU | embryonic cells, adult ovary and testis | (retinoic acid) | Most probably, Oct-3, 4, and 5 are identical proteins. Exists in a minor form of 35 kDa. Maternal factor that is also implicated in DNA replication. | 233, 234, 235, 236 |
| Oct-6[m] | Tst1[r], SCIP[r] | ATGCAAAT TAATGARAT | 45[a] POU | embryonic stem cells, germ cells, adult brain and nerve cells | retinoic acid | May be identical to N-Oct-3. May control events at very early and late stages of development. | 236, 237, 238 |
| Oct-R[f] | | ATGCAAAC/T | | ubiquitous | | Binds to the motif only in the context of the H2B box. | 239 |
| Pax-1[h,m] | | CACCGTTCCGCTCTAGATATCTC | 42[a] 37.9[c] | | | Mutation of this factor leads to altered DNA-binding specificity and is associated to malformations of the vertebral column in mice. | 240 |

| Factor [1] | Synonyms, Homologs[2] | Binding sequence[3] | $M_r$ (kDa);[4] domains[5,6] | Tissue specificity | Inducers (repressors)[7] | Features | References |
|---|---|---|---|---|---|---|---|
| PCF$^{m}$ | | AGAAAGGGAAAGGA | | plasmocytoma | | Negative regulating factor of c-myc gene expression. | 241 |
| PEA3$^{h,m,r,ch}$ | | AGGAA$^{G}/_{A}$ | | | TPA, EGF, serum, v-src, c-Ha-ras, v-mos, v-raf, Py-mt | The factor binding to this motif has not yet been identified (Ets-1 has been shown to bind this motif in vitro). The factor is not induced by fos. Represents a primary target of signal transduction. | 103, 243, 244, 245 |
| PPAR$^{m}$ | | AGGTCA | 52.4$^{c}$ zinc f. | liver, kidney heart, brown adipose tissue | peroxisome proliferators | Member of the steroid hormone receptor superfamily. Important for triglyceride and cholesterol homeostasis. May play a role in the development of liver tumors. | 246 |
| PR$^{h, ch}$ | | AGAACAN$_3$TGTTCT | h: 94$^{a}$/120$^{a}$ ch: 79$^{a}$/109$^{a}$ zinc f. | | progesterone (hsp90) | Progesterone receptor, member of the steroid hormone superfamily. Exists in two forms with different promoter specificities. Dimerization is inhibited by the hsp90 heat shock protein. | 29, 247, 248 |
| PRDI-BF1$^{h}$ | | AAGTGAAAGT | 88$^{c}$ zinc f. | | virus infection | Potent repressor of INFß gene expression. | 249 |
| PTF | | TCAGAGTATAAATACT | 40$^{b}$ | pituitary | | May be a modified form of TFIID. Responsible for pituitary-specific expression of the transcription factor GHF1. | 250 |
| PTF1$^{m,r}$ | | ATGGGAN$_x$CTCAGCTGTGC | 64$^{a}$ + 48$^{a}$ | fetal and adult pancreas (from day 15 of gestation) | | May be implicated in the coordinate expression of genes transcribed in the acinar pancreas and in differentiation of the pancreas. | 251, 252, 253 |
| Pu.1$^{ch}$ | Sfpi-1$^{ch}$ | AGAGGAACT | | Most abundant in B lymphocytes and macrophages | | Related to members of the Ets family. Might block proerythroblast differentiation, thereby causing immortalization. | 254, 255 |
| PuF$^{h}$ | | GGGTGGG | | | | Acts on c-myc gene promoter. | 256 |

| Factor [1] | Synonyms, Homologs[2] | Binding sequence[3] | $M_r$ (kDa);[4] domains[5,6] | Tissue specificity | Inducers (repressors)[7] | Features | References |
|---|---|---|---|---|---|---|---|
| RAR$^{h,s,m,f}$ | | AGGTCATGACCT | 48.5[a], 49.9[c] zinc f. | | retinoic acid | Retinoic acid receptor. Member of the steroid hormone receptor superfamily. Heterodimerizes with TR. May compete with AP1. Also binds to the VDR site. Three subtypes (α,β,γ) exist. Developmentally regulated. | 242, 257, 258, 259, 311 |
| RFX$^{h}$ | | CCCCTAGCAACAGATG | | | interferon γ | Binds as a monomer or as a dimer. Acts on X boxes of MHC class II α-chain gene promoters. RFX is defective in MHC class II-deficient combined immunodeficiency. | 202, 260 |
| RVF$^{h,m,r}$ | | AAGATAAAACC | 60[a] | | | Acts on neu gene promoter. | 261 |
| SEF-1$^{m}$ | S-CBF$^{m}$ | TCTGTGGTTAA | 30[a]-35[a] | ubiquitous | | Activates SL3-3 virus promoter. | 262, 263 |
| SIF$^{m,r}$ | | CCCGT$^{C}/_{A}$ | | | c-sis/PDGF | Activates c-fos gene expression in the same time course as SRF. | 264 |
| Sp1$^{h,s,m,r,ch}$ | | $^{G}/_{T}{}^{G}/_{A}$GGC$^{G}/_{T}{}^{G}/_{A}{}^{G}/_{A}{}^{G}/_{T}$ | 95[a]/105[a] zinc f. (Ph, O-glycol.) | ubiquitous | SV40 infection | Has a rather loose binding specificity to G-rich sequences upstream of TATA boxes. Also binds to methylated DNA, and is phosphorylated in situ by a DNA-binding kinase. Does not increase the number of initiation complexes, but the number of productive transcription complexes. Developmentally regulated. DNA-bound Sp1 can self-associate, bringing together distant DNA segments. | 265, 266, 267, 268, 269, 270, 271 |
| SRF$^{h,m,ch,f}$ | | GGATGTCCATATTAGGACATCT | 67[a] (Ph) | ubiquitous | serum | Binds to the serum response element (SRE). Is suggested to adopt different conformations depending on the SRE to which it is bound. Depending on its conformation it is recognized by other proteins in order to confer protein kinase C-dependent or -independent signals. Phosphorylation alters the conformation of the factors DNA-binding domain. | 272, 46, 273, 274 |

| Factor [1] | Synonyms, Homologs[2] | Binding sequence[3] | $M_r$ (kDa);[4] domains[5,6] | Tissue specificity | Inducers (repressors)[7] | Features | References |
|---|---|---|---|---|---|---|---|
| TBP[h,m,r] | | TATAAA | h: 38[a]<br>m: 35[a] | ubiquitous | | TATA box-binding factor. TBP is part of the TFIID protein complex implicated in RNA polymerase II positioning. TFIID-binding to the TATA box is stimulated by TFIIA and TFIIB. Binds as a monomer. | 281, 282, 283, 284 |
| TCF-1[h] | TCF-1α[h]<br>LEF-1[m] | $C/_AA C/_AAG$ | 53[a]-57[a]<br>HMG | T cells | | Distally related to the Ets family. Exists in three alternative splice forms. The DNA-binding domain is similar to that of high mobility group proteins. | 275, 276, 277, 278 |
| TCF-2α[h] | | $G/_CAGGAAGT/_C$ | 63[a] | T cells | | Member of the Ets family. | 277 |
| TEF-1[h] | | $AAGT/_CATGCA$<br>TGGAATGT | 53[a] | | | Binds cooperatively to the Sph- and tandem repeats of the GTIIC motifs on the SV40 promoter. | 279, 280 |
| TEF-2[h] | | GGGTGTGG | 57[a] | | | Binds to the GT-IC motif on the SV40 promoter. May be related to AP3. | 279, 24 |
| TFE3[m] | | GCCACATGACC | 59[c]<br>b/HLH/ZIP | | | Binds to IgH μE3 motif and the USF binding site. Probably different from NF-μE3. Closely related to TFEB. | 73, 200 |
| TFEB[h] | | GGCCACGTGACC | 60[a]<br>b/HLH/ZIP | | | Closely related to TFE3. Binds to E boxes of IgH gene promoters. | 285 |
| TGT3[h] | | AAGTGTTTGC | | liver | | Acts on hepatitis B virus enhancer. | 286 |
| TIN-1[r] | | AGGAAGTTCC | 43[a] /45[a] | testis | | Acts as a transcriptional inhibitor. | 287 |

| Factor [1] | Synonyms, Homologs[2] | Binding sequence[3] | $M_r$ (kDa);[4] domains[5,6] | Tissue specificity | Inducers (repressors)[7] | Features | References |
|---|---|---|---|---|---|---|---|
| TR$^{h,s,m,ch}$ | c-ErbA$^{h,m,r,ch}$ | $(AGGTCA)_2$ | 46$^a$ zinc f. (Ph) | ubiquitous | thyroid hormone | Thyroid hormone receptor. Member of the steroid hormone receptor superfamily. Vertebrates express two different forms, TRα and TRß, with different functions in early embryonic brain as well as during the late phase of hormone requirement. Binds to DNA as a monomer or as a homo- or heterodimer. Binds to head-to-head or tail-to-tail palindromes or to direct repeats of the half-site shown. | 29, 288, 289, 290, 291, 292 |
| TTF-1$^{h,m,r,c}$ | TgTF-1$^r$ T/EBP$^r$ | GNNCACTCAAG | 38$^a$ HD | thyroid, lung | (ras) | Is largely responsible for thyroid-specific gene expression and may be implicated in the differentiation of the thyroid. | 293, 294, 295 |
| UBP-1$^h$ | | CTCTCTGG | 61$^a$-63$^a$ | | | Binds to the HIV tar element, but also to the TATA box. | 86 |
| USF$^{h,m,r}$ | MLTF$^{h,m,r}$ B1$^f$ | GG$^G/_C$CAC$^G/_A$TGAC | 43$^a$/44$^a$ b/HLH/ZIP | ubiquitous | high mobility group proteins 1 and 2 (DNA methylation) | Heat-stable, may be implicated in the regulation of tissue-specific and developmentally regulated genes. Has been suggested to be related to the centromere binding protein CBF-1. USF mRNA is alternatively spliced. Increases rate or stability of TFIID binding during in vitro chromatin assembly. | 50, 296, 297, 298, 299, 300 |
| VBP$^{ch}$ | | GTTTACATAAAC | bZIP | ubiquitous, most abundant in the oviduct | | Appears to play a pitoval role in the estrogen-dependent regulation of the chicken vitellogenin gene. | 301 |
| VDR$^{h,m,r,ch}$ | | AGGTCATGACCT | h: 48.3$^c$ ch:58$^a$/60$^a$ zinc f. (Ph) | | vitamin D | Vitamin D receptor, member of the steroid hormone receptor superfamily. | 242, 302 |

| Factor [1] | Synonyms, Homologs[2] | Binding sequence[3] | $M_r$ (kDa);[4] domains[5,6] | Tissue specificity | Inducers (repressors)[7] | Features | References |
|---|---|---|---|---|---|---|---|
| WT-ZFP[h] | WT1[m] | CGCCCCCGC | h: 21,5[a]<br>m: 47/49[c]<br>zinc f. | developing kidney and Bowman's capsule, meta-nephric blastema | | Encoded by the Wilm's tumor locus. Could act as antagonistic to EGR-1 and EGR-2. Reveals homology to EGR-1. Exists in two alternative splice forms. May regulate transcription during nephroblast development. Acts as a transcriptional repressor. | 303, 304, 305, 306 |
| XF1/2[m,r] | | TCTTCTCACGCAACT | | | (cycloheximide) | Binds to the xenobiotic response element (XRE) of the cytochrome P450c (CYP1A1) gene promoter. Not responsive to polycyclic compounds. Distinct from Ahr. | 307 |
| XPF-1[m] | | CACCTGN$_4$TTTCCC | 60[a] | exocrine pancreas | | Implicated in transcriptional activation of exocrine pancreas-specific gene expression. | 308 |
| YB-1[h] | | ATTTTTCTGATTGGCCAAAG | 35[c] | | (PMA, INFγ) | May be a Y-box binding protein, but is also suspected to be involved in maintenance of chromatin structure or DNA repair as a non-specific DNA-binding protein. | 309, 315 |