

# IV

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## CELLULAR PROTEINS

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Epoc1 . . . . .	IV-2
FTA . . . . .	IV-4
KGF . . . . .	IV-5
p12 <sup>I</sup> . . . . .	IV-6
PEPB2 . . . . .	IV-7

# Epoc1

LOCUS MUSEPOC1A 1587 bp mRNA ROD 18-MAR-1994  
DEFINITION Mus musculus Epoc-1 mRNA, complete cds.  
ACCESSION L14677  
NID g388913  
KEYWORDS DNA binding protein; POU-domain protein.  
SOURCE Mus musculus (mouse).  
ORGANISM Mus musculus  
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;  
Murinae; Mus.  
REFERENCE 1 (bases 1 to 1587)  
AUTHORS Yukawa,K., Yasui,T., Yamamoto,A., Shiku,H., Kishimoto,T. and  
Kikutani,H.  
TITLE Epoc-1: a POU-domain gene expressed in murine epidermal basal cells  
and thymic stromal cells  
JOURNAL Gene 133 (2), 163-169 (1993)  
COMMENT Yukawa and coworkers, in J. Virol. 70:10-16 (1996), demonstrate that  
Epoc1/skn-1a directly activates HPV16 and 18 E6/E7 promoters by binding  
to the viral transcriptional control region. The interpretation is that  
Epoc1 contributes to the differentiation-dependent activation of E6 and E7  
expression. In the absence of a human Epoc1 sequence, the GenBank  
entry for a mouse sequence is provided below.  
FEATURES Location/Qualifiers  
source 1..1587  
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/strain="BALB/c"  
/sub\_species="domesticus"  
/dev\_stage="adult"  
/tissue\_type="thymus"  
/tissue\_lib="lambda gt-10"  
misc\_feature 1..63  
/note="region distinct from oct-11"  
/evidence=experimental  
CDS 73..1368  
/gene="Epoc-1"  
/note="base pairs 546-752 correspond to the POU-specific  
domain of the protein; base pairs 546-995 correspond to  
the POU-domain of the protein; base pairs 753-818  
correspond to a linker on the protein; base pairs 819-995  
correspond to the POU-homeodomain of the protein; base  
pairs 846-884 correspond to helical domain 1 of the  
protein; base pairs 900-935 correspond to helical domain 2  
of the protein; base pairs 945-995 correspond to helical  
domain 3 of the protein"  
/codon\_start=1  
/db\_xref="PID:g388914"  
/translation="MVNLEPMHTEIKMSGDVADSTDTRSTFGQVEPGNDRNGLDFNRQ  
IKTEDLGDSLQQTLSHRPCHLSQGPTMMPGNQMSGDMASLHPLQQLVLPVPHLQSVSQ  
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QTTISRFEALNLSFKNMCKLKPILLEKWLNDPESSPSDPSASTPSSYPTLSEVFGRRK  
KRTSIETNIRLTLEKRFQDNPKPSSEEISMIAEQLSMEKEVVRVWFNRRQKEKRINC  
PVATPVKPPPIYNSRLVSPSGSLGPLSVPPVHSTMPGTVTSSCSPGNNSRSPSPGSLH  
ASSPTASQNNKAAMNSSSSSSFNSSGWSYRWNHPTYLH"  
misc\_feature 1258..1587  
/note="region distinct from oct-11"  
/evidence=experimental  
BASE COUNT 382 a 497 c 398 g 310 t  
ORIGIN  
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61 cgctggggcga ggatggtgaa tctggagccc atgcacacag agatcaagat gagtggggat  
121 gtcgctgatt ccacggacac cgcgacact ttcggtcaag tggagccagg aatgatcga  
181 aatggcctag atttcaacag acagattaag acggaggatc tgggtgactc tctacagcag  
241 accctctccc acaggccatg ccacctgagc caaggaccta ccatgatgcc tggaaaccaa

301 atgtctgggg acatggcttc tctccatcca ctccagcagc tegtgtggt cctggccac  
361 ttgcagtctg tatcccagtt cctgctttcc cagaccccac ctgggcagca aggtctgcag  
421 ccgaatcttc tctcctttcc acagcaacaa agcactctac tcctcccaca gacagggcct  
481 ggcttctgct cccaggcagt tgggcccctt gggctatcag gatcctcttt agagccccac  
541 ctggacgctc ctcaaacctt gccagggcc c aagcatctgc ctggccccgg agggaatgat  
601 gagcccactg acctggagga gctggagaag ttcgccaaga ccttcaagca gagacgcatt  
661 aagctaggct tcacacaggg agatgtggga ctggcgatgg gaaagctgta tggcaatgac  
721 ttcagccaga ctaccatctc gcgatttgag gccctcaacc tgagcttcaa gaacatgtgc  
781 aaactcaagc cactgctgga gaagtggttg aatgatccag agtcctcccc gtcagaccct  
841 tcagcgagca caccagctc ctaccccact ctacagcgaag tgtttggcag gaagaggaag  
901 aaacggacca gcatcgagac caacatacgc ctgactttgg agaagcgatt tcaagataac  
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1021 gtggtgagag tctggttctg caatcgagc caaaaggaga agagaatcaa ctgccccgtg  
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1141 gggcccctct cagtccctcc tgtccacagc accatgcctg gaacagtaac gtcacctctg  
1201 tcccctggga acaacagcag gccttcgtct cctggttcag gactccatgc cagcagcccc  
1261 acagcatctc aaaataactc caaagcagca atgaactcct cctcctcctc cagctttaa  
1321 tcctcgggat catggtaccg ttggaatcat cctacctacc tccactgaga ccaaaaactt  
1381 cctcccttcc cacctggccc ctagttocca agaggaggaa gagagtcgtg ccttccacat  
1441 agggacagac actttgagaa gaatgggagc aatggccact gctgaagagc aaacccatag  
1501 tcttgccctc tcctggatcc agagctttcg gagaacataa ctgtgaccaaa aggccgcact  
1561 cttgccttgg gctcttcatc acccgct

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FTA

LOCUS HUMFTA 1644 bp mRNA PRI 30-JAN-1996  
 DEFINITION Human farnesyltransferase alpha-subunit mRNA, complete cds.  
 ACCESSION L10413  
 KEYWORDS farnesyl-protein transferase alpha-subunit; farnesyltransferase.  
 SOURCE Homo sapiens (human).  
 ORGANISM Homo sapiens  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1644)  
 AUTHORS Andres,D.A., Milatovich,A., Ozcelik,T., Wenzlau,J.M., Brown,M.S.,  
 Goldstein,J.L. and Francke,U.  
 TITLE cDNA cloning of the two subunits of human CAAX farnesyltransferase  
 and chromosomal mapping of FNTA and FNTB loci and related sequences  
 JOURNAL Genomics 18 (1), 105-112 (1993)  
 COMMENT The murine FTA (farnesylytransferase alpha) cDNA was successfully  
 cloned and sequenced from a cell line which expresses the HPV16 E6  
 (Shirasawa et al., Gene 164:373-374,1995). The human cDNA sequence  
 is shown below.  
 FEATURES Location/Qualifiers  
 source 1..1644  
 /organism="Homo sapiens"  
 /map="8p22-q11"  
 /tissue\_type="retina"  
 CDS 7..1146  
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 /product="farnesyl-protein transferase alpha-subunit"  
 /db\_xref="PID:g388756"  
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 EAVASPMDDGFVSLDPSYVLYRDRAEWADIDPVPQNDGPNPVVQIIYSDKFRDVIYDY  
 FRAVLQRDERSERAFKLRDAIELNAANYTVWHFRVLLKSLQKDLHEEMNYITAIIE  
 EQPKNYQVWHRRVLEWLRDPSQLEFIADILNQDAKNYHAWQHRQWVIQEFKLWDN  
 ELQYVDQLLKEDVRNNSVWNQRYFVI SNTTGYNDRAVLREVEQYTLKLVPHNESA  
 WNYLKGILQDRGLSKYPNLLNQLLDLQPSHSSPYLIAFLVDIYEDMLENQCDNKEDIL  
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 BASE COUNT 497 a 338 c 388 g 421 t  
 ORIGIN  
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 61 ccggcgcaac ccccgcccca gccgcaccca ccgcccggcc agcagcagca caaggaagag  
 121 atggcggccg aggctgggga agccgtggcg tccccatgg acgacgggtt tgtgagcctg  
 181 gaactgcgct cctatgtcct gtacagggac agagcagaat gggctgat atagatccggtg  
 241 ccgcagaatg atggcccca tcccgtggtc cagatcatt atagtacaa atttagagat  
 301 gtttatgatt acttccgagc tgtcctgcag cgtgatgaaa gaagtgaacg agcttttaag  
 361 ctaaccggg atgctattga gttaaagca gccaaatata cagtgtggca ttccgggaga  
 421 gttcttttga agtcacttca gaaggatcta catgaggaaa tgaactacat cactgcaata  
 481 attgaggagc agcccaaaaa ctatcaagtt tggcatcata ggcgagatt agtggaaatg  
 541 ctaagagatc catctcagga gcttgaattt attgctgata ttcttaata ggatgcaaa  
 601 aattatcatg cctggcagca tcgacaatgg gttattcagg aatttaaact ttgggataat  
 661 gagctgcagt atgtggacca acttctgaaa gaggatgtga gaaataactc tgtctggaac  
 721 caagatact tcgttatttc taacaccact ggctacaatg atcgtgctgt attggagaga  
 781 gaagtccaat acactctgga aatgattaaa ctagtaccac ataataagaa gcatggaac  
 841 tatttgaaag ggattttgca ggatcgtggt ctttccaaat atcctaactc gttaaatcaa  
 901 ttacttgatt tacaaccaag tcatagttcc ccctacctaa ttgctttct tgtggatata  
 961 tatgaagaca tgctagaaaa tcagtgtgac aataaggaag acattcttaa taagcatta  
 1021 gagttatgtg aatcctagc taaagaaaag gacactataa gaaaggaata ttggagatac  
 1081 attggaagat ccttcaaaag caaacacagc acagaaaatg actcaccaac aatgtacag  
 1141 caataacacc atccagaaga acttgatgga atgcttttat tttttattaa gggaccctgc  
 1201 aggagtttca cagcagagtg gtcctccct ttgctgtggt tgtaaaagt catcacacag  
 1261 gtattgcttt ttaacaagaa ctgatgctcc ttgggtgctg ctgctactca gactagctct  
 1321 aagtaatgtg attcttctaa agcaaatgca ttggatggga ggaggaagaa aaagtcccat  
 1381 aaaggaactt ttgtagtctt atcaacatat aatctaactc cttagcatca gctcctcct  
 1441 cagtgtgaca tgcgtcaaga tttgtagcag taataactgc aggtcacttg tatgtaatgg  
 1501 atgtgaggtg gccgaagttt ggttcagtaa gcaggaata cagtctgctc atcagagctg  
 1561 gtctgcacac tcacattatc ttgctatcac tgtaaccaac taatgcaaaa agaacgggtt  
 1621 tgtaataaaa ttatagctgt atct

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LOCUS S81661 1200 bp mRNA PRI 10-JUL-1992  
DEFINITION Keratinocyte growth factor [human, mRNA, 1200 nt].  
ACCESSION S81661  
SOURCE human.  
REFERENCE 1 (bases 1 to 1200)  
AUTHORS Aaronson,S.A., Bottaro,D.P., Miki,T., Ron,D., Finch,P.W.,  
Fleming,T.P., Ahn,J., Taylor,W.G. and Rubin,J.S.  
TITLE Keratinocyte growth factor. A fibroblast growth factor family  
member with unusual target cell specificity  
JOURNAL Ann. N. Y. Acad. Sci. 638, 62-77 (1991)  
COMMENT Keratinocyte growth facto (KGF) appears to have a role in the  
transformation process of epithelial cells. It also appears to be  
a negative regulator of HPV16 early gene transcription (Zheng et al.,  
J. Cell Biol. 129:843-851, 1995).  
REMARK GenBank staff at the National Library of Medicine created this  
entry [NCBI gibbsq 81661] from the original journal article.  
This sequence comes from fig 2.  
FEATURES Location/Qualifiers  
source 1..1200  
/organism="Homo sapiens"  
CDS 446..1030  
/note="Description: Keratinocyte growth factor, KGF; This  
sequence comes from fig 2B. KGF"  
/codon\_start=1  
/product="Keratinocyte growth factor"  
/db\_xref="PID:g245439"  
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BASE COUNT 432 a 209 c 243 g 316 t  
ORIGIN

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1 acgcgctcac acacagagag aaaatccttc tgcctgttga tttatggaaa caattatgat
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121 gcaccaggca gacaacagac atggaattct tatatatcca gctgttagca acaaaacaaa
181 agtcaaatag caaacagcgt cacagcaact gaacttacta cgaactgttt ttatgaggat
241 ttatcaacag agttatntaa ggaggaatcc tgtgttgta tcaggaacta aaaggataag
301 gctaacaatt tggaaagagc aagtactctt tcttaaatca atctacaatt cacagatagg
361 aagagggtcaa tgacctagga gtaacaatca actcaagatt cattttcatt atgttattca
421 tgaacacccg gagcactaca ctataatgca caaatggata ctgacatgga tcctgccaac
481 tttgctctac agatcatgct ttcacattat ctgtctagtg ggtactatat ctttagcttg
541 caatgacatg actccagagc aaatggctac aaatgtgaac tgttccagcc ctgagcgaca
601 cacaagaagt tatgattaca tgggaaggagg ggatataaga gtgagaagac tcttctgtcg
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721 gaataattac aatatcatgg aaatcaggac agtggcagtt ggaattgtgg caatcaaagg
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901 atcagctaaa tggacacaca acggagggga aatgtttggt gccttaaatc aaaaggggat
961 tcctgtaaga ggaaaaaaaa cgaagaaga acaaaaaaca gccactttc ttcctatggc
1021 aataacttaa ttgcatatgg tatataaaga acccagttcc agcagggaga tttctttaag
1081 tggactgttt tctttcttct caaaattttc tttcctttta ttttttagta atcaagaaag
1141 gctggaaaaa ctactgaaaa actgatcaag ctggacttgt gcatttatgt ttgttttaag

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p12<sup>I</sup>

LOCUS HMVORFA 514 bp mRNA VRL 18-MAY-1993  
DEFINITION Human lymphotropic virus type 1 proviral mRNA sequence.  
ACCESSION L08432  
NID g291296  
KEYWORDS p12 protein.  
SOURCE Human lymphotropic virus type I (strain laf) cDNA to mRNA.  
ORGANISM Human T-cell lymphotropic virus type 1  
Viruses; Retroid viruses; Retroviridae; BLV-HTLV retroviruses.  
REFERENCE 1 (bases 1 to 514)  
AUTHORS Koralnik,I.J., Fullen,J. and Franchini,G.  
TITLE The p12I. p13II, snf p30II proteins encoded by human T-cell  
leukemia/lymphotropic virus type I open reading frames I and II are  
localized in three different cellular compartments  
JOURNAL J. Virol. 67, 2360-2366 (1993)  
MEDLINE 93188190  
COMMENT The HTLV p12I, encoded by an orf in the sequence shown below, is  
a 12 kDa protein that resembles BPV1 E5 and is similarly located in  
the cell. Franchini and coworkers, in J. Virol.67:7701, 1993, show  
that p12I functionally cooperates with E5. The p12I protein is also  
known to bind to the vacuolar H+ATPase 16kDa subunit (Koralnik et al.,  
J. Gen. Virol. 76:1909,1995). See pp. III-86 and -87 of this  
compendium for cautionary results.  
FEATURES Location/Qualifiers  
source 1..514  
/organism="Human T-cell lymphotropic virus type 1"  
/proviral  
/strain="laf"  
/cell\_line="HTLV-I laf"  
BASE COUNT 78 a 203 c 95 g 138 t  
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61 aagaaaaaga ccaccaacac catggcaact tcctccggtc agcctccaag gactccacct  
121 cgcttccaa ctgtctagta tagccatcaa tcccgaactc ctgcattttt tctttcctag  
181 cactatgctg tttcgcttc tcagcccctt gtctccactt gcgctcacgg cgctcctgct  
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361 gctctttttt tcgcttctc ttctctcag cccgtcgtg ccgctcacga tgcgtttccc  
421 cgcgaggtgg cgctttctc cctggaaggc cccgtcgcag ccggccgcgg ctttctctt  
481 ctaaggatag caaacctca agcacagcgg atcc

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LOCUS MUSPEBP2AA 188 bp DNA ROD 20-MAY-1994  
 DEFINITION Mouse gene.  
 ACCESSION D26531  
 SOURCE Mus musculus (strain 129) DNA, clone PEBP2aB2.  
 ORGANISM Mus musculus  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;  
 Murinae; Mus.  
 REFERENCE 1 (sites)  
 AUTHORS Bae,S.-C., Ogawa,E., Maruyama,M., Oka,H., Satake,M., Shigesada,K.,  
 Jenkins,N.A., Gilbert,D.J., Copeland,N.G. and Ito,Y.  
 TITLE PEBP2.alpha.B/mouse AML1 consist of multiple isoforms that possess  
 differential transactivation potentials  
 JOURNAL Mol. Cell. Biol. 14, 3242-3252 (1994)  
 MEDLINE 94217721  
 COMMENT PEPB2, a transcription factor, exists as many isoforms. The murine aB2  
 is shown below. Jackson and Campo, in J.Virol. 69:6038-6046, 1995,  
 argue that PEPB2 binds to the second consensus E2 binding site of the  
 BPV4 LCR. Mutations at this binding site reduce basal promoter activity.  
 Submitted (14-Jan-1994) to DDBJ by: Suk-Chul Bae  
 Institute for Virus Research  
 Dept. of Viral Oncology  
 Kyoto University  
 Shogoin, Sakyo-ku  
 Kyoto 606  
 Japan  
 Phone: 075-751-4028  
 Email: yito@virus.kyoto-u.ac.jp  
 Fax: 075-752-3232.  
 FEATURES Location/Qualifiers  
 source 1..188  
 /organism="Mus musculus"  
 /strain="129"  
 /sub\_species="domesticus"  
 BASE COUNT 49 a 22 c 33 g 84 t  
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 1 caaaatgatc tggttgtttg gatttttctt ttggtgtttt gttttttaat gtaccttta  
 61 aattagttga agtgatgtca ggtcaactcc gaagagcgtt tcaaagcagg acttcagcac  
 121 agtgtttgat ttttttatta ttattaatat tattttataa atttaagcat tcagattaga  
 181 tctttggc

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