Nucleotide sequence of human elongation factor-1β cDNA

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Submitted July 19, 1991

EMBL accession no. X60489

Elongation factor-1, which is composed of four subunits: α, β, γ and δ, participates in protein synthesis by binding aminoacyl-tRNAs to 80S ribosomes under hydrolysis of GTP. The complex is composed of two complementary factors with a distinct function: EF-1α, binding GTP and aminoacyl-tRNA and EF-1βγ, serving as a GDP/GTP exchange enhancer; the two factors are functionally equivalent to prokaryotic EF-Tu and EF-Ts. The actual GDP/GTP exchange activity in EF-1βγ resides in the EF-1β subunit. The functions of EF-1γ and the more recently discovered EF-1δ are less well defined. Since our goal is to have at our disposal a human in vivo system for functional studies on Elongation Factors, we started, after having isolated human EF-1α cDNAs (1), to look for similar EF-1βγ and -δ cDNA sequences. We decided to get protein sequence information first from pig EF-1β to which the Artemia purification procedure was applied (2). As a result, a mixed oligonucleotide corresponding to the peptide sequence KPWDDE, which is completely conserved between Artemia EF-1β and EF-1δ, Xenopus EF-1β and EF-1δ (3) and pig EF-1β was synthesised and used to screen a human lambda gt10 cDNA library. A 400 bp partial EF-1β cDNA clone was isolated and then used as a probe to rescreen the library yielding a lambda gt10 phage with a 1 kb insert. All techniques were carried out according to standard procedures as described in (4). Direct sequencing was performed on the PCR-amplified phage insert using the chain-termination method of Sanger *et al.* (5). The nucleotide sequence contains the AUG translation start codon at position 236 as part of the consensus Kozak sequence ACCAUGG (6). The coding region extends to nucleotide 910 and defines a protein 225 amino acids in length with a calculated mass of 24 kD, the human protein being more than 96% homologous to the pig EF-1β sequence of which 173 amino acids have been determined (to be published). The overall homology of the human protein to Artemia EF-1β (7) is 58%, the conservation in the C-terminal domain (see fig. 1), being much higher. The deduced human EF-1β sequence is 19 amino-acids longer than its homologue in Artemia; the actual number being 18 or 19 depending on the presence or absence of the initiator methionine, which is absent in the pig sequence. Interestingly, the consensus sequence for the casein kinase II-dependent phosphorylation of serine at position 89 in Artemia EF-1β (8) is also present in the human and porcine EF-1β sequences. Phosphorylation of this serine in the EF-1β protein of Artemia influences the GDP/GTP exchange rate on EF-1α (8) and may be a conserved control element for regulation of translation. During preparation of this manuscript another human EF-1β cDNA sequence was published by H. von der Kammer *et al.* in *Biochem. Biophys. Res. Commun.* **177**, 312–317 (1991) having an identical coding region but different 5′ sequences.

ACKNOWLEDGEMENTS

We are grateful to J. Kriek and A. Schipper for use of their pig EF-1β data, G.C.M. van der Zon for donation of the lambda gt10 cDNA library and G.M.C. Janssen for helpful discussion. This work was supported in part by grants from the Netherlands Foundation for Chemical Research (SON/NWO).

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hum    1 MGFGDLKSPAGLQVLNDYLADKSYIEGYVPSQADVAVFEAVSSPPPADLC 50
Art    1  ANIDLKAEKGQEQLNELLANKSYLQGYEPSQEDVAAFNQLNKAPSDKFP 49

hum   51 HALRWYNHIKSY.EKEKASLPGVKKALGKYGPADVEDTTGSGATDSKDDD 99
Art   50 YLLRWYKHISSFSDAEKKGFPGIPTSASK.....................EEDD 82

hum  100 DIDLFGSDDEEESEEAKRLREERLAQYESKKAKKPALVAKSSILLDVKPW 149
Art   83 DVDLFGSDEED..EEAEKIKAERMKAYSDKKSKKPAIVAKSSVILDIKPW 130

hum  150 DDETDMAKLEECVRSIQADGLVWGSSKLVPVGYGIKKLQIQCVVEDDKVG 199
Art  131 DDETDMAEMEKLVRSVQMDGLVWGAAKLIPLAYGIKKLSIMCVVEDDKVS 180

hum  200 TDMLEEQITAFEDYVQSMDVAAFNKI 225
Art  181 IDELQEKISEFEDFVQSVDIAAFNKV 206
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Figure 1. Comparison of the Artemia EF-1β and the deduced human EF-1β sequence. The serine phosphorylated by casein kinase II in the Artemia sequence is underlined.

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