

DNA sequence of a genomic clone encoding an *Arabidopsis* acyl carrier protein (ACP)

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Acyl carrier protein (ACP), an essential cofactor for plant lipid biosynthesis, is involved in fatty acid biosynthesis, desaturation, and acyl transfer (1). ACPs contain a phosphopantetheine prosthetic group which is attached to a central serine residue. Of the 19 amino acids surrounding this attachment site, 18 are conserved in all known plant ACPs. We have isolated an ACP gene from a genomic library of *Arabidopsis thaliana*. The clone was identified using a *Brassica* ACP cDNA as a heterologous probe. The *A. thaliana* ACP coding sequence including the transit peptide has 80% identity with ACP coding sequences of *B. napus* (2) and *B. campestris* (3). A likely TATA box in the *Arabidopsis* ACP genomic sequence is underlined. The sequence around the suggested ATG is in agreement with the proposed plant consensus translational start (4). Based on comparisons to *Brassica* cDNA sequences, we suggest that the ACP gene of *Arabidopsis* has 3 introns. Placement and sizes of the introns are proposed by analogy with the genomic *B. campestris* ACP gene (5) and proposed consensus splice site sequences (6). Intron-I in *Arabidopsis* is located within the transit peptide and is slightly larger than the *B. campestris* intron-I (445 vs 306 bp). Intron-II and intron-III are very similar to those in *B. campestris*. Intron-II (80 bp) is positioned just after the putative transit peptide cleavage site. Intron-III (76 bp) is located within the conserved prosthetic group attachment region. The putative transit peptide in *Arabidopsis* is 54 amino acids compared to 51 for *Brassica*, 56 for spinach ACP-I (7), and 59 for barley ACP-I (8). The putative cleavage site for the transit peptide is indicated by an arrow and is located similarly for the *Brassica* ACPs. A polyadenylation consensus sequence (9) is indicated by a heavy line.

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cgctcaatagaataaaaaaacctgtatgaatagaataatcngtttaaatggccagctgaaatgcgaatgggctgagtcattcattatggaag
cccattgtgattggtagggaacgacgctcgggtgaaaggagggaagagcttataaatgaaagcagcaagcagtcagcttccagcttcttgcaca
                                     H A T Q F S A
ctccgccctctctccccctctcttttgcagacatctctctctctctctctgctgttccacgaaca ATG GCG ACT CAA TTC AGG GGT
S V S L Q T S C L
TCT GTC TGA TTG CAA ACT TCT TGT CTG gtaatecaaatctctctctcttcatTTTaaacaattgecttagagatcgtcttggatctta
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gcatggacattcattggctaaagaattggcttgattgaaattcagaacaagaattctttagaatgcaatgctttttttttttttttttttgtgtgt
      A T T R I S F Q K P A L I S N H G K T
ttgataaacaatag GCA ACA ACA AGG ATT AGT TTC CAA AAG CCA GCT TTG ATT TGC AAG CAT GGA AAG ACT
N L S F N L R R S I P S R R L S V S C A
AAT CTA TCC TTC AAC CTC CGC CGT TCA ATC CGA TCT CGC CGC CTC TCT GTT TCT TGC GCG gtatgagcatttt
ttttcaagtttggtaactatataatagggtcctcaagtttttaaaagacattatatttgggtttatag GCA AAA CAA GAG ACG ATA
E K V S A I V K Q L S L T P D K K V V A E T
GAG AAA GTG TCT GCT ATA GTT AAG AAG CAA CTA TCA CTT ACA CCG GAT AAA AAA GTC GTT GCA GAA ACC
K F A D L G A D S L D T
AAA TTT GCT GAC CTT GGA GCA GAT TCT CTC GAC ACG tatccattcactcaagtggaactaaacccaattcttaattttct
      V E I V M G L E E E F N I Q H
tgatactgatcaactgagtgctttttcttcag GTT GAG ATA GTA ATG GGT TTA GAG GAA GAG TTT AAC ATC CAA ATG
A E E K A Q K I A T V E Q A A E L I E E L I N
GCC CAA CAG AAA CCA CAG AAG ATT GCC ACA GTT GAG CAA GCT GCT GAA CTC ATT CAA GAG CTC ATC AAC
E K K *
GAG AAG AAG taa ttttagctttataaaatgcccttaataaaactaaaaaagcaaaaaaacaggcgttgagttgtttctt
attatgttgatttctctctcattcttcttaatgtgtctagcagctctgctcttgccttgcctcaatgggttagtatctcatccacggatctc
tattt
    
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