

Nucleotide sequence of pea cDNA encoding chloroplast carbonic anhydrase

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A 1.3 kb cDNA was isolated from a pea (*Pisum sativum* L.) cDNA library by immunoscreening with rabbit antiserum to spinach carbonic anhydrase (E.C. 4.2.1.1). The 984 bp open reading frame contained the entire coding region of the mature chloroplast protein and its transit peptide. The identity of the protein is verified by the strong homology with carbonic anhydrase from spinach (1). There is little sequence homology with mammalian isozymes (2). The transit peptide, based on Edman degradation of the mature polypeptide, is 104 amino acids. This is longer than commonly found for nuclear-encoded chloroplast proteins (3). Also unusual, even for the serine- and

theonine-rich chloroplast transit peptides, is a region of seven consecutive Ser residues bounded by Thr residues (amino acid residues 36–43). The molecular mass of the deduced 224 amino acid mature chloroplast polypeptide is 24.2 kd.

REFERENCES

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GGTTTGAATCTTCATTGCACCA ATG TCT ACC TCT TCA ATA AAC GGC TTT AGT CTT TCT TCT TTG TCC CCT GCC
                               M  S  T  S  S  I  N  G  F  S  L  S  S  L  S  P  A      17
AAA ACT TCT ACC AAA AGA ACT ACA TTG AGA CCC TTT GTT TCT GCA TCT CTT AAC ACT TCT TCT TCA TCT
K  T  S  T  K  R  T  T  L  R  P  F  V  S  A  S  L  N  T  S  S  S  S      40
TCT TCC TCG ACT TTC CCT TCT CTT ATT CAA GAC AAG CCG GTT TTC GCT TCT TCT TCT CCT ATC ATC ACC
S  S  S  T  F  P  S  L  I  Q  D  K  P  V  F  A  S  S  S  P  I  I  T      63
CCA GTT TTG AGA GAA GAA ATG GGA AAG GGC TAT GAT GAA GCT ATT GAA GAA CTC CAA AAG TTG TTG AGG
P  V  L  R  E  E  M  G  K  G  Y  D  E  A  I  E  E  L  Q  K  L  L  R      86
ACA GCT GCT GAG AAG GTT GAG CAA ATC GAG AAG ACT GAA CTG AAA GCC ACA GCT CAG CTA GGA ACA ACA
E  K  T  E  L  K  A  T  A  A  E  K  V  E  Q  I  T  A  Q  L  G  T  T      109
TCA TCA TCT GAT GGC ATT CCA AAA TCT GAA GCC TCT GAA AGG ATC AAA ACT GGT TTC CTT CAC TTC AAG
S  S  S  D  G  I  P  K  S  E  A  S  E  R  I  K  T  G  F  L  H  F  K      132
AAA GAG AAA TAT GAC AAG AAT CCA GCT TTG TAT GGT GAA CTT GCC AAA GGC CAA AGC CCT CCG TTT ATG
K  E  K  Y  D  K  N  P  A  L  Y  G  E  L  A  K  G  Q  S  P  P  F  M      155
GTG TTT GCA TGT TCA GAC TCA AGA GTC TGC CCA TCT CAT GTG CTA GAT TTC CAG CCA GGT GAA GCC TTT
V  F  A  C  S  D  S  R  V  C  P  S  H  V  L  D  F  Q  P  G  E  A  F      178
GTG GTC AGA AAT GTT GCT AAC TTG GTT CCA CCA TAT GAC CAG CGA AAA TAT GCC GGA ACT GGT GCT GCA
V  V  R  N  V  A  N  L  V  P  P  Y  D  Q  A  K  Y  A  G  T  G  A  A      201
ATT GAG TAC GCA GTT CTG CAT CTC AAG GTT TCC AAC ATT GTT GTC ATT GGA CAC AGT GCT TGT GGT GGT
I  E  Y  A  V  L  H  L  K  V  S  N  I  V  V  I  G  H  S  A  C  G  G      224
ATT AAG GGA CTT TTG TCC TTT CCA TTT GAT GGA ACC TAC TCC ACT GAT TTC ATT GAG GAG TGG GTC AAA
I  K  G  L  L  S  F  P  F  D  G  T  Y  S  T  D  F  I  E  E  W  V  K      247
ATT GGT TTA CCT GCA AAG GCG AAG GTG AAA GCA CAA CAT GGA GAT GCA CCT TTT GCA GAG CTA TGC ACA
I  G  L  P  A  K  A  K  V  K  A  Q  H  G  D  A  P  F  A  E  L  C  T      270
CAC TGT GAG AAG GAA GCT GTG AAT GCT TCC CTT GGA AAC CTT CTC ACC TAC CCA TTT GTG AGA GAG GGA
H  C  E  K  E  A  V  N  A  S  L  G  N  L  L  T  Y  P  F  V  R  E  G      293
TTG GTG AAC AAG ACA TTG GCA CTC AAA GTA GGA TAC TAT GAC TTT GTG AAA GGA TCC TTT GAG CTT TGG
L  V  N  K  T  L  A  L  K  G  G  Y  Y  D  F  V  K  G  S  F  E  L  W      316
GGA CTT GAA TTT GGC CTT TCG TCC ACT TTC TCC GFA TGAACATCAACCATATATCAATGACCACATCTTGATTACTAAG
G  L  E  F  G  L  S  S  T  F  S  V      328
TATTCTTCTCCCTAAAATGTCAAAGATGTGGCCACGATTCTACATTGGAAGCTATAATCTCGTGGTTAAAGGTCGTGTCTGCAATGAAG
AAGCCTACCAACTTTCATCATATGATATTTATATATATGAGAATCTATGAACCTGTATTATGTACTATATATCATGTATCCCATCTTAA
TAAGAGTTTCTAATTCCTATTGAGGCAAAAATTTCAAGAGTTTGTTCAAAAA

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