Chaperonins are a family of proteins that are involved in the correct folding of newly synthesized proteins in prokar
yotes, mitochondria, and plastids (Hemmingsen et al., 1988; Ellis, 1991). Two cpn-60 polypeptides have been purified
from plastids, cpn-60α and cpn-60β (Martel et al., 1990). Sequence comparisons of cpn-60α and cpn-60β from Brassica
napus and Arabidopsis thaliana show that the individual subunits are more closely conserved between species than are
the two subunits within each species (Martel et al., 1990). However, the Brassica cpn-60α cDNA clone reported by
Martel et al. (1990) and used in the above comparisons was not full length.

We have isolated a full-length B. napus cDNA clone encoding cpn-60α (Table I) that is nearly identical with the one
reported by Martel et al. (1990). This clone is 1975 bp in length and encodes an additional 38 amino acid residues at
the NH₂ terminus. The cDNA includes 53 bp of 5' and 145 bp of 3' untranslated sequences. The deduced amino acid
sequence of the full-length protein was 583 amino acids and had a predicted molecular mass of 61,605 D. This protein
appears to have a transit peptide of 45 amino acids which, if cleaved at an Asn residue, would yield the mature form of
the protein, which has been found to be 56,768 D (Martel et al., 1990). A comparison of this cDNA and that reported by
Martel et al. (1990) shows them to be closely related (88% nucleotides, 95% amino acids identity). This suggests that
these are products of two genes, and therefore cpn-60α may be encoded by a gene family.

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Abbreviation: cpn-60, 60-kD chaperonin.

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Table I. Characteristics of a cDNA encoding cpn-60 from B. napus

| Organism: | Brassica napus L. |
| Source: | cDNA, full length. |
| Method of Identification: | The deduced amino acid sequence was compared with the SwissProt, PDB, PIR, Genpept, SPUdatabase, and GPUpdate data bases at National Center for Biotechnology Information using the BLAST network service. |
| Sequencing Methods: | The EcoRI-Nol fragment was subcloned into the pGEM11+ and pGEM11- vectors. Single-strand DNA was produced and sequenced using the T7 sequencing kit (Pharmacia). |
| Features of the cDNA: | This cDNA contains a 1749-bp open reading frame, 53 bp of a 5' untranslated sequence, and 157 bp of a 3' untranslated sequence. Two polyadenylation signals (AATAAA) are found within the 3' untranslated region, 94 and 137 bp downstream of the stop codon. |
| Structural Features of the Deduced Protein: | The open reading frame encodes 583 amino acids with a predicted molecular mass of 61,605 D. The transit peptide consists of the NH2-terminal 45 amino acids. |