

# Sequence of a cDNA from *Drosophila* coding for the 16kD proteolipid component of the vacuolar H<sup>+</sup>-ATPase

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The vacuolar H<sup>+</sup>-ATPases are a class of endomembrane pumps which acidify the interiors of vacuolar compartments of eukaryotic cells<sup>1</sup>. The major membrane component is a proteolipid of MW 16kD and the deduced amino acid sequences from a yeast gene<sup>2</sup> and from a bovine cDNA<sup>3</sup> show high identity with each other and a lower identity with the 8kD subunit c proteolipid of the F<sub>1</sub>F<sub>0</sub>H<sup>+</sup>-ATP synthase. A related, possibly identical 16kD protein has also been found to be a component of gap junction-like structures isolated from animal tissues<sup>4</sup>. We have isolated a cDNA from *Drosophila* coding for the 16kD proteolipid as part of a study to understand the structure and disposition of this protein in the bilayer.

A bovine cDNA coding for the 16kD proteolipid was first obtained by screening a commercially available cDNA library from adrenal medulla using oligonucleotide probes derived from the published sequence<sup>3</sup>. The *Drosophila* cDNA was identified from a larval library in lambda gt10 by screening with randomly primed probes from the bovine cDNA. The deduced amino acid sequence of the longest open reading frame from the *Drosophila*

cDNA shows a high degree of identity with the bovine and yeast sequences and with the direct amino acid sequence of the gap junction form of the *Nephrops norvegicus* 16kD proteolipid (Finbow *et al.*, unpublished results).

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GGCCGATCCGCGCTTTTAAACGAGCAGCCAGCAGTAACCCGAAGAGGCCACAGAGCCGAATTCGTTTTAAT 73
AGATTCTAATCACCCATAAAAAACACACAACAACAAGCAAAATGCTCTCTGAAGTGAGCAGCGACAACCCC 146
                                     M S S E V S S D N P 10

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I Y G P F F G V M G A A S A I I F S A L G A A Y 34

GGCACTGCTAAGTCTGGTACCGGTATTGCTGCCATGTCAGTGATCGGCCCTGAAGTATGATGAAATCCATC 288
G T A K S G T G I A A M S V M R P E L I M K S I 58

ATTCTGTGGTCAAGCGGGTATCATTGCCATTTACGGTCTGGTGGTGGCTGTGCTTATTGCCGGCGCGCTG 369
I P V V M A G I I A I Y G L V V A V L I A G A L 82

GAAGAGCCATCAAAGTACTCACTATACAGGGGCTTCATTCACTTGGGAGCCGGTCTGGCGGTGGCTTCTCT 440
E E P S K Y S L Y R G F I H L G A G L A V G F S 106

GGTCTGGCAGCTGGTTTTGCGATCGGCATCGTGGGAGAGCCGGTGTCCGTGGCACAGCACAGCAGCCTAGA 511
G L A A G F A I G I V G D A G V R G T A Q Q P R 130

CTGTTCTGGGATGATCCTGATTCTCATCTTCGCCGAAGTGTGGGTCTCTACGGCTTGAATTGTGGCCATT 582
L F V G M I L I L I F A E V L G L Y G L I V A I 154

TACCTGTACAGAAATAAATCAATCAATGCAAAACACACAACAACAGATAGACAACCGGCCCCAGCGGT 653
Y L Y T K * 159
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TTTTTCCATTATTATTATAAATAATGTTTAGTGTATATGTAAGTTCGTTAAACAAAAA 1145

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