Gene and derived peptide sequences for *C.tropicalis* vacuolar ATPase subunit b

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We report here the cloning and sequence determination of the gene encoding the *Candida tropicalis* vacuolar ATPase subunit b. The gene is predicted to encode a polypeptide of 511 residues with a calculated MW of 57,135 dalton. The *Candida* gene carried on pAB107 restored a *Saccharomyces* subunit b deletion mutant (*var2*; ref. 1) to apparently wild-type viability at pH 7.6; when the coding sequence was disrupted at the single XbaI site, the gene failed to restore function.

The deduced amino acid sequence is shown in single letter code. The XbaI site used to disrupt the gene is underlined.

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REFERENCE

1. Yamashiro, C.T., Kane, P.M., Wolczyk, D.F., Preston, R.A. and Stevens, T.H. (1990) *Mol. Cell. Biol.* **10**, 3737-3749.

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AAGCTTGGGGTATCATTGTTAAAAATAATTGTCAACTTTCAAGTGTTTTAAATTTCCACAAGTTATGAAACGGAGTTGAAATCTGAGGAATGGTGAATTTCTACAATATACTTCGAGAG 120
ATCTCCAATCTTGATCAGGTATTTAAAGACAAAATTGCAAAAGAACAGATTTCGAGACCAATAACCAACCAACTGTCGACTGATCTTGAATGAGAGCTAATTCGAAGTACTTATGGAA 240
TTAGTTTATGAGAAGCTCATGACGTCGTCGTACAGTAGAAAACACACAATCGACCTATTGCTTTACAAGATTGAATTTAAAGAAATTAGTATTTAATCTGACCAAACTAAGCGATGAT 360
TGGGACATTGTGACGGGTATGTCATAAAGTTAGTACTGTTCTGAATAGGTGATACGAATTTGGGTGAATGAGTGATTAGTGTGTATAGATAAATTAATATATGTCATGGTGTCAAGCCACT 480
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M S L T D K E L F E L N K K A V
CCGAAGGTTTTAAAAACAACCAAGAAATTAACATATACCCCGTTGGTGGTGTAAATGGTCCATTGGTTATTTTGGATAATGTTAAATCCCACGTTATATGAAATTTGCAACTTGGACTT 960
T E G F K I K P R I N Y T P V G G V N G P L V I L D N V K F P R Y N E I V N L T
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L P D G T V R Q G Q V L E V R G T K A I V Q V F E G T S G I D V K K T R V E F T
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G E N L K I P V S E D M L G R I F D G S G R P I D K G P K I F A E D Y L D I N G
CTCCAATTAATCCATATGCTCGTATTTATCCAGAAGAAATGATTCTACTGGTGTTCGTGATTGATACCATGAATTTCTATTGCTAGAGGTCAAAAGATTCCAATTTTCTGCTCTG 1320
S P I N P Y A R I Y P E E M I S T G V S A I D T M N S I A R G Q K I P I F S A S
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G L P H N E I A A Q I C R Q A G L V R P T K D V H D G H E E N F S I V F A A M G
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P S L S R L M K S A I G E G M T R K D H G D V S N Q L Y A K Y A I G K D A A M
AAGCCGTTGTTGGTGAAGAGCTTTGTCACTGAAGATAAATTTGTCAATGAAATTTTGGAAAAATTCGAAAAAGAAATTCATTCTCAAGGTGCTTATGAAAACAGAACTATTTTGAAT 2160
K A V V G E E A L S T E D K L S L E F L E K F E K N F I S Q G A Y E N R T I F E
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AAGAAGAGATCCAGACAAGTCTGGTGATAAATTAATGACGCTACAGCTTATTACATAAGTTTCATTGATATAAATTTGTTGCTTATGTTTATTTTATTTAGTTTAGTA 2400
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ATTC

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