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Nucleotide sequence of the F_0 subunits of the sodium dependent F_1F_0 ATPase of *Propionigenium modestum*

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Propionigenium modestum is a strictly anaerobic gram negative bacterium which grows from the fermentation of succinate to propionate and CO_2. The energy generated during the decarboxylation of methyl-malonyl CoA is used to generate a sodium ion gradient across the cytoplasmic membrane. The energy of the sodium gradient then drives ATP synthesis catalyzed by a sodium dependent F_1F_0 ATPase. The ATPase of *P. modestum* has been shown to couple translocation of either sodium ions or protons to ATP hydrolysis (1). This enzyme is interesting since other characterized bacterial F_1F_0 ATPases are thought to be strictly proton translocating.

The *Escherichia coli unc* operon, which codes for the ATPase polypeptides, consists of nine genes coding for the F_1 and F_0 domains of the enzyme. The F_0 portion is membrane intrinsic and is encoded by three genes organized in a linear fashion in the *E. coli unc* operon. The F_0 subunits from *P. modestum* have been sequenced and the sequence is shown here. The subunits are termed *uncB, uncE* and *uncF* and their reading frames begin at base numbers 235, 1168 and 1545 respectively in the *P. modestum* nucleotide sequence shown below. The Shine-Dalgarno sequences as well as the stop codons for the individual subunits are underlined. The start codons appear in bold letters. Translation initiation for subunit *b* (coded by *uncF*) probably starts with a UUG start codon as reported for *uncB* in *Bacillus megaterium* or with the AUG located 15 nucleotides further 3′ in the same reading frame.

The sequence was obtained after construction of a bacteriophage λ Dash library with chromosomal *P. modestum* DNA. The library was then screened with an oligonucleotide specific for the ATPase β-subunit (2). Restriction fragments of suitable clones were subcloned into the sequencing vectors pBluescript KS and SK (Stratagene Inc.) from which the sequence was obtained.

REFERENCES

1. Laubinger,W. and Dimroth,P. (1989) *Biochemistry* **28**, 7194–7198.
2. Amann,R., Ludwig,W., Laubinger,W., Dimroth,P. and Schleifer,K.H. (1988) *FEMS Microbiol. Lett.* **56**, 253–260.

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GGGTCACCGT TTAAAATGAC TGTTACAGGC TATATGAAAA GATATGCTAT TTACGGTATA TATTTAGGAA TCCTGGTTAA GTTCTTCGGA   90
TTTCCGGTTT TCTTAGGAGG AGCCGTAGGG CTTCTAAACA TAAAGTTCAA TATTTTTCTC AAGGTGGTTT CAACGCAATT TGAAAAAATA  180
AAGAAGAAAC TAAGCAGTTT AAAATGATTA AAGAAAGGGG GTAAATGGAG AGAAATGAAA AAAATGGGAC CTATCATATT AGCAGTAGTA  270
ATCGCTATTG GAACCTTCGC GTTGAAGATG ATGGGAGTCA TTGGTTTTAA AACTCCGCCT TTAGTGGAGG GGCCAAAGAT AATGTTTTAT  360
GTGCCTCTGC CTGAAGCTAT GCACGATTTT CCTTTTGCAA TGGAAATGGC TAGTGGGGTT TACGGATTCC CGGTAACAAT AACGGTTATA  450
AGTACTTGGT TTGTCATGCT TTTTCTGATA ATGGTATTTA GATGGAGTTC AAAGAATCTG GAAGTGGTTC CTGAAAGGAA ACAAGCCTTT  540
TTTGAAACAA TTTATGGATT TCTTGATGAT CTCATCGGTC AGTTGTTAGG AAATTGGAAG AAAAAATACT TTACTTACAT TGGAACATTG  630
TTCCTATTCC TACTTATTTC AAATATAGTT TCGTTTTTTC CGATTCCAGG CTTCTCATCA GAGAATGGAG TGTTTTCAAT AGCACCGGCC  720
TTAAGAACAC CGACAGCAGA CCTTAATACT ACAGTTGGCC TGGCATTACT TACAACTTAC AGCTTTATAG CTGCCTCGTT TAGGACTTCA  810
GGATTCTTTG GGTTTTTCAA AGGATTATTT GAACCAATGC CTCTTATGTT TCCGATCAAC CTAGCGGGAG AATTTGCAAA ACCAACGAAT  900
ATTTCAATCA GACTTTTTGG TAACATGTTC GCAGGGATGG TAATCTTAGG GCTACTTTAT AAAGCAGCAC CTGTATTAAT CCCAGCACCG  990
CTTCACCTGT ACTTCGATCT TTTCAGTGGA GTGGTACAAA GTTTCGTATT CATCATGCTG ACAATGGTTT ATATTCAAGG ATCTATTGGA 1080
GATGCAGAGT ATTTAGAAGA TTAGTTTTAA ACAGTTTTAA ACAAAATATT AATAAAAAAG AAATTAATTT AAGGAGGGAA TCAAGATATG 1170
GATATGGTAT TAGCTAAAAC TGTAGTATTA GCAGCATCAG CTGTTGGTGC AGGAGCAGCA ATGATCGCAG GTATTGGACC AGGGGTTGGA 1260
CAAGGGTATG CAGCAGGTAA AGCGGTAGAA TCTGTTGCCA GACAACCAGA AGCAAAAGGG GACATCATCT CTACAATGGT ACTAGGACAA 1350
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AAAAGGTTGA CGCTAAGATA GGAGCAAACC TACTTGACCA ATTCATTGGA GAGGTAGGGG AAGAGAAATG ATAGAAGCAC AAGTTGGTA  2069
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