

Sequence of the gene encoding the ATP synthase beta subunit from alkaliphilic *Bacillus firmus* RAB

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GenBank accession no. M31107

A genomic library of *Bacillus firmus* RAB was probed with the genes encoding the γ and β subunits of the *B. megaterium* ATP synthase (1). A 1.8 kb fragment containing the entire β subunit gene of *B. firmus* RAB was subcloned and sequenced. The deduced amino acid sequence shares 93% homology with the β subunit sequence of *B. megaterium*.

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REFERENCE

1. Brusilow, W.S.A., Scarpetta, M.A., Hawthorne, C.A. and Clark, W.P. (1989) *J. Biol. Chem.* **264**, 1528–1533.

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-30  TGGCTAGGAGCATTAGGAGGGACGGAATACATGGAATACAGGTACACATATCTCAGTAATGGGTCGGGTTGTTGACGTAAAGTTCAAGAGCGGCAATATCCTGAATCAATA
      M E Y R S H I S V M G P V V D V K F K S G Q Y P E S I
82  AACGCATTAAGTCGACAAGTAGGGTCAGACAAAATGCGGTTGATGTTACAGTTACACTTGAAGTTGCAATTGCCTTAGGTGATGATTCAGTTCGTACCGTTGCAATGGGT
      N A L K S T S R V R Q N A V D V T V T L E V A I A L G D D S V R T V A M G
193  TCAACAGACGGCGTGTACGTGTACAGAGGCACTGATACAGGCGCTCCAATCAGCGTCCAGTTGGAGAAGCGACTCTGGTCGTGATTCACAGTATTAGGAGAAGCAATC
      S T D G L Y V Y R G T D T G A P I S V P V G E A T L G R V F N V L G E A I
304  GACTTAGGTGAGCCGGTTCAGCTGATGATAAGCGTGACCCAATCCATCGTGAAGCTCCTAAATTTGAAGAGCTTCAACAACACTGAAATCTTGAGACAGGGATTA
      D L G E P V A A D D K R D P I H R E A P K F E E L S T T T E I L E T G I K
415  GTAGTAGATCTTCTAGCACCTTACATTATAGGTGGTAAGATCGGTCTATTTGGTGGCGGTGATAGGTAACAGTCTTATCCAAGAACCTATCAATAACATCGCTCAA
      V V D L L A P Y I I G G K I G L F G G A G V G K T V L I Q E L I N N I A Q
526  GAGCACGGCGTAATCTCTGTATTGCTGGTGTAGGTGAGCGTACTCGTGAAGGGAATGACCTTTACCACGAGATGACTGACTCTGGCGTTATCAAAAAGTCTGCCATGGTA
      E H G V I S V F A G V G E R T R E G N D L Y H E M T D S G V I K K S A M V
637  TTTGGTCAAATGAATGAGCCGCTGGTGGCGGTATGGCTGTTGCTTTCTGGTCTTACAATGGCAGAGCACTTCCGTGACCCGATGGTCAGGATGACTTCTTTTCGTT
      F G Q M N E P P G A R M A V A L S G L T M A E H F R D R D G Q D V L L F V
748  GATAACATCTCGTTCACACAAGCAGGTTCTGAGGTATCAGCCCTACTAGCCGTTGCCTTCCAGCCGTTGGTTACCAGCCGACACTTGCTACAGAGATGGTCAGCTACAA
      D N I S F T Q A G S E V S A L L G R M P S A V G Y Q P T L A T E M G Q L Q
859  GAGCGTATCACATCGACAAAAGTTGGTTCGGTTACATCAATCCAAGCGATCTATGTACCAGCCGATGACTATACAGATCCAGCGCCAGCGACAAACATTCGCTCAGTTGGAT
      E R I T S T K V G S V T S I Q A I Y V P A D D Y T D P A P A T T F A H L D
970  GCAACAACAACTTAGAACGTAATATCTGAGATGGGTATCTACCCCTGCCGTTGATCCACTTGCAATCAACATCTCGTGCACTTCTCCTGAAATCGTTGGAGAAGAGCAC
      A T T N L E R K L S E M G I Y P A V D P L A S T S R A L S P E I V G E E H
1081  TACAGTGTGCTCGTCAAGTTCAACAAACGCTTCAAAAGTATAAAGAATCAAGATATCATCGCAATCCTAGGTATGGATGAGCTTCTGAGGAAGATAAGCTTGTGTGA
      Y S V A R Q V Q Q T L Q K Y K E L Q D I I A I L G M D E L S E E D K L V V
1192  CACCGTGGCGTGTATCCAGTTCCTTCTTCTCAAAAACCTCCACGTAAGTGTGAGCGTCTGAGTGGTTCAGAAAGGTTCTTACGTGCCAGTTAAAGAGACAATCAAAGGATTC
      H R A R R I Q F F L S Q N F H V A E Q F T G Q K G S Y V P V K E T I K G F
1303  AAAGAATCCCTTGATGGTAAATATGATGATCTCCTGAAGATGCATCCGCTTCTGCGGCCGATTGAAGAGGTTATCGAAAAAGGAAAACAACAGCGCGTAA
      K E S L D G K Y D D L P E D A F R L V G R I E E V I E K G K Q T A *

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