Nucleic Acids Research

Nucleotide sequence of the phosphoenolpyruvate carboxykinase gene from *Saccharomyces cerevisiae*

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pMV1, a clone carrying the gene for phosphoenolpyruvate carboxykinase was isolated from a S.cerevisiae library constructed in pFL1 (1) by complementation experiments using a derivative of the mutant JPM2 (2) and characterized biochemically (3). A 2.2 kb HindIII/EcoRI-fragment shown to complement all functions was sequenced by the dideoxy chain termination method (4). The coding sequence for the putative protein of 553 amino acid residues is flanked by canonical yeast signal sequences. Computer-assisted searches revealed no significant homologies between the yeast gene sequence and sequences for the corresponding enzyme from rat liver (5) or chicken (6), respectively.

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   1  AAGCTTAGACGCTTCTGGTTGGACAATGGTACGTTTGTGTATTAAGTAAGGCTTGGCTGGGGATAGCAACATTGGGCAGAGTATAGAAGACCACAAAAAAAGGTATATAAGGGCAGAGA

 121  AGTCTTTGTAATGTGTGTAACTTCTCTTCCATGTGTAATCAGTATTTCTACTTACTTCTTAAATATACAGAAGTAAGACAGATAACCAACAGGCTTTCCCAGATATACATATATATCTTT

 241  ATTTCAGCTTAAACAATAATTATATTTGTTTAACTCAAAAATAAAAAAAAAAAACCAAACTCACGCAACTAATTATTCCATAATAAAATAACAACATGTCCCCTTCTAAAATGAATGCTA
   1                                                                                                      M  S  P  S  K  M  N  A

 361  CAGTAGGATCTACTTCCGAAGTTGAACAAAAAATCAGACAGAAATTGGCTCTTAGTGACGAAGTCACCACCATCAGACGCAATGCTCCAGCTGCCGTTTTGTATGAAGATGGTCTAAAAG
  10   V  G  S  T  S  E  V  E  Q  K  I  R  Q  E  L  A  L  S  D  E  V  T  T  I  R  R  N  A  P  A  A  V  L  Y  E  D  G  L  K  E

 481  AAAATAAAACTGTCATTTCATCAAGCGGTGCATTGATCGCTTATTCCGGTGTTAAAACCGGAAGATCTCCAAAGGACAAACGTATTGTTGAAGAACCTACTTCGAAAGACGAAATTTGGT
  50   N  K  T  V  I  S  S  S  G  A  L  I  A  Y  S  G  V  K  T  G  R  S  P  K  D  K  R  I  V  E  E  P  T  S  K  D  E  I  W  W

 601  GGGGTCCGGTCAATAAACATGTTCTGAAAGAACATGGTCTATCAACCGTGAAAGCTGCAGATTACTTGAGAACGAAGACCACATTTATATTGTCGATCGATTCGCTGGATGGGATCCAA
  90   G  P  V  N  K  H  V  L  K  E  H  G  L  S  T  V  K  A  A  D  Y  L  R  T  R  D  H  I  Y  I  V  D  R  F  A  G  W  D  P  K

 721  AATACAGAATCAAAGTCCGTGTTGTTGTGCCAGGGCTTACCACGCTTTATTCATGACAAATATGCTTATTAGACCTACAGAAGAAGAATTAGCCCATTTTGGAGAACCTGATTTTACTG
 130   Y  R  I  K  V  R  V  V  C  A  R  A  Y  H  A  L  F  M  T  N  M  L  I  R  P  T  E  E  E  L  A  H  F  G  E  P  D  F  T  V

 841  TCTGGAACGCTGGTCAGTTCCCAGCCAATTTACACACCCAGGATATGTCTTCAAAGAGTACTATAGAAATTAACTTCAAAGCAATGGAAATGATCATTTTAGGTACCGAATACGCCGGTG
 170   W  N  A  G  Q  F  P  A  N  L  H  T  Q  D  M  S  S  K  S  T  I  E  I  N  F  K  A  M  E  M  I  I  L  G  T  E  Y  A  G  E

 961  AAATGAAAAAAGGTATTTTCACAGTTATGTTTTACTTGATGCCTGTGCACCATAACGTTTTAACTTTGCACTCTTCCGCCAACCAGGGTATTCAAAACGGTGACGTTACTTTATTCTTTG
 210   M  K  K  G  I  F  T  V  M  F  Y  L  M  P  V  H  H  N  V  L  T  L  H  S  S  A  N  Q  G  I  Q  N  G  D  V  T  L  F  F  G

1081  GCCTAAGTGGTACCGGGAAAACCACTTTATCCGCAGACCCACATAGATTGTTGATCGGCGATGATGAACATTGTTGGTCCGACCATGGTGTCTTCAATATCGAAGGTGGTTGTTACGCCA
 250   L  S  G  T  G  K  T  T  L  S  A  D  P  H  R  L  L  I  G  D  D  E  H  C  W  S  D  H  G  V  F  N  I  E  G  G  C  Y  A  K

1201  AGTGTATTAATCTATCTGCTGAAAAGGAGCCTGAAATTTTCGACGCTATCAAGTTTGGTTCTGTATTAGAAAACGTTATCTATGACGAGAAGTCGCAAGTAGTCGACTATGACGACTCTT
 290   C  I  N  L  S  A  E  K  E  P  E  I  F  D  A  I  K  F  G  S  V  L  E  N  V  I  Y  D  E  K  S  Q  V  V  D  Y  D  D  S  S

1321  CTATTACTGAAAATACTAGATGTGCCTACCCAATTGACTACATTCCAAGTGCCAAGATTCCATGTTTGGCGGACTCTCATCCAAAGAACATTATCCTGCTAACTTGTGATGCTTCGGGTG
 330   I  T  E  N  T  R  C  A  Y  P  I  D  Y  I  P  S  A  K  I  P  C  L  A  D  S  H  P  K  N  I  I  L  L  T  C  D  A  S  G  V

1441  TTTTACCACCAGTATCTAAATTGACTCCTGAACAAGTCATGTACCATTTCATCTCTGGTTACACTTCTAAAATGGCTGGTACTGAGCAAGGTGTCACTGAACCTGAACCAACATTTTCAT
 370   L  P  P  V  S  K  L  T  P  E  Q  V  M  Y  H  F  I  S  G  Y  T  S  K  M  A  G  T  E  Q  G  V  T  E  P  E  P  T  F  S  S

1561  CTTGTTTCGGACAACCCTTCCTAGCCTTACACCCTATTAGATACGCAACCATGTTAGCTACAAAGATGTCTCAACATAAAGCTAATGCGTACTTAATCAACACCGGCTGGACTGGTTCTT
 410   C  F  G  Q  P  F  L  A  L  H  P  I  R  Y  A  T  M  L  A  T  K  M  S  Q  H  K  A  N  A  Y  L  I  N  T  G  W  T  G  S  S

1681  CCTACGTATCTGGTGGTAAACGTTGCCCATTGAAGTACACAAGGGCCATTCTGGATTCTATTCATTGACTGGTTCGTTAGCCAATGAAACGTACGAAACTTTACCGATTTTCAATCTTCAAG
 450   Y  V  S  G  G  K  R  C  P  L  K  Y  T  R  A  I  L  D  S  I  H  D  G  S  L  A  N  E  T  Y  E  T  L  P  I  F  N  L  Q  V

1801  TACCTACCAAGGTTAACGGTGTTCCAGCTGAGCTCTTGAATCCTGCTAAAAACTGGTCTCAAGGTGAATCCAAATACGAGGGTGCAGTTACCAACTTGGCCAACTTGTTTGTTCAAAATT
 490   P  T  K  V  N  G  V  P  A  E  L  L  N  P  A  K  N  W  S  Q  G  E  S  K  Y  R  G  A  V  T  N  L  A  N  L  F  V  Q  N  F

1921  TCAAGATTTATCAAGACAGAGCCACACCAGATGTATTAGCCGACTGGTCCTCAATTCGAGTAAACGAAACATGTTAGTTCGATATGTTCAATCCAAAAAAAAAAAAAAAAAAAAGAAT
 530   K  I  Y  Q  D  R  A  T  P  D  V  L  A  D  W  S  S  I  R  V  N  E  T  C  *   553

2041  TAGAATTATTCGACATAGTAAATGTTAGTAATATATTATTTTGCAATTTTTTCTCTTCCCATTTCAGTTTTTTTTGATAACTGAAACTGGATCAACAAGCACATGTTTTCTAATTAA

2161  TCTTTCAAACATATTTATGTATATACATAAGGAAAATTCAAAAATCCGATGCAATTAAACAAAAAGAATTC  2231
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