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Sequence of a human fetal skeletal muscle potassium channel cDNA related to RCK4

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Complementary DNA cloning has revealed that mammalian voltage dependent K^+channels are encoded by a family of genes elated to the *Shaker* gene of *Drosophila* (1). Expression of these cloned genes has shown that they have unique biophysical and pharmacological properties. We screened a human fetal skeletal muscle cDNA library (2) with a probe, hKC1, derived from a K^+channel cDNA expressed in a human insulinoma (3). A 4 kb clone was isolated (λhPCN2) that encodes a polypeptide of 653 amino acids, 96.7% identical to the deduced RCK4 protein (1). Shown in the figure is the sequence of hPCN2, a 3.3 kb *Eco*RI/*Hinc*II fragment of the cDNA clone. When expressed in *Xenopus* oocytes, hPCN2 K^+channels have similar properties to that of RCK4 (Hice,R.E., Philipson,L.H.,Steiner,D.F., and Nelson,D.J., in preparation).

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-1155  TTAACAAGTGATCGCTGCTGTCTAGGATTTTGTTTCTTTTCGGGGGAACCTTGACTTCCTTTCCCAGGCAATCCCTCCTGTGCTGAACTCCAGAGGAACCAGGAGTCTTGGGGTCTTCTC
-1035  TGGGGCAGCCCCAACCCCCACCCCCAGGCTCCAGCCGCGAGGACTCTGTGCACCCCTCGGGCCAGGCAACAGAACTTGTTCCGTGGATATTTGGAGCCTCCACCTGCCAAACCCGAGTGA
-915   TTCCTTTTACCACCCCCCGCCCCCCACCCAGGATCATTCTTCCCCTCCTCCAGCTGTTGCAGCTTGAGGGGGAAAAACAAGCCAGCCGGTGGATTTTCTTTATTTTTATTTTTCGCCCCG
-795   CCGGGGAAGGGTGAAGTGCTTCTTCTGCATGATTTTGGCTGAAGAATGCTCTGCATTTCCTTGATTTCTATGGAGACCTCAGAGCTGGTTTTGCTTCTGCTGACACCTCATCTAGCACCT
-675   TCTCTACCTCCCAGGGTCTTTGCCTCTATCTGTGGTTTGGCATTGTACCTGGGTACAGGAAGCCTTTGATGAACTTAAAAGGAGAGCCTGGAGAATCATCCTGATAGACTTTGAGTAGAA
-555   ATGGCTGGACATACTTCAAACCACATCTTAACATGGTTCGAGCCATCACTAGAAGGCAAGTGCTAACAGTAAAGGCTTATTTGCATTTTATTTACATTTAATGGACTGAGCATTGGCCAA
-435   TTTCCATGGCAGAAAAATATATTTCATTTTCTAGGCACAACTTCTGGCTGTCAGACACTTGCTGCCTTTGAATCTTGCAGCAACATCACTAACCACATCCCAGACATATTTCCAAATTTC
-315   AACATCTACCCCCAAAACATAGGTGTCTGAGAGACTCCAGCATTTTCGGACTTCTTAGTCTTGAGAGTGCCAGGCTATTTATCTCGACCAGCCAAGCTCTGGAGAGCAATGTTGAATCCC
-195   TGAGAAGAGAGAGGCATGGGGCGTGCTGATTTAAAAACAGAAAATGCAAAGTTGGAGCTGAAAATATCCTTAGTCTTCCAAGCAATCTGCTTAAGGGTTCCAAACTTACCTTAATTTGGT
                                                                                                  M  E  V  A  M  V  S  A  E  S  S  G  C  N  S  H    400
 -75   GAGAAAAGAAGCTGCCCTATTTTTCTTTCTTCTTCTTCTACAACTGGAACCAGCCATTTCCGAAAACCACCACCATGGAGGTTGCAATGGTGAGTGCGGAGAGCTCAGGGTGCAACAGTC    44
 401    M  P  Y  G  Y  A  A  Q  A  R  A  R  E  R  E  R  L  A  H  S  R  R  A  A  A  R  A  V  A  A  A  T  A  A  V  E  G  S  G  G    440
  45   ACATGCCTTATGGTTATGCTGCCCAGGCCCGGGCCCGGGAGCGGGAGAGGCTTGCTCACTCCAGGCGAGCTGCAGCACGTGCTGTTGCAGCGGCCACAGCTGCTGTCGAAGGTAGCGGGG   164
 441    S  G  G  G  S  H  H  H  H  Q  S  R  G  A  C  T  S  H  D  P  Q  S  S  R  G  S  R  E  E  E  A  T  R  S  E  K  K  K  A  H    480
 165   GTTCTGGTGGGGGCTCCCACCACCACCACCAGTCACGCGGGGCCTGTACCTCCCATGACCCTCAGAGCAGCCGGGGTAGTCGGGAGGAGGAGGCGACACGGTCTGAGAAGAAGAAAGCCC   284
 481    Y  R  Q  S  S  F  P  H  C  S  D  L  M  P  S  G  S  E  E  K  I  L  R  E  L  S  E  E  E  E  D  E  E  E  E  E  E  E  E  E    520
 285   ACTACCGGCAGAGCAGCTTCCCTCATTGCTCTGACCTGATGCCCAGTGGCTCTGAGGAGAAGATCCTGAGGGAGCTGAGTGAGGAGGAGGAAGATGAGGAGGAGGAGGAAGAGGAGGAAG   404
 521    E  G  R  F  Y  Y  S  E  D  D  H  G  D  E  C  S  Y  T  D  L  L  P  Q  D  E  G  G  G  G  Y  S  S  V  R  Y  S  D  C  C  E    560
 405   AGGAGGGAAGGTTTTACTATAGTGAAGATGACCATGGTGATGAGTGTTCCTACACGGATCTGCTGCCTCAGGATGAGGGCGGTGGCGGCTACAGTTCAGTCCGCTACAGTGACTGTTGTG   524
 561    R  V  V  I  N  V  S  G  L  R  F  E  T  Q  M  K  T  L  A  Q  F  P  E  T  L  L  G  D  P  E  K  R  T  Q  Y  F  D  P  L  R    600
 525   AACGTGTGGTGATAAATGTGTCAGGCCTACGCTTTGAGACCCAAATGAAAACTCTGGCCCAGTTTCCAGAGACTTTGTTGGGAGACCCTGAAAAGAGGACTCAGTACTTTGACCCTTTGC   644
 601    N  E  Y  F  F  D  R  N  R  P  S  F  D  A  I  L  Y  Y  Y  Q  S  G  G  R  L  K  R  P  V  N  V  P  F  D  I  F  T  E  E  V    640
 645   GCAATGAGTATTTTTTTGACAGGAACCGCCCCAGCTTTGATGCCATCTTGTATTATTATCAATCAGGAGGCCGCCTGAAGAGGCCAGTCAATGTCCCCTTTGATATCTTCACTGAGGAGG   764
 641    K  F  Y  Q  L  G  E  E  A  L  L  K  F  R  E  D  E  G  F  V  R  E  E  E  D  R  A  L  P  E  N  E  F  K  K  Q  I  W  L  L    680
 765   TGAAGTTCTATCAGTTGGGGGAGGAGGCCCTGTTGAAGTTTCGGGAGGACGAGGGCTTTGTGAGAGAAGAGGAAGACAGGGCCCTCCCCGAGAATGAATTTAAAAAGCAGATTTGGCTCC   884
 681    F  E  Y  P  E  S  S  D  P  A  R  G  I  A  I  V  S  V  L  V  I  L  I  S  I  V  I  F  C  L  E  T  L  P  E  F  R  D  D  R    720
 885   TCTTTGAATATCCAGAGAGCTCCGATCCTGCAAGGGGCATAGCCATTGTGTCCGTCCTGGTCATCTTAATCTCCATTGTCATCTTTTGCCTGGAAACCTTGCCTGAGTTTAGGGACGACA   1004
 721    D  L  V  M  A  L  S  A  G  G  H  G  G  L  L  N  D  T  S  A  P  H  L  E  N  S  G  H  T  I  F  N  D  P  F  F  I  V  E  T    760
1005   GGGATCTCGTCATGGCACTGAGTGCTGGCGGGCATGGTGGGTTGTTGAATGATACTTCAGCACCCCATCTGGAGAACTCAGGGCACACAATATTCAATGACCCCTTCTTCATCGTGGAAA   1124
 761    V  C  I  V  W  F  S  F  E  F  V  V  R  C  F  A  C  P  S  Q  A  L  F  F  K  N  I  M  N  I  I  D  I  V  S  I  L  P  Y  F    800
1125   CAGTCTGTATTGTATGGTTTTCCTTTGAGTTTGTGGTTCGCTGCTTTGCTTGTCCCAGCCAAGCACTCTTCTTCAAAAACATCATGAACATCATTGACATTGTCTCCATTTTGCCTTACT   1244
 801    I  T  L  G  T  D  L  A  Q  Q  Q  G  G  G  N  G  Q  Q  Q  Q  A  M  S  F  A  I  L  R  I  I  R  L  V  R  V  F  R  I  F  K    840
1245   TCATCACACTGGGCACTGACCTGGCCCAGCAACAGGGGGGTGGCAATGGTCAGCAGCAGCAGGCCATGTCCTTTGCCATCCTCAGAATCATTCGTCTGGTCCGAGTATTCCGGATCTTCA   1364
 841    L  S  R  H  S  K  G  L  Q  I  L  G  H  T  L  R  A  S  M  R  E  L  G  L  L  I  F  F  L  F  I  G  V  I  L  F  S  S  A  V    880
1365   AACTCTCCAGGCACTCCAAAGGCCTGCAGATCCTGGGCCACACCCTCAGAGCCAGCATGCGGGAACTGGGCCTTCTGATCTTCTTCCTCTTCATTGGGGTCATCCTCTTTTCTAGTGCTG   1484
 881    Y  F  A  E  A  D  E  P  T  T  H  F  Q  S  I  P  D  A  F  W  W  A  V  V  T  M  T  T  V  G  Y  G  D  M  K  P  I  T  V  G    920
1485   TGTATTTTGCAGAGGCGGATGAACCTACTACCCATTTCCAAAGCATCCCAGATGCATTTTGGTGGGCTGTGGTGACCATGACAACTGTGGGCTATGGGGACATGAAGCCCATCACTGTAG   1604
 921    G  K  I  V  G  V  L  C  A  I  A  G  V  L  T  I  A  L  P  V  P  V  I  V  S  N  F  N  Y  F  Y  H  R  E  T  E  N  E  E  Q    960
1605   GGGGCAAGATTGTCGGGGTCCTGTGTGCCATTGCGGGTGTCTTAACCATTGCTTTGCCAGTGCCAGTGATTGTCTCTAACTTTAACTATTTCTACCACAGAGAGACTGAAAATGAGGAAC   1724
 961    T  Q  L  T  Q  N  A  V  S  C  P  Y  L  P  S  N  L  L  K  K  F  R  S  S  T  S  S  S  L  G  D  K  S  E  Y  L  E  M  E  E    1000
1725   AGACACAGCTAACGCAGAATGCAGTCAGTTGTCCATACCTCCCCTCTAATTTGCTCAAGAAATTTCGGAGCTCTACTTCTTCTTCCCTGGGGGACAAGTCAGAGTATCTAGAGATGGAAG   1844
1001    G  V  K  E  S  L  C  A  K  E  E  K  C  Q  A  K  G  D  D  S  E  T  D  K  N  N  C  S  N  A  K  A  V  E  T  D  V  *          1040
1845   AAGGAGTTAAGGAATCTCTGTGTGCCAAGGAGGAGAAGTGTCAGGCCAAGGGGGATGACAGTGAGACAGATAAAAACAACTGTTCTAATGCAAAGGCTGTGGAGACTGATGTGTGAATCT   1964
1965   TTTTTTTCCACCTGCCACTGCTCCCCCCTCAGCCATCTTCCAAATATATTTATGCATAGAGAGTGCAGTTATGAAAATGAAATATGCAAATGATCCAATGCATACCAGTAGTACACTATT   2084
2085   TAATGGTTATACATGGCATAATTGTTACTAAACTTGTATTACATATCAAATAAATGATACATCTTGGAGAAGAGGGAGGAATAGGAGCAATCTATCTTTATATTTTTATTAGAATGCAAG   2204
2205   AATTTTCCACATTAACCTGGAAAAGATG  2232
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