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Complete nucleotide sequence of the cDNA for thyroid peroxidase in FRTL5 rat thyroid cells

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Thyroid peroxidase (TPO) is the primary enzyme involved in thyroid hormone synthesis. FRTL5 rat thyroid cells are the only differentiated thyroid cell line available for study of the molecular mechanism involved in the regulation of TPO gene expression by TSH. Unfortunately, human and pig cDNA probes hybridize poorly to rat TPO mRNA. We therefore cloned the complete cDNA for TPO by low stringency screening of an FRTL5 cDNA library. There is 74% homology with human TPO.

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0001 GCACAGCTGCTTCTTCAGTGGAGGAAAAGAAAATGGTCAGAATGAGAACACTTGGAGCTATGGCAGTAATGCTGGTTGTGATGGGAACTGCAATTTTCCTCCCTTTCCTCCTGAGAAGCA
                                                                  M  R  T  L  G  A  M  A  V  M  L  V  V  M  G  T  A  I  F  L  P  F  L  L  R  S

0121 GAGACATCTTGGGGGGGAAGACTATGACATCCCATGTTATCAGTGTTGTAGAAACGAGCCAGCTTCTGGTGGACAATGCAGTCTACAACACCATGAAAAGAAACCTCAAGAAAAGGGGAG
     R  D  I  L  G  G  K  T  M  T  S  H  V  I  S  V  V  E  T  S  Q  L  L  V  D  M  A  V  Y  M  T  M  K  R  N  L  K  K  R  G

0241 TCCTTTCTCCAGCCCAGCTTCTCTCTTTCTCCAAGCTGCCAGAGTCCACCAGTGGAGCTATTTCCCGAGCAGCAGAGATCATGGAAACATCAATACAAGTCATGAAACGTGAACAATCAC
     V  L  S  P  A  Q  L  L  S  F  S  K  L  P  E  S  T  S  G  A  I  S  R  A  A  E  I  M  E  T  S  I  Q  V  M  K  R  E  Q  S

0361 AGTTCTCCACGGATGCACTATCAGCAGACATCCTGGCCACAATTGCCAACCTGTCAGGATGCTTGCCTTTCATGCTGCCACCGAGATGTCCTGACACCTGCCTGGCAAACAAGTACCGGC
     Q  F  S  T  D  A  L  S  A  D  I  L  A  T  I  A  N  L  S  G  C  L  P  F  M  L  P  P  R  C  P  D  T  C  L  A  N  K  Y  R

0481 CCATCACAGGGGTGTGCAACAACAGAGATCACCCCAGATGGGGAGCCTCCAACACAGCCCTAGCAAGATGGCTGCCTCCTGTCTACGAAGATGGTTTCAGTCAGCCCAGAGGCTGGAACC
     P  I  T  G  V  C  N  N  R  D  H  P  R  W  G  A  S  N  T  A  L  A  R  W  L  P  P  V  Y  E  D  G  F  S  Q  P  R  G  W  N

0601 CTAATTTCTTATACCATGGCTTCCCACTGCCCCCGGTACGGGAGGTGACAAGACACCTCATTCAAGTTTCAAATGAGGCTGTGACTGAAGATGACCAGTACTCTGATTTTCTGCCGGTGT
     P  N  F  L  Y  H  G  F  S  L  P  P  V  R  E  V  T  R  N  L  I  Q  V  S  N  E  A  V  T  E  D  D  Q  Y  S  D  F  L  P  V

0721 GGGGCAGTACATCATCATGACACTGCTCTCACACCACAGAGCACCAGCACAGCAGCCTTCTGGGGAGGTGTCGACTGCCAGTTGACCTGTGAGAACCAAAACCCCTGCTTCCCCATAC
     W  G  Q  Y  I  D  H  D  I  A  L  T  P  Q  S  T  S  T  A  A  F  W  G  G  V  D  C  Q  L  T  C  E  N  Q  N  P  C  F  P  I

0841 AGCTTCCCTCAAACTCCTCACGGACCACTGCATGCCTACCTTTCTACCGCTCCTCAGCCGCCTGTGGCACTGGGGACCAAGGAGCACTCTTTGGCAACCTGTCTGCAGCCAATCCGAGGC
     Q  L  P  S  N  S  S  R  Y  T  A  C  L  P  F  Y  R  S  S  A  A  C  G  T  G  D  Q  G  A  L  F  G  N  L  S  A  A  N  P  R

0961 AGCAGATGAATGGCTTGACCTCCTTCCTTGATGCTTCCACGGTGTATGGCAGCTCCCCAGGTGTTGAGAAGCAGTTGCGCAACTGGAGCAGCTCTGCAGGGCTGCTGCGTGTCAACACCC
     Q  Q  M  N  G  L  T  S  F  L  D  A  S  T  V  Y  G  S  S  P  G  V  E  K  Q  L  R  N  W  S  S  A  G  L  L  R  V  N  T

1081 TCCACCTAGACTCTGGCCGTGCCTACCTGCCCTTCGCATCAGCCGCCTGTGCTCCAGAGCCTGGTGCTCCACACGCCAACCGCACGCCCTGCTTCCTGGCTGGTGATGGCCGCGCCAGCG
     L  H  L  D  S  G  R  A  Y  L  P  F  A  S  A  A  C  A  P  E  P  G  A  P  N  A  N  R  T  P  C  F  L  A  G  D  G  R  A  S

1201 AGGTCCCCGCCCTGGCAGCAGTGCACACCTTGTGGCTGCGCGAGCACAACCGCCTGGCTACAGCTTTCAAAGCCATCAACACACATTGGAGCGCCAACCACTGCCTACCAGGAGGCACGCA
     E  V  P  A  L  A  A  V  H  T  L  W  L  R  E  H  N  R  L  A  T  A  F  K  A  I  N  T  H  W  S  A  N  T  A  Y  Q  E  A  R

1321 AGGTGGTAGGGGCATTGCACCAGATCATCACCATGAGGGATTATATCCCCAAGATCCTGGGTCCCGATGCCTTCAGGCAGTATGTGGGCCCCTATGAAGGCTATAACCCCACGGTGAACC
     K  V  V  G  A  L  H  Q  I  I  T  M  R  D  Y  I  P  K  I  L  G  P  D  A  F  R  Q  Y  V  G  P  Y  E  G  Y  N  P  T  V  N

1441 CTACTGTGTCCAACGTCTTCTCTACTGCTGCCTTCCGCTTTGGCCATGCCACAGTCCATCCACTGGTGAGACGACTAAACACGGACTTCCAGGACCACACAGAGCTCCCCAGGCTGCAGC
     P  T  V  S  N  V  F  S  T  A  A  F  R  F  G  H  A  T  V  H  P  L  V  R  R  L  N  T  D  F  Q  D  H  T  E  L  P  R  L  Q

1561 TGCACGACGTCTTCTTCAGGCCCTGGAGGCTTATCCAGGAAGGTGGTTTGGATCCAATAGTAAGAGGCCTCCTGGCAAGACCAGCCAAGCTGCAAGTACAGGAGCAACTGATGAATGAGG
     L  H  D  V  F  F  R  P  W  R  L  I  Q  E  G  G  L  D  P  I  V  R  G  L  A  R  P  A  K  L  Q  V  Q  E  Q  L  M  N  E

1681 AACTGACCGAGAGGCTCTTTGTGTTGTCTAATGTGGGCACCTTGGATCTGGCATCACTGAACTTGCAGAGGGGCCGGGACCACGGCTTACCAGGCTACAATGAGTGGAGAGAGTTCTGTG
     E  L  T  E  R  L  F  V  L  S  N  V  G  T  L  D  L  A  S  L  N  L  Q  R  G  R  D  H  G  L  P  G  Y  N  E  W  R  E  F  C

1801 GCTTGTCACGCCTGGACACAGGAGCTGAGCTGAACAAGGCCATTGCCAACAGAAGCATGGTCAACAAGATAATGGAGTTATACAAGCATGCTGACAACATTGATGTCTGGTTGGGAGGCC
     G  L  S  R  L  D  T  G  A  E  L  N  K  A  I  A  N  R  S  M  V  N  K  I  M  E  L  Y  K  H  A  D  N  I  D  V  W  L  G  G

1921 TGGCTGAAAAGTTCTTACCGGGAGCCCGCACCGGTCCTCTGTTTGCATGTATCATTGGGAAGCAGATGAAGGCTCTGAGGGATGGGGACAGGTTTTGGTGGGAGAACAGCCATGTCTTCA
     L  A  E  K  F  L  P  G  A  R  T  G  P  L  F  A  C  I  I  G  K  Q  M  K  A  L  R  D  G  G  R  F  W  W  E  N  S  H  V  F

2041 CAGACGCTCAGAGGCAGGAACTGGAAAAGCATTCACTACCTCGGGTCATCTGTGACAACACCCGGCCTCACCAGAGTACCTGTGGATGCCTTCCGTATTGGAAAGTTCCCCCAGGACTTTG
     T  D  A  Q  R  Q  E  L  E  K  N  S  L  P  R  V  I  C  D  N  T  G  L  T  R  V  P  V  D  A  F  R  I  G  K  F  P  Q  D  F

2161 AATCCTGTGAGGAAATCCCTAGCATGGACCTCAGACTGTGGAGGGAGACCTTCCCACAAGACGACAAGTGTGTCTTCCCAGAGAAGGTGGACAATGGGAACTTTGTGCACTGTGAAGAAT
     E  S  C  E  E  I  P  S  M  D  L  R  L  W  R  E  T  F  P  Q  D  D  K  C  V  F  P  E  K  V  D  N  G  N  F  V  H  C  E  E

2281 CTGGGAAGCTGGTACTGGTGTATTCCTGTTTCCATGGATACAAGCTGCAAGGCCAGGAGCAGGTCACATGTACCCAGAATGGATGGCACTCAGAGCCTCCTGTCTGTAAAGATGTTAATG
     S  G  K  L  V  L  Y  S  C  F  H  G  Y  K  L  Q  G  Q  E  Q  V  T  C  T  Q  N  G  W  D  S  E  P  P  V  C  K  D  V  N

2401 AGTGTGCAGATCTGACACACCCACCTTGCCACTCCTCCGCAAAGTGCAAGAACACCAAGGGAAGCTTCCAGTGTGTCTGCACAGACCCCTACATGCTAGGTGAGGATGAGAAGACCTGCA
     E  C  A  D  L  T  H  P  P  C  H  S  S  A  K  C  K  N  T  K  G  S  F  Q  C  V  C  T  D  P  Y  M  L  G  E  D  E  K  T  C

2521 TAGATTCTGGCAGGCTACCTCGGGCATCCTGGGTCTCCATTGCATTGGGTGCACTTCTCATTGGTGGTTTGGCCAGTCTCAGCTGGACTGTAATTTGCAGGTGGACACATGCTGATAAGA
     I  D  S  G  R  L  P  R  A  S  W  V  S  I  A  L  G  A  L  L  I  G  G  L  A  S  L  S  W  T  V  I  C  R  W  T  H  A  D  K

2641 AGTCCACATTGCTGATCACCGAGAGAGTGACCATGGAGTCAGGATTCAGAAAGAGTCAGGAGAGTGGGATTTCACCACAAAAGGCCGAGGTTCAAGATGCTGAACAGGAACCGGCTTATG
     K  S  T  L  L  I  T  E  R  V  T  M  E  S  G  F  R  K  S  Q  E  S  G  I  S  P  Q  K  A  E  V  Q  D  A  E  Q  E  P  A  Y

2761 GATCCAGAGTCCTCCTGTGTGAATAGAAGTCCTCACTGCTTTGGAGCCAGACATTGGCTAATTCAAGTCTCAAGCTGCCTGGGCAAAGAAAGACATGATACATGTTGAAGTCAGAGGCTT
     G  S  R  V  L  L  C  E  .

2881 GAGGACACCAGATGGTTAATCTTATCAGTCCAAGGCTGCATAGCTGAGTTCCATCTCATGTTTTTCCACAGGAGCAGGCCAGGCCAGACTGTGCTAATGCCTCTCCTACACAGTAAGGCT

3001 AATGGATAAGTAGGTGGAAGGATAGGAGAATTGCATAAGCCTGAAAGCGTTGAGAGAAGCTAGCATAGACTCCAGATCCTTCCAGACAATTCCACGTTCATTCAGAATCAGAATGTATCT

3121 CTTCCAGATACATTCAGTTCTCTCATTATGTTCCAGTCACCACAAAGCACAGACGAATAAATGCCACAGCCCTTCTCTGGTCTAGCTCAGATATCCTCTTCCTCTAGGCTTGCATTA(n)
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