

Nucleotide and predicted protein sequence of rat retinal degeneration slow (rds)

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The cDNA for mouse rds has been cloned (1). Using oligomers corresponding to the mouse sequence we purified and sequenced in both directions a 1574 bp clone from a rat retina cDNA library in lambda gt10. An open reading frame with 95.0% identity to the mouse extended from nucleotides 123 (ATG) to 1160. A CATAAA consensus (box; cf. mouse) occurred 16 bp upstream from a 12-base poly A tract. The predicted rat rds protein (M_r = 39.3K) is 97.1% identical with the mouse, has two N-glycosylation sites (N*) and four hydrophobic regions (2; underlined, bold). The rds product in cattle has been identified as peripherin (3), a 38K glycosylated, membrane-bound protein. We have used the rat clone as a probe to purify human rds clones from a human retina cDNA library.

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   1  CACTCCCTGCAGCTTGGGCCCATGGTGCTCTTCCCAAGACCCTGAGTGGTCCAGCCCCTAAGCTCATTCGGGCTTGGAGT
  81  GGAAGCTGAACTAGGGGAGGCTGCTGAACCCCCTCGGTAAGCATGGCGCTGCTCAAAGTCAAGTTTGACCAGAAGAAGCG
                                                  M  A  L  L  K  V  K  F  D  Q  K  K  R   13
 161  GGTCAAGTTGGCCCAGGGGCTATGGCTTATGAACTGGCTGTCCGTGTTGGCCGGCATCGTCCTCTTCAGCCTGGGGCTGT
         V  K  L  A  Q  G  L  W  L  M  N  W  L  S  V  L  A  G  I  V  L  F  S  L  G  L   39
 241  TCCTGAAGATTGAACTCCGCAAGAGGAGTGACGTGATGGATAACTCCGAGAGCCACTTTGTGCCCAACTCCCTGATTGGG
         F  L  K  I  E  L  R  K  R  S  D  V  M  D  N  S  E  S  H  F  V  P  N  S  L  I  G   66
 321  GTGGGGGTCCTGTCCTGTGTCTTCAACTCTCTGGCTGGGAAGATCTGCTATGACGCCCTGGACCCTGCCAAGTACGCCAA
         V  G  V  L  S  C  V  F  N  S  L  A  G  K  I  C  Y  D  A  L  D  P  A  K  Y  A  K   93
 401  GTGGAAGCCCTGGCTGAAGCTGTACCTGGCCGTCTGCGTCTTCTTTAACGTCATCCTCTTCCTGGTGGCGCTCTGCTGCT
         W  K  P  W  L  K  L  Y  L  A  V  C  V  F  F  N  V  I  L  F  L  V  A  L  C  C   119
 481  TTCTGCTGCGAGGCTCCCTGGAGAGCACCCTGGCGTACGGGCTCAAGAACGGGATGAAGTACTATCGGGACACGGACACG
         F  L  L  R  G  S  L  E  S  T  L  A  Y  G  L  K  N  G  M  K  Y  Y  R  D  T  D  T   146
 561  CCAGGCCGGTGCTTCATGAAAAAGACCATCGACATGCTCCAGATCGAGTTCAAGTGCTGTGGGAACAACGGCTTCCGGGA
         P  G  R  C  F  M  K  K  T  I  D  M  L  Q  I  E  F  K  C  C  G  N  N  G  F  R  D   173
 641  CTGGTTCGAGATTCAGTGGATCAGCAATCGCTATCTGGACTTTTCCTCCAAGGAGGTCAAAGACCGCATCAAGAGTAATG
         W  F  E  I  Q  W  I  S  N  R  Y  L  D  F  S  S  K  E  V  K  D  R  I  K  S  N   199
 721  TGGATGGGAGGTACCTGGTGGACGGCGTCCCCTTCAGCTGCTGCAACCCCAGCTCCCCGCGGCCCTGTATTCAGTACCAG
         V  D  G  R  Y  L  V  D  G  V  P  F  S  C  C  N*  P  S  S  P  R  P  C  I  Q  Y  Q   226
 801  CTCACCAACAACTCTGCGCACTACAGCTATGACCACCAGACCGAGGAGCTCAACCTCTGGCTGCGGGGTTGCAGGGCTGC
         L  T  N*  N  S  A  H  Y  S  Y  D  H  Q  T  E  E  L  N  L  W  L  R  G  C  R  A  A   253
 881  CCTGCTGAATTACTACAGCAGCCTCATGAACTCCATGGGCGTTGTCACGCTTCTCATCTGGCTCTTTGAGGTGAGCATCA
         L  L  N  Y  Y  S  S  L  M  N  S  M  G  V  V  T  L  L  I  W  L  F  E  V  S  I   279
 961  CTGCCGGACTCCGCTTCCTCCACACAGCGCTGGAGAGCGTGTCCAACCCGGAGGACCCTGAGTGTGAGAGCGAGGGCTGG
         T  A  G  L  R  F  L  H  T  A  L  E  S  V  S  N  P  E  D  P  E  C  E  S  E  G  W   306
1041  TTGCTGGAGAATAGCGTGTCCGAGACCTGGAAGGCCTTTCTGGAGAGCTTTAAAAAACTGGGCAAGAGCAATCAGGTGGA
         L  L  E  N  S  V  S  E  T  W  K  A  F  L  E  S  F  K  K  L  G  K  S  N  Q  V  E   333
1121  GGCTGAAGCTGCAGACGCAGGCCAGGCCCCAGAGGCTGGCTGACGGCCTGGGGCGTCTCCCTTCCTCACCACTTAGTGGA
         A  E  A  A  D  A  G  Q  A  P  E  A  G  #
1201  CTCCAGGGAATGTGGATACCCCTTGTCCAGCTGAAGGTCCAAATTTCCCAAGAAAGCTGGTCACCTACTGACTCTCCTTG
1281  ACGTGGGCCTTGAAGTTCAGAGTCCTTAGGGCACACTATGCTACAAACATCGGTGAAATGGCTGCCTGCAAATGTGAGTG
1361  ACTGAACAAACACTCCCAGTGGATGCCTGTCTCACAGGACTGGCTAGTCAGGGCTCTGACCAAGTGTGAGCCCAGTTCTC
1441  CCATAGGTGACTGGCCACACCAAGGGCCTCCCCCTCCTTAGTAGTTAGTGTCTGCCTCTTTTTAAGCTCTAAGTTTCTGC
1521  ATCCCAACCATTATTTGACACATAAAATCAAGGTGAAAAAACAAAAAAAAAAAA
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