

Prokineticin Receptor (PROKR2) in pcDNA3.1+
Sequence Range: 1 to 1221

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                >KpnI   >BamHI
                |       |
          10      20      30      40      50
TTAACTTAGCTTGGTACCGAGCTCGGATCCACCATGGCAGCCCAGAATGG
                                M A A Q N G>
                                PROKR2>

          60      70      80      90     100
AAACACCAGTTTCACACCCAACTTTAATCCACCCCAAGACCATGCCTCCT
  N T S F T P N F N P P Q D H A S>
          PROKR2>

        110      120      130      140      150
CCCTCTCCTTTAACTTCAGTTATGGTGATTATGACCTCCCTATGGATGAG
S L S F N F S Y G D Y D L P M D E>
          PROKR2>

        160      170      180      190      200
GATGAGGACATGACCAAGACCCGACCTTCTTCGCAGCCAAGATCGTCAT
  D E D M T K T R T F F A A K I V I>
          PROKR2>

        210      220      230      240      250
TGGCATTGCACTGGCAGGCATCATGCTGGTCTGCGGCATCGGTAACTTTG
  G I A L A G I M L V C G I G N F>
          PROKR2>

        260      270      280      290      300
TCTTTATCGCTGCCCTCACCCGCTATAAGAAGTTGCGCAACCTCACCAAT
V F I A A L T R Y K K L R N L T N>
          PROKR2>

        310      320      330      340      350
CTGCTCATTGCCAACCTGGCCATCTCCGACTTCCTGGTGGCCATCATCTG
  L L I A N L A I S D F L V A I I C>
          PROKR2>

        360      370      380      390      400
CTGCCCCCTTCGAGATGGACTACTACGTGGTACGGCAGCTCTCCTGGGAGC
  C P F E M D Y Y V V R Q L S W E>
          PROKR2>

        410      420      430      440      450
ATGGCCACGTGCTCTGTGCCTCCGTCAACTACCTGCGCACCGTCTCCCTC
H G H V L C A S V N Y L R T V S L>
          PROKR2>

                                >EcoRV
                                |
          460      470      480      490      500
TACGTCTCCACCAATGCCTTGCTGGCCATTGCCATTGACAGATATCTTGC
  Y V S T N A L L A I A I D R Y L A>
          PROKR2>
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      510      520      530      540      550
CATCGTTTCACCCCTTGAAACCACGGATGAATTATCAAACGGCCTCCTTCC
  I  V  H  P  L  K  P  R  M  N  Y  Q  T  A  S  F>
      _____PROKR2_____>

      560      570      580      590      600
TGATCGCCTTGGTCTGGATGGTGTCCATTCTCATTGCCATCCCATCGGCT
  L  I  A  L  V  W  M  V  S  I  L  I  A  I  P  S  A>
      _____PROKR2_____>

      610      620      630      640      650
TACTTTGCAACAGAAACCGTCCTCTTTATTGTCAAGAGCCAGGAGAAGAT
  Y  F  A  T  E  T  V  L  F  I  V  K  S  Q  E  K  I>
      _____PROKR2_____>

      660      670      680      690      700
CTTCTGTGGCCAGATCTGGCCTGTGGATCAGCAGCTCTACTACAAGTCCT
  F  C  G  Q  I  W  P  V  D  Q  Q  L  Y  Y  K  S>
      _____PROKR2_____>

      710      720      730      740      750
ACTTCCTCTTCATCTTTGGTGTGCGAGTTCGTGGGCCCTGTGGTCACCATG
  Y  F  L  F  I  F  G  V  E  F  V  G  P  V  V  T  M>
      _____PROKR2_____>

      760      770      780      790      800
ACCCTGTGCTATGCCAGGATCTCCCGGGAGCTCTGGTTCAAGGCAGTCCC
  T  L  C  Y  A  R  I  S  R  E  L  W  F  K  A  V  P>
      _____PROKR2_____>

      810      820      830      840      850
TGGGTTCCAGACGGAGCAGATTTCGCAAGCGGCTGCGCTGCCGCAGGAAGA
  G  F  Q  T  E  Q  I  R  K  R  L  R  C  R  R  K>
      _____PROKR2_____>

      860      870      880      890      900
CGGTCCTGGTGCTCATGTGCATTCTCACGGCCTATGTGCTGTGCTGGGCA
  T  V  L  V  L  M  C  I  L  T  A  Y  V  L  C  W  A>
      _____PROKR2_____>

      910      920      930      940      950
CCCTTCTACGGTTTCACCATCGTTCGTGACTTCTTCCCCACTGTGTTCGT
  P  F  Y  G  F  T  I  V  R  D  F  F  P  T  V  F  V>
      _____PROKR2_____>

      960      970      980      990     1000
GAAGGAAAAGCACTACCTCACTGCCTTCTACGTGGTCGAGTGCATCGCCA
  K  E  K  H  Y  L  T  A  F  Y  V  V  E  C  I  A>
      _____PROKR2_____>

      >V330M
      |
    1010 |    1020      1030      1040      1050
TGAGCAACAGCATGATCAACACCATGTGCTTCGTGACGGTCAAGAACAAC
  M  S  N  S  M  I  N  T  M  C  F  V  T  V  K  N  N>
      _____PROKR2_____>

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      1060      1070      1080      1090      1100
ACCATGAAGTACTTCAAGAAGATGATGCTGCTGCACTGGCGTCCCTCCCA
  T  M  K  Y  F  K  K  M  M  L  L  H  W  R  P  S  Q>
_____PROKR2_____>

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      1110      1120      1130      1140      1150
GCGGGGGAGCAAGTCCAGTGCTGACCTTGACCTCAGAACCAATGGGGTGC
  R  G  S  K  S  S  A  D  L  D  L  R  T  N  G  V>
_____PROKR2_____>

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                                     >EcoRI   >PstI
                                     |         |
      1160      1170      1180      1190      1200
CCACAACAGAAGAGGTGGACTGTATCAGGCTGAAGTGAGAATTCTGCAGA
P  T  T  E  E  V  D  C  I  R  L  K  *>
_____PROKR2_____>

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>EcoRV      >BstXI
|            |
|            |
|      1210|      1220
TATCCAGCACAGTGGCGGCCG

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