

Sequence Range: 1 to 1192

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                                >HindIII  >KpnI  >BamHI
                                |      |      |
          10          20          30          40          50
GTTGCCGGGGCAGGGGGTTTAACTTAAGCTTGGTACCGAGCTCGGATCCA

                                >EcoRI
                                |
          >BstXI
          |
        60          70          80          90          100
CTAGTCCAGTGTGGTGAATTCACCATGGGCAACCACACGTGGGAGGGCT
          M G N H T W E G>
          _____GPR4_____>

        110          120          130          140          150
GCCACGTGGACTCGCGCGTGGACCACCTCTTTCCGCCATCCCTCTACATC
C H V D S R V D H L F P P S L Y I>
          _____GPR4_____>

                                >BstXI
                                |
        160          170          180          190          200
TTTGTTCATCGGCGTGGGGCTGCCCACCAACTGCCTGGCTCTGTGGGCGGC
F V I G V G L P T N C L A L W A A>
          _____GPR4_____>

        210          220          230          240          250
CTACCGCCAGGTGCAACAGCGCAACGAGCTGGGCGTCTACCTGATGAACC
Y R Q V Q Q R N E L G V Y L M N>
          _____GPR4_____>

        260          270          280          290          300
TCAGCATCGCCGACCTGCTGTACATCTGCACGCTGCCGCTGTGGGTGGAC
L S I A D L L Y I C T L P L W V D>
          _____GPR4_____>

                                >BamHI
                                |
        310          320          330          340          350
TACTTCCTGCACCACGACAACCTGGATCCACGGCCCCGGGTCCTGCAAGCT
Y F L H H D N W I H G P G S C K L>
          _____GPR4_____>

        360          370          380          390          400
CTTTGGGTTTCATCTTCTACACCAATATCTACATCAGCATCGCCTTCCTGT
F G F I F Y T N I Y I S I A F L>
          _____GPR4_____>

        410          420          430          440          450
GCTGCATCTCGGTGGACCGCTACCTGGCTGTGGCCCACTCCGCTTC
C C I S V D R Y L A V A H P L R F>
          _____GPR4_____>

        460          470          480          490          500
GCCCCGCTGCGCCGCTCAAGACCGCCGTGGCCGTGAGCTCCGTGGTCTG
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A R L R R V K T A V A V S S V V W>
_____GPR4_____>

      >BstXI
      |
      510      520      530      540      550
GGCCACGGAGCTGGGCGCCAACTCGGCGCCCCTGTTCCATGACGAGCTCT
  A T E L G A N S A P L F H D E L>
_____GPR4_____>

      560      570      580      590      600
TCCGAGACCGCTACAACCACACCTTCTGCTTTGAGAAGTTCCCCATGGAA
F R D R Y N H T F C F E K F P M E>
_____GPR4_____>

      610      620      630      640      650
GGCTGGGTGGCCTGGATGAACCTCTATCGGGTGTTCTGTTGGCTTCCTCTT
  G W V A W M N L Y R V F V G F L F>
_____GPR4_____>

      660      670      680      690      700
CCCGTGGGCGCTCATGCTGCTGCTACCGGGGCATCCTGCGGGCCGTGC
  P W A L M L L S Y R G I L R A V>
_____GPR4_____>

      710      720      730      740      750
GGGGCAGCGTGTCCACCGAGCGCCAGGAGAAGGCCAAGATCAAGCGGCTG
R G S V S T E R Q E K A K I K R L>
_____GPR4_____>

      >BstXI
      |
      760      770      780      790      800
GCCCTCAGCCTCATCGCCATCGTGCTGGTCTGCTTTGCGCCCTATCACGT
  A L S L I A I V L V C F A P Y H V>
_____GPR4_____>

      >BstXI
      |
      810      820      830      840      850
GCTCTTGCTGTCCCGCAGCGCCATCTACCTGGGCGGCCCTGGGACTGCG
  L L L S R S A I Y L G R P W D C>
_____GPR4_____>

      860      870      880      890      900
GCTTCGAGGAGCGCGTCTTTTCTGCATACCACAGCTCACTGGCTTTCACC
G F E E R V F S A Y H S S L A F T>
_____GPR4_____>

      910      920      930      940      950
AGCCTCAACTGTGTGGCGGACCCCATCCTCTACTGCCTGGTCAACGAGGG
  S L N C V A D P I L Y C L V N E G>
_____GPR4_____>

      960      970      980      990      1000
CGCCCGCAGCGATGTGGCCAAGGCCCTGCACAACCTGCTCCGCTTTTCTGG
  A R S D V A K A L H N L L R F L>

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____GPR4____>

      1010      1020      1030      1040      1050
CCAGCGACAAGCCCCAGGAGATGGCCAATGCCTCGCTCACCCCTGGAGACC
A S D K P Q E M A N A S L T L E T>
____GPR4____>

      1060      1070      1080      1090      1100
C C A C T C A C C T C C A A G A G G A A C A G C A C A G C C A A G C C A T G A C T G G C A G C T G
P L T S K R N S T A K A M T G S W>
____GPR4____>

      1110      1120      1130      1140      1150
G G C G G C C A C T C C G C C C T C C C A G G G G G A C C A G G T G C A G C T G A A G A T G C T G C
A A T P P S Q G D Q V Q L K M L>
____GPR4____>

      >XhoI      >XbaI      >ApaI
      |         |         |
      1160      | 1170      | 1180      | 1190
CGCCAGCACAATGACTCGAGTCTAGAGGGCCCCGTAAACCCT
P P A Q *>
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