

Homo sapiens G protein-coupled receptor 39 (GPR39) in pcDNA3.1+
Sequence Range: 1 to 1488

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>HindIII      >KpnI  
|             |  
>AflIII      >Asp718I    >BamHI  
|             |           |  
|             |           |  
          10         20        30          40          50  
ACTTAAGCTTGGTACCGAGCTCGGATCCACCATGGCTTCACCCAGCCTCC  
                                     M A S P S L>  
                               _____ GPR39 _____>  
  
              60            70            80            90            100  
CGGGCAGTGACTGCTCCCAAATCATTTGATCACAGTCATGTCCCCGAGTTTT  
P   G   S   D   C   S   Q     I   I   D   H   S   H   V   P   E   F>  
_____ GPR39 _____>  
  
              110           120           130           140           150  
GAGGTGGCCACCTGGATCAAAATCACCCCTTATTCTGGTGTACCTGATCAT  
E   V   A   T   W   I   K   I   T   L   I   L   V   Y   L   I   I>  
_____ GPR39 _____>  
  
              160           170           180           190           200  
CTTCGTGATGGGCCTTCTGGGGAACAGCGCCACCATTTCGGGTACCCCAGG  
F   V   M   G   L   L   G   N   S   A   T   I   R   V   T   Q>  
_____ GPR39 _____>  
  
              210           220           230           240           250  
TGCTGCAGAAGAAAAGGATACTTGCAGAAGGAGGTGACAGACCACATGGTG  
V   L   Q   K   K   G   Y   L   Q   K   E   V   T   D   H   M   V>  
_____ GPR39 _____>  
  
              260           270           280           290           300  
AGTTTGGCTTGCTCGGACATCTTGGTGTTCCTCATCGGCATGCCCATGGA  
S   L   A   C   S   D   I   L   V   F   L   I   G   M   P   M   E>  
_____ GPR39 _____>  
  
              310           320           330           340           350  
GTTCTACAGCATCATCTGGAATCCCCTGACCAGTCCAGCTACACCCTGT  
F   Y   S   I   I   W   N   P   L   T   T   S   S   Y   T   L>  
_____ GPR39 _____>  
  
              360           370           380           390           400  
CCTGCAAGCTGCACACTTTCTCTTCGAGGCCTGCAGCTACGCTACGCTG  
S   C   K   L   H   T   F   L   F   E   A   C   S   Y   A   T   L>  
_____ GPR39 _____>  
  
              410           420           430           440           450  
CTGCACGTGCTGACA CTCTTTCGAGCGCTACATCGCCATCTGTACCCC  
L   H   V   L   T   L   S   F   E   R   Y   I   A   I   C   H   P>  
_____ GPR39 _____>  
  
              460           470           480           490           500  
CTTCAGGTACAAGGCTGTGTCGGGACCTTGCCAGGTGAAGCTGCTGATTG  
F   R   Y   K   A   V   S   G   P   C   Q   V   K   L   L   I>  
_____ GPR39 _____
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      510      520      530      540      550
GCTTCGTCTGGGTACCTCCGCCCTGGTGGCACTGCCCTTGCTGTTTGCC
G F V W V T S A L V A L P L L F A>
      GPR39>

      560      570      580      590      600
ATGGGTACTGAGTACCCCTGGTGAACGTGCCCAGCCACCGGGGTCTCAC
M G T E Y P L V N V P S H R G L T>
      GPR39>

      610      620      630      640      650
TTGCAACCGCTCCAGCACCCGCCACCACGAGCAGCCCAGACCTCCAATA
C N R S S T R H H E Q P E T S N>
      GPR39>

      660      670      680      690      700
TGTCCATCTGTACCAACCTCTCCAGCCGCTGGACCGTGTTCCAGTCCAGC
M S I C T N L S S R W T V F Q S S>
      GPR39>

      710      720      730      740      750
ATCTTCGGCGCCTTCGTGGTCTACCTCGTGGTCCTGCTCTCCGTAGCCTT
I F G A F V V Y L V V L L S V A F>
      GPR39>

      760      770      780      790      800
CATGTGCTGGAACATGATGCAGGTGCTCATGAAAAGCCAGAAGGGCTCGC
M C W N M M Q V L M K S Q K G S>
      GPR39>

      810      820      830      840      850
TGGCCGGGGGCACGCGGCCTCCGCAGCTGAGGAAGTCCGAGAGCGAAGAG
L A G G T R P P Q L R K S E S E E>
      GPR39>

      860      870      880      890      900
AGCAGGACCGCCAGGAGGCAGACCATCATCTTCCTGAGGCTGATTGTTGT
S R T A R R Q T I I F L R L I V V>
      GPR39>

      910      920      930      940      950
GACATTGGCCGTATGCTGGATGCCCAACCAGATTCCGAGGATCATGGCTG
T L A V C W M P N Q I R R I M A>
      GPR39>

      960      970      980      990     1000
CGGCCAAACCCAAGCACGACTGGACGAGGTCCTACTTCCGGGCGTACATG
A A K P K H D W T R S Y F R A Y M>
      GPR39>

     1010     1020     1030     1040     1050
ATCCTCCTCCCCTTCTCGGAGACGTTTTTCTACCTCAGCTCGGTCATCAA
I L L P F S E T F F Y L S S V I N>
      GPR39>

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      1060      1070      1080      1090      1100
CCCCGCTCCTGTACACGGTGTCTCGCAGCAGTTTCGGCGGGTGTTCGTGC
  P  L  L  Y  T  V  S  S  Q  Q  F  R  R  V  F  V>
_____GPR39_____>

      1110      1120      1130      1140      1150
AGGTGCTGTGCTGCCGCCTGTCTGCTGCAGCACGCCAACCACGAGAAGCGC
  Q  V  L  C  C  R  L  S  L  Q  H  A  N  H  E  K  R>
_____GPR39_____>

      1160      1170      1180      1190      1200
CTGCGCGTACATGCGCACTCCACCACCGACAGCGCCCGCTTTGTGCAGCG
  L  R  V  H  A  H  S  T  T  D  S  A  R  F  V  Q  R>
_____GPR39_____>

      1210      1220      1230      1240      1250
CCCGTTGCTCTTCGCGTCCCGGCCAGTCCTCTGCAAGGAGAACTGAGA
  P  L  L  F  A  S  R  R  Q  S  S  A  R  R  T  E>
_____GPR39_____>

      >AflIII
      |
      1260      1270      1280      1290      1300
AGATTTTCTTAAGCACTTTTCAGAGCGAGGCCGAGCCCCAGTCTAAGTCC
  K  I  F  L  S  T  F  Q  S  E  A  E  P  Q  S  K  S>
_____GPR39_____>

      >XhoI
      |
      1310      1320      1330      1340      1350
CAGTCATTGAGTCTCGAGTCACTAGAGCCCAACTCAGGCGCGAAACCAGC
  Q  S  L  S  L  E  S  L  E  P  N  S  G  A  K  P  A>
_____GPR39_____>

      >EcoRI
      |
      1360      1370      1380      1390      1400
CAATTCTGCTGCAGAGAATGGTTTTTCAGGAGCATGAAGTTTGAGAATTCT
  N  S  A  A  E  N  G  F  Q  E  H  E  V  *>
_____GPR39_____>

      >NotI
      |
      >EcoRV      >BstXI      >XhoI      >XbaI
      |          |          |          |
      1410      1420      1430      1440      1450
GCAGATATCCAGCACAGTGGCGGCCGCTCGAGTCTAGATGACTAACTATA

      1460      1470      1480
GTGTCACCTAAATCGTATGTCCCTTTAGTGAGGGTTAA

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