

Human orphan g protein coupled receptor 31 (GPR31), wild type, cloned into pcDNA3.1+

Sequence Range: 1 to 1074

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                                     >EcoRI
                                     |
          >KpnI      >BamHI      >BstXI
          |          |          |
    10      20      30      40      50
TACTTAGCTTGGTACCGAGCTCGGATCCACTAGTCCAGTGTGGTGGAATT

                                     >BstXI
                                     |
    60      70      80      90     100
CACCATGCCATTCCCAAACCTGCTCAGCCCCCAGCACTGTGGTGGCCACAG
  M  P  F  P  N  C  S  A  P  S  T  V  V  A  T>
      _____GPR31_____>

>BstXI
|
110      120      130      140      150
CTGTGGGTGTCTTGCTGGGGCTGGAGTGTGGGCTGGGTCTGCTGGGCAAC
A  V  G  V  L  L  G  L  E  C  G  L  G  L  L  G  N>
      _____GPR31_____>

160      170      180      190      200
GCGGTGGCGCTGTGGACCTTCCTGTTCCGGGTCAGGGTGTGGAAGCCGTA
A  V  A  L  W  T  F  L  F  R  V  R  V  W  K  P  Y>
      _____GPR31_____>

210      220      230      240      250
CGCTGTCTACCTGCTCAACCTGGCCCTGGCTGACCTGCTGTTGGCTGCGT
A  V  Y  L  L  N  L  A  L  A  D  L  L  L  A  A>
      _____GPR31_____>

260      270      280      290      300
GCCTGCCTTTCTGGCCGCCTTCTACCTGAGCCTCCAGGCTTGGCATCTG
C  L  P  F  L  A  A  F  Y  L  S  L  Q  A  W  H  L>
      _____GPR31_____>

          >ApaI
          |
          >nt272_A->G_(aa._H->R)
          |          |
    310      320      330      340      350
GGCCGTGTGGGCTGCTGGGCCCTGCGCTTCCTGCTGGACCTCAGCCGCAG
G  R  V  G  C  W  A  L  R  F  L  L  D  L  S  R  S>
      _____GPR31_____>

                                     >KpnI
                                     |
    360      370      380      390     400
CGTGGGGATGGCCTTCCTGGCCGCGCTGGCTTTGGACCGGTACCTCCGTG
V  G  M  A  F  L  A  A  V  A  L  D  R  Y  L  R>
      _____GPR31_____>

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410 420 430 440 450
TGGTCCACCCTCGGCTTAAGGTCAACCTGCTGTCTCCTCAGGCGGCCCTG
V V H P R L K V N L L S P Q A A L>
GPR31>

460 470 480 490 500
GGGGTCTCGGGCCTCGTCTGGCTCCTGATGGTCGCCCTCACCTGCCCCGG
G V S G L V W L L M V A L T C P G>
GPR31>

510 520 530 540 550
CTTGCTCATCTCTGAGGCCGCCAGAACTCCACCAGGTGCCACAGTTTCT
L L I S E A A Q N S T R C H S F>
GPR31>

560 570 580 590 600
ACTCCAGGGCAGACGGCTCCTTCAGCATCATCTGGCAGGAAGCACTCTCC
Y S R A D G S F S I I W Q E A L S>
GPR31>

610 620 630 640 650
TGCCTTCAGTTTGTCTCCCTTTGGCCTCATCGTGTCTGCAATGCAGG
C L Q F V L P F G L I V F C N A G>
GPR31>

660 670 680 690 700
CATCATCAGGGCTCTCCAGAAAAGACTCCGGGAGCCTGAGAAACAGCCCA
I I R A L Q K R L R E P E K Q P>
GPR31>

710 720 730 740 750
AGCTTCAGCGGGCCCAGGCACTGGTCACCTTGGTGGTGGTGCTGTTTGTCT
K L Q R A Q A L V T L V V V L F A>
GPR31>

760 770 780 790 800
CTGTGCTTTCTGCCCTGCTTCCTGGCCAGAGTCCTGATGCACATCTTCCA
L C F L P C F L A R V L M H I F Q>
GPR31>

810 820 830 840 850
GAATCTGGGGAGCTGCAGGGCCCTTTGTGCAGTGGCTCATACCTCGGATG
N L G S C R A L C A V A H T S D>
GPR31>

860 870 880 890 900
TCACGGGCAGCCTCACCTACCTGCACAGTGTGCTCAACCCCGTGGTATAC
V T G S L T Y L H S V L N P V V Y>
GPR31>

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          910          920          930          940          950
TGCTTCTCCAGCCCCACCTTCAGGAGCTCCTATCGGAGGGTCTTCCACAC
  C  F  S  S  P  T  F  R  S  S  Y  R  R  V  F  H  T>
_____GPR31_____>
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          960          970          980          990          1000
CCTCCGAGGCAAAGGGCAGGCAGCAGAGCCCCCAGATTTCAACCCAGAG
  L  R  G  K  G  Q  A  A  E  P  P  D  F  N  P  R>
_____GPR31_____>
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          >XhoI    >XbaI
          |      |
        1010    | 1020|      1030      1040      1050
ACTCCTATTCTGACTCGAGTCTAGATGACTAACTATAGTGTCACCTAAA
D  S  Y  S  *>
_____>
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        1060      1070
TCGTATGTCCCTTTAGTGAGGGTT
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