

Prostaglandin D2 Receptor (PTGDR) in pcDNA3.1+: Type = cDNA
Sequence Range: 1 to 1153

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      >HindIII   >KpnI   >BamHI
      |         |         |
      10        20        30        40        50
CGTTTACTTAAGCTTGGTACCGAGCTCGGATCCACCATGAAGTCGCCGTT
                                     M K S P F>
                                     _____>

                                >BstXI
                                |
                                60        70        80        90        100
CTACCGCTGCCAGAACACCACCTCTGTGGAAAAAGGCAACTCGGCGGTGA
  Y R C Q N T T S V E K G N S A V>
_____PTGDR_____>

      110        120        130        140        150
TGGGCGGGGTGCTCTTCAGCACCGGCCTCCTGGGCAACCTGCTGGCCCTG
M G G V L F S T G L L G N L L A L>
_____PTGDR_____>

      160        170        180        190        200
GGGCTGCTGGCGCGCTCGGGGCTGGGGTGGTGCTCGCGGCGTCCACTGCG
  G L L A R S G L G W C S R R P L R>
_____PTGDR_____>

      210        220        230        240        250
CCCCTGCCCCTCGGTCTTCTACATGCTGGTGTGTGGCCTGACGGTCACCG
  P L P S V F Y M L V C G L T V T>
_____PTGDR_____>

      260        270        280        290        300
ACTTGCTGGGCAAGTGCCTCCTAAGCCCGGTGGTGCTGGCTGCCTACGCT
D L L G K C L L S P V V L A A Y A>
_____PTGDR_____>

      310        320        330        340        350
CAGAACCGGAGTCTGCGGGTGCTTGCGCCCGCATTGGACAACCTCGTTGTG
  Q N R S L R V L A P A L D N S L C>
_____PTGDR_____>

      360        370        380        390        400
CCAAGCCTTCGCCTTCTTCATGTCCTTCTTTGGGCTCTCCTCGACACTGC
  Q A F A F F M S F F G L S S T L>
_____PTGDR_____>

                                >BstXI
                                |
                                410        420        430        440        450
AACTCCTGGCCATGGCACTGGAGTGCTGGCTCTCCCTAGGGCACCCCTTTC
Q L L A M A L E C W L S L G H P F>
_____PTGDR_____>

      460        470        480        490        500
TTCTACCGACGGCACATCACCTGCGCCTGGGCGCACTGGTGGCCCCGGT
  F Y R R H I T L R L G A L V A P V>
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PTGDR>

510 520 530 540 550
GGTGAGCGCCTTCTCCCTGGCTTTCTGCGCGCTACCTTTTCATGGGCTTCG
V S A F S L A F C A L P F M G F>

PTGDR>

560 570 580 590 600
GGAAGTTCGTGCAGTACTGCCCCGGCACCTGGTGCTTTATCCAGATGGTC
G K F V Q Y C P G T W C F I Q M V>

PTGDR>

>nucleotide_C576T_Silent_Mutation

610 620 630 640 650
CACGAGGAGGGTTCGCTGTGCGGTGCTGGGGTACTCTGTGCTCTACTCCAG
H E E G S L S V L G Y S V L Y S S>
PTGDR>

>BstXI

660 670 680 690 700
CCTCATGGCGCTGCTGGTCCTCGCCACCGTGCTGTGCAACCTCGGCGCCA
L M A L L V L A T V L C N L G A>
PTGDR>

>PstI

710 720 730 740 750
TGCGCAACCTCTATGCGATGCACCGGCGGCTGCAGCGGCACCCGCGCTCC
M R N L Y A M H R R L Q R H P R S>
PTGDR>

760 770 780 790 800
TGCACCAGGGAAGTGTGCCGAGCCGCGCGGACGGGAGGGAAGCGTCCCC
C T R D C A E P R A D G R E A S P>
PTGDR>

810 820 830 840 850
TCAGCCCCTGGAGGAGCTGGATCACCTCCTGCTGCTGGCGCTGATGACCG
Q P L E E L D H L L L L A L M T>
PTGDR>

860 870 880 890 900
TGCTCTTCACTATGTGTTCTCTGCCCCGTAATTTATCGCGCTTACTATGGA
V L F T M C S L P V I Y R A Y Y G>
PTGDR>

910 920 930 940 950
GCATTTAAGGATGTCAAGGAGAAAAACAGGACCTCTGAAGAAGCAGAAGA
A F K D V K E K N R T S E E A E D>
PTGDR>

960 970 980 990 1000
CCTCCGAGCCTTGCGATTTCTATCTGTGATTTCAATTGTGGACCCTTGGA
L R A L R F L S V I S I V D P W>
PTGDR>

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      1010      1020      1030      1040      1050
TTTTTATCATTTCAGATCTCCAGTATTTTCGGATATTTTTTTCACAAGATT
I  F  I  I  F  R  S  P  V  F  R  I  F  F  H  K  I>
_____PTGDR_____>

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                                                    >BstXI
                                                    |
      1060      1070      1080      1090      1100
TTCATTAGACCTCTTAGGTACAGGAGCCGGTGCAGCAATTCCACTAACAT
F  I  R  P  L  R  Y  R  S  R  C  S  N  S  T  N  M>
_____PTGDR_____>

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                        >EcoRV
                        |
          >EcoRI      >PstI      >BstXI
          |           |           |
      1110      1120      |1130      1140      1150
GGAATCCAGTCTGTGAGAATTCTGCAGATATCCAGCACAGTGGCGGCCGC
E  S  S  L  *>
_____PTGDR_____>

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TCG