



PLD4 (NM_138790.5) - cDNA - 2026-05-18

AGAGAAGAGG AGGTTGGTGT GGAGCACAGG CAGCACCGAG CCTGCCCCGT -63
GAGCTGAGGG CCTGCAGTCT GCGGCTGGAA TCAGGATAGA CACCAAGGCA -13
GGACCCCCAG **AGATG**CTGAA GCCTCTTTGG AAAGCAGCAG TGGCCCCAC 38
ATGGCCATGC TCCATGCCGC CCCGCCGCC GTGGGACAGA GAGGCTGGCA 88
CGTTGCAGGT CCTGGGAGCG CTGGCTGTGC TGTGGCTGGG CTCCGTGGCT 138
CTTATCTGCC TCCTGTGGCA AGTGCCCCGT CCTCCCACCT GGGGCCAGGT 188
GCAGCCCAAG GACGTGCCCA GGTCCTGGGA GCATGGCTCC AGCCCAGCTT 238
GGGAGCCCCCT GGAAGCAGAG GCCAGGCAGC AGAGGGACTC CTGCCAGCTT 288
GTCCTTGTGG AAAGCATCCC CCAGGACCTG CCATCTGCAG CCGGCAGCCC 338
CTCTGCCCAG CCTCTGGGCC AGGCCTGGCT GCAGCTGCTG GACACTGCCC 388
AGGAGAGCGT CCACGTGGCT TCATACTACT GGTCCCTCAC AGGGCCTGAC 438
ATCGGGGTCA ACGACTCGTC TTCCCAGCTG GGAGAGGCTC TTCTGCAGAA 488
GCTGCAGCAG CTGCTGGGCA GGAACATTTT CCTGGCTGTG GCCACCAGCA 538
GCC**C**GACACT GGCCAGGACA TCCACCGA**C**C TGCAGGTTCT GGCTGCCCGA 588 **P181L D189E**
GGTGCCCATG TAC**G**ACAGGT GCCCATGGGG CGGCTCACCA GGGGTGTTTT 638 **R201Q**
GCACTCCAAA TTCTGGGTTG TGGATGGACG GCACATATAC ATGGGCAGTG 688
CCAACATGGA CTGGCGGTCT CTGACGCAGG TGAAGGAGCT TGGCGTGTCT 738
ATCT**A**TAACT GCAGCCACCT GGCCCAAGAC CTGGAGAAGA CCTTCCAGAC 788 **Y248C**
CTACTGGGTA CTGGGGGTGC CCAAGGCTGT CCTCCCCAAA ACCTGGCCTC 838
AGAACTTCTC ATCTCACTTC AACCCTTTCC AGCCCTTCCA CGGCCTCTTT 888
GATGGGGTGC CCACCCTGC CTACTTCTCA GCGTCGCCAC CAGCACTCTG 938
TCCCCAGGGC CGCACCCGGG ACCTGGAGG**C** GCTGCTGGCG GTGATGGGGA 988 **A323V**

GCGCCCAGGA GTTCATCTAT GCCTCCGTA TGGAGTATTT CCCACCACG 1038
CGCTTCAGCC ACCCCCCGAG GTACTGGCCG GTGCTGGACA ACGCGCTGCG 1088
GCGCGCAGCC TTCGGCAAGG GCGTGC GCGCTGCTG GTCGGCTGCG 1138 [A364Rfs*45](#)
GACTCAACAC GGACCCACC ATGTTCCCT ACCTGCGGTC CCTGCAGGCG 1188
CTCAGCAACC CCGCGGCCAA CGTCTCTGTG GACGTGAAAG TCTTCATCGT 1238
GCCGGTGGGG AACCATTCCA ACATCCCATT CAGCAGGGTG AACCACAGCA 1288
AGTTCATGGT CACGGAGAAG GCAGCCTACA TAGGCACCTC CAACTGGTCG 1338
GAGGATTACT TCAGCAGCAC GCGGGGGTG GGCTTGGTGG TCACCCAGAG 1388 [G457D](#)
CCCTGGCGCG CAGCCC GGGCCACGGT GCAGGAGCAG CTGCGGCAGC 1438
TCTTTGAGCG GGACTGGAGT TCGCGCTACG CCGTCGGCCT GGACGGACAG 1488
GCTCCGGGCC AGGACTGCGT TTGGCAGGGC TGAAGGGGGC CTCTTTTCT *17
CTCGGCGACC CCGCCCCGCA CGCGCCCTCC CCTCTGACCC CGGCCTGGGC *67
TTCAGCCGCT TCCTCCCGCA AGCAGCCCGG GTCCGCACTG CGCCAGGAGC *117
CGCCTGCGAC CGCCCGGGCG TCGCAAACCG CCCGCTGCT CTCTGATTTC *167
CGAGTCCAGC CCCCCCTGAG CCCACCTCC TCCAGGGAGC CCTCCAGGAA *217
GCCCCTTCCC TGACTCCTGG CCCACAGGCC AGGCCTAAAA AAAACTCGTG *267
GCTTC

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