



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

AGAGAAGAGG AGGTTGGTGT GGAGCACAGG CAGCACCGAG CCTGCCCCGT -63
GAGCTGAGGG CCTGCAGTCT GCGGCTGGAA TCAGGATAGA CACCAAGGCA -13
GGACCCCCAG **AGATGCTGAA** GCCTCTTTGG AAAGCAGCAG TGGCCCCAC 38
MetLeuLy sProLeuTrp LysAlaAlaV alAlaProTh 13

ATGGCCATGC TCCATGCCGC CCCGCCGCC GTGGGACAGA GAGGCTGGCA 88
rTrpProCys SerMetProP roArgArgPr oTrpAspArg GluAlaGlyT 30

CGTTGCAGGT CCTGGGAGCG CTGGCTGTGC TGTGGCTGGG CTCCGTGGCT 138
hrLeuGlnVa lLeuGlyAla LeuAlaValL euTrpLeuGl ySerValAla 46

CTTATCTGCC TCCTGTGGCA AGTGCCCCGT CCTCCCACCT GGGCCAGGT 188
LeuIleCysL euLeuTrpGl nValProArg ProProThrT rpGlyGlnVa 63

GCAGCCCAAG GACGTGCCCA GTCTCTGGGA GCATGGCTCC AGCCCAGCTT 238
lGlnProLys AspValProA rgSerTrpGl uHisGlySer SerProAlaT 80

GGGAGCCCCCT GGAAGCAGAG GCCAGGCAGC AGAGGGACTC CTGCCAGCTT 288
rpGluProLe uGluAlaGlu AlaArgGlnG lnArgAspSe rCysGlnLeu 96

GTCCTTGTGG AAAGCATCCC CCAGGACCTG CCATCTGCAG CCGGCAGCCC 338
ValLeuValG luSerIlePr oGlnAspLeu ProSerAlaA laGlySerPr 113

CTCTGCCCAG CCTCTGGGCC AGGCCCTGGCT GCAGCTGCTG GACACTGCCC 388
oSerAlaGln ProLeuGlyG lnAlaTrpLe uGlnLeuLeu AspThrAlaG 130

AGGAGAGCGT CCACGTGGCT TCATACTACT GGTCCCTCAC AGGGCCTGAC 438
lnGluSerVa lHisValAla SerTyrTyrT rpSerLeuTh rGlyProAsp 146

ATCGGGGTCA ACGACTCGTC TTCCCAGCTG GGAGAGGCTC TTCTGCAGAA 488
IleGlyValA snAspSerSe rSerGlnLeu GlyGluAlaL euLeuGlnLy 163

GCTGCAGCAG CTGCTGGGCA GGAACATTC CCTGGCTGTG GCCACCAGCA 538
sLeuGlnGln LeuLeuGlyA rgAsnIleSe rLeuAlaVal AlaThrSerS 180

GCCCGACACT GGCCAGGACA TCCACCGACC TGCAGTTTCT GGCTGCCCGA 588 [P181L](#) [D189E](#)
erProThrLe uAlaArgThr SerThrAspL euGlnValLe uAlaAlaArg 196

GGTGCCCATG TACGACAGGT GCCCATGGGG CGGCTCACCA GGGGTGTTTT 638 [R201Q](#)
GlyAlaHisV alArgGlnVa lProMetGly ArgLeuThrA rgGlyValLe 213

GCACTCCAAA TTCTGGGTTG TGGATGGACG GCACATATAC ATGGGCAGTG 688
uHisSerLys PheTrpValV alAspGlyAr gHisIleTyr MetGlySerA 230

CCAACATGGA CTGGCGGTCT CTGACGCAGG TGAAGGAGCT TGGCGCTGTC 738
laAsnMetAs pTrpArgSer LeuThrGlnV alLysGluLe uGlyAlaVal 246

ATCTATAACT GCAGCCACCT GGCCCAAGAC CTGGAGAAGA CCTTCCAGAC 788 [Y248C](#)
IleTyrAsnC ysSerHisLe uAlaGlnAsp LeuGluLysT hrPheGlnTh 263

CTACTGGGTA CTGGGGGTGC CCAAGGCTGT CCTCCCCAAA ACCTGGCCTC 838

rTyrTrpVal LeuGlyValP roLysAlaVa lLeuProLys ThrTrpProG 280

AGAACTTCTC ATCTCACTTC AACCGTTTCC AGCCCTTCCA CGGCCTCTTT 888

lnAsnPheSe rSerHisPhe AsnArgPheG lnProPheHi sGlyLeuPhe 296

GATGGGGTGC CCACCACTGC CTACTTCTCA GCGTCGCCAC CAGCACTCTG 938

AspGlyValP roThrThrAl aTyrPheSer AlaSerProP roAlaLeuCy 313

TCCCCAGGGC CGCACCCGGG ACCTGGAGGC GCTGCTGGCG GTGATGGGGA 988 [A323V](#)

sProGlnGly ArgThrArgA spLeuGluAl aLeuLeuAla ValMetGlyS 330

GCGCCCAGGA GTTCATCTAT GCCTCCGTA TGGAGTATTT CCCCACCACG 1038

erAlaGlnGl uPheIleTyr AlaSerValM etGluTyrPh eProThrThr 346

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ArgPheSerH isProProAr gTyrTrpPro ValLeuAspA snAlaLeuAr 363

GCGCGCAGCC TTCGGCAAGG GCGTGC GCGCTGCTG GTCGGCTGCG 1138 [A364Rfs*45](#)

gAlaAlaAla PheGlyLysG lyValArgVa lArgLeuLeu ValGlyCysG 380

GACTCAACAC GGACCCACCT ATGTTCCCTT ACCTGCGGTC CCTGCAGGCG 1188

lyLeuAsnTh rAspProThr MetPheProT yrLeuArgSe rLeuGlnAla 396

CTCAGCAACC CCGCGGCCAA CGTCTCTGTG GACGTGAAAG TCTTCATCGT 1238

LeuSerAsnP roAlaAlaAs nValSerVal AspValLysV alPheIleVa 413

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lProValGly AsnHisSerA snIleProPh eSerArgVal AsnHisSerL 430

AGTTCATGGT CACGGAGAAG GCAGCCTACA TAGGCACCTC CAACTGGTCG 1338

ysPheMetVa lThrGluLys AlaAlaTyrI leGlyThrSe rAsnTrpSer 446

GAGGATTACT TCAGCAGCAC GGCGGGGGTG GGCTTGGTGG TCACCCAGAG 1388 [G457D](#)

GluAspTyrP heSerSerTh rAlaGlyVal GlyLeuValV alThrGlnSe 463

CCCTGGCGCG CAGCCCGCGG GGGCCACGGT GCAGGAGCAG CTGCCGCAGC 1438

rProGlyAla GlnProAlaG lyAlaThrVa lGlnGluGln LeuArgGlnL 480

TCTTTGAGCG GGACTGGAGT TCGCGCTACG CCGTCGGCCT GGACGGACAG 1488

euPheGluAr gAspTrpSer SerArgTyrA laValGlyLe uAspGlyGln 496

GCTCCGGGCC AGGACTGCGT TTGGCAGGGC TGAAGGGGGC CTCTTTTCT *17

AlaProGlyG lnAspCysVa lTrpGlnGly Stop

CTCGGCGACC CCGCCCCGCA CGCGCCCTCC CCTCTGACCC CGGCCTGGGC *67

TTCAGCCGCT TCCTCCCGCA AGCAGCCCGG GTCCGCACTG CGCCAGGAGC *117

CGCCTGCGAC CGCCCGGGCG TCGCAAACCG CCCGCCTGCT CTCTGATTTC *167

CGAGTCCAGC CCCCCCTGAG CCCACCTCC TCCAGGGAGC CCTCCAGGAA *217

GCCCCTTCCC TGACTCCTGG CCCACAGGCC AGGCCTAAAA AAAACTCGTG *267

GCTTC

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