



*PLD4* (NM\_138790.5) - cDNA + Protein - 2026-04-02

AGAGAAGAGG AGGTTGGTGT GGAGCACAGG CAGCACCGAG CCTGCCCCGT -63  
GAGCTGAGGG CCTGCAGTCT GCGGCTGGAA TCAGGATAGA CACCAAGGCA -13  
GGACCCCCAG **AGATGCTGAA** GCCTCTTTGG AAAGCAGCAG TGGCCCCCAC 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 GGGGCCAGGT 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 GACTCTGCCC 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

GCCCGACT GGCCAGGACA TCCACCGACC TGCAGTTCT GGCTGCCCGA 588  
erProThrLe uAlaArgThr SerThrAspL euGlnValLe uAlaAlaArg 196

GGTGCCCATG TACGACAGGT GCCCATGGGG CGGCTCACCA GGGGTGTTTT 638  
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  
IleTyrAsnC ysSerHisLe uAlaGlnAsp LeuGluLysT hrPheGlnTh 263

[P181L](#) [D189E](#)

[R201Q](#)

[Y248C](#)

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

GCGCCAGGA GTTCATCTAT GCCTCCGTA TGGAGTATTT CCCCACCACG 1038

erAlaGlnGl uPheIleTyr AlaSerValM etGluTyrPh eProThrThr 346

CGCTTCAGCC ACCCCCCGAG GTACTGGCCG GTGCTGGACA ACGCGCTGCG 1088

ArgPheSerH isProProAr gTyrTrpPro ValLeuAspA snAlaLeuAr 363

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

gAlaAlaAla PheGlyLysG lyValArgVa lArgLeuLeu ValGlyCysG 380

GACTCAACAC GGACCCACCC ATGTTCCCTT ACCTGCGGTC CCTGCAGGCG 1188

lyLeuAsnTh rAspProThr MetPheProT yrLeuArgSe rLeuGlnAla 396

CTCAGCAACC CCGCGGCCAA CGTCTCTGTG GACGTGAAAG TCTTCATCGT 1238

LeuSerAsnP roAlaAlaAs nValSerVal AspValLysV alPheIleVa 413

GCCGGTGGGG AACCATTTCA ACATCCCATT CAGCAGGGTG AACACAGCA 1288

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 CTGCGGCAGC 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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