PLD4 (NM_138790.5) - cDNA + Protein - 2026-07-04

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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 CCCGCCGCCC 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 GGTCCTGGGA GCATGGCTCC AGCCCAGCTT 238
lGlnProLys AspValProA rgSerTrpGl uHisGlySer SerProAlaT 80

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

GTCCTTGTGG AAAGCATCCC CCAGGACCTG CCATCTGCAG CCGGCAGCCC 338
ValLeuValG luSerIlePr oGlnAspLeu ProSerAlaA laGlySerPr 113
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CTCTGCCCAG CCTCTGGGCC AGGCCTGGCT 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 GGAACATTTC CCTGGCTGTG GCCACCAGCA 538
sLeuGlnGln LeuLeuGlyA rgAsnIleSe rLeuAlaVal AlaThrSerS 180

GCCCGACACT GGCCAGGACA TCCACCGACC TGCAGGTTCT 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

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IleTyrAsnC ysSerHisLe uAlaGlnAsp LeuGluLysT hrPheGlnTh 263
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rTyrTrpVal LeuGlyValP roLysAlaVa lLeuProLys ThrTrpProG 280

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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 GCCTCCGTGA TGGAGTATTT CCCCACCACG 1038
erAlaGlnGl uPheIleTyr AlaSerValM etGluTyrPh eProThrThr 346

CGCTTCAGCC ACCCCCCGAG GTACTGGCCG GTGCTGGACA ACGCGCTGCG 1088
ArgPheSerH isProProAr gTyrTrpPro ValLeuAspA snAlaLeuAr 363

GGCGGCAGCC TTCGGCAAGG GCGTGCGCGT GCGCCTGCTG GTCGGCTGCG 1138 A364Rfs*45
gAlaAlaAla PheGlyLysG lyValArgVa lArgLeuLeu ValGlyCysG 380

GACTCAACAC GGACCCCACC ATGTTCCCCT ACCTGCGGTC CCTGCAGGCG 1188
lyLeuAsnTh rAspProThr MetPheProT yrLeuArgSe rLeuGlnAla 396

CTCAGCAACC CCGCGGCCAA CGTCTCTGTG GACGTGAAAG TCTTCATCGT 1238
LeuSerAsnP roAlaAlaAs nValSerVal AspValLysV alPheIleVa 413

GCCGGTGGGG AACCATTCCA ACATCCCATT CAGCAGGGTG AACCACAGCA 1288
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lProValGly AsnHisSerA snIleProPh eSerArgVal AsnHisSerL 430

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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 TGAGGGGGGC CTCTTTTTCT *17
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CTCGGCGACC CCGCCCCGCA CGCGCCCTCC CCTCTGACCC CGGCCTGGGC *67
TTCAGCCGCT TCCTCCCGCA AGCAGCCCGG GTCCGCACTG CGCCAGGAGC *117
CGCCTGCGAC CGCCCGGGCG TCGCAAACCG CCCGCCTGCT CTCTGATTTC *167
CGAGTCCAGC CCCCCCTGAG CCCCACCTCC TCCAGGGAGC CCTCCAGGAA *217
GCCCCTTCCC TGACTCCTGG CCCACAGGCC AGGCCTAAAA AAAACTCGTG *267
GCTTC
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