



PLCG1 (NM_002660.3) - cDNA + Protein - 2025-01-07

GTCTGCCGCC TCAGCCTCAG CCCAACCTC AGCCGCCGCC GTTGCCTTG -50

CTCCCGGGCG GTCCTGGCCT GTGCCGCCG CGCCCCAGC GTCGGAGCCA 1

M 1

TGGCGGGCGC CGCGTCCCCT TGCCCAACG GCTGCGGGCC CGGCGCGCCC 51

etAlaGlyAl aAlaSerPro CysAlaAsnG lyCysGlyPr oGlyAlaPro 17

TCGGACGCCG AGGTGCTGCA CCTCTGCCG AGCCTCGAGG TGGGCACCGT 101

SerAspAlaG luValLeuHi sLeuCysArg SerLeuGluV alGlyThrVa 34

CATGACTTTG TTCTACTCCA AGAAGTCGA GCGACCCGAG CGGAAGACCT 151

lMetThrLeu PheTyrSerL ysLysSerGl nArgProGlu ArgLysThrP 51

TCCAGGTCAA GCTGGAGACG CGCCAGATCA CGTGGAGCCG GGGCGCCGAC 201

heGlnValLy sLeuGluThr ArgGlnIleT hrTrpSerAr gGlyAlaAsp 67

AAGATCGAGG GGGCCATTGA CATTTCGTGAA ATTAAGGAGA TCCGCCCAGG 251

LysIleGluG lyAlaIleAs pIleArgGlu IleLysGluI leArgProGl 84

GAAGACCTCA CGGGACTTTG ATCGCTATCA AGAGGACCCA GCTTTCGGC 301

yLysThrSer ArgAspPheA spArgTyrGl nGluAspPro AlaPheArgP 101

CGGACCAGTC ACATTGCTTT GTCATTCTCT ATGGAATGGA ATTTCGCCTG 351

roAspGlnSe rHisCysPhe ValIleLeuT yrGlyMetGl uPheArgLeu 117

AAAACGCTGA GCCTGCAAGC CACATCTGAG GATGAAGTGA ACATGTGGAT 401

LysThrLeuS erLeuGlnAl aThrSerGlu AspGluValA snMetTrpIl 134

CAAGGGCTTA ACTTGGCTGA TGGAGGATAC ATTGCAGGCA CCCACACCCC 451

eLysGlyLeu ThrTrpLeuM etGluAspTh rLeuGlnAla ProThrProL 151

TGCAGATTGA GAGGTGGCTC CGGAAGCAGT TTTACTCAGT GGATCGGAAT 501

euGlnIleGl uArgTrpLeu ArgLysGlnP heTyrSerVa lAspArgAsn 167

CGTGAGGATC GTATATCAGC CAAGGACCTG AAGAACATGC TGTCCCAGGT 551

ArgGluAspA rgIleSerAl aLysAspLeu LysAsnMetL euSerGlnVa 184

CAACTACCGG GTCCCCAACA TGCCTTCCT CCGAGAGCGG CTGACGGACC 601

lAsnTyrArg ValProAsnM etArgPheLe uArgGluArg LeuThrAspL 201

TGGAGCAGCG CAGCGGGGAC ATCACCTACG GGCAGTTTGC TCAGCTGTAC 651

euGluGlnAr gSerGlyAsp IleThrTyrG lyGlnPheAl aGlnLeuTyr 217

CGCAGCCTCA TGTACAGCGC CCAGAAGACG ATGGACCTCC CCTTCTTGGA 701

ArgSerLeuM etTyrSerAl aGlnLysThr MetAspLeuP roPheLeuGl 234

AGCCAGTACT CTGAGGGCTG GGGAGCGGCC GGAGCTTTGC CGAGTGTCCC 751

uAlaSerThr LeuArgAlaG lyGluArgPr oGluLeuCys ArgValSerL 251

TTCCTGAGTT CCAGCAGTTC CTTCTTGACT ACCAGGGGGA GCTGTGGGCT 801

euProGluPh eGlnGlnPhe LeuLeuAspT yrGlnGlyGl uLeuTrpAla 267

GTTGATCGCC TCCAGGTGCA GGAGTTCATG CTCAGCTTCC TCCGAGACCC 851
ValAspArgL euGlnValGl nGluPheMet LeuSerPheL euArgAspPr 284

CTTACGAGAG ATCGAGGAGC CATACTTCTT CCTGGATGAG TTTGTCACCT 901
oLeuArgGlu IleGluGluP roTyrPhePh eLeuAspGlu PheValThrP 301

TCCTGTTCTC CAAAGAGAAC AGTGTGTGGA ACTCGCAGCT GGATGCAGTA 951
heLeuPheSe rLysGluAsn SerValTrpA snSerGlnLe uAspAlaVal 317

TGCCCCGACA CCATGAACAA CCCTCTTTCC CACTACTGGA TCTCCTCCTC 1001
CysProAspT hrMetAsnAs nProLeuSer HisTyrTrpI leSerSerSe 334

GCACAACACG TACCTGACCG GGGACCAGTT CTCCAGTGAG TCCTCCTTGG 1051
rHisAsnThr TyrLeuThrG lyAspGlnPh eSerSerGlu SerSerLeuG 351

AAGCCTATGC TCGCTGCCTG CGGATGGGCT GTCGCTGCAT TGAGTTGGAC 1101
luAlaTyrAl aArgCysLeu ArgMetGlyC ysArgCysIl eGluLeuAsp 367

TGCTGGGACG GCCCGGATGG GATGCCAGTT ATTTACCATG GGCACACCCT 1151
CysTrpAspG lyProAspGl yMetProVal IleTyrHisG lyHisThrLe 384

TACCACCAAG ATCAAGTTCT CAGATGTCCT GCACACCATC AAGGAGCATG 1201
uThrThrLys IleLysPheS erAspValLe uHisThrIle LysGluHisA 401

CCTTTGTGGC CTCAGAGTAC CCAGTCATCC TGTCCATTGA GGACCACTGC 1251
laPheValAl aSerGluTyr ProValIleL euSerIleGl uAspHisCys 417

AGCATTGCCC AGCAGAGAAA CATGGCCCAA TACTTCAAGA AGGTGCTGGG 1301
SerIleAlaG lnGlnArgAs nMetAlaGln TyrPheLysL ysValLeuGl 434

GGACACACTC CTCACCAAGC CCGTGGAGAT CTCTGCCGAC GGGCTCCCCT 1351
yAspThrLeu LeuThrLysP roValGluIl eSerAlaAsp GlyLeuProS 451

CACCCAACCA GCTTAAGAGG AAGATCCTCA TCAAGCACAA GAAGCTGGCT 1401
erProAsnGl nLeuLysArg LysIleLeuI leLysHisLy sLysLeuAla 467

GAGGGCAGTG CCTACGAGGA GGTGCCTACA TCCATGATGT ACTCTGAGAA 1451
GluGlySerA laTyrGluGl uValProThr SerMetMetT yrSerGluAs 484

CGACATCAGC AACTCTATCA AGAATGGCAT CCTCTACCTG GAGGACCCTG 1501
nAspIleSer AsnSerIleL ysAsnGlyIl eLeuTyrLeu GluAspProV 501

TGAACCACGA ATGGTATCCC CACTACTTTG TTCTGACCAG CAGCAAGATC 1551
alAsnHisGl uTrpTyrPro HisTyrPheV alLeuThrSe rSerLysIle 517

TACTACTCTG AGGAGACCAG CAGTGACCAG GGCAACGAGG ATGAGGAGGA 1601
TyrTyrSerG luGluThrSe rSerAspGln GlyAsnGluA spGluGluGl 534

GCCCAAGGAG GTCAGCAGCA GCACAGAGCT GCACTCCAAT GAGAAGTGGT 1651
uProLysGlu ValSerSerS erThrGluLe uHisSerAsn GluLysTrpP 551

TCCATGGGAA GCTAGGGGCA GGGCGTGACG GGCGTCACAT CGCTGAGCGC 1701
heHisGlyLy sLeuGlyAla GlyArgAspG lyArgHisIl eAlaGluArg 567

CTGCTTACTG AGTACTGCAT CGAGACCGGA GCCCCTGACG GCTCCTTCCT 1751

LeuLeuThrG luTyrCysIl eGluThrGly AlaProAspG lySerPheLe 584

CGTGCGAGAG AGTGAGACCT TCGTGGGCGA CTACACGCTC TCTTTCTGGC 1801

uValArgGlu SerGluThrP heValGlyAs pTyrThrLeu SerPheTrpA 601

GGAACGGGAA AGTCCAGCAC TGCCGTATCC ACTCCCGGCA AGATGCTGGG 1851

rgAsnGlyLy sValGlnHis CysArgIleH isSerArgGl nAspAlaGly 617

ACCCCAAGT TCTTCTTGAC AGACAACCTC GTCTTTGACT CCCTCTATGA 1901

ThrProLysP hePheLeuTh rAspAsnLeu ValPheAspS erLeuTyrAs 634

CCTCATCAGC CACTACCAGC AGGTGCCCCCT GCGCTGTAAT GAGTTTGAGA 1951

pLeuIleThr HisTyrGlnG lnValProLe uArgCysAsn GluPheGluM 651

TGCGACTTTC AGAGCCTGTC CCACAGACCA ACGCCCACGA GAGCAAAGAG 2001

etArgLeuSe rGluProVal ProGlnThrA snAlaHisGl uSerLysGlu 667

TGGTACCACG CGAGCCTGAC CAGAGCACAG GCTGAGCACA TGCTAATGCG 2051

TrpTyrHisA laSerLeuTh rArgAlaGln AlaGluHisM etLeuMetAr 684

CGTCCCCTCGT GATGGGGCCT TCCTGGTGCG GAAGCGGAAT GAACCCAACT 2101

gValProArg AspGlyAlaP heLeuValAr gLysArgAsn GluProAsnS 701

CATATGCCAT CTCTTTCCGG GCTGAGGGCA AGATCAAGCA TTGCCGTGTC 2151

erTyrAlaIl eSerPheArg AlaGluGlyL ysIleLysHi sCysArgVal 717

CAGCAAGAGG GCCAGACAGT GATGCTAGGG AACTCGGAGT TCGACAGCCT 2201

GlnGlnGluG lyGlnThrVa lMetLeuGly AsnSerGluP heAspSerLe 734

TGTTGACCTC ATCAGCTACT ATGAGAAACA CCCGCTATAC CGCAAGATGA 2251
uValAspLeu IleSerTyrT yrGluLysHi sProLeuTyr ArgLysMetL 751

AGCTGCGCTA TCCCATCAAC GAGGAGGCAC TGGAGAAGAT TGGCACAGCT 2301
ysLeuArgTy rProIleAsn GluGluAlaL euGluLysIl eGlyThrAla 767

GAGCCTGACT ACGGGGCCCT GTATGAGGGA CGCAACCCTG GCTTCTATGT 2351
GluProAspT yrGlyAlaLe uTyrGluGly ArgAsnProG lyPheTyrVa 784

AGAGGCAAAC CCTATGCCAA CTTTCAAGTG TGCAGTCAA GCCCTCTTTG 2401
lGluAlaAsn ProMetProT hrPheLysCy sAlaValLys AlaLeuPheA 801

ACTACAAGGC CCAGAGGGAG GACGAGCTGA CCTTCATCAA GAGCGCCATC 2451
spTyrLysAl aGlnArgGlu AspGluLeuT hrPheIleLy sSerAlaIle 817

ATCCAGAATG TGGAGAAGCA AGAGGGAGGC TGGTGGCGAG GGGACTACGG 2501
IleGlnAsnV alGluLysGl nGluGlyGly TrpTrpArgG lyAspTyrGl 834

AGGGAAGAAG CAGCTGTGGT TCCCATCAAA CTACGTGGAA GAGATGGTCA 2551
yGlyLysLys GlnLeuTrpP heProSerAs nTyrValGlu GluMetValA 851

ACCCCGTGGC CCTGGAGCCG GAGAGGGAGC ACTTGGACGA GAACAGCCCC 2601
snProValAl aLeuGluPro GluArgGluH isLeuAspGl uAsnSerPro 867

CTAGGGGACT TGCTGCGGGG GGTCTTGGAT GTGCCGGCTT GTCAGATTGC 2651
LeuGlyAspL euLeuArgGl yValLeuAsp ValProAlaC ysGlnIleAl 884

CATCCGTCCT GAGGGCAAGA ACAACCGGCT CTCGTCCTC TCCATCAGCA 2701
aIleArgPro GluGlyLysA snAsnArgLe uPheValPhe SerIleSerM 901

TGGCGTCGGT GGCCCACTGG TCCCTGGATG TTGCTGCCGA CTCACAGGAG 2751
etAlaSerVa lAlaHisTrp SerLeuAspV alAlaAlaAs pSerGlnGlu 917

GAGCTGCAGG ACTGGGTGAA AAAGATCCGT GAAGTGGCCC AGACAGCAGA 2801
GluLeuGlnA spTrpValLy sLysIleArg GluValAlaG lnThrAlaAs 934

CGCCAGGCTC ACTGAAGGGA AGATAATGGA ACGGAGGAAG AAGATTGCC 2851
pAlaArgLeu ThrGluGlyL ysIleMetGl uArgArgLys LysIleAlaL 951

TGGAGCTCTC TGAACTTGTC GTCTACTGCC GGCCTGTTCC CTTTGATGAA 2901
euGluLeuSe rGluLeuVal ValTyrCysA rgProValPr oPheAspGlu 967

GAGAAGATTG GCACAGAACG TGCTTGCTAC CGGGACATGT CATCCTTCCC 2951
GluLysIleG lyThrGluAr gAlaCysTyr ArgAspMetS erSerPhePr 984

GGAAACCAAG GCTGAGAAAT ACGTGAACAA GGCCAAAGGC AAGAAGTTCC 3001
oGluThrLys AlaGluLysT yrValAsnLy sAlaLysGly LysLysPheL 1001

TTCAGTACAA TCGACTGCAG CTCTCCCGCA TCTACCCCAA GGGCCAGCGA 3051
euGlnTyrAs nArgLeuGln LeuSerArgI leTyrProLy sGlyGlnArg 1017

CTGGATTCCCT CCAACTACGA TCCTTTGCC ATGTGGATCT GTGGCAGTCA 3101 [S1021F](#)
LeuAspSerS erAsnTyrAs pProLeuPro MetTrpIleC ysGlySerGl 1034

GCTTGTGGCC CTCAACTTCC AGACCCCTGA CAAGCCTATG CAGATGAACC 3151
nLeuValAla LeuAsnPheG lnThrProAs pLysProMet GlnMetAsnG 1051

AGGCCCTCTT CATGACGGGC AGGCACTGTG GCTACGTGCT GCAGCCAAGC 3201
lnAlaLeuPh eMetThrGly ArgHisCysG lyTyrValLe uGlnProSer 1067

ACCATGCGGG ATGAGGCCTT CGACCCCTTT GACAAGAGCA GCCTCCGCGG 3251
ThrMetArgA spGluAlaPh eAspProPhe AspLysSerS erLeuArgGl 1084

GCTGGAGCCA TGTGCCATCT CTATTGAGGT GCTGGGGGCC CGACATCTGC 3301
yLeuGluPro CysAlaIleS erIleGluVa lLeuGlyAla ArgHisLeuP 1101

CAAAGAATGG CCGAGGCATT GTGTGTCCTT TTGTGGAGAT TGAGGTGGCT 3351
roLysAsnGl yArgGlyIle ValCysProP heValGluIl eGluValAla 1117

GGAGCTGAGT ATGACAGCAC CAAGCAGAAG ACAGAGTTTG TGGTGGACAA 3401
GlyAlaGluT yrAspSerTh rLysGlnLys ThrGluPheV alValAspAs 1134

TGGACTCAAC CCTGTATGGC CAGCCAAGCC CTTCCACTTC CAGATCAGTA 3451
nGlyLeuAsn ProValTrpP roAlaLysPr oPheHisPhe GlnIleSerA 1151

ACCCTGAATT TGCCTTCTTG CGCTTCGTGG TGTATGAGGA AGACATGTTT 3501
snProGluPh eAlaPheLeu ArgPheValV alTyrGluGl uAspMetPhe 1167

AGTGACCAGA ATTTCTGGC TCAGGCTACT TTCCCAGTAA AAGGCCTGAA 3551
SerAspGlnA snPheLeuAl aGlnAlaThr PheProValL ysGlyLeuLy 1184

GACAGGATAC AGAGCAGTGC CTTTGAAGAA CAACTACAGT GAGGACCTGG 3601

sThrGlyTyr ArgAlaValP roLeuLysAs nAsnTyrSer GluAspLeuG 1201

AGTTGGCCTC CCTGCTGATC AAGATTGACA TTTTCCCTGC CAAGCAGGAG 3651

luLeuAlaSe rLeuLeuIle LysIleAspI lePheProAl aLysGlnGlu 1217

AATGGTGACC TCAGTCCCTT CAGTGGTACG TCCCTGCGGG AGCGGGGCTC 3701

AsnGlyAspL euSerProPh eSerGlyThr SerLeuArgG luArgGlySe 1234

AGATGCCTCA GGCCAGCTGT TTCATGGCCG AGCCCGGGAA GGCTCCTTTG 3751

rAspAlaSer GlyGlnLeuP heHisGlyAr gAlaArgGlu GlySerPheG 1251

AATCCCGCTA CCAGCAGCCG TTTGAGGACT TCCGCATCTC CCAGGAGCAT 3801

luSerArgTy rGlnGlnPro PheGluAspP heArgIleSe rGlnGluHis 1267

CTCGCAGACC ATTTTGACAG TCGAGAACGA AGGGCCCCAA GAAGGACTCG 3851

LeuAlaAspH isPheAspSe rArgGluArg ArgAlaProA rgArgThrAr 1284

GGTCAATGGA GACAACCGCC TCTAGTTGTA CCCCAGCCTC GTTGGAGAGC *25

gValAsnGly AspAsnArgL euStop

AGCAGGTGCT GTGCGCCTTG TAGAATGCCG CGAACTGGGT TCTTTGGAAG *75

CAGCCCCCTG TGGCGGCCTT CCGGGTCTCG CAGCCTGAAG CCTGGATTCC *125

AGCAGTGAAT GCTAGACAGA AACCAAGCCA TTAATGAGAT GTTATTACTG *175

TTTTGGGCCT CCATGCCCCA GCTCTGGATG AAGGCAAAA CTGTACTGTG *225

TTTCGCATTA AGCACACACA TCTGGCCCTG ACTTCTGGAG ATGGATCCTT *275

CCATCTTG TG GGGCCAGGAC CATGGCCGAA GCCCCTTGGA GAGAGAGGCT *325

GCCTCAGCCA GTGGCACAGG AGACTCCAAG GAGCTACTGA CATTCCCTAAG *375

AGTGGAGGAG GAGGAGGAG CTTGCTGGGC CAGGAAACA AAGTTTACAT *425

TGTCCTGTAG CTTTAAAACC ACAGCTGGGC AGGGTGAGAA GCTAGATGCC *475
CCTGCAGTTT GGCCCTGGAG CCAGGGCAGA GGAATGTAGG GCCTGCATGG *525
AGAAGGGTTC TGCCCTGCCT GAGGAGGAGG ACACAGCACA AGGGCACATT *575
GCCCATGGCT GGGAACATGA CCCAGCCTGA AAGATACAGG GGATCATGTT *625
AAAAATAGCA GTATTATTTT TCGTCTCAAT GGTATTGTAA CTAAGTTATT *675
TACTCCTCCT GCTCCTCACC CCTGTAGGGA AACCTTGGAG AGGAGAGTGG *725
CAGGTGGGCT GCCTGCTGTG TTAAGAGGAC TTAGTTTGTG ATGTAAGGCA *775
CTGTCAGGAA TGGGGGGCGG GCCAGGGTGG GAAGAGAAGA AATAGCAGAG *825
CCTATTTTGG TGAGGTTTTT TGTTTTTAAG TCAAAGAAGA CTCAGTATGC *875
TTTCCCTGAG GAATGAAAAA GGGATTGAGG AGTTGCCTGA CTCCTGGGTG *925
GGTGGGGTAC AGGCAGTTAG GTGCTGAATG AAGCTGCCAT CCTTGCTGCA *975
GCTTCTAACT GGTA AAAAGA TCCAGGGATG GAGATGGGAA GGTTAGAAAAG *1025
GCAGCCCTCA CCTCTGAGGA CAGAGGCCGG GTCCAGGCC CGTGGGCGCA *1075
AAGGTGCCCTC ATAGCATAGC CAGCATTAG CACACACAAA CCTACTGCCC *1125
ACATTTGGGC TCAGGGTTGG CCATTTGCTA GTTCTGCTGC CCTCTTAAGA *1175
TCTGACTGCC AAATAAATCA TCCTCATGTC CTTTTTCCTT TGACTTGTAT *1225
GCTCTTTCGG GGGCTCAGGA AAGCCTGTTG CATGGGACAT GCTCACTAGA *1275
AACAGTCGCC AGATGATTAT TCTGCAGTAG AAGCAGGTAG GAAATTTCTG *1325
GAAATTTCTC AGGTTAAGCA GCAAGAGCTG TAACCCCTCC TCTGGGCTAA *1375
CAGGAGTTGT GGGTCCACTC TCTCCTGCCC ACCCTCTGAG GGTGTGTCTG *1425
AGCAGAGTAC ATCCTGCCTG GGTTCTTTGT GGCCAGCCAG TTTTGGTGGT *1475
GAGCTGGAAA CAACCAGAGC CCCTTTCCAG TTCCACAGAA ACCTCTCCTT *1525
TCAAAAATGT TGCATTCAGT TCGTTAACAC TGCCAGGTGC CATTCTGATT *1575
GCCTCTAGGA CTTGGCAGCT GAAATCTCTG GGCCCTTTCA ACACAGTTGA *1625
AAGGCCCTTC TCTTCTGAA GCTCTGTTTC CATAGTTGGC TGTGCTGGGA *1675
TGGAACAAAA ATGACGCCAC AAAAAAATT TAAGATAGAT CCGGTTCCGT *1725
GGATGACATG AACTGATGAT AGCCAGTATC AAACAGCGAT AGTGCTCAGG *1775
TTCTTGTGTG ACTTCTTTT ACAGCTTCAC AGTCCCAGTT CATAGAGAGG *1825

AGGGTGGCTT TTTCCCATAC ACAAGAAGGT GGTGGGTGGG AATTCACCTG *1875
GGCCCTCATG ATCCATGTTT CCTCTCTAGG TTTTATGGC CTGGAGAGAA *1925
AGGTTTCCTA TCAGAGAAGG AAGAGGACTG TGTAGGCCCT TCTGTTAGGG *1975
CCCATCCACG TTGGTTAGGA CGTCCTTGGC GTGTTTGTTA GTGTTGACCC *2025
TTTTAGTTTT CATCAATACG TATCTCTATT TGCTGAACAA GTGTCTTTCT *2075
GGAACACAAC CTGGGGAACA GACAGCTCTG CCTTCTTAA GGCAGCTTTG *2125
TAGACCTGAG GCTCACCTCT CTTGGGCTCT GTAAGACATT GCCTTGCCT *2175
CACTGCAAAT GTTTTGATTG TTCTTCCTAG TGGAAAACGT GCCAACTCTC *2225
AAGCAAATTT AAAGATCATT TTCACTTCAA GATTCCTCCA GACCTGACAA *2275
ATGTTGATTG ACCCAGAAGG CAGAGTGTTT GTTGGTGGGG AAGACCCTTA *2325
CTTGGGGCCG AATGCTTTGG CATCAGGAGT TGTTTGCCCC ATCCCATGCA *2375
TGCAGGCCGT GTCCCTACAG TCGCAGAGCT CAGGGTTATG ACCTGTGGAG *2425
TCTCAACCCCT AACAGCACAT TAGCACCCT TGGGGAGCTT CTGAAAAATA *2475
CTGGTACCCG GGGCCTTAGC ATAGGTATTG TTCAAAACCT CTCAAGGTGA *2525
TTTAAATGAG TAACAAGGGT TGAAAAACCC TGATTTTGGC AGCACAAACC *2575
AAAAGAGCAG GCAGGGCCGG GAGAGGGAAG TCAGTGGTAC CAGAAGGTAG *2625
ATGGGCTCCC TTGCAGGCTC CTTGTTCTCC TGCCATCACC AGTAGAACCT *2675
TCTGGCTGAC AGACCAGGGA CAAGTAGACT GGGTTCAAAG TGACAGACCT *2725
TTCACTTTCA ACAGCTTTGG CTCAGCAGAC ATGTACACAT ACAAAGTAGA *2775
GCC'TACAAGG TCAGGGGCAT TCTGCCCCCG CCACAGGACT AAAGACTGCC *2825
CTGCGGGAAG ATGGCAGGAG CAGTTTCTGA CCTCAGTTGA GTATCTGTGG *2875
CCATGAGCAG AAAAGGCAGG GGTCTGCCTC CTGACCAAGC ACATCTTGAA *2925
CATCACCTGA GAGCTTGAAC ATCACTAAGG ACCTAGACAC TCACTTGTCT *2975
TTCAACTTGA GCCCATCACT CACCATGTGA GTTCTGTTGA GGGTGGGTAG *3025
AAAGCAAATA GGTTCAGGTT ATCCCACCAG ACTAACTCGG TGAATGAAAG *3075
GATCATGCCT TCTTCACATT TTAATTAAT GGATCAAGCA CA

PLCG1 (NM_002660.3) - cDNA + Protein - 2025-01-07

