PLCG2 (NM_002661.5) - cDNA + Protein - 2026-02-01

```
AGAAGTAGCG AGCGCCGGCG GCGGAGGGCG TGAGCGGCGC TGAGTGACCC -132
GAGTCGGGAC GCGGGCTGCG CGCGCGGGAC CCCGGAGCCC AAACCCGGGG -82
CAGGCGGGCA GCTGTGCCCG GGCGGCACGG CCAGCTTCCT GATTTCTCCC -32
GATTCCTTCC TTCTCCCTGG AGCGGCCGAC AATGTCCACC ACGGTCAATG 19
                                 MetSerThr ThrValAsnV 7

TAGATTCCCT TGCGGAATAT GAGAAGAGCC AGATCAAGAG AGCCCTGGAG 69   A21V
alAspSerLe uAlaGluTyr GluLysSerG lnIleLysAr gAlaLeuGlu 23

CTGGGGACGG TGATGACTGT GTTCAGCTTC CGCAAGTCCA CCCCCGAGCG 119  T26M M28L
LeuGlyThrV alMetThrVa lPheSerPhe ArgLysSerT hrProGluAr 40

GAGAACCGTC CAGGTGATCA TGGAGACGCG GCAGGTGGCC TGGAGCAAGA 169  R50W
gArgThrVal GlnValIleM etGluThrAr gGlnValAla TrpSerLysT 57

CCGCTGACAA GATCGAGGGC TTCTTGGATA TCATGGAAAT AAAAGAAATC 219  D59G
hrAlaAspLy sIleGluGly PheLeuAspI leMetGluIl eLysGluIle 73

CGCCCAGGGA AGAACTCCAA AGATTTCGAG CGAGCAAAAG CAGTTCGCCA 269  R84X R89C
ArgProGlyL ysAsnSerLy sAspPheGlu ArgAlaLysA laValArgGl 90

GAAAGAAGAC TGCTGCTTCA CCATCCTATA TGGCACTCAG TTCGTCCTCA 319  V105I
```

```
nLysGluAsp CysCysPheT hrIleLeuTy rGlyThrGln PheValLeuS 107

GCACGCTCAG CTTGGCAGCT GACTCTAAAG AGGATGCAGT TAACTGGCTC 369
erThrLeuSe rLeuAlaAla AspSerLysG luAspAlaVa lAsnTrpLeu 123

TCTGGCTTGA AAATCTTACA CCAGGAAGCG ATGAATGCGT CCACGCCCAC 419  A133V A136V P139S
SerGlyLeuL ysIleLeuHi sGlnGluAla MetAsnAlaS erThrProTh 140

CATTATCGAG AGTTGGCTGA GAAAGCAGAT ATATTCTGTG GATCAAACCA 469
rIleIleGlu SerTrpLeuA rgLysGlnIl eTyrSerVal AspGlnThrA 157

GAAGAAACAG CATCAGTCTC CGAGAGTTGA AGACCATCTT GCCCCTGATC 519  R164Q I169V L170F
rgArgAsnSe rIleSerLeu ArgGluLeuL ysThrIleLe uProLeuIle 173

AACTTTAAAG TGAGCAGTGC CAAGTTCCTT AAAGATAAGT TTGTGGAAAT 569  L183F
AsnPheLysV alSerSerAl aLysPheLeu LysAspLysP heValGluIl 190

AGGAGCACAC AAAGATGAGC TCAGCTTTGA ACAGTTCCAT CTCTTCTATA 619  H193Q
eGlyAlaHis LysAspGluL euSerPheGl uGlnPheHis LeuPheTyrL 207

AAAAACTTAT GTTTGAACAG CAAAAATCGA TTCTCGATGA ATTCAAAAAG 669  S216L
ysLysLeuMe tPheGluGln GlnLysSerI leLeuAspGl uPheLysLys 223

GATTCGTCCG TGTTCATCCT GGGGAACACT GACAGGCCGG ATGCCTCTGC 719  V227M P236L
AspSerSerV alPheIleLe uGlyAsnThr AspArgProA spAlaSerAl 240

TGTTTACCTG CATGACTTCC AGAGGTTTCT CATACATGAA CAGCAGGAGC 769  H244R
aValTyrLeu HisAspPheG lnArgPheLe uIleHisGlu GlnGlnGluH 257
```

ATTGGGCTCA GGATCTGAAC AAAGTCCGTG AGCGGATGAC AAAGTTCATT 819 R268W
isTrpAlaGl nAspLeuAsn LysValArgG luArgMetTh rLysPheIle 273

GATGACACCA TGCGTGAAAC TGCTGAGCCT TTCTTGTTTG TGGATGAGTT 869 T276N
AspAspThrM etArgGluTh rAlaGluPro PheLeuPheV alAspGluPh 290

CCTCACGTAC CTGTTTTCAC GAGAAAACAG CATCTGGGAT GAGAAGTATG 919 T292M
eLeuThrTyr LeuPheSerA rgGluAsnSe rIleTrpAsp GluLysTyrA 307

ACGCGGTGGA CATGCAGGAC ATGAACAACC CCCTGTCTCA TTACTGGATC 969 P317L
spAlaValAs pMetGlnAsp MetAsnAsnP roLeuSerHi sTyrTrpIle 323

TCCTCGTCAC ATAACACGTA CCTTACAGGT GACCAGCTGC GGAGCGAGTC 1019
SerSerSerH isAsnThrTy rLeuThrGly AspGlnLeuA rgSerGluSe 340

GTCCCCAGAA GCTTACATCC GCTGCCTGCG CATGGGCTGT CGCTGCATTG 1069 Y345H
rSerProGlu AlaTyrIleA rgCysLeuAr gMetGlyCys ArgCysIleG 357

AACTGGACTG CTGGGACGGG CCCGATGGGA AGCCGGTCAT CTACCATGGC 1119
luLeuAspCy sTrpAspGly ProAspGlyL ysProValIl eTyrHisGly 373

TGGACGCGGA CTACCAAGAT CAAGTTTGAC GACGTCGTGC AGGCCATCAA 1169 Q387P
TrpThrArgT hrThrLysIl eLysPheAsp AspValValG lnAlaIleLy 390

AGACCACGCC TTTGTTACCT CGAGCTTCCC AGTGATCCTG TCCATCGAGG 1219 A393T
sAspHisAla PheValThrS erSerPhePr oValIleLeu SerIleGluG 407

AGCACTGCAG CGTGGAGCAA CAGCGTCACA TGGCCAAGGC CTTCAAGGAA 1269
luHisCysSe rValGluGln GlnArgHisM etAlaLysAl aPheLysGlu 423

GTATTTGGCG ACCTGCTGTT GACGAAGCCC ACGGAGGCCA GTGCTGACCA 1319 P425S D427N
ValPheGlyA spLeuLeuLe uThrLysPro ThrGluAlaS erAlaAspGl 440

GCTGCCCTCG CCCAGCCAGC TGCGGGAGAA GATCATCATC AAGCATAAGA 1369
nLeuProSer ProSerGlnL euArgGluLy sIleIleIle LysHisLysL 457

AGCTGGGCCC CCGAGGCGAT GTGGATGTCA ACATGGAGGA CAAGAAGGAC 1419
ysLeuGlyPr oArgGlyAsp ValAspValA snMetGluAs pLysLysAsp 473

GAACACAAGC AACAGGGGGA GCTGTACATG TGGGATTCCA TTGACCAGAA 1469 Y482H M483Ifs
GluHisLysG lnGlnGlyGl uLeuTyrMet TrpAspSerI leAspGlnLy 490

ATGGACTCGG CACTACTGCG CCATTGCCGA TGCCAAGCTG TCCTTCAGTG 1519 H494Y A501S
sTrpThrArg HisTyrCysA laIleAlaAs pAlaLysLeu SerPheSerA 507

ATGACATTGA ACAGACTATG GAGGAGGAAG TGCCCCAGGA TATACCCCCT 1569 I509T
spAspIleGl uGlnThrMet GluGluGluV alProGlnAs pIleProPro 523

ACAGAACTAC ATTTTGGGGA GAAATGGTTC CACAAGAAGG TGGAGAAGAG 1619
ThrGluLeuH isPheGlyGl uLysTrpPhe HisLysLysV alGluLysAr 540

GACGAGTGCC GAGAAGTTGC TGCAGGAATA CTGCATGGAG ACGGGGGGCA 1669 K545R T554M
gThrSerAla GluLysLeuL euGlnGluTy rCysMetGlu ThrGlyGlyL 557

AGGATGGCAC CTTCCTGGTT CGGGAGAGCG AGACCTTCCC CAATGACTAC 1719 E565D N571S

ysAspGlyTh rPheLeuVal ArgGluSerG luThrPhePr oAsnAspTyr 573

ACCCTGTCCT TCTGGCGGTC AGGCCGGGTC CAGCACTGCC GGATCCGCTC 1769

ThrLeuSerP heTrpArgSe rGlyArgVal GlnHisCysA rgIleArgSe 590

CACCATGGAG GGCGGGACCC TGAAATACTA CTTGACTGAC AACCTCACCT 1819 M592R G595R

rThrMetGlu GlyGlyThrL euLysTyrTy rLeuThrAsp AsnLeuThrP 607

TCAGCAGCAT CTATGCCCTC ATCCAGCACT ACCGCGAGAC GCACCTGCGC 1869 R623L

heSerSerIl eTyrAlaLeu IleGlnHisT yrArgGluTh rHisLeuArg 623

TGCGCCGAGT TCGAGCTGCG GCTCACGGAC CCTGTGCCCA ACCCCAACCC 1919 R630Q N639S

CysAlaGluP heGluLeuAr gLeuThrAsp ProValProA snProAsnPr 640

CCACGAGTCC AAGCCGTGGT ACTATGACAG CCTGAGCCGC GGAGAGGCAG 1969 del Exon19 5.9kb del Exon19 4.8kb

oHisGluSer LysProTrpT yrTyrAspSe rLeuSerArg GlyGluAlaG 657

AGGACATGCT GATGAGGATT CCCCGGGACG GGGCCTTCCT GATCCGGAAG 2019

luAspMetLe uMetArgIle ProArgAspG lyAlaPheLe uIleArgLys 673

CGAGAGGGGA GCGACTCCTA TGCCATCACC TTCAGGGCTA GGGGCAAGGT 2069 del Exon20-22

ArgGluGlyS erAspSerTy rAlaIleThr PheArgAlaA rgGlyLysVa 690

AAAGCATTGT CGCATCAACC GGGACGGCCG GCACTTTGTG CTGGGGACCT 2119 R697W G699S R700Q H701L H701Q T706I S707P

lLysHisCys ArgIleAsnA rgAspGlyAr gHisPheVal LeuGlyThrS 707

CCGCCTATTT TGAGAGTCTG GTGGAGCTCG TCAGTTACTA CGAGAAGCAT 2169 S707Y A708P E721K K722E

erAlaTyrPh eGluSerLeu ValGluLeuV alSerTyrTy rGluLysHis 723

TCACTCTACC GAAAGATGAG ACTGCGCTAC CCCGTGACCC CCGAGCTCCT 2219 V735M

SerLeuTyrA rgLysMetAr gLeuArgTyr ProValThrP roGluLeuLe 740

GGAGCGCTAC AATATGGAAA GAGATATAAA CTCCCTCTAC GACGTCAGCA 2269 R742C R742H

uGluArgTyr AsnMetGluA rgAspIleAs nSerLeuTyr AspValSerA 757

GAATGTATGT GGATCCCAGT GAAATCAATC CGTCCATGCC TCAGAGAACC 2319

rgMetTyrVa lAspProSer GluIleAsnP roSerMetPr oGlnArgThr 773

GTGAAAGCTC TGTATGACTA CAAAGCCAAG CGAAGCGATG AGCTGAGCTT 2369

ValLysAlaL euTyrAspTy rLysAlaLys ArgSerAspG luLeuSerPh 790

CTGCCGTGGT GCCCTCATCC ACAATGTCTC CAAGGAGCCC GGGGGCTGGT 2419 N798S

eCysArgGly AlaLeuIleH isAsnValSe rLysGluPro GlyGlyTrpT 807

GGAAAGGAGA CTATGGAACC AGGATCCAGC AGTACTTCCC ATCCAACTAC 2469 N822T N822K

rpLysGlyAs pTyrGlyThr ArgIleGlnG lnTyrPhePr oSerAsnTyr 823

GTCGAGGACA TCTCAACTGC AGACTTCGAG GAGCTAGAAA AGCAGATTAT 2519 V824I E833K

ValGluAspI leSerThrAl aAspPheGlu GluLeuGluL ysGlnIleIl 840

TGAAGACAAT CCCTTAGGGT CTCTTTGCAG AGGAATATTG GACCTCAATA 2569 E841G L845 L848del L845S L848P

eGluAspAsn ProLeuGlyS erLeuCysAr gGlyIleLeu AspLeuAsnT 857

CCTATAACGT CGTGAAAGCC CCTCAGGGAA AAAACCAGAA GTCCTTTGTC 2619

hrTyrAsnVa lValLysAla ProGlnGlyL ysAsnGlnLy sSerPheVal 873

TTCATCCTGG AGCCCAAGCA GCAGGGCGAT CCTCCGGTGG AGTTTGCCAC 2669 E887K E887A
PheIleLeuG luProLysGl nGlnGlyAsp ProProValG luPheAlaTh 890

AGACAGGGTG GAGGAGCTCT TTGAGTGGTT TCAGAGCATC CGAGAGATCA 2719
rAspArgVal GluGluLeuP heGluTrpPh eGlnSerIle ArgGluIleT 907

CCTGGAAGAT TGACACCAAG GAGAACAACA TGAAGTACTG GGAGAAGAAC 2769
hrTrpLysIl eAspThrLys GluAsnAsnM etLysTyrTr pGluLysAsn 923

CAGTCCATCG CCATCGAGCT CTCTGACCTG GTTGTCTACT GCAAACCAAC 2819
GlnSerIleA laIleGluLe uSerAspLeu ValValTyrC ysLysProTh 940

CAGCAAAACC AAGGACAACT TAGAAAATCC TGACTTCCGA GAAATCCGCT 2869 R956C
rSerLysThr LysAspAsnL euGluAsnPr oAspPheArg GluIleArgS 957

CCTTTGTGGA GACGAAGGCT GACAGCATCA TCAGACAGAA GCCCGTCGAC 2919
erPheValGl uThrLysAla AspSerIleI leArgGlnLy sProValAsp 973

CTCCTGAAGT ACAATCAAAA GGGCCTGACC CGCGTCTACC CAAAGGGACA 2969 T983I
LeuLeuLysT yrAsnGlnLy sGlyLeuThr ArgValTyrP roLysGlyGl 990

AAGAGTTGAC TCTTCAAACT ACGACCCCTT CCGCCTCTGG CTGTGCGGTT 3019 D993Y L1002F
nArgValAsp SerSerAsnT yrAspProPh eArgLeuTrp LeuCysGlyS 1007

CTCAGATGGT GGCACTCAAT TTCCAGACGG CAGATAAGTA CATGCAGATG 3069 L1012V D1018G
erGlnMetVa lAlaLeuAsn PheGlnThrA laAspLysTy rMetGlnMet 1023

AATCACGCAT TGTTTTCTCT CAATGGGCGC ACGGGCTACG TTCTGCAGCC 3119 S1029C

AsnHisAlaL euPheSerLe uAsnGlyArg ThrGlyTyrV alLeuGlnPr 1040

TGAGAGCATG AGGACAGAGA AATATGACCC GATGCCACCC GAGTCCCAGA 3169 P1050L

oGluSerMet ArgThrGluL ysTyrAspPr oMetProPro GluSerGlnA 1057

GGAAGATCCT GATGACGCTG ACAGTCAAGG TTCTCGGTGC TCGCCATCTC 3219

rgLysIleLe uMetThrLeu ThrValLysV alLeuGlyAl aArgHisLeu 1073

CCCAAACTTG GACGAAGTAT TGCCTGTCCC TTTGTAGAAG TGGAGATCTG 3269 C1082R

ProLysLeuG lyArgSerIl eAlaCysPro PheValGluV alGluIleCy 1090

TGGAGCCGAG TATGACAACA ACAAGTTCAA GACGACGGTT GTGAATGATA 3319 N1097del

sGlyAlaGlu TyrAspAsnA snLysPheLy sThrThrVal ValAsnAspA 1107

ATGGCCTCAG CCCTATCTGG GCTCCAACAC AGGAGAAGGT GACATTTGAA 3369

snGlyLeuSe rProIleTrp AlaProThrG lnGluLysVa lThrPheGlu 1123

ATTTATGACC CAAACCTGGC ATTTCTGCGC TTTGTGGTTT ATGAAGAAGA 3419 A1130S F1131L R1133C E1139del

IleTyrAspP roAsnLeuAl aPheLeuArg PheValValT yrGluGluAs 1140

TATGTTCAGC GATCCCAACT TTCTTGCTCA TGCCACTTAC CCCATTAAAG 3469 M1141K M1141I

pMetPheSer AspProAsnP heLeuAlaHi sAlaThrTyr ProIleLysA 1157

CAGTCAAATC AGGATTCAGG TCCGTTCCTC TGAAGAATGG GTACAGCGAG 3519 K1168N

laValLysSe rGlyPheArg SerValProL euLysAsnGl yTyrSerGlu 1173

GACATAGAGC TGGCTTCCCT CCTGGTTTTC TGTGAGATGC GGCCAGTCCT 3569 I1175K

AspIleGluL euAlaSerLe uLeuValPhe CysGluMetA rgProValLe 1190

GGAGAGCGAA GAGGAACTTT ACTCCTCCTG TCGCCAGCTG AGGAGGCGGC 3619 E1191Q
uGluSerGlu GluGluLeuT yrSerSerCy sArgGlnLeu ArgArgArgG 1207

AAGAAGAACT GAACAACCAG CTCTTTCTGT ATGACACACA CCAGAACTTG 3669
lnGluGluLe uAsnAsnGln LeuPheLeuT yrAspThrHi sGlnAsnLeu 1223

CGCAATGCCA ACCGGGATGC CCTGGTTAAA GAGTTCAGTG TTAATGAGAA 3719
ArgAsnAlaA snArgAspAl aLeuValLys GluPheSerV alAsnGluAs 1240

CCAGCTCCAG CTGTACCAGG AGAAATGCAA CAAGAGGTTA AGAGAGAAGA 3769 E1247X
nGlnLeuGln LeuTyrGlnG luLysCysAs nLysArgLeu ArgGluLysA 1257

GAGTCAGCAA CAGCAAGTTT TACTCATAGA AGCTGGGGTA TGTGTGTAAG *21
rgValSerAs nSerLysPhe TyrSerStop

GGTATTGTGT GTGTGCGCAT GTGTGTTTGC ATGTAGGAGA ACGTGCCCTA *71 *35T>C
TTCACACTCT GGGAAGACGC TAATCTGTGA CATCTTTTCT TCAAGCCTGC *121
CATCAAGGAC ATTTCTTAAG ACCCAACTGG CATGAGTTGG GGTAATTTCC *171
TATTATTTTC ATCTTGGACA ACTTTCTTAA CTTATATTCT TTATAGAGGA *221
TTCCCCAAAA TGTGCTCCTC ATTTTTGGCC TCTCATGTTC CAAACCTCAT *271
TGAATAAAAG CAATGAAAAC CTTGATCAAT TAAGCCTTCT GTTGCACGAC *321
CTGTGCAGTG AACAGGATTT CTTTTCTGGC CAAGAAGATT CTACCTCTAA *371
TGATCCAGGT AACTGATGTC CATGGAGGAT GAGCTGGAAA TGTAAGAAAC *421
TATTCATGAG ATTCTGAAAA GGATTTTAAC TCAAAGGCAA ATGATTCCAT *471
AAGGGCCCAA AGAGAAGCCC TACCCACAGG CAGCCTGCTC AGTTCAATGT *521
ACTTTAACTA CCACCGGCTG CCTGCTGCAG TCCACAAGAA AATGGCTGAG *571
TGATGGGATC TGTTCATTAA GACAATTTCT AATTAATGGT GACAGCTTGT *621

TTTGTGACTA GAGTTACTGG GATGGAGGGT AGGAATCTTG GGGCCTCTTT *671

GTTTTAAAAA GCCCATCAGA GAGACCAGAG CCGTGCTGCA GGGGCAGGTT *721

CTCACTTGCC CCTGGCTCTG CCAGCTGCTG GGAGGCTCTG GCCCCACTAG *771

TCCCTCATGG CCCTACTGAA CTGGCTGGGA GGCTGCTGGA ATGGCCCTTG *821

GTCCACAGCT CTCCACAGGC AAGAGGTCAA CTGCTGCTTG AAAGAGGTAG *871

ACAAAAGTTA GGTTGATGGC GAAATGTCTC TGGGTTACCC AGTCTTCTGG *921

AGCAGCAAGC TGAGCTTTAA TGGGCTAAGC ATTAGGGTGT TACAGAAAAT *971

TTCAAATGCA GCCATCTCCC TTGGGGCAGA TCTACCTAGT TCATGACAGT *1021

ATGTGCGGCT GGCCAGGGCT TTACACCTCT GCATCTTAAG TTGTTAATAC *1071

ATACCAATAA TGTAATATGG CTTTTTAAAG GAGAGGAGAG TGCTGGGTTG *1121

GGAAGGGAGG TGGTTGGTAG AGTCACAACT TCTCAATGAG TGAATTTACA *1171

GCTGATGGGA AAAGGAGTGT AACTGTGAAA AACGATGGCT GTGGTGGGGA *1221

AGAACAAACC AGCAGTAAGC CTGATGTTTG ATGTGGATGG AACTGGCCCC *1271

TAGAAACCCA TCTGACCCTC CTCTTGTTAC CCGAAATGCT GGGCTTAGTA *1321

TGCATGTACT GCTGAAAAGC AGGGCAGAAC AAATCAGGCT CTGACCAGAA *1371

GATCCTTCTG GTCCCTTCAC TCTACAAAAA CTTACTGATC ACCTCCACAT *1421

GCCAAATACA GTGCCAAGAT TTGGGGGTGT GGATGTTTAA ACAAAAAGCT *1471

GTGGGTCTCA TCAATCATCT CCATCCACAA GCTCCTAAAA GAAAGCCATT *1521

TACCTCGCTT GAAGCCAGGA ACACAGGGAA CAGCAGTCTG GCCAAGGAAG *1571

GGCTGTTATC TGGTGCTATC ACTCCAGTTA CTCCTCCAAC TGGGAGCTGC *1621

TATTTTATTT GGCAGTCAGC AACTGAAGAA AGAACATTCC TCTTAGTGGC *1671

AGATGTTCAA AGCAACTTTC AAGAAAGGCT AGGTGAGAAA GGCACTGGGA *1721

TGAGTGCTGC AGGCACTCTG TAGCCAGGGC CCCATTAGCC TTTGGCCAGG *1771

TAGCCACCAG AACCTATTTA TTGCACCTGG CATCTCCCCC AACCCCTCTC *1821

AGCTCTGTTA GGACTTCCAC ACAGCAGAGC TCAGGTGTTG CTGTCATTAC *1871

CTCCTTTCAG CTCCTCACTT CATTCTACTT TAAAGCCACA GTGCTAAGGC *1921

CTGCATCCCC TTTCTGCCCA AATGGGTTTT TTGCTACCAT ATCAAAGAAC *1971

CTGACATATG GCGGCATAGG AAGCAGAAGC TAAGCCTCTC TCCAGCTGCT *2021

GCTGTGTAAA ATCCATGCGT GGCCAAAGAG AAGTCAGGGG ATTATGACAT *2071

AAATGGTGCT GGGAAGAACC CTCTGCCTAA AACTGTCTCC TTCTCCTGGT *2121

GCTACAACCG GAATCCACCA TGAGAGAGTA CTTTCTTCGG TTCTTTCCTC *2171

CTGTCCTTGA CAGAGTAACA CGTTAATCTG GTTCTTGGTG GTGTTAGGGA *2221

CTGATTCTCT CAGGAAAGGC ACACATGGTA TGATGGCTCT TCCCAGAGTC *2271

TATGTGATGC TACATAACTT CAGTATCTAG CTGAGACATG CTTCCTACAT *2321

GACTGTTAAA GCACAGCCAA TCCAGGCCAA GAAGACTAGT AACAGGCACA *2371

TTCTGAAAGA TGGAAGCAGC ACTGATAGAT CAAAACCACC ACTGCATATG *2421

TATTACACTG TTTTTGTTCA CCATTTTCCT AAGTGTGTTA TTTAGAATAT *2471

TGGTTATTAC AAGGAAAAAT AAAGTGGGGA GGCTGGTTAG GCCTTGTGAG *2521

TTTGGGAAAC TTAGGTTATA AAAACTAAAT AAAGTTTTTC TACTGTGAGA *2571

CTAGATGTGC AGGAGTGAAA GGTGTAGAGG GTCTTGTTTT CCAAATTCGA *2621

TCTCAGAATC TTTTTGCCAG AAGTGTCTCA TGGGACTTAT CTATAGTGGA *2671

ACACATTTGA AGACCTACTG CTCTATTAAG AAGGCAGCCG GACAACATGT *2721

TCTAATACTT CGTATGCTTT GTGACCTAGT TAAAATCTAA ACTTAAGTCG *2771

CCATGGCCAG TGGCCTTTAG ATTAAGCTAG CCTTACCCCT GGGAGTATAC *2821

CAGAGCTTTC CAAGGAATAC ACAGACTCCA GTACTCTCAG GGGAGCAGTG *2871

TTCAGAGCCT CATCTTCCTG TTATATTCTT CTCTAAGATT CATCTGCCTG *2921

AGAAAATGCC CTTTTCTCAC CTTACAAAAG AAAATATGGC TGTCTCCACC *2971

TCTAGTCTTA CTGTAGAGCA TGTCCCAAGG TGTAAAAATT CAAAATGTGG *3021

ATATTTGGAA AGTGAAAGAC TTATCAACAG GGCACAAATC TTTTTGCAAA *3071

TGGATTTTCC AAGTTTTTCT GGTGGTTCCA AATTTTTTGC TTTCAACAAA *3121

GTGGGAGGAA CAGCCTGTAG ATTTCTGAGT CTCTTAGCAT GTAACTACAA *3171

AGGGGTTGGA AGAATTCAGT GATTCTGCTA TCATAAAGCT TCCGTTCCCA *3221

TTGATGTATC TGTGTGAACA AGGATCAACA TCTCCATAAA TGAAATTGAA *3271

AACGGAAAAT AGAATTGATG ATGAACTTTG GCTCAATCTT AAGATGTTAT *3321

CAATCTACAT AGATGAAATA ATTGTGGAGA AAAGCCCTCT TTATCTCATT *3371

AAGTGATACA TTTCCAAAGA AGTTTTACTA TGTTTAATAA TTTAGTGAAA *3421

TTTGGGCTAT GTGTTTATTG ATTCAGCTCA ATCCAGAGGA AAATTTTAAA *3471

GGCTTACAGC CTTAGGATTA TAGGATACTA TATAATACTT TTGGTACAGA *3521

GATAGAATTA AATAACATAA AAATCAAAAA TTTATTAGGC TAAAATTTTG *3571

AGGGAGAAGT GGTATGAAAA TACAAATTCA AGGAGTAAAA GGAAAAGTGG *3621

GGCATTCCTT GCTACTAAAA ATTGCCTTGT TCCAGGTAAG ACTGATCATA *3671

AAAAAATGGC CCTGTTCATA AAATTTTTAA AAAGATCATA GTATCTATCA *3721

AATAACTTAT ATTAAGAACC TCCTGGGCTA AATTTAAAAA GTAATACAAC *3771

AGTTTTATTT AAACATGTAG TGTCTACGGT ATGCCAGCAC TTTGCAGCTA *3821

TTTATAATGA GAAATTTTAG ATGTCAATAT AGCAATGTGC AAGAAGATAG *3871

AGATTTTCAA AATTCACTTA AGAGTATCTG AGCATAAAAT GTTAAGATTG *3921

CTGATCGGAT GTGAGGGCGA TCTGGCTGCG ACATCTGTCA CCCCATTGAT *3971

CGCCAGGGTT GATTCGGCTG ATCTGGCTGG CTAGGTGGGT GTCCCCTTCC *4021

TACCTCACCG CTCCATGTGC GTCCCTCCCG AAGCTGCGCG CTCCGTCGAA *4071

GAGGACGACC AACCCCGATA GAGGAGGACC GGTCTTCGGT CAAGGGTATA *4121

CGAGTAGCTG CGCTCCCCTG CTGGAACCTC CAAACAAGCT CTCAAGATTG *4171

CTGATCTAGG GCCACTAAGT GATGAATTGT ATTTGGAAGC AAAAAGGATG *4221

GCTAAAAAGG ACCTCAACCC TTTTGACTTT AAAAGGAAAA TAGCTTAACC *4271

TTCAACCTGT GTGACATTTA ACTTTTTGAA CCCAACCGTA AAAGCTATCT *4321

TCTAACCAAC AAAAAGTTAA TAATTAGATT TGGAATTATA CAGAATTAGA *4371

AAATTGGCAT TTAAAAATAC TCAATAATTT GTCCCTGGTT TTTAATTTTC *4421

AAAATATTTT CTTTTTGAAG AGCCAGATTC CAGTGATCCT GCCTCTCAGA *4471

AATTTCCACA TTTCTTATTT TTCATTAGGC CTTAAGAAGC TGCATTTGTA *4521

AACTTGTGTT TCATTATTAA AGCTTAATTT ATTTTTTATA TAAATAGTAT *4571

GTGCTTTGTG TACATAGAGA ATTAAGTGAA TGAGTCACAC AGATGTTGGC *4621

TGTTGTTAAT GTGAAAATTA AACAGCTGTA TCACATTTTG AAAAATAAAA *4671

GTTTCATCTG AATGAA

PLCG2 (NM_002661.5) - cDNA + Protein - 2026-02-01