LPIN2 (NM_014646.2) - cDNA + Protein - 2025-04-02

```
GAGAAGAAGT GGCAGGTGAT GCTGAAGCGG GGGAGAAGCG GCAGAGCCGG -190

CCACACAGTG CAGGGGATGG AGACAGGTGC TGGGCTGGTC CTCCTGCAGC -140  c.-173A>T

ATCCTCAGTT GTTGGAGGGC AGTCATCCTC AGGCCGTACC CAGCCAGAGA -90

AGAAAAAGAA CAGTGTGAAG CCACGTGTGA TAGCCGTCCA ACATCGGCTC -40

TTCCCTCCAA TTACATTGTA GTTGATTGTG TCTCAAACCA TGAATTATGT 11
                                          M etAsnTyrVa 4


GGGACAGCTG GCTGGGCAGG TGATTGTCAC TGTGAAGGAA CTCTACAAGG 61
lGlyGlnLeu AlaGlyGlnV alIleValTh rValLysGlu LeuTyrLysG 21


GCATTAACCA GGCCACCCTC TCTGGGTGCA TTGATGTCAT CGTGGTACAG 111
lyIleAsnGl nAlaThrLeu SerGlyCysI leAspValIl eValValGln 37


CAGCAGGATG GCAGCTATCA GTGTTCACCT TTTCACGTTC GGTTTGGAAA 161  Q44Hfs*13
GlnGlnAspG lySerTyrGl nCysSerPro PheHisValA rgPheGlyLy 54


GCTGGGAGTC CTGAGATCCA AAGAGAAAGT GATTGATATA GAAATCAACG 211
sLeuGlyVal LeuArgSerL ysGluLysVa lIleAspIle GluIleAsnG 71


GCAGTGCAGT GGATCTTCAC ATGAAGTTGG GTGATAACGG AGAAGCTTTC 261
lySerAlaVa lAspLeuHis MetLysLeuG lyAspAsnGl yGluAlaPhe 87
```

```
TTTGTTGAGG AGACTGAAGA AGAATATGAA AAGCTTCCTG CTTACCTTGC 311
PheValGluG luThrGluGl uGluTyrGlu LysLeuProA laTyrLeuAl 104

CACCTCACCA ATTCCTACTG AAGATCAGTT CTTTAAAGAT ATTGACACCC 361
aThrSerPro IleProThrG luAspGlnPh ePheLysAsp IleAspThrP 121

CTTTGGTGAA ATCGGGTGGA GATGAAACAC CATCTCAGAG TTCAGACATC 411
roLeuValLy sSerGlyGly AspGluThrP roSerGlnSe rSerAspIle 137

TCACACGTCT TGGAAACAGA GACAATTTTT ACTCCAAGTT CTGTGAAAAA 461
SerHisValL euGluThrGl uThrIlePhe ThrProSerS erValLysLy 154

GAAAAAACGA AGGAGAAAGA AATACAAACA GGACAGTAAG AAGGAAGAGC 511
sLysLysArg ArgArgLysL ysTyrLysGl nAspSerLys LysGluGluG 171

AGGCCGCATC TGCTGCTGCA GAAGACACAT GTGATGTAGG CGTGAGCTCC 561  T180fs
lnAlaAlaSe rAlaAlaAla GluAspThrC ysAspValGl yValSerSer 187

GATGATGACA AGGGGGCCCA GGCAGCACGA GGATCTTCAA ATGCTTCCTT 611
AspAspAspL ysGlyAlaGl nAlaAlaArg GlySerSerA snAlaSerLe 204

GAAAGAAGAA GAATGTAAAG AGCCTTTGCT CTTCCATTCT GGGGATCATT 661
uLysGluGlu GluCysLysG luProLeuLe uPheHisSer GlyAspHisT 221

ACCCCTTATC TGATGGAGAT TGGTCCCCTT TAGAGACCAC CTATCCCCAG 711
yrProLeuSe rAspGlyAsp TrpSerProL euGluThrTh rTyrProGln 237

ACAGCGTGTC CTAAGAGTGA TTCAGAGCTG GAGGTGAAAC CTGCGGAGAG 761
```

```
ThrAlaCysP roLysSerAs pSerGluLeu GluValLysP roAlaGluSe 254

CCTGCTCAGA TCAGAGTCTC ACATGGAGTG GACGTGGGGC GGATTCCCAG 811
rLeuLeuArg SerGluSerH isMetGluTr pThrTrpGly GlyPheProG 271

AGTCCACCAA GGTCAGCAAA AGAGAACGAT CTGACCATCA TCCTAGGACA 861  p.16kbdel
luSerThrLy sValSerLys ArgGluArgS erAspHisHi sProArgThr 287

GCTACAATTA CACCATCAGA AAATACTCAT TTTCGGGTAA TTCCCAGTGA 911  R299W
AlaThrIleT hrProSerGl uAsnThrHis PheArgValI leProSerGl 304

GGACAACCTC ATCAGTGAAG TTGAGAAGGA TGCTTCCATG GAAGACACTG 961
uAspAsnLeu IleSerGluV alGluLysAs pAlaSerMet GluAspThrV 321

TCTGTACCAT AGTGAAGCCC AAACCCAGAG CCCTGGGTAC ACAGATGAGC 1011 A331S
alCysThrIl eValLysPro LysProArgA laLeuGlyTh rGlnMetSer 337

GACCCAACAT CTGTGGCAGA GCTTCTCGAA CCTCCTCTTG AGAGTACTCA 1061 P348L
AspProThrS erValAlaGl uLeuLeuGlu ProProLeuG luSerThrGl 354

GATTTCATCT ATGTTAGATG CTGACCACCT TCCCAACGCA GCCTTAGCGG 1111
nIleSerSer MetLeuAspA laAspHisLe uProAsnAla AlaLeuAlaG 371

AGGCGCCCTC AGAATCCAAA CCGGCAGCTA AAGTAGACTC GCCGTCAAAG 1161 K387E
luAlaProSe rGluSerLys ProAlaAlaL ysValAspSe rProSerLys 387

AAGAAAGGTG TTCACAAAAG AAGCCAACAC CAGGGACCTG ATGATATTTA 1211
LysLysGlyV alHisLysAr gSerGlnHis GlnGlyProA spAspIleTy 404
```

```
CCTTGATGAC TTAAAGGGTC TAGAACCTGA AGTTGCAGCT CTTTATTTCC 1261
rLeuAspAsp LeuLysGlyL euGluProGl uValAlaAla LeuTyrPheP 421

CTAAAAGTGA ATCGGAGCCC GGTTCCAGGC AGTGGCCCGA GTCTGACACA 1311 G428S
roLysSerGl uSerGluPro GlySerArgG lnTrpProGl uSerAspThr 437

CTCTCTGGCT CCCAGTCCCC ACAGTCCGTG GGAAGCGCAG CTGCAGATAG 1361 p.Ser439Trpfs*15
LeuSerGlyS erGlnSerPr oGlnSerVal GlySerAlaA laAlaAspSe 454

CGGCACCGAG TGCCTCTCAG ATTCTGCCAT GGACTTGCCT GACGTTACCC 1411
rGlyThrGlu CysLeuSerA spSerAlaMe tAspLeuPro AspValThrL 471

TCTCCCTTTG CGGGGGCCTC AGTGAAAATG GAGAAATTTC AAAAGAAAAA 1461 E486Kfs*20
euSerLeuCy sGlyGlyLeu SerGluAsnG lyGluIleSe rLysGluLys 487

TTCATGGAGC ATATCATTAC TTATCACGAA TTTGCAGAAA ACCCTGGACT 1511 L504F
PheMetGluH isIleIleTh rTyrHisGlu PheAlaGluA snProGlyLe 504

TATAGACAAT CCTAACCTTG TAATAAGGAT ATATAATCGT TACTATAACT 1561 R517H
uIleAspAsn ProAsnLeuV alIleArgIl eTyrAsnArg TyrTyrAsnT 521

GGGCTTTGGC AGCTCCCATG ATCCTTAGCT TGCAAGTATT CCAGAAGAGC 1611
rpAlaLeuAl aAlaProMet IleLeuSerL euGlnValPh eGlnLysSer 537

TTGCCTAAGG CCACAGTTGA GTCCTGGGTG AAAGACAAGA TGCCAAAGAA 1661
LeuProLysA laThrValGl uSerTrpVal LysAspLysM etProLysLy 554
```

```
ATCTGGTCGC TGGTGGTTTT GGCGAAAGAG AGAAAGCATG ACCAAACAGC 1711 R562Q R564Kfs*3 c.1691_1694delGAGA
sSerGlyArg TrpTrpPheT rpArgLysAr gGluSerMet ThrLysGlnL 571

TGCCAGAATC CAAGGAGGGA AAATCTGAGG CACCGCCAGC CAGTGACCTG 1761 S579P
euProGluSe rLysGluGly LysSerGluA laProProAl aSerAspLeu 587

CCATCCAGCT CCAAGGAGCC GGCCGGTGCC AGGCCGGCCG AGAATGACTC 1811 G596S P599L E601K
ProSerSerS erLysGluPr oAlaGlyAla ArgProAlaG luAsnAspSe 604

CTCGAGTGAC GAGGGATCAC AGGAGCTCGA AGAATCCATC ACAGTGGACC 1861
rSerSerAsp GluGlySerG lnGluLeuGl uGluSerIle ThrValAspP 621

CCATCCCCAC AGAGCCCCTG AGCCACGGCA GCACAACTTC ATATAAGAAG 1911 P626S
roIleProTh rGluProLeu SerHisGlyS erThrThrSe rTyrLysLys 637

TCTCTCCGCC TCTCCTCAGA CCAGATCGCA AAACTGAAGC TCCACGATGG 1961 D644G G654D
SerLeuArgL euSerSerAs pGlnIleAla LysLeuLysL euHisAspGl 654

CCCAAATGAT GTTGTGTTTA GTATTACAAC CCAGTATCAA GGCACCTGTC 2011
yProAsnAsp ValValPheS erIleThrTh rGlnTyrGln GlyThrCysA 671

GCTGTGCAGG GACCATTTAC CTGTGGAACT GGAATGACAA GATCATCATT 2061 W681Gfs*14
rgCysAlaGl yThrIleTyr LeuTrpAsnT rpAsnAspLy sIleIleIle 687

TCTGATATTG ATGGGACAAT AACCAAGTCG GATGCTTTGG GACAGATTCT 2111
SerAspIleA spGlyThrIl eThrLysSer AspAlaLeuG lyGlnIleLe 704

CCCACAGCTG GGCAAAGACT GGACCCACCA GGGTATAGCA AAGCTCTACC 2161
```

```
uProGlnLeu GlyLysAspT rpThrHisGl nGlyIleAla LysLeuTyrH 721

ATTCCATCAA TGAGAATGGC TACAAGTTTC TGTACTGCTC GGCTCGTGCC 2211 Y732Stop S734L R736C R736H
isSerIleAs nGluAsnGly TyrLysPheL euTyrCysSe rAlaArgAla 737

ATCGGCATGG CCGACATGAC CCGTGGCTAC CTGCACTGGG TCAATGACAA 2261 A741A Y747*
IleGlyMetA laAspMetTh rArgGlyTyr LeuHisTrpV alAsnAspLy 754

GGGCACAATC TTGCCCCGGG GCCCCCTGAT GCTGTCCCCC AGCAGCTTGT 2311
sGlyThrIle LeuProArgG lyProLeuMe tLeuSerPro SerSerLeuP 771

TCTCCGCCTT CCACAGAGAA GTGATAGAAA AGAAACCAGA GAAGTTCAAA 2361
heSerAlaPh eHisArgGlu ValIleGluL ysLysProGl uLysPheLys 787

ATTGAGTGTC TAAATGATAT CAAGAATCTG TTTGCCCCGT CTAAGCAGCC 2411
IleGluCysL euAsnAspIl eLysAsnLeu PheAlaProS erLysGlnPr 804

CTTCTATGCT GCCTTTGGAA ACCGTCCAAA TGATGTCTAT GCCTACACAC 2461
oPheTyrAla AlaPheGlyA snArgProAs nAspValTyr AlaTyrThrG 821

AAGTTGGAGT TCCAGACTGT AGAATATTCA CCGTGAACCC CAAGGGTGAA 2511 G823A
lnValGlyVa lProAspCys ArgIlePheT hrValAsnPr oLysGlyGlu 837

TTAATACAAG AAAGAACCAA AGGAAACAAG TCATCGTATC ACAGGCTGAG 2561
LeuIleGlnG luArgThrLy sGlyAsnLys SerSerTyrH isArgLeuSe 854

TGAGCTCGTG GAGCATGTGT TCCCCCTTCT CAGTAAGGAG CAGAATTCCG 2611
rGluLeuVal GluHisValP heProLeuLe uSerLysGlu GlnAsnSerA 871
```

```
CTTTTCCCTG CCCGGAGTTC AGCTCCTTCT GCTACTGGCG AGACCCGATC 2661 C874F P875P
laPheProCy sProGluPhe SerSerPheC ysTyrTrpAr gAspProIle 887

CCTGAAGTGG ACCTGGATGA CCTGTCTTGA GGCGGCACCT CAGTGGGTGG *20  c.*3C>T
ProGluValA spLeuAspAs pLeuSerSto p

GCAGGGCTTG GTCCCCCTCC CCACAGCAAG GGAAGGCAGC TGGCTCTTCT *70
GCTGACCTCA GATACCAGCC TTCCCCAGCG GGGACGGGTG CTTCTGGAGC *120
TGGTCCCGCC ATCCTCCTTT GCCTTCCCAG GCCAGCTGCT CAGGCTCGGC *170
AGGTCTGCAG CTCAGCTCCT GGAAGGAGAA GGGAGGAACT GGGCCTGGGG *220
CTGGAGGCCT GGGATCCCTC CTTTGTGGGT CGCACACATG TTTCCTGCTG *270
TGAGCTGGGG CCTCCTTCCA TTGCATCATT TTAAAGGAAG AAAAAAGCAG *320
CTAAAAAAGA GTGGACCAAA ACACTGCACA CAGTGAAGTG TTCCAGTTTC *370
CACTGGGCAG TTGAGGTGGC TTCTGTAACC AGGGCTGTCT TCAGATGTCA *420
GGGTCCCTGA ACTGCTGCGG GCCCAGTCAG TGATGCTGGC TGAAGCTGCC *470
TGTGCACGTT TCTTCTCTGG TCGCCTCATT TCCTGCTACA CTGAAGGGGT *520
CAGCTGCTCC AGTGGGCCAA GTTGGGCAGG ACCCCCGCCC CTGCAGGGCC *570
CATGCACCAG AGCCACTGAG CCCAGTCCCA TAAACCTGGC CCTCTTTGGG *620
GAAAGATCCC CACAGAGCAT CCTCCTCTCA TCTGTGACAA CTCCACGAGC *670
CCTTAATTTC TTAGTCCTCA CCAGAAGAAC AGGTCTCACA AGTATATATT *720
TGATGTCTGT AATAAAAGTG GGAAGGTGGG TCTTAAAACA GACCAAACCC *770
CGCCCCGCCC CCAACAACTC TGCTTTTAGG GAGGCCTCCG AAATGCAGAT *820
AGGCGGTTGA GTGGGGTCCT GGGAAGAGCG CTGAATCCCT CTGCTTGCTG *870
CCTGGTGTGG GCCTTTGGAA AGCATCTTGC CTTGGGACAG GATTTCTAAA *920
ATTCTGTGAT TCAGATTTGT CAGGGAAGCA CAGTGAAGCT TGCTTAAAGG *970
CACTGGCCAG CAGTGTGTGA CTTTGGCTTT TGGGATCACA CCCTGTAATC *1020
GGGCCCGTGG AAGCAGCGTC AAAGAGGGGT CTTGGAGCTC CTATGGAGCA *1070
```

```
GACTGCCCCC CGAGCAGTGT CCCCAGCCTA GCCCTGTGAG ACCCCATGGG *1120
GACACGGGTG CCTATGTATT TTCACTAAAA TATACATGGT AGCTCCATTT *1170
ACTGATGCGG TTGTAATGAG CTCACATCGT GTCTGAAGAG ATGGCACCAG *1220
GGAAAGGTGT GCCATAAGCT GCTCCAGAGC TTTTGGTATG CTGAGTGTTG *1270
ACAGAGCTGC ACTCTTAACA TCAAGAGAAC TGTCAGGAGC CCAGAACCAA *1320
CCCCAGGTCT TGGTCTCCAT TGGCGAGAAC ACAGGACGTG GTGGTTCCTG *1370
AGCAGAGAGG GATCTGCAGA TACAGGCTTG GCGCTCGGGG TGGTCTCGTG *1420
GCCAACTCTT CATGCCCCTG CCGTTGTAGT GGAACCTCTA CATGTTTTAG *1470
TTTGCTTCAC CTAAAATAAT GCTGATCTAG AGATAGAGAA ATAGGGGTGG *1520
TTATTTTTCC AGATTGGAGA GTTGAAAGTC CCTGACTGAT TTCAGCCATT *1570
TTCCTAGTGC TTGTCGGATG CAGAGACAAT GTTGAAATCC CCTAAACACA *1620
GTTCTCAGTG GCAAAACCTA GGAAGGCTCA TGTTCCCAGA GAAGGGACCA *1670
CATGAGCCTT CTCCCATGCA AAGCTTCCCC CAGCTTAAAT AGTTGATAAG *1720
GACTAATTGT TTAATGAGTT TATTTATCTA CAGTAGGTTA GGGATCCTGG *1770
GTTCTGTTTA TATGAAGTTC TTCCCAGTTT GTGAATTCTA GTACAGCAGC *1820
CATGCAGCCA CCTTATTTCA TAGATGCCAT CTGTGTGTCC TCTTGACTAC *1870
CTTCTATTTA GAGGAAGAAT GAGAGCTTTG TGTGTTTAAC TGAGCTTATA *1920
GTAGGACTTC TTTGCATATG TATGGTACTG AAAAATCTTA ATATACATCT *1970
TTAATCCTTT TTAGGTTGTC CTTTAAAGAG TTTTTGACTA GTTTCTTTTT *2020
CTTGACAGCT CTTCTCTTTG GACACATGGG CCTTCTTAGA GGGTTCAGTC *2070
TAGGACCCGG CTCTCCTGGC CCTGTGTTGA GGGTAGCTGG TCCCTCTGTC *2120
CCTGTGTCTG CTAGCACTAG ACTTTGTTGC TGCAGATTGA TCCAGTGGGT *2170
ACATAGGCTA ATTAATGTGA GTCTTTTTCC TTGTTTAAAG GAGTCCCTCT *2220
TGCTGAAAGT AGATGATTAC TATTGCTGTA GTGTTAGGAA AGTATTAAGT *2270
TTGTGCTGAA AATCCATTGC CATTTGGTAC AAATGACATT TGTTCTTTCT *2320
GTGAAAGAGA TGCCCTCGAG TGTGTTTGTA CACAAACCCT TAGGATGGTG *2370
AGTTGAAGCA TCACCCTCGC GCTATCTTCA GTGACGGGTG ACGGCTCAGG *2420
GAGATGGCAG GCAGATTGGG CTCTAAGTCA TTATTCTCTC AGTTACTCCA *2470
```

```
TTGGTGAAAT GGCCCTTTCC CTCTTTGCAG TTCAGTCTAA GTCTCGTATT *2520
TGCTTTGCTG TCTGTGTGCT GAAGCTCGTC CCGTGTGAGT TGCTGTCTGC *2570
CCCTTGTCAG GCTGTGAGGT GCTCGTGTAG ACCTGGAGCA TGCAGGCTGC *2620
CTCCGTTTTT GGGTACTGTG TTGTGTTTTG CTCTGTCTAA AAACATCTGC *2670
ATAGTTTTCA ACTGGAAAAA GAAAAAACTT AAAAATGGGA TGTCCTAAAA *2720
TGAAAGCTGC TCAAAGTCAC AGAACAACCG AGGGACAAAG GAGATTGGAT *2770
GACTGGGAAG CGCTGGCCCG GAACAGCCCC TGCAACTGTG GGGCCTGCAC *2820
ACAGCCCTTC CACAGTTGGC ACTGCAGGTG CAGGCCAACC CTTTAAAGAA *2870
TAAACAAGGA AGTCAGCTCT TTCACTTTTT ACAAGTTGGC AAAAACAGAC *2920
TTCCGGGGAA TTTCGATGTT TTCCCGTGTT GTAGAGCTTC CAGGGTTTAA *2970
TAAAACTGGT TAAAAATTGA GTCTTTCCCT GAAGTAAGTG CTCTTTCCAG *3020
ATGAAAACTA CTCTTTTGGT TTTGTTTGAA AGTAAGAAAG GGAGGGGAAA *3070
CTTTGCTCTT TTAATAATTA TGTTCAGCCT ATGATGAAGT ATTTGATTAT *3120
TAGACAGCAA TGTCACTAAT AAGTTTTAAG TTGTCCAAAG TTAATTGTAA *3170
ACATCATCAG TACAGTACTC TTAGTTACAG TAAAGCAATT GTTGCAAGAT *3220
GAATGGCTAA TATTTTGGTG CAGTGTTTGA TGTTCAAAAC AAAATGTTAC *3270
AACAATAAAC GAACATAACA TAAACTGAA
```

LPIN2 (NM_014646.2) - cDNA + Protein - 2025-04-02