



LPIN2 (NM_014646.2) - cDNA + Protein - 2026-03-03

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

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lGlyGlnLeu AlaGlyGlnV alIleValTh rValLysGlu LeuTyrLysG 21

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

CAGCAGGATG GCAGCTATCA GTGTTACCT TTTCACGTTT GGTGGGAAA 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

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PheValGluG luThrGluG1 uGluTyrGlu LysLeuProA laTyrLeuAl 104

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aThrSerPro IleProThrG luAspGlnPh ePheLysAsp IleAspThrP 121

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roLeuValLy sSerGlyGly AspGluThrP roSerGlnSe rSerAspIle 137

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SerHisValL euGluThrGl uThrIlePhe ThrProSerS erValLysLy 154

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lnAlaAlaSe rAlaAlaAla GluAspThrC ysAspValGl yValSerSer 187

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AspAspAspL ysGlyAlaGl nAlaAlaArg GlySerSerA snAlaSerLe 204

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uLysGluGlu GluCysLysG luProLeuLe uPheHisSer GlyAspHist 221

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rLeuLeuArg SerGluSerH isMetGluTr pThrTrpGly GlyPheProG 271

AGTCCACCAA GGTCAGCAA AGAGAACGAT CTGACCATCA TCCTAGGACA 861 [p.16kdel](#)

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

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alCysThrIl eValLysPro LysProArgA laLeuGlyTh rGlnMetSer 337

GACCCAACAT CTGTGGCAGA GCTTCTCGAA CCTCCTCTTG AGAGTACTCA 1061 [P348L](#)

AspProThrS erValAlaGl uLeuLeuGlu ProProLeuG luSerThrGl 354

GATTTTCATCT 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

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