



LPIN2 (NM_014646.2) - cDNA + Protein - 2024-12-04

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 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

TCACACGTCT TGGAAACAGA GACAATTTTT ACTCCAAGTT CTGTGAAAAA 461

SerHisValL euGluThrGl uThrIlePhe ThrProSerS erValLysLy 154

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sLysLysArg ArgArgLysL ysTyrLysGl nAspSerLys LysGluGluG 171

AGGCCGCATC TGCTGCTGCA GAAGACACA^AT GTGATGTAGG CGTGAGCTCC 561 [T180fs](#)

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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yrProLeuSe rAspGlyAsp TrpSerProL euGluThrTh rTyrProGln 237

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ThrAlaCysP roLysSerAs pSerGluLeu GluValLysP roAlaGluSe 254

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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

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uAspAsnLeu IleSerGluV alGluLysAs pAlaSerMet GluAspThrV 321

TCTGTACCAT AGTGAAGCCC AAACCCAGAG CCCCTGGGTAC ACAGATGAGC 1011 [A331S](#)

alCysThrIl eValLysPro LysProArgA laLeuGlyTh rGlnMetSer 337

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

AspProThrS erValAlaGl uLeuLeuGlu ProProLeuG luSerThrGl 354

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nIleSerSer MetLeuAspA laAspHisLe uProAsnAla AlaLeuAlaG 371

AGGCGCCCTC AGAATCCAAA CCGGCAGCTA AAGTAGACTC GCCGTCAAAG 1161 [K387E](#)

luAlaProSe rGluSerLys ProAlaAlaL ysValAspSe rProSerLys 387

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LysLysGlyV alHisLysAr gSerGlnHis GlnGlyProA spAspIleTy 404

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TGCCAGAATC CAAGGAGGGA AAATCTGAGG CACCGCCAGC CAGTGACCTG 1761 [S579P](#)

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rSerSerAsp GluGlySerG lnGluLeuGl uGluSerIle ThrValAspP 621

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yProAsnAsp ValValPheS erIleThrTh rGlnTyrGln GlyThrCysA 671

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TAGACAGCAA TGTCACAAAT AAGTTTTAAG TTGTCCAAAG TTAATTGTAA *3170
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AACATAAAC GAACATAACA TAAACTGAA

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