



LYN (NM_002350.4) - cDNA + Protein - 2026-05-30

AGTTCCTCTC CCGCCGCGCC GGGCCGCGCT GCCGCTCGCT CCCC GGCCGT -225
GGCGCCTCCG GGCCAGACGC GCTGCAGCCT CCAGCCCGCG GCAAGCGGGG -175
CGGCCGCGCC ACCCCCGGCC CCGCGCCAGC AGCCCCTCGC CGCGCGTCCA -125
GCGTTCCCGG CCAGCAGCCT CCCCATACGC AGGTCCTGCT GGGCCGCCCC -75
GTCGCGCCCC CCACTCTGAA CTCAAGTCAC CGTGGAGCTC CGCCGCCCCG -25
AAACTTTCAC CGCGAGCGGG AAATATGGGA TGTATAAAAT CAAAAGGGAA 26
MetGly CysIleLysS erLysGlyLy 9

AGACAGCTTG AGTGACGATG GAGTAGATTT GAAGACTCAA CCAGTACGTA 76
sAspSerLeu SerAspAspG lyValAspLe uLysThrGln ProValArgA 26

ATACTGAAAG AACTATTTAT GTGAGAGATC CAACGTCCAA TAAACAGCAA 126
snThrGluAr gThrIleTyr ValArgAspP roThrSerAs nLysGlnGln 42

AGGCCAGTTC CAGAATCTCA GCTTTTACCT GGACAGAGGT TTCAA ACTAA 176
ArgProValP roGluSerGl nLeuLeuPro GlyGlnArgP heGlnThrLy 59

AGATCCAGAG GAACAAGGAG ACATTGTGGT AGCCTTGTAC CCCTATGATG 226
sAspProGlu GluGlnGlyA spIleValVa lAlaLeuTyr ProTyrAspG 76

GCATCCACCC GGACGACTTG TCTTTCAAGA AAGGAGAGAA GATGAAAGTC 276
lyIleHisPr oAspAspLeu SerPheLysL ysGlyGluLy sMetLysVal 92

CTGGAGGAGC ATGGAGAATG GTGGAAAGCA AAGTCCCTTT TAACAAAAAA 326
LeuGluGluH isGlyGluTr pTrpLysAla LysSerLeuL euThrLysLy 109

AGAAGGCTTC ATCCCCAGCA ACTATGTGGC CAAACTCAAC ACCTTAGAAA 376
sGluGlyPhe IleProSerA snTyrValAl aLysLeuAsn ThrLeuGluT 126

CAGAAGAGTG GTTTTTCAAG GATATAACCA GGAAGGACGC AGAAAGGCAG 426
hrGluGluTr pPhePheLys AspIleThrA rgLysAspAl aGluArgGln 142

CTTTTGGCAC CAGGAAATAG CGCTGGAGCT TTCCTTATTA GAGAAAGTGA 476
LeuLeuAlaP roGlyAsnSe rAlaGlyAla PheLeuIleA rgGluSerGl 159

AACATTAAAA GGAAGCTTCT CTCTGTCTGT CAGAGACTTT GACCCTGTGC 526
uThrLeuLys GlySerPheS erLeuSerVa lArgAspPhe AspProValH 176

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isGlyAspVa lIleLysHis TyrLysIleA rgSerLeuAs pAsnGlyGly 192

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TyrTyrIleS erProArgIl eThrPhePro CysIleSerA spMetIleLy 209

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sHisTyrGln LysGlnAlaA spGlyLeuCy sArgArgLeu GluLysAlaC 226

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CCCCGGGAGT CCATCAAGTT GGTGAAAAGG CTTGGCGCTG GGCAGTTTGG 776
ProArgGluS erIleLysLe uValLysArg LeuGlyAlaG lyGlnPheGl 259

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yGluValTrp MetGlyTyrT yrAsnAsnSe rThrLysVal AlaValLysT 276

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hrLeuLysPr oGlyThrMet SerValGlnA laPheLeuGl uGluAlaAsn 292

CTCATGAAGA CCCTGCAGCA TGACAAGCTC GTGAGGCTCT ACGCTGTGGT 926
LeuMetLysT hrLeuGlnHi sAspLysLeu ValArgLeuT yrAlaValVa 309

CACCAGGGAG GAGCCCATT ACATCATCAC CGAGTACATG GCCAAGGGCA 976
lThrArgGlu GluProIleT yrIleIleTh rGluTyrMet AlaLysGlyS 326

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LysLeuIleA spPheSerAl aGlnIleAla GluGlyMetA laTyrIleGl 359

GCGGAAGAAC TACATTCACC GGGACCTGCG AGCAGCTAAT GTTCTGGTCT 1126
uArgLysAsn TyrIleHisA rgAspLeuAr gAlaAlaAsn ValLeuValS 376

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pThrAlaPro GluAlaIleA snPheGlyCy sPheThrIle LysSerAspV 426

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alTrpSerPh eGlyIleLeu LeuTyrGluI leValThrTy rGlyLysIle 442

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etLysMetCy sTrpLysGlu LysAlaGluG luArgProTh rPheAspTyr 492

TTACAGAGCG TCCTGGATGA TTTCTACACA GCCACGGAAG GGCAATACCA 1526 Q507* Y508H Y508F Y508*

LeuGlnSerV alLeuAspAs pPheTyrThr AlaThrGluG lyGlnTyrGl 509

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