



*SH3BP2* (NM\_001122681.2) - cDNA + Protein - 2026-06-18

GAGTCAAGCC GCCGCCTCGA CCCAGGGCCC GCGGGCCAGG AGAGCGCTCG -9  
GCGGCTTCAT GCGGGCTGAA GAGATGCATT GGCCTGTCCC TATGAAGGCC 42  
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ATTGGTGCCC AGAACCTGCT AACCATGCCT GGGGGCGTGG CCAAGGCTGG 92  
IleGlyAlaG lnAsnLeuLe uThrMetPro GlyGlyValA laLysAlaGl 31

CTACCTGCAC AAGAAGGGCG GTACCCAGCT GCAGCTGCTG AAATGGCCCC 142  
yTyrLeuHis LysLysGlyG lyThrGlnLe uGlnLeuLeu LysTrpProL 48

TGCGCTTTGT CATCATCCAC AAACGCTGCG TCTACTACTT CAAGAGTAGC 192 ~~408delC~~  
euArgPheVa lIleIleHis LysArgCysV alTyrTyrPh eLysSerSer 64

ACCTCTGCCT CCCCGCAGGG CGCCTTCTCC CTGAGTGGCT ATAACC~~G~~GGT 242 ~~R80Q~~  
ThrSerAlaS erProGlnGl yAlaPheSer LeuSerGlyT yrAsnArgVa 81

GATGCGGGCG GCTGAGGAGA CCACGTCCAA CAACGTTTTC CCCTTCAAGA 292  
lMetArgAla AlaGluGluT hrThrSerAs nAsnValPhe ProPheLysI 98

TCATCCATAT CAGCAAGAAG CACCGCA~~C~~GT GGTTCCTTCTC GGCCTCCTCC 342 ~~T107M~~  
leIleHisIl eSerLysLys HisArgThrT rpPhePheSe rAlaSerSer 114

GAGGAGGAGC GCAAGAGCTG GATGGCCTTG CTGCGCAGGG AGATTGGCCA 392

GluGluGluA rgLysSerTr pMetAlaLeu LeuArgArgG luIleGlyHi 131

CTTCCACGAA AAGAAAGACC TGCCCTTGGA CACCAGCGAC TCCAGCTCGG 442

sPheHisGlu LysLysAspL euProLeuAs pThrSerAsp SerSerSerA 148

ACACAGACAG CTTCTACGGC GCAGTTGAGC GGCCTGTGGA TATCAGCCTT 492 [A155V](#)

spThrAspSe rPheTyrGly AlaValGluA rgProValAs pIleSerLeu 164

TCCCCGTACC CCACGGACAA TGAAGACTAT GAGCACGACG ATGAGGATGA 542

SerProTyrP roThrAspAs nGluAspTyr GluHisAspA spGluAspAs 181

CTCCTACCTG GAGCCTGACT CCCCAGGACC CGGAAGGCTT GAGGATGCCC 592

pSerTyrLeu GluProAspS erProGluPr oGlyArgLeu GluAspAlaL 198

TGATGCACCC ACCGGCTTAC CCACCACCCC CAGTGCCAC GCCCAGGAAG 642

euMetHisPr oProAlaTyr ProProProP roValProTh rProArgLys 214

CCAGCCTTCT CTGACATGCC CCGGGCCCAC TCCTTTACCT CCAAGGGCCC 692

ProAlaPheS erAspMetPr oArgAlaHis SerPheThrS erLysGlyPr 231

CGGTCCCCCTA CTGCCACCCC CGCCCCCTAA GCACGGCCTC CCAGATGTTG 742

oGlyProLeu LeuProProP roProProLy sHisGlyLeu ProAspValG 248

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GAGCCTTGCC CCAGGGTACC TGCTACCCCC CGAAGGATGA GCGATCCCC 842

GluProCysP roArgValPr oAlaThrPro ArgArgMetS erAspProPr 281

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oLeuSerThr MetProThrA laProGlyLe uArgLysPro ProCysPheA 298

GGGAGAGTGC CAGCCCCAGC CCGGAGCCCT GGACCCCTGG CCACGGGGCC 942 [G313R](#)

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TGCTCCACTT CCAGTGCTGC CATCATGGCC ACTGCCACCT CCAGAAACTG 992

CysSerThrs erSerAlaAl aIleMetAla ThrAlaThrs erArgAsnCy 331

TGACAAACTC AAGTCCTTCC ACCTGTCCCC CCGAGGACCA CCCACATCTG 1042

sAspLysLeu LysSerPheH isLeuSerPr oArgGlyPro ProThrSerG 348

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luProProPr oValProAla AsnLysProL ysPheLeuLy sIleAlaGlu 364

GAGGACCCCC CAAGGGAGGC AGCCATGCCC GGACTCTTTG TGCCCCCGT 1142

GluAspProP roArgGluAl aAlaMetPro GlyLeuPheV alProProVa 381

GGCTCCCCGG CCTCCTGCGC TGAAGCTGCC AGTGCCTGAG GCCATGGCGC 1192

lAlaProArg ProProAlaL euLysLeuPr oValProGlu AlaMetAlaA 398

GGCCCGCAGT CCTGCCCAGG CCAGAGAAGC CGCAGCTCCC GCACCTCCAG 1242

rgProAlaVa lLeuProArg ProGluLysP roGlnLeuPr oHisLeuGln 414

[CGATCACCCC](#) [CCGATGGGCA](#) [GAGTTTCAGG](#) [AGCTTCTCCT](#) [TTGAAAAGCC](#) 1292 [c.1243C>T](#) [R415P](#) [R415O](#) [P418T](#) [P418L](#) [P418H](#) [P418R](#) [P418Ha](#) [D419N](#) [D419Y](#) [D419G](#) [G420R](#) [G>C](#)

[G420R](#) [G>A](#) [G420E](#)

ArgSerProP roAspGlyGl nSerPheArg SerPheSerP heGluLysPr 431

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ATGAGAAGGT GCCACTGCCC AACTCGGTCT TCGTCAACAC CACGGAGTCC 1392

yrGluLysVa lProLeuPro AsnSerValP heValAsnTh rThrGluSer 464

TGCGAAGTGG AAAGGTTGTT CAAGGCTACA AGCCCCGGG GAGAGCCCCA 1442 [O481L](#)

CysGluValG luArgLeuPh eLysAlaThr SerProArgG lyGluProGl 481

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euValValTr pAspGluThr SerAsnLysV alArgAsnTy rArgIlePhe 514

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GluLysAspS erLysPheTy rLeuGluGly GluValLeuP heValSerVa 531

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lGlySerMet ValGluHisT yrHisThrHi sValLeuPro SerHisGlnS 548

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ATGCTA

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