



*F12 (NM\_000505.3) - cDNA + Protein - 2024-11-24*

CTATTGATCT GGACTCCTGG ATAGGCAGCT GGACCAACGG ACGGATGCCA 1  
M 1

TGAGGGCTCT GCTGCTCCTG GGGTTCCTGC TGGTGAGCTT GGAGTCAACA 51  
etArgAlaLe uLeuLeuLeu GlyPheLeuL euValSerLe uGluSerThr 17

CTTTCGATTC CACCTTGGGA AGCCCCCAAG GAGCATAAGT ACAAAGCTGA 101  
LeuSerIleP roProTrpGl uAlaProLys GluHisLysT yrLysAlaGl 34

AGAGCACACA GTCGTTCTCA CTGTCACCGG GGAGCCCTGC CACTTCCCCT 151  
uGluHisThr ValValLeuT hrValThrGl yGluProCys HisPheProP 51

TCCAGTACCA CCGGCAGCTG TACCACAAAT GTACCCACAA GGGCCGGCCA 201  
heGlnTyrHi sArgGlnLeu TyrHisLysC ysThrHisLy sGlyArgPro 67

GGCCCTCAGC CCTGGTGTGC TACCACCCCC AACTTTGATC AGGACCAGCG 251  
GlyProGlnP roTrpCysAl aThrThrPro AsnPheAspG lnAspGlnAr 84

ATGGGGATAC TGTTTGGAGC CCAAGAAAGT GAAAGACCAC TGCAGCAAAC 301  
gTrpGlyTyr CysLeuGluP roLysLysVa lLysAspHis CysSerLysH 101

ACAGCCCCTG CCAGAAAGGA GGGACCTGTG TGAACATGCC AAGCGGCCCC 351

isSerProCy sGlnLysGly GlyThrCysV alAsnMetPr oSerGlyPro 117

CACTGTCTCT GTCCACAACA CCTCACTGGA AACCACTGCC AGAAAGAGAA 401

HisCysLeuC ysProGlnHi sLeuThrGly AsnHisCysG lnLysGluLy 134

GTGCTTTGAG CCTCAGCTTC TCCGGTTTTT CCACAAGAAT GAGATATGGT 451

sCysPheGlu ProGlnLeuL euArgPhePh eHisLysAsn GluIleTrpT 151

ATAGAACTGA GCAAGCAGCT GTGGCCAGAT GCCAGTGCAA GGGTCCTGAT 501

yrArgThrGl uGlnAlaAla ValAlaArgC ysGlnCysLy sGlyProAsp 167

GCCCACTGCC AGCGGCTGGC CAGCCAGGCC TGCCGCACCA ACCCGTGCCT 551

AlaHisCysG lnArgLeuAl aSerGlnAla CysArgThrA snProCysLe 184

CCATGGGGGT CGCTGCCTAG AGGTGGAGGG CCACCGCCTG TGCCACTGCC 601

uHisGlyGly ArgCysLeuG luValGluGl yHisArgLeu CysHisCysP 201

CGGTGGGCTA CACCGGAGCC TTCTGCGACG TGGACACCAA GGCAAGCTGC 651

roValGlyTy rThrGlyAla PheCysAspV alAspThrLy sAlaSerCys 217

TATGATGGCC GCGGGCTCAG CTACCGCGGC CTGGCCAGGA CCACGCTCTC 701

TyrAspGlyA rgGlyLeuSe rTyrArgGly LeuAlaArgT hrThrLeuSe 234

GGGTGCGCCC TGTCAGCCGT GGGCCTCGGA GGCCACCTAC CGGAACGTGA 751

rGlyAlaPro CysGlnProT rpAlaSerGl uAlaThrTyr ArgAsnValT 251

CTGCCGAGCA AGCGCGGAAC TGGGGACTGG GCGGCCACGC CTTCTGCCCG 801

hrAlaGluGl nAlaArgAsn TrpGlyLeuG lyGlyHisAl aPheCysArg 267

AACCCGGACA ACGACATCCG CCCGTGGTGC TTCGTGCTGA ACCGCGACCG 851  
AsnProAspA snAspIleAr gProTrpCys PheValLeuA snArgAspAr 284

GCTGAGC**TGG** GAGTACTGCG ACCTGGCACA GTGCCAGACC CCAACCCAGG 901 **W268R**  
gLeuSerTrp GluTyrCysA spLeuAlaGl nCysGlnThr ProThrGlnA 301

CGGCGCCTCC GACCCCGGTG TCCCCTAGGC TTCATGTCCC ACTCATGCCC 951  
laAlaProPr oThrProVal SerProArgL euHisValPr oLeuMetPro 317

GCGCAGCCGG CACCGCCGAA GCCTCAGCCC ACGACCCGGA CCCC GCCTCA 1001  
AlaGlnProA laProProLy sProGlnPro ThrThrArgT hrProProGl 334

GTCCCAGACC CCGGGAGCCT TGCCGGCGAA GCGGGAGCAG CCGCCTTCCC 1051  
nSerGlnThr ProGlyAlaL euProAlaLy sArgGluGln ProProSerL 351

TGACCAGGAA CGGCCCACTG AGCTGCGGGC AGCGGCTCCG CAAGAGTCTG 1101  
euThrArgAs nGlyProLeu SerCysGlyG lnArgLeuAr gLysSerLeu 367

TCTTCGATGA CCCGCGTCGT TGGCGGGCTG GTGGCGCTAC GCGGGGCGCA 1151  
SerSerMetT hrArgValVa lGlyGlyLeu ValAlaLeuA rgGlyAlaHi 384

CCCCTACATC GCCGCGCTGT ACTGGGGCCA CAGTTTCTGC GCCGGCAGCC 1201  
sProTyrIle AlaAlaLeuT yrTrpGlyHi sSerPheCys AlaGlySerL 401

TCATCGCCCC CTGCTGGGTG CTGACGGCCG CTCACTGCCT GCAGGACCGG 1251  
euIleAlaPr oCysTrpVal LeuThrAlaA laHisCysLe uGlnAspArg 417

CCCGCACCCG AGGATCTGAC GGTGGTGCTC GGCCAGGAAC GCCGTAACCA 1301

ProAlaProG luAspLeuTh rValValLeu GlyGlnGluA rgArgAsnHi 434

CAGCTGTGAG CCGTGCCAGA CGTTGGCCGT GCGCTCCTAC CGCTTGCACG 1351

sSerCysGlu ProCysGlnT hrLeuAlaVa lArgSerTyr ArgLeuHisG 451

AGGCCTTCTC GCCCGTCAGC TACCAGCAGC ACCTGGCTCT GTTGCGCCTT 1401

luAlaPheSe rProValSer TyrGlnHisA spLeuAlaLe uLeuArgLeu 467

CAGGAGGATG CGGACGGCAG CTGCGCGCTC CTGTCGCCTT ACGTTCAGCC 1451

GlnGluAspA laAspGlySe rCysAlaLeu LeuSerProT yrValGlnPr 484

GGTGTGCCTG CCAAGCGGCG CCGCGCGACC CTCCGAGACC ACGCTCTGCC 1501

oValCysLeu ProSerGlyA laAlaArgPr oSerGluThr ThrLeuCysG 501

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lnValAlaGl yTrpGlyHis GlnPheGluG lyAlaGluGl uTyrAlaSer 517

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PheLeuGlnG luAlaGlnVa lProPheLeu SerLeuGluA rgCysSerAl 534

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aProAspVal HisGlySerS erIleLeuPr oGlyMetLeu CysAlaGlyP 551

TCCTCGAGGG CGGCACCGAT GCGTGCCAGG GTGATTCCGG AGGCCCGCTG 1701

heLeuGluGl yGlyThrAsp AlaCysGlnG lyAspSerGl yGlyProLeu 567

GTGTGTGAGG ACCAAGCTGC AGAGCGCCGG CTCACCCTGC AAGGCATCAT 1751

ValCysGluA spGlnAlaAl aGluArgArg LeuThrLeuG lnGlyIleIl 584

CAGCTGGGGA TCGGGCTGTG GTGACCGCAA CAAGCCAGGC GTCTACACCG 1801

eSerTrpGly SerGlyCysG lyAspArgAs nLysProGly ValTyrThrA 601

ATGTGGCCTA CTACCTGGCC TGGATCCGGG AGCACACCGT TTCC**TGATTG** \*3

spValAlaTy rTyrLeuAla TrpIleArgG luHisThrVa lSerStop

CTCAGGGACT CATCTTTCCC TCCTTGGTGA TTCCGCAGTG AGAGAGTGGC \*53

TGGGGCATGG AAGGCAAGAT TGTGTCCCAT TCCCCCAGTG CGGCCAGCTC \*103

CGCGCCAGGA TGGCGCAGGA ACTCAATAAA GTGCTTTGAA AATGCTGAGA \*153

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