



PSTPIP1 (NM_003978.5) - cDNA + Protein - 2026-03-03

AAACCTTCCT GCGCAGGCCT CGGGCTGCCT GCCTGCCTGC CTGCCTGGCC -399
CGGCCCGAGC TCCAGCCTGC CTCTTCCACT GGCCACTGCC TCCCACCCAG -349
GGCTGGCATC CCTGCTCCCT GCCCTGGGTC CCAGACTGTG TCCTCCATCA -299
CCGCAGGGTC GGTGAGGGC TGGGCTGGAC ACCAGGGCCC GCCCTCCCAT -249 -282G>T
CACTGAGCTC CACTCCTTCC TCATTTTGTCT GCTGATTCTA GCCCCAAACA -199
AAACAGGTTG AGCTTTTTTCC TCCCCTCAGA AGCTCCTCTC TGGCTCGTGG -149 c.262G>A
CTGCCTTCTG AGTGTTGCAG ACGGCGCCGG CCGGGAAGGG GGGCCTGGGC -99
CAGCCCTGCC AGGACTGGGA CGCTGCTGCT GGCGCCTGGC CCTCCATCAG -49
GCCAGCCTGT GGCAGGAGAG TGAGCTTTGC CGCGGCAGAC GCCTGAGGAT 2
Me 1

GATGCCCCAG CTGCAGTTCA AAGATGCCTT TTGGTGCAGG GACTTCACAG 52 M2T
tMetProGln LeuGlnPheL ysAspAlaPh eTrpCysArg AspPheThrA 18

CCCACACGGG CTACGAGGTG CTGCTGCAGC GGCTTCTGGA TGGCAGGAAG 102 T20M K34T
laHisThrGl yTyrGluVal LeuLeuGlnA rgLeuLeuAs pGlyArgLys 34

ATGTGCAAAG ACATGGAGGA GCTACTGAGG CAGAGGGCCC AGGCGGAGGA 152 A49Y
MetCysLysA spMetGluGl uLeuLeuArg GlnArgAlaG lnAlaGluGl 51

GCGGTACGGG AAGGAGCTGG TGCAGATCGC ACGGAAAGGCA GGTGGCCAGA 202 E51D R52Q L57R R62W A64T
uArgTyrGly LysGluLeuV alGlnIleAl aArgLysAla GlyGlyGlnT 68

CGGAGATCAA CTCCCTGAGG GCCTCCTTTG ACTCCTTGAA GCAGCAAATG 252 T68M

hrGluIleAs nSerLeuArg AlaSerPheA spSerLeuLy sGlnGlnMet 84

GAGAATGTGG GCAGCTCACA CATCCAGCTG GCCCTGACCC TGCGTGAGGA 302

GluAsnValG lySerSerHi sIleGlnLeu AlaLeuThrL euArgGluGl 101

GCTGCGGAGT CTCGAGGAGT TTCGTGAGAG GCAGAAGGAG CAGAGGAAGA 352 E110D

uLeuArgSer LeuGluGluP heArgGluAr gGlnLysGlu GlnArgLysL 118

AGTATGAGGC CGTCATGGAC CGGGTCCAGA AGAGCAAGCT GTCGCTCTAC 402 Y119C V122I M123 L416delinsT M123 K128delinsTMLLSQ D124 K128delinsGMLLS

L133 K136delinsPPDP)

ysTyrGluAl aValMetAsp ArgValGlnL ysSerLysLe uSerLeuTyr 134

AAGAAGGCCA TGGAGTCCAA GAAGACATAC GAGCAGAAGT GCCGGGACGC 452 D150E

LysLysAlaM etGluSerLy sLysThrTyr GluGlnLysC ysArgAspAl 151

GGACGACGCG GAGCAGGCCT TCGAGCGCAT TAGCGCCAAC GGCCACCAGA 502

aAspAspAla GluGlnAlaP heGluArgIl eSerAlaAsn GlyHisGlnL 168

AGCAGGTGGA GAAGAGTCAG AACAAAGCCA GGCAGTGCAA GGACTCGGCC 552 G543A

ysGlnValGl uLysSerGln AsnLysAlaA rgGlnCysLy sAspSerAla 184

ACCGAGGCAG AGCGGGTATA CAGGCAGAGC ATTGCGCAGC TGGAGAAGGT 602

ThrGluAlaG luArgValTy rArgGlnSer IleAlaGlnL euGluLysVa 201

CCGGGCTGAG TGGGAGCAGG AGCACCGGAC CACCTGTGAG GCCTTTCAGC 652 R202W R210W

lArgAlaGlu TrpGluGlnG luHisArgTh rThrCysGlu AlaPheGlnL 218

TGCAAGAGTT TGACCGGCTG ACCATTCTCC GCAACGCCCT GTGGGTGCAC 702 [c.C850T: p.Q284X](#) [Q219H](#) [E220_I226delinsDROFHPG](#) [D222_L416delinsSTRKCGI](#) [R228C](#) [A230T](#)
euGlnGluPh eAspArgLeu ThrIleLeuA rgAsnAlaLe uTrpValHis 234

AGCAA~~C~~AGC TCTCCATGCA GTGTGTCAAG GATGATGAGC TCTACGAGGA 752 [N236K](#) [Q237](#) [M240delinsRHRO](#) [S239P](#) [Q241R](#) [D246N](#) [E250Q](#) [E250K](#)
SerAsnGlnL euSerMetGl nCysValLys AspAspGluL euTyrGluGl 251

AGTGC GGCTG ACGCTGGAAG GCTGCAGCAT AGACGCCGAC ATCGACAGTT 802 [V252A](#) [T255M](#) [E257K](#) [E256G](#) [G258R](#) [G258S](#) [G258A](#) [D266N](#)
uValArgLeu ThrLeuGluG lyCysSerIl eAspAlaAsp IleAspSerP 268

TCATCCAGGC CAAGAGCA~~C~~G GGCACAGA~~G~~C CCCCCGCTCC GGTG~~C~~CCTAC 852 [T274M](#) [E277D](#) [P283S](#)
heIleGlnAl aLysSerThr GlyThrGluP roProAlaPr oValProTyr 284

CAGAACTATT ACGATCGGGA GGTCACCCCG CTGACCAGCA GCCCTGGCAT 902 [D289H](#) [P299S](#)
GlnAsnTyrT yrAspArgGl uValThrPro LeuThrSerS erProGlyIl 301

ACAGCCGTCC TG~~C~~GGCATGA TAAAGAGGTT CTCTGGACTG CTGCACGGAA 952 [C305C](#)
eGlnProSer CysGlyMetI leLysArgPh eSerGlyLeu LeuHisGlyS 318

GTCCCAAGAC CACTT~~C~~GTTG GCAGCTTCTG CTG~~C~~GTCCAC AGAGACCCTG 1002 [S323L](#) [A329V](#)
erProLysTh rThrSerLeu AlaAlaSerA laAlaSerTh rGluThrLeu 334

ACCC~~C~~ACCC CCGAGCGGAA TGAGGGT~~G~~TC TACACAGCCA TCGCAGTGCA 1052 [T337Pfs*52](#) [P338](#) [A347delinsLSERRVHTS](#) [E339](#) [D341delinsGGM](#) [Val344Ile](#) [Y345C](#)
ThrProThrP roGluArgAs nGluGlyVal TyrThrAlaI leAlaValGl 351

GGAGATACAG GGAAACCCCG CCTCACCAGC CCAGGAGTAC CGGGCGCTCT 1102 [E352K](#) [E352A](#) [R365W](#)
nGluIleGln GlyAsnProA laSerProAl aGlnGluTyr ArgAlaLeuT 368

ACGATTATAC AGCGCAGAAC CCAGATGAGC TGGACCTGTC CGCGGGAGAC 1152 D369G A372Y D384G

yrAspTyrTh rAlaGlnAsn ProAspGluL euAspLeuSe rAlaGlyAsp 384

AUCCTGGAGG TGATCCTGGA AGGGGAGGAT GCGCTGGTGA CTGTGGAGAG 1202 c.1154T>C G1179A G395S

IleLeuGluV alIleLeuGl uGlyGluAsp GlyTrpTrpT hrValGluAr 401

GAACGGGCAG CGTGGCTTCG TCCCTGGTTC CTACCTGGAG AAGCTTGTAG *1 G403R G403E R405C F407L V408I

gAsnGlyGln ArgGlyPheV alProGlySe rTyrLeuGlu LysLeuStop 418

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CCCCCAGCAC TGTCCCCACC TTGCTAGGGC CCAGAACCAA GCGTCCCCCA *101

GCCCCGAGAG GGAGCCTGTC GTCTCCAGG GAATAAAGGA GTGCGTTCTG *151

TTCTCCTTGG TGTGCTGGGG TCCCGTTCTC TTTTCTCCT GCTCCAGTGT *201 c.*156_158del

CCGAGTGCTC AGTTCAGAGG AGGCAAAGGA ACAAGGGAAG GAGCCTGGAT *251

GTGGAGCTCC CCAACTCAGC CGAGGCTCA GCTATAGTTG GAGAAGAG

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