



PSTPIP1 (NM_003978.5) - cDNA + Protein - 2024-05-14

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 TCATTTTGCT GCTGATTCTA GCCCCAAACA -199
AAACAGGTTG AGCTTTTTCC TCCCCTCAGA AGCTCCTCTC TGGCTCGTGG -149 c.262G>A
CTGCCTTCTG AGTGTTCAG ACGGCGCCGG CCGGGAAGGG GGGCCTGGGC -99
CAGCCCTGCC AGGACTGGGA CGCTGCTGCT GGC GCCTGGC CCTCCATCAG -49
GCCAGCCTGT GGCAGGAGAG TGAGCTTTGC CGCGGCAGAC GCCTGAGGAT 2

Me 1

GATGCCCCAG CTGCAGTTCA AAGATGCCTT TTGGTGCAGG GACTTCACAG 52 M2I
tMetProGln LeuGlnPheL ysAspAlaPh eTrpCysArg AspPheThrA 18

CCCACA~~C~~GGG CTACGAGGTG CTGCTGCAGC GGCTTCTGGA TGGCAGGA~~A~~G 102 T20M K34I
laHisThrG1 yTyrGluVal LeuLeuGlnA rgLeuLeuAs pGlyArgLys 34

ATGTGCAAAG ACATGGAGGA GCTACTGAGG CAGAGGGCCC AGG~~C~~GGAGGA 152 A49V
MetCysLysA spMetGluG1 uLeuLeuArg GlnArgAlaG lnAlaGluG1 51

GCGGTACGGG AAGGAGCTGG TGCAGATCGC A~~C~~GGAAAG~~G~~CA GGTGGCCAGA 202 E51D R52Q L57R R62W A64I
uArgTyrGly LysGluLeuV alGlnIleAl aArgLysAla GlyGlyGlnT 68

CGGAGATCAA CTCCCTGAGG GCCTCCTTTG ACTCCTTGAA GCAGCAAATG 252 **T68M**

hrGluIleAs nSerLeuArg AlaSerPheA spSerLeuLy sGlnGlnMet 84

GAGAATGTGG GCAGCTCACA CATCCAGCTG GCCCTGACCC TGCCTGAGGA 302

GluAsnValG lySerSerHi sIleGlnLeu AlaLeuThrL euArgGluGl 101

GCTGCGGAGT CTCGAGGAGT TTCGTGA**GAG** **GCAGAAGGAG CAGAGGAAGA** 352 **E110D**

uLeuArgSer LeuGluGluP heArgGluAr gGlnLysGlu GlnArgLysL 118

AGT**A**TGAGGC **C****G**TC**A**T**G****G****A**C **CGGGTCCAGA AGAGCAAGCT GTCGC****I**CTAC 402 **Y119C V122I M123 L416delinsI M123 K128delinsTMLLSQ D124 K128delinsGMLLS**
L133 K136delinsPPDP)

ysTyrGluAl aValMetAsp ArgValGlnL ysSerLysLe uSerLeuTyr 134

AAGAAGGCCA TGGAGTCCAA GAAGACATAC GAGCAGAAGT GCCGGGACGC 452

LysLysAlaM etGluSerLy sLysThrTyr GluGlnLysC ysArgAspAl 151

GGACGACGCG GAGCAGGCCT TCGAGCGCAT TAGCGCCAAC GGCCACCAGA 502

aAspAspAla GluGlnAlaP heGluArgIl eSerAlaAsn GlyHisGlnL 168

AGCAGGTGGA GAAGAGTCAG AACAAAGCCA GGCAGTGCAA **G**GACTCGGCC 552 **G543A**

ysGlnValGl uLysSerGln AsnLysAlaA rgGlnCysLy sAspSerAla 184

ACCGAGGCAG AGCGGGTATA CAGGCAGAGC ATTGCGCAGC TGGAGAAGGT 602

ThrGluAlaG luArgValTy rArgGlnSer IleAlaGlnL euGluLysVa 201

CGGGCTGAG **T**GGGAGCAGG **AGCAC****C**GGAC **CACCTGTGAG GCCTTTCAGC** 652 **R202W R210W**

lArgAlaGlu TrpGluGlnG luHisArgTh rThrCysGlu AlaPheGlnL 218

TGCAAGATT TGACCGGCTG ACCATTCTCC GCAACGCCCT GTGGGTGCAC 702 [c.C850T: p.Q284X](#) [Q219H](#) [E220_I226delinsDRQFHPG](#) [D222_L416delinsSTRKCG](#) [R228C](#) [A230T](#)
euGlnGluPh eAspArgLeu ThrIleLeuA rgAsnAlaLe uTrpValHis 234

AGCAAACAGC TCTCCATGCA GTGTGTCAAG GATGATGAGC TCTACGAGGA 752 [N236K](#) [Q237_M240delinsRHRQ](#) [S239P](#) [Q241R](#) [D246N](#) [E250Q](#) [E250K](#)
SerAsnGlnL euSerMetGl nCysValLys AspAspGluL euTyrGluGl 251

AGTGCGGCTG ACCTGTGAAG GCTGCAGCAT AGACGCCGAC ATCGACAGTT 802 [T255M](#) [E257K](#) [E256G](#) [G258R](#) [G258S](#) [G258A](#) [D266N](#)
uValArgLeu ThrLeuGluG lyCysSerIl eAspAlaAsp IleAspSerP 268

TCATCCAGGC CAAGAGCACG GGCACAGAGC CCCCCGCTCC GGTGCCCTAC 852 [T274M](#) [E277D](#)
heIleGlnAl aLysSerThr GlyThrGluP roProAlaPr oValProTyr 284

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

ACAGCCGTCC TGCGGCATGA TAAAGAGGTT CTCTGGACTG CTGCACGGAA 952 [C915T](#)
eGlnProSer CysGlyMetI leLysArgPh eSerGlyLeu LeuHisGlyS 318

GTCCCAAGAC CACTTCGTTG GCAGCTTCTG CTGCGTCCAC AGAGACCCTG 1002 [S323L](#) [A329V](#)
erProLysTh rThrSerLeu AlaAlaSerA laAlaSerTh rGluThrLeu 334

ACCCCACCC CCGAGCGGAA TGAGGGTGTC TACACAGCCA TCGCAGTGCA 1052 [T337Pfs*52](#) [P338_A347delinsLSERRVHTS](#) [E339_D341delinsG6M](#) [Val344Ile](#) [Y345C](#)
ThrProThrP roGluArgAs nGluGlyVal TyrThrAlaI leAlaValGl 351

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

ACGATTATAC AGCGCAGAAC CCAGATGAGC TGGACCTGTC CGCGGGAGAC 1152 D369G A372V D384G

yrAspTyrTh rAlaGlnAsn ProAspGluL euAspLeuSe rAlaGlyAsp 384

ATCCTGGAGG TGATCCTGGA AGGGGAGGAT GGCTGGTGGG CTGTGGAGAG 1202 c.1154T>C G1179A G395S

IleLeuGluV alIleLeuGl uGlyGluAsp GlyTrpTrpT hrValGluAr 401

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

gAsnGlyGln ArgGlyPheV alProGlySe rTyrLeuGlu LysLeuStop 418

GAAGGGCCAG GAGCCCCTTC GGACCTGCCC TGCCAGTGGA GCCAGCAGTG *51

CCCCCAGCAC TGTCCCCACC TTGCTAGGGC CCAGAACCAA GCGTCCCCCA *101

GCCCCGAGAG GGAGCCTGTC GTCTCCCAGG GAATAAAGGA GTGCGTTCTG *151

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

CCGAGTGCTC AGTTCAGAGG AGGCAAAGGA ACAAGGGAAG GAGCCTGGAT *251

GTGGAGCTCC CCAACTCAGC CGAGGCTTCA GCTATAGTTG GAGAAGAG

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