

PSTPIP1 (NM_003978.5) - cDNA - 2026-11-23

AAACCTTCCT GCGCAGGCCT CGGGCTGCCT GCCTGCCTGC CTGCCTGGCC -399

CGGCCCGAGC TCCAGCCTGC CTCTTCCACT GGCCACTGCC TCCCACCCAG -349

GGCTGGCATC CCTGCTCCCT GCCCTGGGTC CCAGACTGTG TCCTCCATCA -299

CCGCAGGGTC GGTGAGGGGC TGGGCTGGAC ACCAGGGCCC GCCCTCCCAT -249 -282G>T

CACTGAGCTC CACTCCTTCC TCATTTTGCT GCTGATTCTA GCCCCAAACA -199

AAACAGGTTG AGCTTTTTCC 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

GATGCCCCAG CTGCAGTTCA AAGATGCCTT TTGGTGCAGG GACTTCACAG 52 M2T

CCCACACGGG CTACGAGGTG CTGCTGCAGC GGCTTCTGGA TGGCAGGAAG 102 T20M K34T

ATGTGCAAAG ACATGGAGGA GCTACTGAGG CAGAGGGCCC AGGCGGAGGA 152 A49V

GCGGTACGGG AAGGAGCTGG TGCAGATCGC ACGGAAGGCA GGTGGCCAGA 202 E51D R52Q L57R R62W A64T

CGGAGATCAA CTCCCTGAGG GCCTCCTTTG ACTCCTTGAA GCAGCAAATG 252 T68M

GAGAATGTGG GCAGCTCACA CATCCAGCTG GCCCTGACCC TGCGTGAGGA 302

GCTGCGGAGT CTCGAGGAGT TTCGTGAGAG GCAGAAGGAG CAGAGGAAGA 352 E110D

AGTATGAGGC CGTCATGGAC CGGGTCCAGA AGAGCAAGCT GTCGCTCTAC 402 Y119C V122I M123_L416delinsT M123_K128delinsTMLLSQ D124_K128delinsGMLLS L133_K136delinsPPDP)

AAGAAGGCCA TGGAGTCCAA GAAGACATAC GAGCAGAAGT GCCGGGACGC 452 D150E

GGACGACGCG GAGCAGGCCT TCGAGCGCAT TAGCGCCAAC GGCCACCAGA 502

AGCAGGTGGA GAAGAGTCAG AACAAAGCCA GGCAGTGCAA GGACTCGGCC 552 G543A

ACCGAGGCAG AGCGGGTATA CAGGCAGAGC ATTGCGCAGC TGGAGAAGGT 602

CCGGGCTGAG TGGGAGCAGG AGCACCGGAC CACCTGTGAG GCCTTTCAGC 652 R202W R210W

TGCAAGAGTT TGACCGGCTG ACCATTCTCC GCAACGCCCT GTGGGTGCAC 702 c.C850T: p.Q284X Q219H E220_I226delinsDRQFHPG D222_L416delinsSTRKCG) R228C A230T

AGCAACCAGC TCTCCATGCA GTGTGTCAAG GATGATGAGC TCTACGAGGA 752 N236K Q237_M240delinsRHRQ) S239P Q241R D246N E250Q E250K

AGTGCGGCTG ACGCTGGAAG GCTGCAGCAT AGACGCCGAC ATCGACAGTT 802 V252A T255M E257K E256G G258R G258S G258A D264N D266N

TCATCCAGGC CAAGAGCACG GGCACAGAGC CCCCCGCTCC GGTGCCCTAC 852 T274M E277D P283S

CAGAACTATT ACGATCGGGA GGTCACCCCG CTGACCAGCA GCCCTGGCAT 902 D289H P299S

ACAGCCGTCC TGCGGCATGA TAAAGAGGTT CTCTGGACTG CTGCACGGAA 952 C305C

GTCCCAAGAC CACTTCGTTG GCAGCTTCTG CTGCGTCCAC AGAGACCCTG 1002 T321P S323L A329V

ACCCCCACCC CCGAGCGGAA TGAGGGTGTC TACACAGCCA TCGCAGTGCA 1052 T337Pfs*52 P338_A347delinsLSERRVHTS E339_D341delinsGGM Val344Ile Y345C

GGAGATACAG GGAAACCCGG CCTCACCAGC CCAGGAGTAC CGGGCGCTCT 1102 E352K E352A R365W

ACGATTATAC AGCGCAGAAC CCAGATGAGC TGGACCTGTC CGCGGGAGAC 1152 D369G A372V D384G

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

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

GAAGGGCCAG GAGCCCCTTC GGACCTGCCC TGCCAGTGGA GCCAGCAGTG *51

CCCCCAGCAC TGTCCCCACC TTGCTAGGGC CCAGAACCAA GCGTCCCCCA *101

GCCCCGAGAG GGAGCCTGTC GTCTCCCAGG GAATAAAGGA GTGCGTTCTG *151

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

CCGAGTGCTC AGTTCAGAGG AGGCAAAGGA ACAAGGGAAG GAGCCTGGAT *251

GTGGAGCTCC CCAACTCAGC CGAGGCTTCA GCTATAGTTG GAGAAGAG

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