

PSMA6 (NM_002791.3) - cDNA + Protein - 2026-11-14

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GGAAGCAGTC GCTGCAACTT CCGGGAGGTG CTTGTGTGCC TGGTGCGGGA -46
GCTACGGGGC CCAGGGATTG TGTTTAAAGT AGTGCTTCTA CCAACATGTC 5
                                                MetSe 2

CCGTGGTTCC AGCGCCGGTT TTGACCGCCA CATTACCATT TTTTCACCCG 55
rArgGlySer SerAlaGlyP heAspArgHi sIleThrIle PheSerProG 19

AGGGTCGGCT CTACCAAGTA GAATATGCTT TTAAGGCTAT TAACCAGGGT 105
luGlyArgLe uTyrGlnVal GluTyrAlaP heLysAlaIl eAsnGlnGly 35

GGCCTTACAT CAGTAGCTGT CAGAGGGAAA GACTGTGCAG TAATTGTCAC 155
GlyLeuThrS erValAlaVa lArgGlyLys AspCysAlaV alIleValTh 52

ACAGAAGAAA GTACCTGACA AATTATTGGA TTCCAGCACA GTGACTCACT 205  EX3Del
rGlnLysLys ValProAspL ysLeuLeuAs pSerSerThr ValThrHisL 69

TATTCAAGAT AACTGAAAAC ATTGGTTGTG TGATGACCGG AATGACAGCT 255
euPheLysIl eThrGluAsn IleGlyCysV alMetThrGl yMetThrAla 85

GACAGCAGAT CCCAGGTACA GAGGGCACGC TATGAGGCAG CTAACTGGAA 305
AspSerArgS erGlnValGl nArgAlaArg TyrGluAlaA laAsnTrpLy 102

ATACAAGTAT GGCTATGAGA TTCCTGTGGA CATGCTGTGT AAAAGAATTG 355
sTyrLysTyr GlyTyrGluI leProValAs pMetLeuCys LysArgIleA 119

CCGATATTTC TCAGGTCTAC ACACAGAATG CTGAAATGAG GCCTCTTGGT 405
laAspIleSe rGlnValTyr ThrGlnAsnA laGluMetAr gProLeuGly 135

TGTTGTATGA TTTTAATTGG TATAGATGAA GAGCAAGGCC CTCAGGTATA 455
CysCysMetI leLeuIleGl yIleAspGlu GluGlnGlyP roGlnValTy 152

TAAGTGTGAT CCTGCAGGTT ACTACTGTGG GTTTAAAGCC ACTGCAGCGG 505
rLysCysAsp ProAlaGlyT yrTyrCysGl yPheLysAla ThrAlaAlaG 169

GAGTTAAACA AACTGAGTCA ACCAGCTTCC TTGAAAAAAA AGTGAAGAAG 555
lyValLysGl nThrGluSer ThrSerPheL euGluLysLy sValLysLys 185

AAATTTGATT GGACATTTGA ACAGACAGTG GAAACTGCAA TTACATGCCT 605
LysPheAspT rpThrPheGl uGlnThrVal GluThrAlaI leThrCysLe 202
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GTCTACTGTT CTATCAATTG ATTTCAAACC TTCAGAAATA GAAGTTGGAG 655
uSerThrVal LeuSerIleA spPheLysPr oSerGluIle GluValGlyV 219

TAGTGACAGT TGAAAATCCT AAATTCAGGA TTCTTACAGA AGCAGAGATT 705
alValThrVa lGluAsnPro LysPheArgI leLeuThrGl uAlaGluIle 235

GATGCTCACC TTGTTGCTCT AGCAGAGAGA GACTAAACAT TGTCGTTAGT *14
AspAlaHisL euValAlaLe uAlaGluArg AspStop

TTACCAGATC CGTGATGCCA CTTACCTGTG TGTTTGGTAA CAACAAACCA *64
ACATCATGGA GGTCCCTGGA TTGAAAAAGG AGCCTCTCCC ACTCCTCCTA *114
CCACCGAAGT GGTTAGGACT CTATATAAAT AAAAACAAGG CTTTTGGAAA *164
ATAATTGCAT CCTGTTGTTT TCA
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