```
AGTTGGTCCT TAGTACTGCG GCCGTGTGGG TGAGTTGGCT GCCGGTGAGT -69

TGGGTGCCGG TGGAGTCGTG TTGGTCCTCA GAATCCCCGC GTAGCCGCTG -19

CCTCCTCCTA CCCTCGCCAT GTTTCTTACC CGGTCTGAGT ACGACAGGGG 32
           Me tPheLeuThr ArgSerGluT yrAspArgGl 11


CGTGAATACT TTTTCTCCCG AAGGAAGATT ATTTCAAGTG GAATATGCCA 82
yValAsnThr PheSerProG luGlyArgLe uPheGlnVal GluTyrAlaI 28


TTGAGGCTAT CAAGCTTGGT TCTACAGCCA TTGGGATCCA GACATCAGAG 132
leGluAlaIl eLysLeuGly SerThrAlaI leGlyIleGl nThrSerGlu 44


GGTGTGTGCC TAGCTGTGGA GAAGAGAATT ACTTCCCCAC TGATGGAGCC 182
GlyValCysL euAlaValGl uLysArgIle ThrSerProL euMetGluPr 61


CAGCAGCATT GAGAAAATTG TAGAGATTGA TGCTCACATA GGTTGTGCCA 232
oSerSerIle GluLysIleV alGluIleAs pAlaHisIle GlyCysAlaM 78


TGAGTGGGCT AATTGCTGAT GCTAAGACTT TAATTGATAA AGCCAGAGTG 282
etSerGlyLe uIleAlaAsp AlaLysThrL euIleAspLy sAlaArgVal 94


GAGACACAGA ACCACTGGTT CACCTACAAT GAGACAATGA CAGTGGAGAG 332
GluThrGlnA snHisTrpPh eThrTyrAsn GluThrMetT hrValGluSe 111
```

```
TGTGACCCAA GCTGTGTCCA ATCTGGCTTT GCAGTTTGGA GAAGAAGATG 382
rValThrGln AlaValSerA snLeuAlaLe uGlnPheGly GluGluAspA 128

CAGATCCAGG TGCCATGTCT CGTCCCTTTG GAGTAGCATT ATTATTTGGA 432
laAspProGl yAlaMetSer ArgProPheG lyValAlaLe uLeuPheGly 144

GGAGTTGATG AGAAAGGACC CCAGCTGTTT CATATGGACC CATCTGGGAC 482
GlyValAspG luLysGlyPr oGlnLeuPhe HisMetAspP roSerGlyTh 161

CTTTGTACAG TGTGATGCTC GAGCAATTGG CTCTGCTTCA GAGGGTGCCC 532    p.Arg168*
rPheValGln CysAspAlaA rgAlaIleGl ySerAlaSer GluGlyAlaG 178

AGAGCTCCTT GCAAGAAGTT TACCACAAGT CTATGACTTT GAAAGAAGCC 582
lnSerSerLe uGlnGluVal TyrHisLysS erMetThrLe uLysGluAla 194

ATCAAGTCTT CACTCATCAT CCTCAAACAA GTAATGGAGG AGAAGCTGAA 632
IleLysSerS erLeuIleIl eLeuLysGln ValMetGluG luLysLeuAs 211

TGCAACAAAC ATTGAGCTAG CCACAGTGCA GCCTGGCCAG AATTTCCACA 682
nAlaThrAsn IleGluLeuA laThrValGl nProGlyGln AsnPheHisM 228

TGTTCACAAA GGAAGAACTT GAAGAGGTTA TCAAGGACAT TTAAGGAATC *6
etPheThrLy sGluGluLeu GluGluValI leLysAspIl eStop

CTGATCCTCA GAACTTCTCT GGGACAATTT CAGTTCTAAT AATGTCCTTA *56
AATTTTATTT CCAGCTCCTG TTCCTTGGAA AATCTCCATT GTATGTGCAT *106
TTTTTAAATG ATGTCTGTAC ATAAAGGCAG TTCTGAAATA AAGAAAATTT *156
```

```
TAAAATATTT GTTAATAGAC TGTTCTCTTC TAATAGTCTT TTTTTTTTTT *206

TTTTTTTTAA GAGATGAGGT CTCACTATAT TGCCCAGGCT GGTTTCAAAC *256

TCCTGGGTTC AAGTGATCTT CCCGCCTCTG CCTCCTGAAG TGCTAGGATT *306

ATAGGCGAGA GCCACTGTGC CCAGCCATTG TAATACAGTC TTTTGTTTGA *356

AATGCAAATG TTAGTGGGCC AAAAGGACAG TGTTATTAAT ATCCCTATTC *406

TATGAAGATG TCTGTTCTAA AACTGTTTTA GTGATGCTCT ATAACAGAAT *456

CAACTATATC CATTAATCCC ATGGTGTTGA TAAATGAACT AGTCCAGCTC *506

TTCCCAGTGG TTAATAGATG TTAACAGCAC TGTAAATCCA TTTCGGCCCT *556

ATAATTTCTG GAGCAAACGT GTATTTTGC TGCTTTTCTT ATAAGGAGAT *606

GCTACTAATT GACTATCAGA AGAACATGTT TTGAGGTCCT CCTCAAAACA *656

TTGATGGGTT GGAATCAGCC ATCAACAGTG TTGTACCAGT TCTTGGGTCT *706

TGATAGACAA TTTGGAAAGA GATTCCTTG TTTACGAAGT GAAGGACTAA *756

GAATTAAATT AATGACCTTG GCCTCACTGG CAATCAATTA CAAATCTCTA *806

TATCAGTAAG AGAATTGTAA AATTCAGAAG CAGTTTACAT TAGACTTTGG *856

AATGAATGAT GAACTTTCCC CATTAGAGCT GCCATCATAT GATTGGTGGA *906

GATTGTTTAA AGAATCATTC TATCTCAGCC TCAAAAATTA CCACGGGAAG *956

ATGGTATCAG TATCACTACT TAACAGATGA AGAATCTAAT GCTGTGTGCC *1006

CATGGACACA CAAAATTAAG CTGTTGGGAC TTGAACAGCT CAAATTTTCT *1056

TGTTTCAGAT CACCAGCTCT TGAGTAATAG GGAAATCTGG AGATTTGAAA *1106

AGTACTTGCA CTGTCCACAA CATGGCTAAT CCATATGTGG ATGATGCAGA *1156

ATTGATTTAA TTCACTAACA GGGACCCCAT AATTATTTGC TGGGCTCTGG *1206

GTATATTGAT GTGTAGGAAG TTGTACTATA TGTTAATAAA TTATGACTAT *1256

TTGGATAGGC TGAATTCATA CTAAATCCAT ACTGTAGTTC AACAAAAAAC *1306

AACATGTTTA TATACATTTG GAAACTGCAA TGATAGGAAA CATTTGGAAG *1356

AAAGGGATTT TGCCCTAGAA TAACACATAA GGAAAGCAGA GAATTAGAGT *1406

ATATTGTTAC TGAATGTTCC AGAGACTTCT AGTGATTTTA ACACTTATTA *1456

AGTATAGCAT GTTGATGGGG AGATTTGTTT CTCTAAAGAT CACTTTGTTT *1506

TATTAAATCC TAATAGAAAA TACCCTTGAA AATCCTATCT CATTTATTCC *1556
```

```
TGTAACAAAT TTATTGAGCA CCTACCTACT ATATGCCAAG AAATGTATTA *1606

GCCATCAGGC AGAGAGCTGT TCAAATGGTA GATATGATCT GTGCTCCTGT *1656

GAAACTTCTA GTGGGGAGAG CCAAACAATA AACAATATTC CTTTTTAACT *1706

CTAGGTTAAT GCAGAAATGG ATAAAGCCCA TGTTGCTTTT GGGAGAGGTG *1756

AGTTGTGTCT CTGAATCACA TGCATTTCAT AGGGGGAAAA ATGCCCAAAT *1806

ACTAAGGAGT AGCTCTTAGC CTATGTCCGT TCGCCTCAGC TTAAGTTGTT *1856

TTCCCTCCCA CTGGCTGGGC AGCATATTTG TGTTTTACCT GGTAAAACAG *1906

TAAATTTCGT ACCTTCTATA ATTGGCATTC TTCAAAGAGG TAGAACTTTG *1956

ATTTTTTTGT AGAATATTAA AACAAGCTTT CTTAGGTTAA AGAAGTGATC *2006

TTACTACGAA CAGCAATGGT TTCATGATGT GTAATTGCTT TATGTTATCT *2056

TTCTGCTATA GAATGTTTCC TGGAGAAAGG TACGGTTTTT AGTAATAAGA *2106

TAAATTTACT TTAGTCCTGC AAATAAGGTG AAATCTTATG TCCAGTATCT *2156

CACAAAGGAG AACTGACAGT GCCACTTTTA TATTTAATGT CAATCTCATT *2206

AGACAAAAAT GAAATATAGT TCCTAGGGTT TCCAATTTAA AAAGTGAAAT *2256

AATAAATATA TTCACTCAAA CATTTTCTCA GTGCCATATG CAAGTTACCA *2306

TGTCCCAGAA GCTGATACAG TTTGAAGAAG GAAATATATA AGTACTGTAA *2356

GCCTGTGATA ACTAAAAGCA ACATACTAAA AAGTGAAGGT ACAGATAATT *2406

GGAACAAATT TAATAGCGTT TAAAAGTGTA TTTGGTAATT CTCCAGGAG *2456

GTGGCACTGT TGAGTTGTTT TTTCTTTTCA GACAGTAAGA CAATAGACCA *2506

TTCATCTTTG TGTCACCCAA ACAAAGAAAT ATTCCTTTAT AACCCCCTTT *2556

CCTCCCCCCA CCTAATCACA TGCTACTGGA ACTGACTGTC TTGTGATCTA *2606

CTCCCATAGT TGGCATAGAT TTAAAAATAA TCTTTTTTAA ATTAATCTGA *2656

TAGTAGTTAT GGAAAGGAAC AAATTGTTCA CCAATTTTCA TCAGCTTTAT *2706

CTTTTCAGTC CAGTAACTGA GAACTTAAAA AGACTATTCT AGTGATTTTA *2756

CTATCCTGCT CAGATGGCAT TCAAAAACAT TTTTCACTTC TCACGTCTTG *2806

GAAAAATTTG TAAATTCGTT AAGTCTTTTT GTTTGAAAGT TAATGTGACT *2856

GGAAATATTT TAATGTAAAT ATCGGGTTGG GTGCATTGTA TCATTTTGCT *2906

CTACAATGAC TATATCCTCA TTTGGGTTTA TGGCCAGTTT ATAATTAAAA *2956
```

PSMA5 (NM_002790.4) - cDNA + Protein - 2026-05-13