



NCSTN (NM_015331.3) - cDNA + Protein - 2024-05-03

AGCAGAGAGG CAAG**ATGGCT** ACGGCAGGGG GTGGCTCTGG GGCTGACCCG 36

MetAla ThrAlaGlyG lyGlySerG1 yAlaAspPro 12

GGAAGTCGGG GTCTCCTTCG CCTTCTGTCT TTCTGCGTCC TACTAGCAGG 86

GlySerArgG lyLeuLeuAr gLeuLeuSer PheCysValL euLeuAlaG1 29

TTTGTGCAGG **GGAAACTCAG** TGGAGAGGAA GATATATATC CCCTTAAATA 136 **G33R**

yLeuCysArg GlyAsnSerV alGluArgLy sIleTyrIle ProLeuAsnL 46

AAACAGCTCC CTGTGTTCGC CTGCTCAACG CCACTCATCA GATTGGCTGC 186

ysThrAlaPr oCysValArg LeuLeuAsnA laThrHisG1 nIleGlyCys 62

CAGT**CTTCAA** TTAGTGGAGA CAC**AGGGTT** ATCCAC**GTAG** TAGAGAAAGA 236 **Thr70fsx18 V75I**

GlnSerSerI leSerGlyAs pThrGlyVal IleHisValV alGluLysG1 79

GGAGGACCTA CAGTGGGTAT TGACTGATGG CCCCAACCCC **CCTTACATGG** 286 **p.P73Lfs*15**

uGluAspLeu GlnTrpValL euThrAspG1 yProAsnPro ProTyrMetV 96

TTCTGCTGGA GAGCAAGCAT TTTACCAGGG ATTAAATGGA GAAGCTGAAA 336

alLeuLeuG1 uSerLysHis PheThrArgA spLeuMetG1 uLysLeuLys 112

GGGAGAAC**CCA** GC**CGAATTGC** TGGTCTTGCA GTGTCCTGCA CCAAGCCAG 386 **T115fs R117X**

GlyArgThrS erArgIleAl aGlyLeuAla ValSerLeuT hrLysProSe 129

TCCTGCCTCA GGCTTCTCTC CTAGTGTACA GTGCCAAAT GATGGGTTG 436

rProAlaSer GlyPheSerP roSerValG1 nCysProAsn AspGlyPheG 146

GTTTTACTC CAATTCTAT GGGCCAGAGT TTGCTCACTG CAGAGAAATA 486 I162Yfs*57

lyValTyrSe rAsnSerTyr GlyProGluP heAlaHisCy sArgGluIle 162

CAGTGGATT CGCTGGCAA TGGTTGGCT TATGAAGACT TTAGTTCCC 536 p.Gln163SerfsX39 S166X

GlnTrpAsnsS erLeuGlyAs nGlyLeuAla TyrGluAspP heSerPhePr 179

CATCTTTCTT CTTGAAGATG AAAATGAAAC CAAAGTCATC AAGCAGTGCT 586 F181S D185N

oIlePheLeu LeuGluAspG luAsnGluTh rLysValIle LysGlnCysT 196

ATCAAGATCA CAACCTGAGT CAGAATGGCT CAGCACCAAC CTTCCCACTA 636 P211R

yrGlnAspHi sAsnLeuSer GlnAsnGlyS erAlaProTh rPheProLeu 212

TGTGCCATGC AGCTCTTTC ACACATGCAT GCTGTCATCA GCACTGCCC 686 Q216P S219Ffs*31 c.687insCC

CysAlaMetG lnLeuPheSe rHisMetHis AlaValIleS erThrAlaTh 229

CTGCATGCGG CGCAGCTCCA TCCAAAGCAC CTTCAGCATC AACCCAGAAA 736

rCysMetArg ArgSerSerI leGlnSerTh rPheSerIle AsnProGluI 246

TCGTCTGTGA CCCCTGTCT GATTACAATG TGTGGAGCAT GCTAAAGCCT 786

leValCysAs pProLeuSer AspTyrAsnV alTrpSerMe tLeuLysPro 262

ATAAAATACAA CTGGGACATT AAAGCCTGAC GACAGGGTTG TGGTTGCTGC 836

IleAsnThrT hrGlyThrLe uLysProAsp AspArgValV alValAlaAl 279

CACCCGGCTG GATAGTCGTT CCTTTTCTG GAATGTGGCC CCAGGGGCTG 886

aThrArgLeu AspSerArgS erPhePheTr pAsnValAla ProGlyAlaG 296

AAAGCGCAGT GGCTTCCTTT GTCACCCAGC TGGCTGCTGC TGAAGCTTTG 936 c.887A>G

luSerAlaVa lAlaSerPhe ValThrGlnL euAlaAlaAl aGluAlaLeu 312

CAAAAGGCAC CTGATGTGAC CACCCTGCC CGCAATGTCA TGTTTGTCTT 986 A315V

GlnLysAlaP roAspValTh rThrLeuPro ArgAsnValM etPheValPh 329

CTTTCAAGGG GAAACTTTG ACTACATTGG CAGCTCGAGG ATGGTCTACG 1036

ePheGlnGly GluThrPheA spTyrIleGl ySerSerArg MetValTyrA 346

ATATGGAGAA GGGCAAGTTT CCCGTGCAGT TAGAGAATGT TGACTCATTT 1086

spMetGluLy sGlyLysPhe ProValGlnL euGluAsnVa lAspSerPhe 362

GTGGAGCTGG GACAGGTGGC CTTAAGAACT TCATTAGAGC TTTGGATGCA 1136 c.1125+1G>A

ValGluLeuG lyGlnValAl aLeuArgThr SerLeuGluL euTrpMetHi 379

CACAGATCCT GTTTCTCAGA AAAATGAGTC TGTACGGAAC CAGGTGGAGG 1186 D381fs*7

sThrAspPro ValSerGlnL ysAsnGluSe rValArgAsn GlnValGluA 396

ATCTCCTGGC CACATTGGAG AAGAGTGGTG CTGGTGTCCC TGCTGTCAT 1236

spLeuLeuAl aThrLeuGlu LysSerGlyA laGlyValPr oAlaValIle 412

CTCAGGAGGC CAAATCAGTC CCAGCCTCTC CCACCATCTT CCCTGCAGCG 1286 Q420X

LeuArgArgP roAsnGlnSe rGlnProLeu ProProSerS erLeuGlnAr 429

ATTTCTTCGA GCTCGAAACA TCTCTGGCGT TGTTCTGGCT GACCACTCTG 1336 p.Arg434X

gPheLeuArg AlaArgAsnI leSerGlyVa lValLeuAla AspHisSerG 446

GTGCCTCCA TAACAAATAT TACCAGAGTA TTTACGACAC TGCTGAGAAC 1386

lyAlaPheHi sAsnLysTyr TyrGlnSerI leTyrAspTh rAlaGluAsn 462

ATTAATGTGA GCTATCCGA ATGGCTGAGC CCTGAAGAGG ACCTGAACCT 1436

IleAsnValS erTyrProG1 uTrpLeuSer ProGluGluA spLeuAsnPh 479

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GTGCTCTGTA TGAGCTTGCA GGAGGAACCA ACTTCAGCGA CACAGTTTAG 1536

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AlaAspProG lnThrValTh rArgLeuLeu TyrGlyPheL euIleLysAl 529

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euGlyAspG1 yProLeuGln HisTyrIleA laValSerSe rProThrAsn 562

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ThrThrTyrV alvalGlnTy rAlaLeuAla AsnLeuThrG lyThrValVa 579

CAACCTCACCGAGAAGT GCCAGGATCC AAGTAAAGTC CCAAGTGAAA 1786 E584DfsX44 c.1768A>G

1AsnLeuThr ArgGluGlnC ysGlnAspPr oSerLysVal ProSerGluA 596

ACAAGGATCT GTATGAGTAC TCATGGGTCC AGGGCCCTTT GCATTCTAAAT 1836 c.1799delTG

snLysAspLe uTyrGluTyr SerTrpValG lnGlyProLe uHisSerAsn 612

GAGACGGACC GACTCCCCG GTGTGTGCGT TCTACTGCAC GATTAGCCAG 1886

GluThrAspA rgLeuProAr gCysValArg SerThrAlaA rgLeuAlaAr 629

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gAlaLeuSer ProAlaPheG luLeuSerG1 nTrpSerSer ThrGluTyrS 646

CTACATGGAC TGAGAGCCGC TGGAAAGATA TCCGTGCCCG GATATTCTC 1986

erThrTrpTh rGluSerArg TrpLysAspI leArgAlaAr gIlePheLeu 662

ATCGCCAGCA AAGAGCTTGA GTTGATCACC CTGACAGTGG GCTTCGGCAT 2036

IleAlaSerL ysGluLeuG1 uLeuIleThr LeuThrValG lyPheGlyIl 679

CCTCATCTTC TCCCTCATCG TCACCTACTG CATCAATGCC AAAGCTGATG 2086

eLeuIlePhe SerLeuIleV alThrTyrCy sIleAsnAla LysAlaAspV 696

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alLeuPheIl eAlaProArg GluProGlyA laValSerTy rStop

CCCCAGCTTT TCTTGCCAGC TCAGCAGTTC ACTTCCTAGA GCATCTGTCC *56

CACTGGGACA CAACCACTAA TTTGTCACTG GAACCTCCCT GGGCCTGTCT *106

CAGATTGGGA TTAACATAAA AGAGTGGAAC TATCCAAAAG AGACAGGGAG *156

AAATAAATAA ATTGCCTCCC TTCCTCCGCT CCCCTTCCC ATCACCCCTT *206

CCCCATTTC CTTTCTTCT CTACTCATGC CAGATTGG GATTACAAAT *256

AGAAGCTTCT TGCTCCTGTT TAACTCCCTA GTTACCCACC CTAATTGCC *306
CTTCAGGACC CTTCTACTTT TTCCTTCCTG CCCTGTACCT CTCTCTGCTC *356
CTCACCCCCA CCCCTGTACC CAGCCACCTT CCTGACTGGG AAGGACATAA *406
AAGGTTAAC GTCAGGGTCA AACTACATTG AGCCCCTGAG GACAGGGGCA *456
TCTCTGGGCT GAGCCTACTG TCTCCTTCCC ACTGTCTTT CTCCAGGGCC *506
TCAGATGGCA CATTAGGGTG GGC GTGCTGC GGGTGGGTAT CCCACCTCCA *556
GCCCACAGTG CTCAGTTGTA CTTTTTATTA AGCTGTAATA TCTATTTTG *606
TTTTGTCTT TTCCCTTAT TCTTTTGTA AATATATATA TAATGAGTTT *656
CATTAAAATA GATTATCCCA CA

NCSTN (NM_015331.3) - cDNA + Protein - 2024-05-03

