



STING1 (NM_198282.4) - cDNA + Protein - 2024-05-18

GTTCATTTTT CACTCCTCCC TCCTAGGTCA CACTTTTCAG AAAAGAATC -253
TGCATCCTGG AAACCAGAAG AAAAATATGA GACGGGGAAT CATCGTGTGA -203
TGTGTGTGCT GCCTTTGGCT GAGTGTGTGG AGTCCTGCTC AGGTGTTAGG -153
TACAGTGTGT TTGATCGTGG TGGCTTGAGG GGAACCCGCT GTTCAGAGCT -103
GTGACTGCGG CTGCACTCAG AGAAGCTGCC CTTGGCTGCT CGTAGCGCCG -53
GGCCTTCTCT CCTCGTCATC ATCCAGAGCA GCCAGTGTCC GGGAGGCAGA -3
AGATGCCCCA CTCCAGCCTG CATCCATCCA TCCCGTGTCC CAGGGGTCAC 48
MetProHi sSerSerLeu HisProSerI leProCysPr oArgGlyHis 16

GGGGCCCAGA AGGCAGCCTT GGTTCCTGCTG AGTGCCTGCC TGGTGACCCT 98
GlyAlaGlnL ysAlaAlaLe uValLeuLeu SerAlaCysL euValThrLe 33

TTGGGGGCTA GGAGAGCCAC CAGAGCACAC TCTCCGGTAC CTGGTGCTCC 148
uTrpGlyLeu GlyGluProP roGluHisTh rLeuArgTyr LeuValLeuH 50

ACCTAGCCTC CCTGCAGCTG GGACTGCTGT TAAACGGGGT CTGCAGCCTG 198 L189V
isLeuAlaSe rLeuGlnLeu GlyLeuLeuL euAsnGlyVa lCysSerLeu 66

GCTGAGGAGC TGCGCACAT CCACTCCAGG TACCGGGGCA GCTACTGGAG 248 H72N
AlaGluGluL euArgHisIl eHisSerArg TyrArgGlyS erTyrTrpAr 83

GACTGTGCGG GCCTGCCTGG GCTGCCCCCT CCGCCGTGGG GCCCTGTTGC 298 R94H

gThrValArg AlaCysLeuG lyCysProLe uArgArgGly AlaLeuLeuL 100

TGCTGTCCAT CTATTTCTAC TACTCCCTCC CAAATGCGGT CGGCCCCGCC 348

euLeuSerIl eTyrPheTyr TyrSerLeuP roAsnAlaVa lGlyProPro 116

TTCACTTGGA TGCTTGCCCT CCTGGGCCTC TCGCAGGCAC TGAACATCCT 398

PheThrTrpM etLeuAlaLe uLeuGlyLeu SerGlnAlaL euAsnIleLe 133

CCTGGGCCTC AAGGGCCTGG CCCCAGCTGA GATCTCTGCA GTGTGTGAAA 448 [V147L](#) [V147M](#)

uLeuGlyLeu LysGlyLeuA laProAlaGl uIleSerAla ValCysGluL 150

AAGGGAATTT CAACGTGGCC CATGGGCTGG CATGGTCATA TTACATCGA 498 [F153V](#) [F153I](#) [N154S](#) [V155M](#) [G158A](#) [G166E](#)

ysGlyAsnPh eAsnValAla HisGlyLeuA laTrpSerTy rTyrIleGly 166

TATCTGCGGC TGATCCTGCC AGAGCTCCAG GCCCGGATTC GAACTTACAA 548

TyrLeuArgL euIleLeuPr oGluLeuGln AlaArgIleA rgThrTyrAs 183

TCAGCATTAC AACAACTGC TACGGGGTGC AGTGAGCCAG CGGCTGTATA 598

nGlnHisTyr AsnAsnLeuL euArgGlyAl aValSerGln ArgLeuTyrI 200

TTCTCCTCCC ATTGGACTGT GGGGTGCCTG ATAACCTGAG TATGGCTGAC 648 [C206G](#) [C206Y](#) [G207E](#)

leLeuLeuPr oLeuAspCys GlyValProA spAsnLeuSe rMetAlaAsp 216

CCCAACATTC GCTTCCTGGA TAAACTGCCC CAGCAGACCG GTGACCATGC 698

ProAsnIleA rgPheLeuAs pLysLeuPro GlnGlnThrG lyAspHisAl 233

TGGCATCAAG GATCGGGTTT ACAGCAACAG CATCTATGAG CTTCTGGAGA 748

aGlyIleLys AspArgValT yrSerAsnSe rIleTyrGlu LeuLeuGluA 250

ACGGGCAGCG GCGGGCACC TGTGCTCTGG AGTACGCCAC CCCCTTGCAG 798
snGlyGlnAr gAlaGlyThr CysValLeuG luTyrAlaTh rProLeuGln 266

ACTTTGTTTG CCATGTCACA ATACAGTCAA GCTGGC**TTT**A G**C**CGGGAGGA 848 F279L S280R R281W R281Q
ThrLeuPheA laMetSerGl nTyrSerGln AlaGlyPheS erArgGluAs 283

TA**G**GCTTGAG CAGGCCAAAC TCTTCTGCCG GACACTTGAG GACATCCTGG 898 R284G R284S
pArgLeuGlu GlnAlaLysL euPheCysAr gThrLeuGlu AspIleLeuA 300

CAGATGCCCC TGAGTCTCAG AACAACTGCC GCCTCATTGC CTACCAGGAA 948
laAspAlaPr oGluSerGln AsnAsnCysA rgLeuIleAl aTyrGlnGlu 316

CCTGCAGATG ACAGCAGCTT CTCGCTGTCC CAGGAGGTTC TCCGGCACCT 998
ProAlaAspA spSerSerPh eSerLeuSer GlnGluValL euArgHisLe 333

GCGGCAGGAG GAAA**A**GGAAG AGGTTACTGT GGGCAGCTTG AAGACCTCAG 1048 K338Rfs*9
uArgGlnGlu GluLysGluG luValThrVa lGlySerLeu LysThrSerA 350

CGGTGCCCAG TACCTCCACG ATGTCCCAAG AGCCTGAGCT CCTCATCAGT 1098
laValProSe rThrSerThr MetSerGlnG luProGluLe uLeuIleSer 366

GGAATGGAAA AGCCCTCCC TCTCCGCACG GATTTCTCT**T** **G**AGACCCAGG *8
GlyMetGluL ysProLeuPr oLeuArgThr AspPheSerS top

GTCACCAGGC CAGAGCCTCC AGTGGTCTCC AAGCCTCTGG ACTGGGGGGCT *58
CTCTTCAGTG GCTGAATGTC CAGCAGAGCT ATTCCTTCC ACAGGGGGCC *108
TTGCAGGGAA GGGTCCAGGA CTTGACATCT TAAGATGCGT CTTGTCCCCT *158

TGGGCCAGTC ATTTCCCCTC TCTGAGCCTC GGTGTCTTCA ACCTGTGAAA *208
TGGGATCATA ATCACTGCCT TACCTCCCTC ACGGTTGTTG TGAGGACTGA *258
GTGTGTGGAA GTTTTTCATA AACTTTGGAT GCTAGTGTAC TTAGGGGGTG *308
TGCCAGGTGT CTTTCATGGG GCCTTCCAGA CCCACTCCCC ACCCTTCTCC *358
CCTTCCTTTG CCCGGGGACG CCGAACTCTC TCAATGGTAT CAACAGGCTC *408
CTTCGCCCTC TGGCTCCTGG TCATGTTCCA TTATTGGGGA GCCCCAGCAG *458
AAGAATGGAG AGGAGGAGGA GGCTGAGTTT GGGGTATTGA ATCCCCCGGC *508
TCCCACCCTG CAGCATCAAG GTTGCTATGG ACTCTCCTGC CGGGCAACTC *558
TTGCGTAATC ATGACTATCT CTAGGATTCT GGCACCACTT CCTTCCCTGG *608
CCCCTTAAGC CTAGCTGTGT ATCGGCACCC CCACCCCACT AGAGTACTCC *658
CTCTCACTTG CGGTTTCCTT ATACTCCACC CCTTTCTCAA CGGTCCTTTT *708
TTAAAGCACA TCTCAGATTA

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