



STING1 (NM_198282.4) - cDNA + Protein - 2025-07-19

GTTCATTTT CACTCCTCCC TCCTAGGTCA CACTTTCA G AAAAAGAAC -253

TGCATCCTGG AAACCAGAAG AAAAATATGA GACGGGAAAT CATCGTGTGA -203

TGTGTGTGCT GCCTTGCT GAGTGTGTGG AGTCCTGCTC AGGTGTTAGG -153

TACAGTGTGT TTGATCGTGG TGGCTTGAGG GGAACCCGCT GTTCAGAGCT -103

GTGACTGCGG CTGCACTCAG AGAAGCTGCC CTTGGCTGCT CGTAGCGCCG -53

GGCCTTCTCT CCTCGTCATC ATCCAGAGCA GCCAGTGTCC GGGAGGCAGA -3

AGATCCCCA CTCCAGCCTG CATCCATCCA TCCCGTGTCC CAGGGGTCAC 48

MetProHi sSerSerLeu HisProSerI leProCysPr oArgGlyHis 16

GGGGCCCAGA AGGCAGCCTT GGTTCTGCTG AGTGCCTGCC TGGTGACCC 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 TGCGCCACAT CCACTCCAGG TACCGGGCA GCTACTGGAG 248 H72N

AlaGluGluL euArgHisIle HisSerArg TyrArgGlyS erTyrTrpAr 83

GACTGTGCGG GCCTGCCTGG GCTGCCCTC CCGCCGTGGG GCCCTGTTGC 298 R94H

gThrValArg AlaCysLeuG lyCysProLe uArgArgGly AlaLeuLeuL 100

TGCTGTCCAT CTATTTCTAC TACTCCCTCC CAAATGCGGT CGGCCCGCCC 348

euLeuSerIleTyrPheTyr TyrSerLeuPro AsnAlaVal GlyProPro 116

TTCACTTGGA TGCTTGCCCT CCTGGGCCTC TCGCAGGCAC TGAACATCCT 398

PheThrTrpMet LeuAlaLeu LeuGlyLeu SerGlnAlaL AsnIleLeu 133

CCTGGGCCTC AAGGGCCTGG CCCCAGCTGA GATCTCTGCA GTGTGTGAAA 448 V147L V147M

uLeuGlyLeu LysGlyLeuA laProAlaG1 uIleSerAla ValCysGluL 150

AAGGGAATT CAACGTGGCC CATGGGCTGG CATGGTCATA TTACATCGGA 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 AACAAACCTGC TACGGGGTGC AGTGAGCCAG CGGCTGTATA 598

nGlnHisTyr AsnAsnLeuL euArgGlyAl aValSerGln ArgLeuTyrI 200

TTCTCCTCCC ATTGGACTTGT GGGGTGCCTG ATAACCTGAG TATGGCTGAC 648 C206G C206Y G207E

leLeuLeuPr oLeuAspCys GlyValProA spAsnLeuSe rMetAlaAsp 216

CCCAACATTC GCTTCCTGGA TAAACTGCC CAGCAGACCG GTGACCATGC 698

ProAsnIleA rgPheLeuAs pLysLeuPro GlnGlnThrG lyAspHisAl 233

TGGCATCAAG GATCGGGTTT ACAGCAACAG CATCTATGAG CTTCTGGAGA 748

aGlyIleLys AspArgValT yrSerAsnSe rIleTyrGlu LeuLeuGluA 250

ACGGGCAGCG GGCGGCACC TGTGCTCTGG AGTACGCCAC CCCCTGCAG 798

snGlyGlnAr gAlaGlyThr CysValLeuG luTyrAlaTh rProLeuGln 266

ACTTTGTTG CCATGTCACA ATACAGTCAA GCTGGCTTA GCCGGGAGGA 848 F279L S280R R281W R281Q

ThrLeuPheA laMetSerG1 nTyrSerGln AlaGlyPheS erArgGluAs 283

TAGGCTTGAG CAGGCCAAC TCTTCTGCCG GACACTTGAG GACATCCTGG 898 R284G R284S

pArgLeuGlu GlnAlaLysL euPheCysAr gThrLeuGlu AspIleLeuA 300

CAGATGCCCC TGAGTCTCAG ACAACTGCC GCCTCATTGC CTACCAGGAA 948

laAspAlaPr oGluSerGln AsnAsnCysA rgLeuIleAl aTyrGlnGlu 316

CCTGCAGATG ACAGCAGCTT CTCGCTGTCC CAGGAGGTT TCCTGGCACCT 998

ProAlaAspA spSerSerPh eSerLeuSer GlnGluValL euArgHisLe 333

GCGGCAGGAG GAAAAGGAAG AGGTTACTGT GGGCAGCTTG AAGACCTCAG 1048 K338Rfs*9

uArgGlnGlu GluLysGluG luValThrVa lGlySerLeu LysThrSerA 350

CGGTGCCAG TACCTCCACG ATGTCCAAG AGCCTGAGCT CCTCATCAGT 1098

laValProSe rThrSerThr MetSerGlnG luProGluLe uLeuIleSer 366

GGAATGGAAA AGCCCCCTCCC TCTCCGCACG GATTTCTCTT **GA**GACCCAGG *8

GlyMetGluL ysProLeuPr oLeuArgThr AspPheSerS top

GTCACCAGGC CAGAGCCTCC AGTGGCTCTCC AAGCCTCTGG ACTGGGGGCT *58

CTCTTCAGTG GCTGAATGTC CAGCAGAGCT ATTTCTTCC ACAGGGGGCC *108

TTGCAGGGAA GGGTCCAGGA CTTGACATCT TAAGATGCGT CTTGTCCCCCT *158

TGGGCCAGTC ATTTCCCCTC TCTGAGCCTC GGTGTCTTCA ACCTGTGAAA *208
TGGGATCATA ATCACTGCCT TACCTCCCTC ACGGTTGTTG TGAGGACTGA *258
GTGTGTGGAA GTTTTCATA AACTTTGGAT GCTAGTGTAC TTAGGGGGTG *308
TGCAGGTGT CTTCATGGG GCCTTCCAGA CCCACTCCCC ACCCTTCTCC *358
CCTTCCTTTG CCCGGGGACG CGAACTCTC TCAATGGTAT CAACAGGCTC *408
CTTCGCCCTC TGGCTCCTGG TCATGTTCCA TTATTGGGA GCCCCAGCAG *458
AAGAATGGAG AGGAGGAGGA GGCTGAGTTT GGGGTATTGA ATCCCCCGGC *508
TCCCACCTCG CAGCATCAAG GTTGCTATGG ACTCTCCTGC CGGGCAACTC *558
TTGCGTAATC ATGACTATCT CTAGGATTCT GGCACCACTT CCTTCCCTGG *608
CCCCCTTAAGC CTAGCTGTGT ATCGGCACCC CCACCCCCACT AGAGTACTCC *658
CTCTCACTTG CGGTTCCCTT ATACTCCACC CCTTCTCAA CGGTCCCTTT *708
TTAAAGCACA TCTCAGATTA

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