STING1 (NM_198282.4) - cDNA + Protein - 2025-04-03

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GTTCATTTTT CACTCCTCCC TCCTAGGTCA CACTTTTCAG AAAAAGAATC -253
TGCATCCTGG AAACCAGAAG AAAAATATGA GACGGGGAAT CATCGTGTGA -203
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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 GGTTCTGCTG 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 TGCGCCACAT CCACTCCAGG TACCGGGGCA GCTACTGGAG 248   H72N
AlaGluGluL euArgHisIl eHisSerArg TyrArgGlyS erTyrTrpAr 83

GACTGTGCGG GCCTGCCTGG GCTGCCCCCT CCGCCGTGGG GCCCTGTTGC 298   R94H
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euLeuSerIl eTyrPheTyr TyrSerLeuP roAsnAlaVa lGlyProPro 116

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PheThrTrpM etLeuAlaLe uLeuGlyLeu SerGlnAlaL euAsnIleLe 133

CCTGGGCCTC AAGGGCCTGG CCCCAGCTGA GATCTCTGCA GTGTGTGAAA 448  V147L V147M
uLeuGlyLeu LysGlyLeuA laProAlaGl uIleSerAla ValCysGluL 150

AAGGGAATTT CAACGTGGCC CATGGGCTGG CATGGTCATA TTACATCGGA 498  F153V F153I N154S V155M G158A G166E
ysGlyAsnPh eAsnValAla HisGlyLeuA laTrpSerTy rTyrIleGly 166

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CCCAACATTC GCTTCCTGGA TAAACTGCCC CAGCAGACCG GTGACCATGC 698
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aGlyIleLys AspArgValT yrSerAsnSe rIleTyrGlu LeuLeuGluA 250
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ThrLeuPheA laMetSerGl nTyrSerGln AlaGlyPheS erArgGluAs 283

TAGGCTTGAG 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 GAAAAGGAAG 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 AGCCCCTCCC TCTCCGCACG GATTTCTCTT GAGACCCAGG *8
GlyMetGluL ysProLeuPr oLeuArgThr AspPheSerS top

GTCACCAGGC CAGAGCCTCC AGTGGTCTCC AAGCCTCTGG ACTGGGGGCT *58
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TTGCAGGGAA GGGTCCAGGA CTTGACATCT TAAGATGCGT CTTGTCCCCT *158
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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
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CCCCTTAAGC CTAGCTGTGT ATCGGCACCC CCACCCCACT AGAGTACTCC *658
CTCTCACTTG CGGTTTCCTT ATACTCCACC CCTTTCTCAA CGGTCCTTTT *708
TTAAAGCACA TCTCAGATTA
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