



## STAT4 (NM\_003151.4) - cDNA + Protein - 2026-08-03

GACTTTGGAC TTGAGCACTG CCTGGGACCT GTGCTGAGAG AGCGCTAGCA 1

M 1

TGTCTCAGTG GAATCAAGTC CAACAGTTAG AAATCAAGTT TTTGGAGCAG 51

etSerGlnTr pAsnGlnVal GlnGlnLeuG luIleLysPh eLeuGluGln 17

GTGGATCAAT TCTATGATGA CAACTTTCCC ATGGAAATTC GGCATCTGTT 101

ValAspGlnP heTyrAspAs pAsnPhePro MetGluIleA rgHisLeuLe 34

GGCCCAATGG ATTGAAAATC AAGACTGGGA GGCAGCTTCT AACAATGAAA 151

uAlaGlnTrp IleGluAsnG lnAspTrpG1 uAlaAlaSer AsnAsnGluT 51

CCATGGCAAC GATTCTTCTT CAAAACCTGT TAATACAACT GGATGAACAG 201

hrMetAlaTh rIleLeuLeu GlnAsnLeuL euIleGlnLe uAspGluGln 67

TTAGGTCGTG TTTCCAAAGA GAAAAACCTA CTCTTGATAC ACAATCTAAA 251

LeuGlyArgV alSerLysG1 uLysAsnLeu LeuLeuIleH isAsnLeuLy 84

AAGAATTAGG AAGGTCCTTC AGGGAAAATT TCATGGAAAT CCAATGCATG 301

sArgIleArg LysValLeuG lnGlyLysPh eHisGlyAsn ProMetHisV 101

TAGCTGTGGT TATTTCAAAC TGTTTAAGGG AAGAGAGGAG AATATTGGCT 351

alAlaValVa lIleSerAsn CysLeuArgG luGluArgAr gIleLeuAla 117

GCAGCCAACA TGCCTGTCCA GGGGCCTCTA GAGAAATCCT TACAAAGTTC 401

AlaAlaAsnM etProValGl nGlyProLeu GluLysSerL euGlnSerSe 134

TTCAGTTTCA GAAAGACAGA GGAATGTGGA GCACAAAGTG GCTGCCATTA 451

rSerValSer GluArgGlnA rgAsnValGl uHisLysVal AlaAlaIleL 151

AAAACAGTGT GCAGATGACA GAACAAGATA CCAAATACTT AGAAGATCTG 501

ysAsnSerVa lGlnMetThr GluGlnAspT hrLysTyrLe uGluAspLeu 167

CAAGACGAAT TTGACTACAG GTATAAAACA ATTCAGACAA TGGATCAGAG 551

GlnAspGluP heAspTyrAr gTyrLysThr IleGlnThrM etAspGlnSe 184

TGACAAGAAT AGTGCCATGG TGAATCAGGA AGTTTTGACA CTGCAGGAAA 601

rAspLysAsn SerAlaMetV alAsnGlnGl uValLeuThr LeuGlnGluM 201

TGCTTAACAG CCTCGATTTT AAGAGAAAGG AGGCTCTCAG TAAAATGACC 651

etLeuAsnSe rLeuAspPhe LysArgLysG luAlaLeuSe rLysMetThr 217

CAAATCATCC ATGAGACAGA CCTGTTAATG AACACCATGC TCATAGAAGA 701

GlnIleIleH isGluThrAs pLeuLeuMet AsnThrMetL euIleGluGl 234

GCTGCAAGAC TGGAAGCGGC GGCAGCAAAT CGCCTGCATC GGGGGTCCAC 751

uLeuGlnAsp TrpLysArgA rgGlnGlnIl eAlaCysIle GlyGlyProL 251

TCCACAATGG GCTCGACCAG CTTCAGAACT GCTTTACACT ATTGGCAGAA 801

euHisAsnGl yLeuAspGln LeuGlnAsnC ysPheThrLe uLeuAlaGlu 267

AGTCTTTTCC AACTGAGAAG GCAATTGGAG AACTAGAGG AGCAATCTAC 851  
SerLeuPheG lnLeuArgAr gGlnLeuGlu LysLeuGluG luGlnSerTh 284

CAAAATGACA TATGAAGGTG ATCCCATTCC AATGCAAAGA ACTCACATGC 901  
rLysMetThr TyrGluGlyA spProIlePr oMetGlnArg ThrHisMetL 301

TAGAAAGAGT CACCTTCTTG ATCTACAACC TTTTCAAGAA CTCATTTGTG 951  
euGluArgVa lThrPheLeu IleTyrAsnL euPheLysAs nSerPheVal 317

GTTGAGCGAC AGCCATGTAT GCCAACCCAC CTCAGAGGC CGTTGGTACT 1001  
ValGluArgG lnProCysMe tProThrHis ProGlnArgP roLeuValLe 334

TAAAACCCTA ATTCAGTTCA CTGTAAACT AAGGCTACTA ATAAAATTGC 1051  
uLysThrLeu IleGlnPheT hrValLysLe uArgLeuLeu IleLysLeuP 351

CAGAACTAAA CTATCAGGTA AAGGTTAAGG CATCAATTGA CAAGAATGTT 1101  
roGluLeuAs nTyrGlnVal LysValLysA laSerIleAs pLysAsnVal 367

TCAACTCTAA GCAACCGAAG ATTTGTACTT TGTGGAATA ATGTCAAAGC 1151  
SerThrLeuS erAsnArgAr gPheValLeu CysGlyThrA snValLysAl 384

CATGTCTATT GAAGAATCTT CCAATGGGAG TCTCTCAGTA GAATTCGAC 1201  
aMetSerIle GluGluSerS erAsnGlySe rLeuSerVal GluPheArgH 401

ATTTGCAACC AAAGGAAATG AAGTCCAGTG CTGGAGGTAA AGGAAATGAG 1251  
isLeuGlnPr oLysGluMet LysSerSerA laGlyGlyLy sGlyAsnGlu 417

GGCTGTCACA TGGTGA CTGA AGAACTTCAT TCCATAACGT TTGAAACACA 1301

GlyCysHisM etValThrGl uGluLeuHis SerIleThrP heGluThrGl 434

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nIleCysLeu TyrGlyLeuT hrIleAspLe uGluThrSer SerLeuProV 451

TGGTGATGAT TTCCAATGTC AGTCAGTTAC CTAATGCTTG GGCATCCATC 1401

alValMetIl eSerAsnVal SerGlnLeuP roAsnAlaTr pAlaSerIle 467

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IleTrpTyrA snValSerTh rAsnAspSer GlnAsnLeuV alPhePheAs 484

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CTGGGCCAAG TTCTGCAAGG AACATTTACC TGGTAAATCA TTTACCTTTT 1651

rTrpAlaLys PheCysLysG luHisLeuPr oGlyLysSer PheThrPheT 551

GGACATGGCT TGAAGCAATA TTGGATCTAA TTAAGAAACA CATTCTTCCC 1701

rpThrTrpLe uGluAlaIle LeuAspLeuI leLysLysHi sIleLeuPro 567

CTTTGGATTG ATGGGTATGT CATGGGCTTT GTTAGCAAAG AGAAGGAACG 1751

LeuTrpIleA spGlyTyrVa lMetGlyPhe ValSerLysG luLysGluAr 584

GCTGTTGCTA AAGGATAAAA TGCCTGGCAC CTTTTTATTA AGATTCAGTG 1801  
gLeuLeuLeu LysAspLysM etProGlyTh rPheLeuLeu ArgPheSerG 601

AAAGCCATCT CGGAGGAATA ACTTTCACCT GGGTGGACCA TTCTGAAAAGT 1851  
luSerHisLe uGlyGlyIle ThrPheThrT rpValAspHi sSerGluSer 617

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GlyGluValA rgPheHisSe rValGluPro TyrAsnLysG lyArgLeuSe 634

TGCTCTGCCA TTCGCTGACA TCCTGCGAGA CTACAAAGTT ATTATGGCTG 1951  
rAlaLeuPro PheAlaAspI leLeuArgAs pTyrLysVal IleMetAlaG 651

AAAACATTCC TGA AACCCCT CTGAAGTACC TATATCCTGA CATTCCCAA 2001  
luAsnIlePr oGluAsnPro LeuLysTyrL euTyrProAs pIleProLys 667

GACAAAGCCT TCGGTAAACA CTACAGCTCT CAGCCTTGCG AAGTTTCAAG 2051  
AspLysAlaP heGlyLysHi sTyrSerSer GlnProCysG luValSerAr 684

ACCAACAGAA AGGGGTGACA AAGTTATGT TCCTTCTGTT TTTATCCCCA 2101  
gProThrGlu ArgGlyAspL ysGlyTyrVa lProSerVal PheIleProI 701

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leSerThrIl eArgSerAsp SerThrGluP roHisSerPr oSerAspLeu 717

CTTCCCATGT CTCCAAGTGT GTATGCGGTG TTGAGAGAAA ACCTGAGTCC 2201  
LeuProMetS erProSerVa lTyrAlaVal LeuArgGluA snLeuSerPr 734

CACAACAATT GAAACTGCAA TGAAGTCTCC TTATTCTGCT GAATGACAGG \*4

oThrThrIle GluThrAlaM etLysSerPr oTyrSerAla GluStop

ATAAACTCTG ACGCACCAAG AAAGGAAGCA AATGAAAAAG TTAAAGACT \*54

GTTCTTTGCC CAATAACCAC ATTTTATTTT TTCAGCTTTG TAAATACCAG \*104

GTTCTAGGAA ATGTTTGACA TCTGAAGCTC TCTTCACACT CCCGTGGCAC \*154

TCCTCAATTG GGAGTGTTGT GACTGAAATG CTTGAAACCA AAGCTTCAGA \*204

TAAACTTGCA AGATAAGACA ACTTTAAGAA ACCAGTGTTA ATAACAATAT \*254

TAACAGAAGA

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