



TRAP1 (NM_016292.3) - cDNA + Protein - 2025-04-03

GCTCTGGGAG TACGACATGG CGCGCGAGCT GCGGGCGCTG CTGCTGTGGG 34

MetA laArgGluLe uArgAlaLeu LeuLeuTrpG 12

GCCGCCGCCT GCGGCCTTTG CTGCGGGCGC CGGCGCTGGC GGCCGTGCCG 84

lyArgArgLe uArgProLeu LeuArgAlaP roAlaLeuAl aAlaValPro 28

GGAGGAAAAC CAATTCTGTG TCCTCGGAGG ACCACAGCCC AGTTGGGCCC 134

GlyGlyLysP roIleLeuCy sProArgArg ThrThrAlaG lnLeuGlyPr 45

CAGGCGAAAC CCAGCCTGGA GCTTGCAGGC AGGACGACTG TTCAGCACGC 184

oArgArgAsn ProAlaTrpS erLeuGlnAl aGlyArgLeu PheSerThrG 62

AGACCGCCGA GGACAAGGAG GAACCCCTGC ACTCGATTAT CAGCAGCACA 234

lnThrAlaGl uAspLysGlu GluProLeuH isSerIleIl eSerSerThr 78

GAGAGCGTGC AGGGTTCCAC TTCCAAACAT GAGTTCCAGG CCGAGACAAA 284

GluSerValG lnGlySerTh rSerLysHis GluPheGlnA laGluThrLy 95

GAAGCTTTTG GACATTGTTG CCCGGTCCCT GTACTCAGAA AAAGAGGTGT 334

sLysLeuLeu AspIleValA laArgSerLe uTyrSerGlu LysGluValP 112

TTATACGGGA GCTGATCTCC AATGCCAGCG ATGCCTTGGG AAAACTGCGT 384 R128H

heIleArgGl uLeuIleSer AsnAlaSerA spAlaLeuGl uLysLeuArg 128

CACAAACTGG TGTCTGACGG CCAAGCACTG CCAGAAATGG AGATTCACCTT 434

HisLysLeuV alSerAspGl yGlnAlaLeu ProGluMetG luIleHisLe 145

GCAGACCAAT GCCGAGAAAG GCACCATCAC CATCCAGGAT ACTGGTATCG 484

uGlnThrAsn AlaGluLysG lyThrIleTh rIleGlnAsp ThrGlyIleG 162

GGATGACACA GGAAGAGCTG GTGTCCAACC TGGGGACGAT TGCCAGATCG 534

lyMetThrGl nGluGluLeu ValSerAsnL euGlyThrIl eAlaArgSer 178

GGGTCAAAGG CCTTCCTGGA TGCTCTGCAG AACCAGGCTG AGGCCAGCAG 584

GlySerLysA laPheLeuAs pAlaLeuGln AsnGlnAlaG luAlaSerSe 195

CAAGATCATC GGCCAGTTTG GAGTGGGTTT CTA CTCAGCT TTCATGGTGG 634

rLysIleIle GlyGlnPheG lyValGlyPh eTyrSerAla PheMetValA 212

CTGACAGAGT GGAGGTCTAT TCCCGCTCGG CAGCCCCGGG GAGCCTGGGT 684

laAspArgVa lGluValTyr SerArgSerA laAlaProGl ySerLeuGly 228

TACCAGTGGC TTTCAGATGG TTCTGGAGTG TTTGAAATCG CCGAAGCTTC 734

TyrGlnTrpL euSerAspGl ySerGlyVal PheGluIleA laGluAlaSe 245

GGGAGTTAGA ACCGGGACAA AAATCATCAT CCACCTGAAA TCCGACTGCA 784

rGlyValArg ThrGlyThrL ysIleIleIl eHisLeuLys SerAspCysL 262

AGGAGTTTTTC CAGCGAGGCC CGGGTGCGAG ATGTGGTAAC GAAGTACAGC 834

ysGluPheSe rSerGluAla ArgValArgA spValValTh rLysTyrSer 278

AACTTCGTCA GCTTCCCCTT GTACTTGAAT GGAAGGCGGA TGAACACCTT 884
AsnPheValS erPheProLe uTyrLeuAsn GlyArgArgM etAsnThrLe 295

GCAGGCCATC TGGATGATGG ACCCCAAGGA TGTCCGTGAG TGGCAACATG 934
uGlnAlaIle TrpMetMetA spProLysAs pValArgGlu TrpGlnHisG 312

AGGAGTTCTA CCGCTACGTC GCGCAGGCTC ACGACAAGCC CCGCTACACC 984 R316H
luGluPheTy rArgTyrVal AlaGlnAlaH isAspLysPr oArgTyrThr 328

CTGCACTATA AGACGGACGC ACCGCTCAAC ATCCGCAGCA TCTTCTACGT 1034
LeuHisTyrL ysThrAspAl aProLeuAsn IleArgSerI lePheTyrVa 345

GCCCGACATG AAACCGTCCA TGTTTGATGT GAGCCGGGAG CTGGGCTCCA 1084
lProAspMet LysProSerM etPheAspVa lSerArgGlu LeuGlySerS 362

GCGTTGCACT GTACAGCCGC AAAGTCCTCA TCCAGACCAA GGCCACGGAC 1134
erValAlaLe uTyrSerArg LysValLeuI leGlnThrLy sAlaThrAsp 378

ATCCTGCCCA AGTGGCTGCG CTTTCATCCGA GGTGTGGTGG ACAGTGAGGA 1184
IleLeuProL ysTrpLeuAr gPheIleArg GlyValValA spSerGluAs 395

CATTCCCCTG AACCTCAGCC GGGAGCTGCT GCAGGAGAGC GCACTCATCA 1234
pIleProLeu AsnLeuSerA rgGluLeuLe uGlnGluSer AlaLeuIleA 412

GGAAACTCCG GGACGTTTTA CAGCAGAGGC TGATCAAATT CTTCATTGAC 1284
rgLysLeuAr gAspValLeu GlnGlnArgL euIleLysPh ePheIleAsp 428

CAGAGTAAAA AAGATGCTGA GAAGTATGCA AAGTTTTTTG AAGATTACGG 1334 ~~Y444N~~

GlnSerLysL ysAspAlaGl uLysTyrAla LysPhePheG luAspTyrGl 445

CCTGTTTCATG CGGGAGGGCA TTGTGACCGC CACCGAGCAG GAGGTCAAGG 1384

yLeuPheMet ArgGluGlyI leValThrAl aThrGluGln GluValLysG 462

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luAspIleAl aLysLeuLeu ArgTyrGluS erSerAlaLe uProSerGly 478

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GluGlnPheA spGluLeuTh rLeuLeuHis LeuArgGluP heAspLysLy 545

GAAGCTGATC TCTGTGGAGA CGGACATAGT CGTGGATCAC TACAAGGAGG 1684

sLysLeuIle SerValGluT hrAspIleVa lValAspHis TyrLysGluG 562

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luLysPheGl uAspArgSer ProAlaAlaG luCysLeuSe rGluLysGlu 578

ACGGAGGAGC TCATGGCCTG GATGAGAAAT GTGCTGGGGT CGCGTGTAC 1784

ThrGluGluL euMetAlaTr pMetArgAsn ValLeuGlyS erArgValTh 595

CAACGTGAAG GTGACCCTCC GACTGGACAC CCACCCTGCC ATGGTCACCG 1834
rAsnValLys ValThrLeuA rgLeuAspTh rHisProAla MetValThrV 612

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alLeuGluMe tGlyAlaAla ArgHisPheL euArgMetGl nGlnLeuAla 628

AAGACCCAGG AGGAGCGCGC ACAGCTCCTG CAGCCCACGC TGGAGATCAA 1934
LysThrGlnG luGluArgAl aGlnLeuLeu GlnProThrL euGluIleAs 645

CCCCAGGCAC GCGCTCATCA AGAAGCTGAA TCAGCTGCGC GCAAGCGAGC 1984
nProArgHis AlaLeuIleL ysLysLeuAs nGlnLeuArg AlaSerGluP 662

CTGGCCTGGC TCAGCTGCTG GTGGATCAGA TATACGAGAA CGCCATGATT 2034
roGlyLeuAl aGlnLeuLeu ValAspGlnI leTyrGluAs nAlaMetIle 678

GCTGCTGGAC TTGTTGACGA CCCTAGGGCC ATGGTGGGCC GCTTGAATGA 2084
AlaAlaGlyL euValAspAs pProArgAla MetValGlyA rgLeuAsnGl 695

GCTGCTTGTC AAGGCCCTGG AGCGACACTG ACAGCCAGGG GGCCAGAAGG *19
uLeuLeuVal LysAlaLeuG luArgHisSt op

ACTGACACCA CAGATGACAG CCCACCTCC TTGAGCTTTA TTTACCTAAA *69
TTTAAAGGTA TTTCTTAACC CGA

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