

ADAM17 (NM_003183.6) - cDNA + Protein - 2026-11-08

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TTCTGGGGGC GTCGAGCCTG GCGGTAGAAT CTTCCCAGTA GGCGGCGCGG -126
GAGGGAAAAG AGGATTGAGG GGCTAGGCCG GGCGGATCCC GTCCTCCCCC -76
GATGTGAGCA GTTTTCCGAA ACCCCGTCAG GCGAAGGCTG CCCAGAGAGG -26
TGGAGTCGGT AGCGGGGCCG GGAACATGAG GCAGTCTCTC CTATTCCTGA 25
                          MetAr gGlnSerLeu LeuPheLeuT 9

CCAGCGTGGT TCCTTTCGTG CTGGCGCCGC GACCTCCGGA TGACCCGGGC 75
hrSerValVa lProPheVal LeuAlaProA rgProProAs pAspProGly 25

TTCGGCCCCC ACCAGAGACT CGAGAAGCTT GATTCTTTGC TCTCAGACTA 125
PheGlyProH isGlnArgLe uGluLysLeu AspSerLeuL euSerAspTy 42

CGATATTCTC TCTTTATCTA ATATCCAGCA GCATTCGGTA AGAAAAAGAG 175
rAspIleLeu SerLeuSerA snIleGlnGl nHisSerVal ArgLysArgA 59

ATCTACAGAC TTCAACACAT GTAGAAACAC TACTAACTTT TTCAGCTTTG 225
spLeuGlnTh rSerThrHis ValGluThrL euLeuThrPh eSerAlaLeu 75

AAAAGGCATT TTAAATTATA CCTGACATCA AGTACTGAAC GTTTTTCACA 275
LysArgHisP heLysLeuTy rLeuThrSer SerThrGluA rgPheSerGl 92
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AAATTTCAAG GTCGTGGTGG TGGATGGTAA AAACGAAAGC GAGTACACTG 325
nAsnPheLys ValValValV alAspGlyLy sAsnGluSer GluTyrThrV 109

TAAAATGGCA GGACTTCTTC ACTGGACACG TGGTTGGTGA GCCTGACTCT 375
alLysTrpGl nAspPhePhe ThrGlyHisV alValGlyGl uProAspSer 125

AGGGTTCTAG CCCACATAAG AGATGATGAT GTTATAATCA GAATCAACAC 425
ArgValLeuA laHisIleAr gAspAspAsp ValIleIleA rgIleAsnTh 142

AGATGGGGCC GAATATAACA TAGAGCCACT TTGGAGATTT GTTAATGATA 475
rAspGlyAla GluTyrAsnI leGluProLe uTrpArgPhe ValAsnAspT 159

CCAAAGACAA AAGAATGTTA GTTTATAAAT CTGAAGATAT CAAGAATGTT 525
hrLysAspLy sArgMetLeu ValTyrLysS erGluAspIl eLysAsnVal 175

TCACGTTTGC AGTCTCCAAA AGTGTGTGGT TATTTAAAAG TGGATAATGA 575
SerArgLeuG lnSerProLy sValCysGly TyrLeuLysV alAspAsnGl 192

AGAGTTGCTC CCAAAAGGGT TAGTAGACAG AGAACCACCT GAAGAGCTTG 625  D201Efs*11
uGluLeuLeu ProLysGlyL euValAspAr gGluProPro GluGluLeuV 209

TTCATCGAGT GAAAAGAAGA GCTGACCCAG ATCCCATGAA GAACACGTGT 675
alHisArgVa lLysArgArg AlaAspProA spProMetLy sAsnThrCys 225

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LysLeuLeuV alValAlaAs pHisArgPhe TyrArgTyrM etGlyArgGl 242

GGAAGAGAGT ACAACTACAA ATTACTTAAT AGAGCTAATT GACAGAGTTG 775
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yGluGluSer ThrThrThrA snTyrLeuIl eGluLeuIle AspArgValA 259

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spAspIleTy rArgAsnThr SerTrpAspA snAlaGlyPh eLysGlyTyr 275

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GlyIleGlnI leGluGlnIl eArgIleLeu LysSerProG lnGluValLy 292

ACCTGGTGAA AAGCACTACA ACATGGCAAA AAGTTACCCA AATGAAGAAA 925
sProGlyGlu LysHisTyrA snMetAlaLy sSerTyrPro AsnGluGluL 309

AGGATGCTTG GGATGTGAAG ATGTTGCTAG AGCAATTTAG CTTTGATATA 975
ysAspAlaTr pAspValLys MetLeuLeuG luGlnPheSe rPheAspIle 325

GCTGAGGAAG CATCTAAAGT TTGCTTGGCA CACCTTTTCA CATACCAAGA 1025
AlaGluGluA laSerLysVa lCysLeuAla HisLeuPheT hrTyrGlnAs 342

TTTTGATATG GGAACTCTTG GATTAGCTTA TGTTGGCTCT CCCAGAGCAA 1075
pPheAspMet GlyThrLeuG lyLeuAlaTy rValGlySer ProArgAlaA 359

ACAGCCATGG AGGTGTTTGT CCAAAGGCTT ATTATAGCCC AGTTGGGAAG 1125
snSerHisGl yGlyValCys ProLysAlaT yrTyrSerPr oValGlyLys 375

AAAAATATCT ATTTGAATAG TGGTTTGACG AGCACAAAGA ATTATGGTAA 1175
LysAsnIleT yrLeuAsnSe rGlyLeuThr SerThrLysA snTyrGlyLy 392

AACCATCCTT ACAAAGGAAG CTGACCTGGT TACAACTCAT GAATTGGGAC 1225
sThrIleLeu ThrLysGluA laAspLeuVa lThrThrHis GluLeuGlyH 409
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AsnGluAspG lnGlyGlyLy sTyrValMet TyrProIleA laValSerGl 442

CGATCACGAG AACAATAAGA TGTTTTCAAA CTGCAGTAAA CAATCAATCT 1375
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yIleMetTyr LeuAsnAsnA spThrCysCy sAsnSerAsp CysThrLeuL 509

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ysGluGlyVa lGlnCysSer AspArgAsnS erProCysCy sLysAsnCys 525

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sLysGlyVal SerTyrCysT hrGlyAsnSe rSerGluCys ProProProG 559
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GlyLysCysI leProPheCy sGluArgGlu GlnGlnLeuG luSerCysAl 592

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lyArgCysVa lProTyrVal AspAlaGluG lnLysAsnLe uPheLeuArg 625

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LysGlyLysP roCysThrVa lGlyPheCys AspMetAsnG lyLysCysGl 642

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ValLeuValP heSerLeuIl ePheTrpIle ProPheSerI leLeuValHi 692

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sCysValAsp LysLysLeuA spLysGlnTy rGluSerLeu SerLeuPheH 709

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CAGTTTTTTT TTATACACTG TAATGAACCG CTGAATATGA GGCATTTGGC *400
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CCCTGTTACT GATAGGGATA CATGCTCTTA GAAAATTCAC TATTGGCTGG *800

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TAGCACTGAT ATCTGCATTA ATAAATACTG TCGAAACACA A

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