ADA2 (NM_001282225.2) - cDNA + Protein - 2026-02-05

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AGTTGGTGAG CTTTTCCGGT GCTCTGCACA GATGCTGGGG CGCTGAGCAA -77
ACAGCCCTCA GTTTCTGGAG CTGTTCCGAG TCCCGTGGAG TCTCCATCTG -27   -43C>T c.-42G>A -31A>G
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                           MetL euValAspGl yProSerGlu 8

CGGCCAGCCC TGTGCTTCTT GCTGTTGGCT GTGGCAATGT CTTTCTTCGG 74    R9W G25C
ArgProAlaL euCysPheLe uLeuLeuAla ValAlaMetS erPhePheGl 25

CTCAGCTCTA TCCATAGATG AAACACGGGC GCATCTGTTG TTGAAAGAAA 124   I30T T33Nfs*29 R34W
ySerAlaLeu SerIleAspG luThrArgAl aHisLeuLeu LeuLysGluL 42

AGATGATGCG GCTGGGGGGG CGGCTGGTGC TGAACACCAA GGAGGAGCTG 174   R45W c.138G>C G47R G47W G47R_GC G47A G47V G48R c.144delG R49Afs*13 R49W c.158del N53N
K13del
ysMetMetAr gLeuGlyGly ArgLeuValL euAsnThrLy sGluGluLeu 58

GCCAATGAGA GGCTCATGAC GCTCAAAATC GCTGAGATGA AGGAGGCCAT 224
AlaAsnGluA rgLeuMetTh rLeuLysIle AlaGluMetL ysGluAlaMe 75

GAGGACCCTG ATATTCCCAC CCAGCATGCA CTTTTTCCAG GCCAAGCATC 274   c.232_322+105delinsATG H91R H91Lfs
tArgThrLeu IlePheProP roSerMetHi sPhePheGln AlaLysHisL 92
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TCATTGAGAG AAGTCAAGTG TTTAATATTC TAAGGATGAT GCCAAAAGGG 324 I93T P106S p.A109Lfs*11
euIleGluAr gSerGlnVal PheAsnIleL euArgMetMe tProLysGly 108

GCTGCCTTGC ACCTCCATGA CATTGGCATC GTGACTATGG ACTGGCTGGT 374 A109D H112Y H112Q 116Lfs*4 M121T
AlaAlaLeuH isLeuHisAs pIleGlyIle ValThrMetA spTrpLeuVa 125

GAGGAATGTC ACCTACAGGC CTCACTGCCA CATCTGTTTC ACCCCAAGGG 424 T129P p.(Y130Sfs*48) R131Sfs c.396_397del C134Y
lArgAsnVal ThrTyrArgP roHisCysHi sIleCysPhe ThrProArgG 142

GGATCATGCA GTTCAGATTT GCTCACCCAA CTCCCCGTCC ATCAGAAAAA 474 I143Sfs*41 P151QfsX P155Hfs*29
lyIleMetGl nPheArgPhe AlaHisProT hrProArgPr oSerGluLys 158

TGTTCCAAGT GGATTCTGCT GGAGGATTAT CGGAAGCGGG TGCAGAACGT 524 C159Y W162R R169G R169Q
CysSerLysT rpIleLeuLe uGluAspTyr ArgLysArgV alGlnAsnVa 175

CACTGAGTTT GATGACAGCT TGCTGAGGAA TTTCACTCTG GTGACCCAGC 574 F178S L183P T187P L188V L188P
lThrGluPhe AspAspSerL euLeuArgAs nPheThrLeu ValThrGlnH 192

ACCCGGAGGT GATTTACACA AACCAAAATG TTGTCTGGTC GAAATTTGAA 624 P193L V203A W204C G>T W204C F207S
isProGluVa lIleTyrThr AsnGlnAsnV alValTrpSe rLysPheGlu 208

ACCATCTTCT TCACCATCTC TGGTCTCATC CATTACGCAC CAGTGTTCAG 674 I210Tfs F212del Y220X
ThrIlePheP heThrIleSe rGlyLeuIle HisTyrAlaP roValPheAr 225

AGACTATGTC TTCCGGAGCA TGCAGGAGTT CTACGAGGAC AACGTGCTCT 724 Y227fs M232T Y236del c.709delC (p.Glu237fs) D238N A247Qfs*16
gAspTyrVal PheArgSerM etGlnGluPh eTyrGluAsp AsnValLeuT 242

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yrMetGluIl eArgAlaArg LeuLeuProV alTyrGluLe uSerGlyGlu 258

CACCATGACG AAGAGTGGTC AGTGAAGACT TACCAGGAAG TAGCTCAGAA 824 D261Pfs*2 W264S W264Ter S265X

HisHisAspG luGluTrpSe rValLysThr TyrGlnGluV alAlaGlnLy 275

GTTTGTGGAA ACTCACCCTG AGTTTATTGG AATCAAAATC ATTTATTCGG 874 F283L S291L

sPheValGlu ThrHisProG luPheIleGl yIleLysIle IleTyrSerA 292

ATCACAGATC CAAAGATGTG GCTGTCATCG CAGAATCCAT CCGAATGGCC 924 R306*

spHisArgSe rLysAspVal AlaValIleA laGluSerIl eArgMetAla 308

ATGGGGCTCC GAATCAAGTT CCCCACGGTG GTGGCAGGGT TTGACCTGGT 974 M309I L311R R312ter T317M G321E G321A delEx7 Dup Exon7

MetGlyLeuA rgIleLysPh eProThrVal ValAlaGlyP heAspLeuVa 325

GGGGCATGAG GACACTGGCC ACTCCTTGCA TGACTACAAG GAAGCTCTGA 1024 G326V E328K E328D D329N H335R

lGlyHisGlu AspThrGlyH isSerLeuHi sAspTyrLys GluAlaLeuM 342

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CCGCAGTCAG GACTTACTCC TGGAAAAAGG ACATCCCCAT AGAAGTCTGT 1224 W399X I405L C408Y

roAlaValAr gThrTyrSer TrpLysLysA spIleProIl eGluValCys 408

CCCATCTCTA ACCAGGTGCT GAAACTGGTG TCTGACTTGA GGAACCACCC 1274 P409S P409H V372M N423K P425A

ProIleSerA snGlnValLe uLysLeuVal SerAspLeuA rgAsnHisPr 425

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oValAlaThr LeuMetAlaT hrGlyHisPr oMetValIle SerSerAspA 442

ACCCAGCTAT GTTTGGTGCC AAAGGCTTGT CCTATGATTT CTATGAGGTC 1374 P443A M445T F404S K449Nfs*2 G450C L451W L451F Y453C Y453Y D454H Y456C V458D

spProAlaMe tPheGlyAla LysGlyLeuS erTyrAspPh eTyrGluVal 458

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PheMetGlyI leGlyGlyMe tLysAlaAsp LeuArgThrL euLysGlnLe 475

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CTTTCATGGA AATCTGGAAG AAGAGATGGG ATAAGTTCAT AGCAGATGTG 1524 W501*

hrPheMetGl uIleTrpLys LysArgTrpA spLysPheIl eAlaAspVal 508

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AlaThrLysS top

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nfevers