ADA2 (NM_001282225.2) - cDNA - 2026-09-13

AGTTGGTGAG CTTTTCCGGT GCTCTGCACA GATGCTGGGG CGCTGAGCAA	-77	
ACAGCCCTCA GTTTCTGGAG CTGTTCCGAG TCCCGTGGAG TCTCCATCTG	-27	-43C>T c.-42G>A -31A>G
AGCCCTTTCC TAGTCCAGGC ATCCCGATGT TGGTGGATGG CCCATCTGAG	24	c.-14G>T M1T P6L
CGGCCAGCCC TGTGCTTCTT GCTGTTGGCT GTGGCAATGT CTTTCTTCGG	74	R9W G25C
CTCAGCTCTA TCCATAGATG AAACACGGGC GCATCTGTTG TTGAAAGAAA	124	I30T T33Nfs*29 R34W
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

GCCAATGAGA GGCTCATGAC GCTCAAAATC GCTGAGATGA AGGAGGCCAT	224	
GAGGACCCTG ATATTCCCAC CCAGCATGCA CTTTTTCCAG GCCAAGCATC	274	c.232_322+105delinsATG H91R H91Lfs
TCATTGAGAG AAGTCAAGTG TTTAATATTC TAAGGATGAT GCCAAAAGGG	324	I93T P106S p.A109Lfs*11
GCTGCCTTGC ACCTCCATGA CATTGGCATC GTGACTATGG ACTGGCTGGT	374	A109D H112Y H112Q 116Lfs*4 M121T
GAGGAATGTC ACCTACAGGC CTCACTGCCA CATCTGTTTC ACCCCAAGGG	424	N127I T129P p.(Y130Sfs*48) R131Sfs c.396_397del C134Y
GGATCATGCA GTTCAGATTT GCTCACCCAA CTCCCCGTCC ATCAGAAAAA	474	I143Sfs*41 P151QfsX P155Hfs*29
TGTTCCAAGT GGATTCTGCT GGAGGATTAT CGGAAGCGGG TGCAGAACGT	524	C159Y W162R R169G R169Q
CACTGAGTTT GATGACAGCT TGCTGAGGAA TTTCACTCTG GTGACCCAGC	574	F178S L183P T187P L188V L188P
ACCCGGAGGT GATTTACACA AACCAAAATG TTGTCTGGTC GAAATTTGAA	624	P193L V203A W204C G>T W204C F207S
ACCATCTTCT TCACCATCTC TGGTCTCATC CATTACGCAC CAGTGTTCAG	674	I210Tfs F212del Y220X
AGACTATGTC TTCCGGAGCA TGCAGGAGTT CTACGAGGAC AACGTGCTCT	724	Y227fs M232T Y236del c.709delC (p.Glu237fs) D238N A247Qfs*16
ACATGGAGAT CAGAGCCAGG CTGCTGCCGG TGTATGAGCT CAGTGGAGAG	774	M243R E244A R246T A247V L249P P251L P251P
CACCATGACG AAGAGTGGTC AGTGAAGACT TACCAGGAAG TAGCTCAGAA	824	D261Pfs*2 W264S W264Ter S265X
GTTTGTGGAA ACTCACCCTG AGTTTATTGG AATCAAAATC ATTTATTCGG	874	F276S F283L S291L

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ATCACAGATC CAAAGATGTG GCTGTCATCG CAGAATCCAT CCGAATGGCC 924  R306*
ATGGGGCTCC GAATCAAGTT CCCCACGGTG GTGGCAGGGT TTGACCTGGT 974  M309I L311R R312ter T317M G321E G321A delEx7 Dup Exon7
GGGGCATGAG GACACTGGCC ACTCCTTGCA TGACTACAAG GAAGCTCTGA 1024 G326V E328K E328D D329N H335R
TGATCCCCGC CAAGGATGGC GTTAAGCTGC CTTACTTCTT CCACGCCGGA 1074 P344L V349I L351Q Y353H F355L A357T G358R
GAAACAGACT GGCAGGGTAC TTCCATAGAC AGGAACATTC TGGATGCTCT 1124 T119A N370K
GATGCTGAAC ACTACCAGAA TCGGCCATGG ATTTGCTTTG AGCAAACACC 1174 G142S G383D H391Q
CCGCAGTCAG GACTTACTCC TGGAAAAAGG ACATCCCCAT AGAAGTCTGT 1224 W399X I405L C408Y
CCCATCTCTA ACCAGGTGCT GAAACTGGTG TCTGACTTGA GGAACCACCC 1274 P409S P409H V372M N423K P425A
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ACCCAGCTAT GTTTGGTGCC AAAGGCTTGT CCTATGATTT CTATGAGGTC 1374 P443A M445T F404S K449Nfs*2 G450C G450= L451W L451F Y453C Y453Y D454H Y456C V458D
TTCATGGGCA TTGGGGGGAT GAAGGCTGAC CTGAGGACCC TCAAACAGCT 1424 p.(M460K) I462T M465fsX K466Tfs*2
GGCCATGAAC TCTATCAAGT ACAGTACCCT GTTGGAGAGT GAGAAAAATA 1474 N478K S479P Y482C S483Pfs* E489Q E489D T492A
CTTTCATGGA AATCTGGAAG AAGAGATGGG ATAAGTTCAT AGCAGATGTG 1524 W501*
GCTACAAAGT GAGGAGAAGC TAGCCAGCCC TCTACAAGCT GTCTTCTTGC *38
ACACGCTGTC ACTTCCTCTC ACTCGTTCTT GAATCAGCTC CATGTGCCCA *88
TGAAATCAAT GGCCTCTGTA TGGAGCGACC CTGTGAGAAG CACTTGGCTG *138
GCTGAGCAAA TTCATCCTCT GGAAATATTC TCTCTCAGCC ACAGTGACAT *188 *159G>A
TGACCCTCTT GGTTTTCTCC TGTCTCTGGC CATTTCTTCC AGTTTCCCTA *238
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AGTCCTGGGC TCTCTTCTAT TCTGGTCTCT TTATTTTTTT ATTTTTGTAT *338
TTTTTCGAGA TGGAGTTTTG CTCTTGTTGC CCAGGCTGGA GTACAATGGT *388
GCGATCTCAG CTCAGTGCAA CCTCCGCCAC CCGGGTTCAG GCAATTCTCT *438
TGCATCAGCC TCGCGAGTAG TTGGAATTAT AGGCATGTGC CACCACACCC *488
AGCTGATTTT TGCATTTTTA GTAGAGACAG GTTTTCACCA TGTTGGCGAG *538
GCTGGTATCC AACTCTTGAC CTCAGGTGAT CCACTCGCCC CTTGGCTCCC *588
AAAGTGCTGG AATTACAGGC ATTAGCCACC ATGCCTGGCC TATTCTGGTC *638
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GGGTGGTCTC ATCCATTCCT TTGCTTTTTC ATACCATTTA TTTGTTAATG *738
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ATTCCCACAT TTATTTATGC ACTTGGAGAG CTCACAGGAA TCTCAGAAAC *788

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GGTCTCCAAC TCAAGTGATC CTCCTGCCGC AGTCTCCCGA AGTGCTGGGA *938

TTACTGACAT GAGCCACCAC ACTCAGCCCT TTAAACCTTT CCCTGGCCTT *988

TCCCATAGCT GGTGAAGGAC ACCTCCATCC ATTCCACGCA GTTGCTCAAA *1038

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GCCTGGGTCT TTTCTCTTTC TCTCTGCCTG GAAGATTCCT TCTTTCCCCT *1888

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CTTGC

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