UBA1 (NM_003334.4) - cDNA + Protein - 2026-04-30

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ATCTTGTGTC GGCGGCTCGG CTGTAAGGAG GTGGCAGGGA CAACCACAAC -147
CACAACGGCC GGGGGAGGAG AAGGCGGCAG CGGCGATTCT AGGCGGCCCA -97
GGCGGCGGGG AGGAGGAGAA GGAGGAGGGT GGCGGCCGGG CTTGGCTTCG -47
GCTCCTTGAG GAGTTGGCGG CGGCGCGACC CGGGGAACCG GCATTGATGT 4
                                                 MetS 2

CCAGCTCGCC GCTGTCCAAG AAACGTCGCG TGTCCGGGCC TGATCCAAAG 54
erSerSerPr oLeuSerLys LysArgArgV alSerGlyPr oAspProLys 18

CCGGGTTCTA ACTGCTCCCC TGCCCAGTCC GTGTTGTCCG AAGTGCCCTC 104
ProGlySerA snCysSerPr oAlaGlnSer ValLeuSerG luValProSe 35

GGTGCCAACC AACGGAATGG CCAAGAACGG CAGTGAAGCA GACATAGACG 154  c.118-1G>C G40A M41V M41L M41L A>T M41T
rValProThr AsnGlyMetA laLysAsnGl ySerGluAla AspIleAspG 52

AGGGCCTTTA CTCCCGGCAG CTGTATGTGT TGGGCCATGA GGCAATGAAG 204  Y55H S56F
luGlyLeuTy rSerArgGln LeuTyrValL euGlyHisGl uAlaMetLys 68

CGGCTCCAGA CATCCAGTGT CCTGGTATCA GGCCTGCGGG GCCTGGGCGT 254
ArgLeuGlnT hrSerSerVa lLeuValSer GlyLeuArgG lyLeuGlyVa 85

GGAGATCGCT AAGAACATCA TCCTTGGTGG GGTCAAGGCT GTTACCCTAC 304
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lGluIleAla LysAsnIleI leLeuGlyGl yValLysAla ValThrLeuH 102

ATGACCAGGG CACTGCCCAG TGGGCTGATC TTTCCTCCCA GTTCTACCTG 354
isAspGlnGl yThrAlaGln TrpAlaAspL euSerSerGl nPheTyrLeu 118

CGGGAGGAGG ACATCGGTAA AAACCGGGCC GAGGTATCAC AGCCCCGCCT 404
ArgGluGluA spIleGlyLy sAsnArgAla GluValSerG lnProArgLe 135

CGCTGAGCTC AACAGCTATG TGCCTGTCAC TGCCTACACT GGACCCCTCG 454
uAlaGluLeu AsnSerTyrV alProValTh rAlaTyrThr GlyProLeuV 152

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alGluAspPh eLeuSerGly PheGlnValV alValLeuTh rAsnThrPro 168

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LeuGluAspG lnLeuArgVa lGlyGluPhe CysHisAsnA rgGlyIleLy 185

GCTGGTGGTG GCAGACACGC GGGGCCTGTT TGGGCAGCTC TTCTGTGACT 604
sLeuValVal AlaAspThrA rgGlyLeuPh eGlyGlnLeu PheCysAspP 202

TTGGAGAGGA AATGATCCTC ACAGATTCCA ATGGGGAGCA GCCACTCAGT 654
heGlyGluGl uMetIleLeu ThrAspSerA snGlyGluGl nProLeuSer 218

GCTATGGTTT CTATGGTTAC CAAGGACAAC CCCGGTGTGG TTACCTGCCT 704  N228S T233I
AlaMetValS erMetValTh rLysAspAsn ProGlyValV alThrCysLe 235

GGATGAGGCC CGACACGGGT TTGAGAGCGG GGACTTTGTC TCCTTTTCAG 754
uAspGluAla ArgHisGlyP heGluSerGl yAspPheVal SerPheSerG 252
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AAGTACAGGG CATGGTTGAA CTCAACGGAA ATCAGCCCAT GGAGATCAAA 804
luValGlnGl yMetValGlu LeuAsnGlyA snGlnProMe tGluIleLys 268

GTCCTGGGTC CTTATACCTT TAGCATCTGT GACACCTCCA ACTTCTCCGA 854
ValLeuGlyP roTyrThrPh eSerIleCys AspThrSerA snPheSerAs 285

CTACATCCGT GGAGGCATCG TCAGTCAGGT CAAAGTACCT AAGAAGATTA 904
pTyrIleArg GlyGlyIleV alSerGlnVa lLysValPro LysLysIleS 302

GCTTTAAATC CTTGGTGGCC TCACTGGCAG AACCTGACTT TGTGGTGACG 954
erPheLysSe rLeuValAla SerLeuAlaG luProAspPh eValValThr 318

GACTTCGCCA AGTTTTCTCG CCCTGCCCAG CTGCACATTG GCTTCCAGGC 1004
AspPheAlaL ysPheSerAr gProAlaGln LeuHisIleG lyPheGlnAl 335

CCTGCACCAG TTCTGTGCTC AGCATGGCCG GCCACCTCGG CCCCGCAATG 1054
aLeuHisGln PheCysAlaG lnHisGlyAr gProProArg ProArgAsnG 352

AGGAGGATGC AGCAGAACTG GTAGCCTTAG CACAGGCTGT GAATGCTCGA 1104
luGluAspAl aAlaGluLeu ValAlaLeuA laGlnAlaVa lAsnAlaArg 368

GCCCTGCCAG CAGTGCAGCA AAATAACCTG GACGAGGACC TCATCCGGAA 1154
AlaLeuProA laValGlnGl nAsnAsnLeu AspGluAspL euIleArgLy 385

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sLeuAlaTyr ValAlaAlaG lyAspLeuAl aProIleAsn AlaPheIleG 402
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GGGGCCTGGC TGCCCAGGAA GTCATGAAGG CCTGCTCCGG GAAGTTCATG 1254
lyGlyLeuAl aAlaGlnGlu ValMetLysA laCysSerGl yLysPheMet 418

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ProIleMetG lnTrpLeuTy rPheAspAla LeuGluCysL euProGluAs 435

CAAAGAGGTC CTCACAGAGG ACAAGTGCCT CCAGCGCCAG AACCGTTATG 1354
pLysGluVal LeuThrGluA spLysCysLe uGlnArgGln AsnArgTyrA 452

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GlnLysTyrP heLeuValGl yAlaGlyAla IleGlyCysG luLeuLeuLy 485

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sAsnPheAla MetIleGlyL euGlyCysGl yGluGlyGly GluIleIleV 502

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PheArgProT rpAspValTh rLysLeuLys SerAspThrA laAlaAlaAl 535

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CCGCCGCTGT GTCTACTACC GGAAGCCACT GCTGGAGTCA GGCACACTGG 1804
pArgArgCys ValTyrTyrA rgLysProLe uLeuGluSer GlyThrLeuG 602

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lyThrLysGl yAsnValGln ValValIleP roPheLeuTh rGluSerTyr 618

AGTTCCAGCC AGGACCCACC TGAGAAGTCC ATCCCCATCT GTACCCTGAA 1904 S621C
SerSerSerG lnAspProPr oGluLysSer IleProIleC ysThrLeuLy 635

GAACTTCCCT AATGCCATCG AGCACACCCT GCAGTGGGCT CGGGATGAGT 1954
sAsnPhePro AsnAlaIleG luHisThrLe uGlnTrpAla ArgAspGluP 652

TTGAAGGCCT CTTCAAGCAG CCAGCAGAAA ATGTCAACCA GTACCTCACA 2004
heGluGlyLe uPheLysGln ProAlaGluA snValAsnGl nTyrLeuThr 668

GACCCCAAGT TTGTGGAGCG AACACTGCGG CTGGCAGGCA CTCAGCCCTT 2054
AspProLysP heValGluAr gThrLeuArg LeuAlaGlyT hrGlnProLe 685

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uGluValLeu GluAlaValG lnArgSerLe uValLeuGln ArgProGlnT 702

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rSerSerGly AlaProPheT rpSerGlyPr oLysArgCys ProHisProL 752

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AlaSerValA spAspSerAr gLeuGluGlu LeuLysAlaT hrLeuProSe 835

CCCAGACAAG CTCCCTGGAT TCAAGATGTA CCCCATTGAC TTTGAGAAGG 2554
rProAspLys LeuProGlyP heLysMetTy rProIleAsp PheGluLysA 852

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spAspAspSe rAsnPheHis MetAspPheI leValAlaAl aSerAsnLeu 868
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uIleAlaGly LysIleIleP roAlaIleAl aThrThrThr AlaAlaValV 902

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alGlyLeuVa lCysLeuGlu LeuTyrLysV alValGlnGl yHisArgGln 918

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ATGTCCGATA CACCATCCGC TGACCCCGTC TGCTCCTCTA GGCTGGCCCC *27
yrValArgTy rThrIleArg Stop

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CTGGCAGTGG CCCAACTAGC CAAGTCTGGT GTTCCCTCAT CATCCCCCTA *127
CCTGAACCCC TCTTGCCACT GCCTTCTACC TTGTTTGAAA CCTGAATCCT *177
AATAAAGAAT TAATAACTCC CA
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