

CEBPE (NM_001805.4) - cDNA + Protein - 2026-11-01

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ACACAGGAGT GGGTGACAGA GGAGACTGCA GAGGGCAGGT CTAGGGCAGA -115
AGATCGAGAG AGGGCAGGCC CAGGTCAGGA GGAGGTAGAG AGAGGGCAGC -65
CGGAGCACCC CAAGGGGTGC CTCAAGAGCA GGTGGGGGCG GGGAGCCGAG -15
GGGGCGGGCC GGCCATGTCC CACGGGACCT ACTACGAGTG TGAGCCCCGG 36
               MetSer HisGlyThrT yrTyrGluCy sGluProArg 12

GGTGGCCAGC AGCCACTCGA GTTCTCAGGG GGCCGAGCTG GGCCCGGGGA 86
GlyGlyGlnG lnProLeuGl uPheSerGly GlyArgAlaG lyProGlyGl 29

GCTAGGGGAC ATGTGTGAGC ATGAGGCCTC CATTGACCTC TCCGCCTACA 136
uLeuGlyAsp MetCysGluH isGluAlaSe rIleAspLeu SerAlaTyrI 46

TCGAGTCTGG GGAAGAGCAG CTTCTCTCCG ATCTCTTTGC CGTGAAGCCA 186
leGluSerGl yGluGluGln LeuLeuSerA spLeuPheAl aValLysPro 62

GCGCCTGAGG CCAGAGGCCT CAAGGGCCCC GGAACCCCTG CCTTCCCCCA 236
AlaProGluA laArgGlyLe uLysGlyPro GlyThrProA laPheProHi 79

CTACTTGCCG CCTGACCCTC GGCCCTTTGC CTACCCTCCA CATACCTTCG 286  delTGACC
sTyrLeuPro ProAspProA rgProPheAl aTyrProPro HisThrPheG 96

GCCCAGACAG GAAGGCGCTG GGGCCTGGCA TCTACAGCAG CCCAGGGAGC 336
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lyProAspAr gLysAlaLeu GlyProGlyI leTyrSerSe rProGlySer 112

TACGACCCCA GGGCTGTGGC GGTGAAGGAG GAGCCCCGGG GGCCAGAGGG 386
TyrAspProA rgAlaValAl aValLysGlu GluProArgG lyProGluGl 129

CAGCCGAGCT GCCAGCCGAG GCAGCTACAA TCCCCTGCAG TACCAAGTGG 436
ySerArgAla AlaSerArgG lySerTyrAs nProLeuGln TyrGlnValA 146

CACACTGTGG GCAGACAGCC ATGCACCTGC CCCCAACTCT GGCAGCACCC 486
laHisCysGl yGlnThrAla MetHisLeuP roProThrLe uAlaAlaPro 162

GGCCAGCCTC TGCGCGTTCT CAAGGCCCCT TTGGCCACTG CCGCACCCCC 536  c.508_509insA
GlyGlnProL euArgValLe uLysAlaPro LeuAlaThrA laAlaProPr 179

CTGCAGTCCC CTCCTGAAGG CGCCCTCCCC GGCTGGCCCC TTACACAAGG 586
oCysSerPro LeuLeuLysA laProSerPr oAlaGlyPro LeuHisLysG 196

GCAAGAAGGC AGTGAACAAA GATAGCCTTG AGTACCGGCT GAGGCGGGAG 636
lyLysLysAl aValAsnLys AspSerLeuG luTyrArgLe uArgArgGlu 212

CGCAACAACA TCGCCGTGCG CAAGAGCCGA GACAAGGCCA AGAGGCGCAT 686  V218A R219H
ArgAsnAsnI leAlaValAr gLysSerArg AspLysAlaL ysArgArgIl 229

TCTGGAGACG CAGCAGAAGG TGCTGGAGTA CATGGCAGAG AACGAGCGCC 736
eLeuGluThr GlnGlnLysV alLeuGluTy rMetAlaGlu AsnGluArgL 246

TCCGCAGCCG CGTGGAGCAG CTCACCCAGG AGCTAGACAC CCTCCGCAAC 786  c.739_744delCGCAGC
euArgSerAr gValGluGln LeuThrGlnG luLeuAspTh rLeuArgAsn 262
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CTCTTCCGCC AGATTCCTGA GGCGGCCAAC CTCATCAAGG GCGTGGGGGG 836
LeuPheArgG lnIleProGl uAlaAlaAsn LeuIleLysG lyValGlyGl 279

TTGCAGCTGA GGCTGGCTGG TGGATTGTGG GCACCAGGCT CCCTGGCACG *40
yCysSerSto p

GCCTAACTCT GCGGACCCCC ATCCTGCTGG GGGCCTAGAA CCCTGAGACA *90
TAGACCATGG ATAAATGGCA ACCGGGGTGG CAAAGAGGGC AGGACCCAGC *140
ATAATGATTA TATGGCTGAA TAAAGTTGCA CTGTGACTGG G
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