



*CEBPE* (NM\_001805.4) - cDNA + Protein - 2026-03-10

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 CCTGACCCCTC GGCCCTTTGC CTACCCCTCA CATACTTCG 286 ~~delTGACC~~  
sTyrLeuPro ProAspProA rgProPheAl aTyrProPro HisThrPheG 96

GCCCAGACAG GAAGGCGCTG GGGCCTGGCA TCTACAGCAG CCCAGGGAGC 336

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 MethHisLeuP roProThrLe uAlaAlaPro 162

GGCCAGCCTC TGC GCGTTCT CAAGGCCCT 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

CTCTTCCGCC AGATTCCCTGA GCGGGCCAAC CTCATCAAGG GCGTGGGGGG 836

LeuPheArgG lnIleProGl uAlaAlaAsn LeuIleLysG lyValGlyGl 279

TTGCAGCTGA GGCTGGCTGG TGGATTGTGG GCACCAGGCT CCCTGGCAGC \*40

yCysSerSto p

GCCTAACTCT GCGGACCCCC ATCCTGCTGG GGCCTAGAA CCCTGAGACA \*90

TAGACCATGG ATAAATGGCA ACCGGGGTGG CAAAGAGGGC AGGACCCAGC \*140

ATAATGATTA TATGGCTGAA TAAAGTTGCA CTGTGACTGG G

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