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Coding sequence of human placenta Cofilin cDNA

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Cofilin is a widely distributed 21-KDa actin-modulating protein that forms intranuclear actin/cofilin rods in cultured cells exposed to heat shock or 10% dimethyl sulfoxide (1, 2). We report a coding sequence of human placenta Cofilin cDNA which was obtained by screening human placenta cDNA library (Clontech Lab., Inc.) with an oligomer corresponding to the porcine brain Cofilin sequence (3), 5′ CCGGAGGAGGTGAAGAAGCGCAAGAAG 3′. The human placenta Cofilin cDNA has an open reading frame of 166 amino acids. Of these 166 amino acids there is only one difference when compared to porcine (3), and two differences when compared to mouse (4). In human placenta Ser 108 is substituted for Cys, Asn in porcine, mouse respectively (3,), and Asp 69 is substituted for Thr in mouse (boxed) (4). For completeness we confirmed differences of amino acids among thee species by direct cloning of human placenta Cofilin cDNA with RT-PCR and its sequencing. Two PCR-primers with restriction endonuclease sites were obtained by modifying near their 5′ ends. 5′ GTGGAATTCAACGACATGAAGGTGC (underlined). 3′ CGTTTTACTAAATACGGCCTAGGCAC (overlined). In the human placenta used for RT-PCR, there is a T→C base substitution at position 205 (marked with *).

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                                                                 GGGAAAC   7

 M  A  S  G  V  A  V  S  D  G  V  I  K  V  F  N  D  M  K  V  R  K  S  S
ATGGCCTCCGGTGTGGCTGTCTCTGATGGTGTCATCAAGGTGTTCAACGACATGAAGGTGCGTAAGTCTTCA  79

 T  P  E  E  V  K  K  R  K  K  A  V  L  F  C  L  S  E  D  K  K  N  I  I
ACGCCAGAGGAGGTGAAGAAGCGCAAGAAGGCGGTGCTCTTCTGCCTGAGTGAGGACAAGAAGAACATCATC 151
                 .
 L  E  E  G  K  E  I  L  V  G  D  V  G  Q  T  V  D  D  P  Y  A  T  F  V
CTGGAGGAGGGCAAGGAGATCCTGGTGGGCGATGTGGGCCAGACTGTCGACGATCCCTACGCCACCTTTGTC 223
                                                     *
 K  M  L  P  D  K  D  C  R  Y  A  L  Y  D  A  T  Y  E  T  K  E  S  K  K
AAGATGCTGCCAGATAAGGACTGCCGCTATGCCCTCTATGATGCAACCTATGAGACCAAGGAGAGCAAGAAG 295

 E  D  L  V  F  I  F  W  A  P  E  S  A  P  L  K  S  K  M  I  Y  A  S  S
GAGGATCTGGTGTTTATCTTCTGGGCCCCCGAGTCTGCGCCCCTTAAGAGCAAAATGATTTATGCCAGCTCC 367

 K  D  A  I  K  K  K  L  T  G  I  K  H  E  L  Q  A  N  C  Y  E  E  V  K
AAGGACGCCATCAAGAAGAAGCTGACAGGGATCAAGCATGAATTGCAAGCAAACTGCTACGAGGAGGTCAAG 439

 D  R  C  T  L  A  E  K  L  G  G  S  A  V  I  S  L  E  G  K  P  L
GACCGCTGCACCCTGGCAGAGAAGCTGGGGGGCAGTGCGGTCATCTCCCTGGAGGGCAAGCCTTTGTGAGCC 511


CCTTC                                                                    516
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