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The nucleotide sequence of a human smooth muscle alpha-actin (aortic type) cDNA

Shinji Kamada* and Takeo Kakunaga#

Department of Oncogene Research, Research Institute for Microbial Disease, Osaka University, Osaka 565, Japan

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To isolate the human smooth muscle (SM) alpha-actin (aortic type) cDNA, we constructed the cDNA library from the artery of umbilical cord. By using the human SM alpha-actin specific probe containing 3' untranslated (UT) region (1), we got a clone (pHSMαA-2) which is 1345 bp long with 5' and 3' UT regions of 47 bp and 149bp, respectively. The amino acid sequence deduced from the nucleotide sequence is composed of 377 amino acid residues containing an initial Met-Cys dipeptide, which is removed post-translationally. The remainder of the amino acid sequence matched those of bovine, rat and chicken SM alpha-actins (2,3,4). In 5' UT region, the 23 bp region immediately preceding the initiation codon is identical with the corresponding sequence of the human SM alpha-actin gene (5), but the initial 24bp region did not match with the corresponding genomic DNA. From this result, the human SM alpha-actin gene has at least one more non-coding exons in 5' upstream region. In 5' UT region, there are 83% sequence conservation between human and mouse genes (6), and 76% between human and rat genes (3). Although the human SM alpha-actin 3' UT region did not have a 32bp long G/C rich segment that is present in the rat SM alpha-actin 3' UT region (3), there are 80% sequence conservation between human and rat genes, 75% between human and mouse genes, and 60% between human and chicken genes (3,6,5).

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GCAGCCCAGCCAAGCACTGTCAGGAATCCTGTGAAGCAGCTCCAGCTATGTGTGAAGAAGAGGACAGCACTGCCTTGGTGTGTGACAATGGCTCTGGGCT 100
                                                MetCysGluGluGluAspSerThrAlaLeuValCysAspAsnGlySerGlyLe

CTGTAAGGCCGGCTTTGCTGGGGACGATGCTCCCAGGGCTGTTTTCCCATCCATTGTGGGACGTCCCAGACATCAGGGGGTGATGGTGGGAATGGGACAA 200
uCysLysAlaGlyPheAlaGlyAspAspAlaProArgAlaValPheProSerIleValGlyArgProArgHisGlnGlyValMetValGlyMetGlyGln

AAAGACAGCTACGTGGGTGACGAAGCACAGAGCAAAAGAGGAATCCTGACCCTGAAGTACCCGATAGAACATGGCATCATCACCAACTGGGACGACATGG 300
LysAspSerTyrValGlyAspGluAlaGlnSerLysArgGlyIleLeuThrLeuLysTyrProIleGluHisGlyIleIleThrAsnTrpAspAspMetG

AAAAGATCTGGCACCACTCTTTCTACAATGAGCTTCGTGTTGCCCCTGAAGAGCATCCCACCCTGCTCACGGAGGCACCCCTGAACCCCAAGGCCAACCG 400
luLysIleTrpHisHisSerPheTyrAsnGluLeuArgValAlaProGluGluHisProThrLeuLeuThrGluAlaProLeuAsnProLysAlaAsnAr

GGAGAAAATGACTCAAATTATGTTTGAGACTTTCAATGTCCCAGCCATGTATGTGGCTATCCAGGCGGTGCTGTCTCTCTATGCCTCTGGACGCACAACT 500
gGluLysMetThrGlnIleMetPheGluThrPheAsnValProAlaMetTyrValAlaIleGlnAlaValLeuSerLeuTyrAlaSerGlyArgThrThr

GGCATCGTGCTGGACTCTGGAGATGGTGTCACCCACAATGTCCCCATCTATGAGGGCTATGCCTTGCCCCATGCCATCATGCGTCTGGATCTGGCTGGCC 600
GlyIleValLeuAspSerGlyAspGlyValThrHisAsnValProIleTyrGluGlyTyrAlaLeuProHisAlaIleMetArgLeuAspLeuAlaGlyA

GAGATCTCACTGACTACCTCATGAAGATCCTGACTGAGCGTGGCTATTCCTTCGTTACTACTGCTGAGCGTGAGATTGTCCGGGACATCAAGGAGAAACT 700
rgAspLeuThrAspTyrLeuMetLysIleLeuThrGluArgGlyTyrSerPheValThrThrAlaGluArgGluIleValArgAspIleLysGluLysLe

GTGTTATGTAGCTCTGGACTTTGAAAATGAGATGGCCACTGCCGCATCCTCATCCTCCCTTGAGAAGAGTTACGAGTTGCCTGATGGGCAAGTGATCACC 800
uCysTyrValAlaLeuAspPheGluAsnGluMetAlaThrAlaAlaSerSerSerSerLeuGluLysSerTyrGluLeuProAspGlyGlnValIleThr

ATCGGAAATGAACGTTTCCGCTGCCCAGAGACCCTGTTCCAGCCATCCTTCATCGGGATGGAGTCTGCTGGCATCCATGAAACCACCTACAACAGCATCA 900
IleGlyAsnGluArgPheArgCysProGluThrLeuPheGlnProSerPheIleGlyMetGluSerAlaGlyIleHisGluThrThrTyrAsnSerIleM

TGAAGTGTGATATTGACATCAGGAAGGACCTCTATGCTAACAATGTCCTATCAGGGGGCACCACTATGTACCCTGGCATTGCCGACCGAATGCAGAAGGA 1000
etLysCysAspIleAspIleArgLysAspLeuTyrAlaAsnAsnValLeuSerGlyGlyThrThrMetTyrProGlyIleAlaAspArgMetGlnLysGl

GATCACGGCCCTAGCACCCAGCACCATGAAGATCAAGATCATTGCCCCTCCGGAGCGCAAATACTCTGTCTGGATCGGTGGCTCCATCCTGGCCTCTCTG 1100
uIleThrAlaLeuAlaProSerThrMetLysIleLysIleIleAlaProProGluArgLysTyrSerValTrpIleGlyGlySerIleLeuAlaSerLeu

TCCACCTTCCAGCAGATGTGGATCAGCAAACAGGAATACGATGAAGCCGGGCCTTCCATTGTCCACCGCAAATGCTTCTAAAACACTTTCCTGCTCCTCT 1200
SerThrPheGlnGlnMetTrpIleSerLysGlnGluTyrAspGluAlaGlyProSerIleValHisArgLysCysPheEnd

CTGTCTCTAGCACACAACTGTGAATGTCCTGTGGAATTATGCCTTCAGTTCTTTTCCAAATCATTCCTAGCCAAAGCTCTGACTCGTTACCTATGTGTTT 1300
TTTAATAAATCTGAAATAGGCTACTGGTAAAAAAAAAAAAAAAAA 1345
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*To whom correspondence should be addressed

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