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Nucleotide sequence of human muscle acetylcholine receptor β-subunit

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We report the nucleotide sequence and deduced amino acid sequence for the human muscle acetylcholine receptor β -subunit. The sequence is derived from a clone isolated from a cDNA library using poly(A)$^+$RNA from human leg muscle.

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        10        20        30        40        50        60        70        80        90
GGCGAGCCGCCAGCGTATGACCCCAGGGGCTCTGCTGATGCTGCTGGGGGCGCTGGGGCCGGCGCTCGCCCCAGGCGTCCGCGGCTCGGA
                MetThrProGlyAlaLeuLeuMetLeuLeuGlyAlaLeuGlyProAlaLeuAlaProGlyValArgGlySerGl
       100       110       120       130       140       150       160       170       180
GGCGGAGGGTCGACTCCGGGAGAAACTTTTCTCTGGCTATGATAGCTCCGTCCGGCCAGCGCGGGAGGTGGGAGACCGTGTCAGGGTCAG
uAlaGluGlyArgLeuArgGluLysLeuPheSerGlyTyrAspSerSerValArgProAlaArgGluValGlyAspArgValArgValSe
       190       200       210       220       230       240       250       260       270
CGTTGGTCTCATCCTGGCGCAACTCATCAGCCTGAACGAGAAGGATGAAGAGATGAGCACAAAGGTGTACTTAGACCTGGAGTGGACTGA
rValGlyLeuIleLeuAlaGlnLeuIleSerLeuAsnGluLysAspGluGluMetSerThrLysValTyrLeuAspLeuGluTrpThrAs
       280       290       300       310       320       330       340       350       360
CTACAGGCTGAGCTGGGACCCTGCGGAGCACGAGGGCATCGATTCGCTCCGCATCACGGCGGAATCCGTGTGGCTCCCTGACGTGGTGCT
pTyrArgLeuSerTrpAspProAlaGluHisGluGlyIleAspSerLeuArgIleThrAlaGluSerValTrpLeuProAspValValLe
       370       380       390       400       410       420       430       440       450
ACTGAACAACAATGATGGGAATTTTGACGTGGCTCTGGACATTAGCGTCGTGGTGTCCTCCGACGGCTCCGTGCGTTGGCAACCCCCGGG
uLeuAsnAsnAsnAspGlyAsnPheAspValAlaLeuAspIleSerValValValSerSerAspGlySerValArgTrpGlnProProGl
       460       470       480       490       500       510       520       530       540
CATCTATCGCAGCAGCTGCAGCATCCAGGTCACCTACTTCCCCTTCGACTGGCAGAATTGCACTATGGTGTTCAGCTCCTACAGCTACGA
yIleTyrArgSerSerCysSerIleGlnValThrTyrPheProPheAspTrpGlnAsnCysThrMetValPheSerSerTyrSerTyrAs
       550       560       570       580       590       600       610       620       630
CAGCTCGGAGGTCACGCTGCAGACAGGCCTGGGTCCTGACGGGCAAGGGACTCAGGAAATCCACATTCATGAAGGGACTTTCATTGAGAA
pSerSerGluValThrLeuGlnThrGlyLeuGlyProAspGlyGlnGlyThrGlnGluIleHisIleHisGluGlyThrPheIleGluAs
       640       650       660       670       680       690       700       710       720
TGGCCAGTGGGAGAATATCCACAAGCCCTCTCGGCTAATCCAGCCTCCAGGCGATCCTAGGGGAGGGAGGGAAGGACAGCGCCAGGAAGT
nGlyGlnTrpGluAsnIleHisLysProSerArgLeuIleGlnProProGlyAspProArgGlyGlyArgGluGlyGlnArgGlnGluVa
       730       740       750       760       770       780       790       800       810
CATCTTCTACCTCATCATCCGCCGCAAGCCTCTCTTCTACCTGGTCAACGTCATTGCCCCATGCATCCTCATCACTCTTCTGGCCATCTT
lIlePheTyrLeuIleIleArgArgLysProLeuPheTyrLeuValAsnValIleAlaProCysIleLeuIleThrLeuLeuAlaIlePh
       820       830       840       850       860       870       880       890       900
CGTCTTCTACCTGCCACCAGATGCAGGAGAGAAGATGGGGCTCTCAATCTTTGCCCTGCTGACCCTTACTGTGTTCCTGCTGCTGCTGGC
eValPheTyrLeuProProAspAlaGlyGluLysMetGlyLeuSerIlePheAlaLeuLeuThrLeuThrValPheLeuLeuLeuLeuAl
       910       920       930       940       950       960       970       980       990
TGACAAAGTACCTGAGACCTCACTATCAGTACCCATTATTATCAAGTACCTCATGTTTACCATGGTCCTCGTCACCTTCTCAGTCATCCT
aAspLysValProGluThrSerLeuSerValProIleIleIleLysTyrLeuMetPheThrMetValLeuValThrPheSerValIleLe
      1000      1010      1020      1030      1040      1050      1060      1070      1080
TAGTGTCGTGGTTCTCAACCTGCACCACCGCTCACCCCACACCCACCAAATGCCCCTTTGGGTCCGTCAGATCTTCATTCACAAACTTCC
uSerValValValLeuAsnLeuHisHisArgSerProHisThrHisGlnMetProLeuTrpValArgGlnIlePheIleHisLysLeuPr
      1090      1100      1110      1120      1130      1140      1150      1160      1170
GCTGTACCTGCGTCTAAAAAGGCCCAAACCCGAGAGAGACCTGATGCCGGAGCCCCCTCACTGTTCTTCTCCAGGAAGTGGCTGGGGTCG
oLeuTyrLeuArgLeuLysArgProLysProGluArgAspLeuMetProGluProProHisCysSerSerProGlySerGlyTrpGlyAr
      1180      1190      1200      1210      1220      1230      1240      1250      1260
GGGAACAGATGAATATTTCATCCGGAAGCCGCCAAGTGATTTTCTCTTCCCCAAACCCAATAGGTTCCAGCCTGAACTGTCTGCCCCTGA
gGlyThrAspGluTyrPheIleArgLysProProSerAspPheLeuPheProLysProAsnArgPheGlnProGluLeuSerAlaProAs
      1270      1280      1290      1300      1310      1320      1330      1340      1350
TCTGCGGCGATTTATCGATGGTCCAAACCGGGCTGTGGCCCTGCTTCCGGAGCTACGGGAGGTCGTCTCCTCTATCAGCTACATCGCTCG
pLeuArgArgPheIleAspGlyProAsnArgAlaValAlaLeuLeuProGluLeuArgGluValValSerSerIleSerTyrIleAlaAr
      1360      1370      1380      1390      1400      1410      1420      1430      1440
ACAGCTGCAGGAACAGGAGGACCACGATGCGCTGAAGGAGGACTGGCAGTTTGTGGCCATGGTAGTGGACGCGCTCTTCCTGTGGACTTT
gGlnLeuGlnGluGlnGluAspHisAspAlaLeuLysGluAspTrpGlnPheValAlaMetValValAspAlaLeuPheLeuTrpThrPh
      1450      1460      1470      1480      1490      1500      1510      1520      1530
CATCATCTTCACCAGCGTTGGGACCCTAGTCATCTTCCTGGACGCCACGTACCACTTGCCCCCTCCAGACCCCTTTCCTTGAAGACTGGA
eIleIlePheThrSerValGlyThrLeuValIlePheLeuAspAlaThrTyrHisLeuProProProAspProPhePro *
      1540      1550      1560      1570      1580      1590      1600      1610      1620
GGGTTGAGACCAGGCCCCCTGCCAGTTGAAGTGAGAGAGTTTGGTGATACTGTCAAGCCCTATCCTTCTCTGCCTCTTAACTCCTTCACG

      1630      1640      1650
AGGAATCTGGGCCTCTTATTTCGTTCTGGG...........3'
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