

Nucleotide sequence of cDNA to mRNA for a cerebellar Ca-binding protein, spot 35 protein

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Submitted 17 July 1986

A cDNA library to enriched mRNA for rat spot 35 protein was screened with [<sup>32</sup>P]-labeled oligodeoxynucleotides. The nucleotide sequence of the longest cDNA (pRS35-1) and the deduced amino acid sequence are described. The amino acid sequence determined with a gas phase sequence is underlined. The synthetic oligodeoxynucleotide probes are indicated by the dotted underline. The initiation codon, the termination codon and polyadenylation signal are double underlined.

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-100                                -50
AGAACUCCGGAGACGCCCGAACGGAGACACCGCGGACAGCGCCGCGCGCCGACGACGUCAGCCUGUCAGCCUUGCCGAGGUGG
      1
CGCUCAGCGCUCUCUACUAGCCCGCUGCACCUUGCAGAAUCCACACUGCAGUCUCUCUGAUCACAGCCUCACAGUUUUUGGAGAUCGGCGUUCAU
      10
      MetAlaGluSerHisLeuGlnSerSerLeuIleThrAlaSerGlnPheGluIleTrpLeuHis
      20
UUGACGCGUUGGAGUGGUUACUGGCAAGGAGCGUCAGAAUCUAGUCAGGAGCUUCUGCAGCCGACGAAGAAGCGCGUAGUGGAGUACA
      30
      PheAspAlaAspGlySerGlyTyrLeuGluGlyLeuGlnAsnLeuIleGlnGluLeuLeuGlnAlaArgLysLysAlaGlyLeuGluLeuSer
      40
      CCGAGAGAAUACCUUUGGUAUUAUUGGGCAGAGGUAUGGGAUUUGAGUUGGCCAUGUCUUAUCCACCGAAGGAGUUAUC
      50
      ProGluMetLysThrPheValAspGlnTyrGlyGlnArgAspAspGlyLysIleGlyIleValGluLeuAlaHisValLeuProThrGluGluAsnPhe
      60
      CUGCUCGCUUUUCGAGCCAGCAUCAGUUCUGCGAGGAUUUCAUGAAGACUUGGAGAAUUGACACACGACACGAGUCUUCUAGAAACGGAG
      70
      LeuLeuLeuPheArsCysGlnGlnLeuLysSerCysGlnGluPheMetLysThrTrpArgLysTyrAspThrAspHisSerGlyPheIleGluThrGlu
      80
      GAACUUAAGAACUUUUUAAAGGACUCUGCUAGAGAAAGCAACAGCCGUGGAGUAUCGAACUUGCUGAGUACACAGCCUUCAGUGAAAGCGUUC
      90
      GluLeuLysAsnPheLeuLysAspLeuLeuGluLysAlaAsnLysThrValAspAspThrLysLeuAlaGluTyrThrAspLeuMetLeuLysLeuPhe
      100
      GACUCAAAUUAUGAUGGGAAGCUGGAGCAGACAGAGUGGCCAGGUUACUACCCAGUCAGGAGAAUUUCCUUCUUAUUAAUCCAGGGAAUAAAUGUGU
      110
      AspSerAsnAsnAspGlyLysLeuGlnLeuThrGluMetAlaArgLeuLeuProValGlnGluAsnPheLeuLeuLysPheGlnGlyIleLysMetCys
      120
      GGGAAAGAGUUAUUAAGGCUUUUUGAGUUUAUGAUCAGGAGGCAACGAAUUAUGAUGAAUAGCUGAUGCCUUCAGGAAUCAAUUGCUGAG
      130
      GlyLysGluPheAsnLysAlaPheGluLeuTyrAspGlnAspGlyAsnGlyTyrIleAspGluAsnGluLeuAspAlaLeuLeuLysAspLeuLysGlu
      140
      AAAACAAACAGGAAUUGGAAUUAUUAACAUUUUUCUACUACGAAAGAAACAUUAUUGGCCUUGUCGGAUGGAGGAGUGUCCGACAGAGAUUGCC
      150
      LysAsnLysGlnGluLeuAspIleAsnAsnIleSerThrTyrLysLysAsnIleMetAlaLeuSerAspGlyGlyLysLeuTyrArgThrAspLeuAla
      160
      CUUAUUCUCUCUGGGGCAACUAGAGUUGGGCCACACACCACUCUAGUGUAUCAUUGUUAUCCAAUACCAUUAUCUGGCCUUAUAAAGGAGUAG
      170
      LeuIleLeuSerAlaGlyAspAsn
      180
      CGCUAUUUUCUUUUUAUUUUAUUUUAUUCUAGAGAAUUAUUCAGGAGUGUGGCACUUCUUUCUGCUGUUUUUCUUAUCUGUUUUUAUU
      190
      GUACAGUUUUUGUAGCAUUUAUUGAAAGAAAGAAAGUUCUUGCUUAGGCCAGUCAGUUAUUAUCCAUUUUCAAAGAUAGAUUACAUAGUUCUUCU
      200
      UCAUUAUUAUCAGAAACACUUGGAUUUCCUUAUAAACUACCAUUCUACAAUUAUUGUUCAGAGUUAUUAUUGCAGUCUGAGUUAUUAAGAU
      210
      AUUUCAGCAACAGCAGUUUUUUUAUUUAGGCAUUAUGAAGCUGCCCAACAGCACUUCUGCUGUUUCUUCUUGUGAAGGAGGUGGUCUCU
      220
      CGUUGAAGACCAAAUUAUUAUAGUUAUCUAGGCCUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
      230
      UAGUCCGCCACUUGUGGUCAAGCUGGUGGCAAGGAGGUGCCAGAGUACACAAUAGUCUGUCUGAUUUAUUAUUAUUAUUAUUAUUAUUAUUAU
      240
      CUUUGCAGAGAGUAGACCUAUAGCCAAUUUUUAUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
      250
      UGUGUUCUCUCAGUUAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
      260
  
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