

```

-1000 AACAGAGAGGTCCCAAATCCCGGTCTGTGGCCTGTCCGCCTAAGCTCTGCCTCCTGCCAGATCAGCAGGCAGCATTAGATTCTCATAGGAGCTGGACGC
-900 CTATTGTGAAGTGCATGATGCGGGATCCAGATTGTGCACTCTTTATGAGAATCTAAGTAAATGCTTGTGATCTATCTGAACCAGAACAAATTCATCCTG
-800 AAACCATCCCCACCAATCCATAGAAATACTGTCTTCCACAAAAATGATCCCTGGTGCCAAAAATGTTAGAGACCACTCCCTAAAACCTCTCTCTTAGC
-700 TCTCACCTCCTGTATTACTATCTCATCTCAGTACATTGAAGCCCCATCTTTTCCCATGGATGCCTCATTTCCATTATTAGGAGGAGCATTTTTTTATTTTT
-600 TGTTTTTATTTTTTCCGAGACGGAGTCTCGCTCTGTGCCTAAGGCTGGAGTGCAGTGGCGCGATCTCGGCTCACTGCAAGCTCCGCCCTCCGGGTTAC
-500 GCCATTCCTCCTGCCTCAGCTCCCAAGTAGTGGGACTACAGGCGCCGCACTACGCGCCGCTAATTTTTTGTATTTTTAGTAGAGACGGGGTTTCACCC
-400 TGGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCGCCCTTGCCCTCCCAAAGTGTGGGATTACAGGCGTGAGACCGCGCCCGGCGTCA
-300 TTGGTATGTCTTAAATGTGCTCAGGACCTAGCACAGTCCCTGGTACCCAGTAGAGACCTATGTAATGTTTGTATTTCAATAATAAATACATGAATTAAAG
-200 AGTGAGAGTGGATTTTGTAAATGTACGACTGATAGAGAAATACTCAGTATTCTAAGGGATGGGAAGAACGGTTGGAGCTAGAGGTTGTGCTCAGGAAA
-100 CTATTAATAGACGTTCCGCAGGAAGGGATTGACGAAGTGTGAGGTTAATGAGGAAGGGAAAATAGAAATATAAAATTTGGTGGTGGAAAAGATCTGATTC
1 ATGATGCCGTGTGAGAGCAAAGCTCCTGTCTTTTGGCCTAATTTGGTGATGCTGTTCTTGGGCTACCACACCTCCTTTTGCCTCCGCAGGAGCCT
. . . . .-24. . . . .-20. . . . .-10. . . . .+1. . . . .
. . . . .M.V.M.G.L.G.V.L.L.L.V.F.V.L.G.L.G.L.T.P.P.T.L.A.Q.D.N.S.R..
101 GTGTTGGAAGAGATGGTGTGATGGGCTGGGCGTTTGTGTGGTCTTCGTGCTGGGCTGACCCACCGACCCTGGCTCAGGATAACTCCAGT
. . . . .10. . . . .20. . . . .30. . . . .
Y.T.H.F.L.T.Q.H.Y.D.A.K.P.Q.G.R.D.D.R.Y.C.E.S.I.M.R.R.R.G.L.T.S.P.C
201 ACACACACTTCTGACCAGCACTATGATGCCAAACCACAGGCGGGATGACAGATACTGTGAAAGCATCATGAGGAGACGGGGCTGACCTCACCTG
..40. . . . .50. . . . .60. . . . .70. . . . .
.K.D.I.N.T.F.I.H.G.N.K.R.S.I.K.A.I.C.E.N.K.N.G.N.P.H.R.E.N.L.R.I.S.
301 CAAAGACATCAACACATTTATTCATGGCAACAAGCGCAGCATCAAGCCATCTGTGAAACAAGAATGGAAACCTCACAGAGAAAACCTAAGAATAAGC
. . . . .80. . . . .90. . . . .100. . . . .
.K.S.S.F.Q.V.T.T.C.K.L.H.G.G.S.P.W.P.P.C.Q.Y.R.A.T.A.G.F.R.N.V.V.V..
401 AAGTCTTCTTTCCAGGTACCACCTTGCAAGCTACATGGAGGTCCCCCTGGCCTCCATGCCAGTACCGACCACAGCGGGGTTCAGAAACGTTGTTGTTG
. . . . .110. . . . .120. . . . .123
A.C.E.N.G.L.P.V.H.L.D.Q.S.I.F.R.R.P
501 CTGTGAAAATGGCTTACCTGTCCACTTGGATCAGTCAATTTTCCGTCGTCCGTAACCAAGCGGGCCCCCTGGTCAAGTGTGGCTCTGCTGTCTTGCCT
600 TCCATTTCCCTCTGCACCAGAACAGTGGTGGCAACATTCATTGCCAAGGGCCCAAAGAAAGAGCTACCTGGACCTTTTGTTTTCTGTTTGACAACATG
700 TTTAATAAATAAAAAATGCTTGTATATCAGTAAGAATCAGAGTCTTCTCACTGATTCTGGGCATATTGATCTTCCCCCATTTTCTCTACTTGGCTGCTCC
800 CTGAGAGGACTGCATAGGATAGAAATGCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
900 GTGCAATGGCACAATCTCGGCTCACTGCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
1000 CACCACACTGGCTAATTTTTGTGTTTTTAGTAGAGACAGGGTTTACCCTTTTGGCCAGGTTGGTCTTGAACCTCTGACCTCGGGAGATCCGCCACCT
1100 TGGCCTCTCTTTGTGCTGGGATTACAGGCATGAGCCACTGAGCCGGGCCACTTTTTCTTATCAGTCAGTTTTTACAAGTCATTAGGGAGGTAGACTTTA
1200 CCTCTCTGTGAAGGAAAGTATGGTATGTTGATCTACAGAGAGAGATGAAAAATTCAGGGCTCGTAGCTACTAAGCAGAATTTCCAAGATAGGCCAAAT
1300 GTTTTTTCTGTCAAATAATAAGCTAATATTACTTCTACAAATATGAGACCTTGGAGAGAAGTTTCCAAGGACCAAGTACCAACATACCAACAGATTATTA
1400 TAGTTTTCTCTACTCTTACACACACACACACACATATACACATATGTAATCCAGCATGAATACCAAAATTCATTACGGGTAGCCACCTTTTGTCTTAATC
1500 GAGAGATAATTTGATGTTTGAATGGAATGCTCCAGGATATCTCTTGTATGTTTATTTATATAAAATTCAAAAACCAATTACATTATTTCTCTGT
1600 AATCTTTTACTTTTATCAACTAATGTCTGGCAAGTGTGATGTTTTGGGGAAGTTATAGAAGATTCGCGCCAGCGCTTATCTCACGCTTGTAATCCAGCAC
1700 TTTGGGAAGCTGAGCGGACAGATCACGAGGTCAAGAGATCAAGACCATCTGGACAACATGGTGAACCTTGTCTCTACTAAAAATGTGAAAATTAGCT
1800 GGCGTGGTGGCACACCTATAGTCCCAGTACTCGGGAGGCTGAGGCAGGAGAAATCGCTTGAACCTAGGAGGCGGAGGTTGCACTGAGCCGAGATCAC
1900 GCCACTGCACTCCAGCTGGGCGACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAAAAAAGAAAGATCCAGTTTTATCCCAGTTTTATCCCTTATCTCTCT

```

Figure 5. Nucleotide sequence of the human angiogenin gene and inferred amino acid sequence. Nucleotides are numbered beginning with +1 at the proposed transcription initiation site; TATA box is boxed; AATAAA and CACTG sequences are underlined with solid bars. The two arrows limit the cDNA sequence. Underlining shows the three Alu repeat sequences in the 5'- and 3'- flanking regions of the gene; dashed underlining indicates the direct repeat sequences flanking each Alu repeat (modified from [69]).