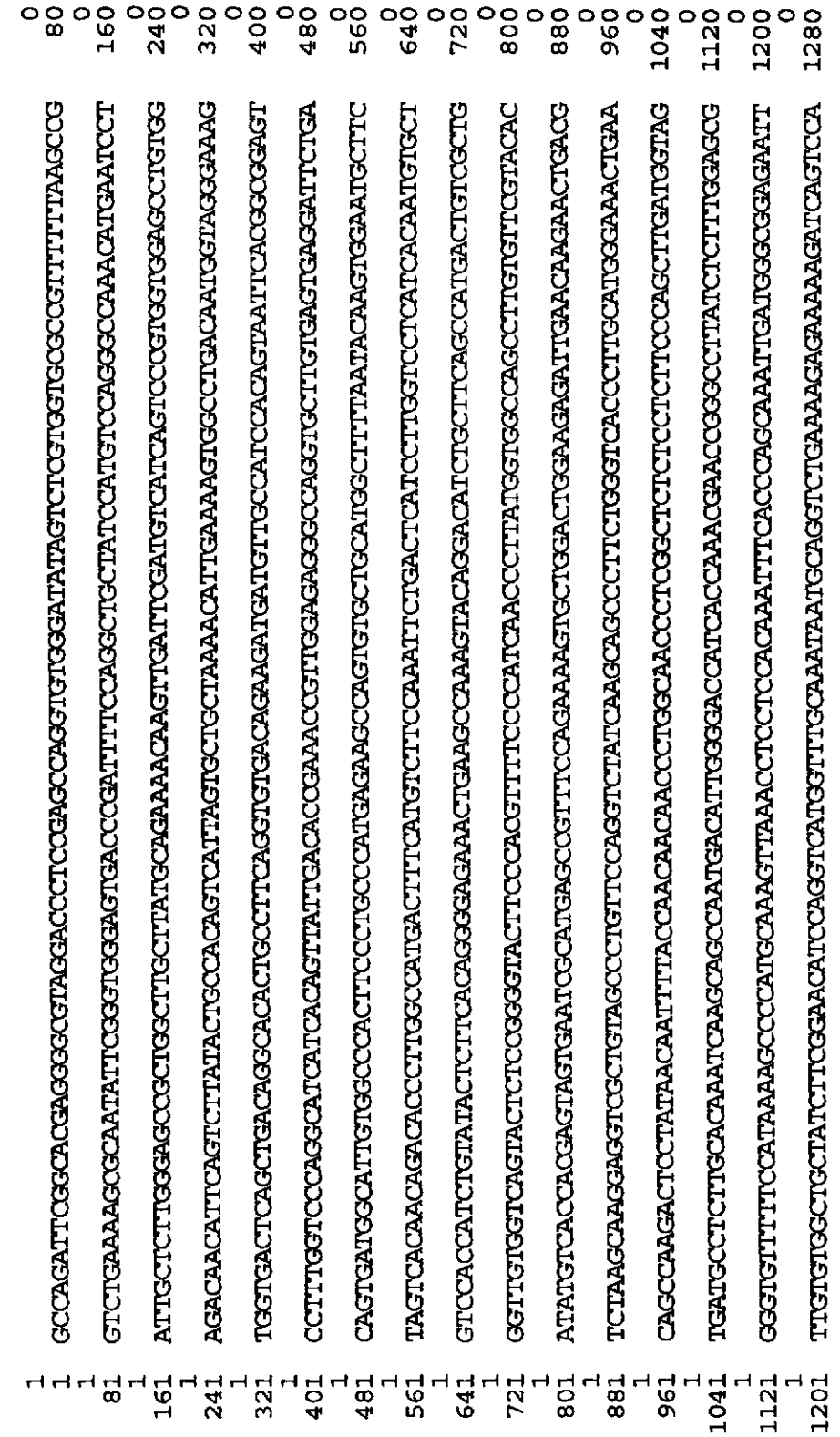

1
1 GCCAGATTCGGCACGAGGGGCGTAGGACCCTCCGAGCCAGGTGTGGATATAGTCTCGTGGTGCGCCGTTTTTTAAGCCG 80
1 0
1
81 GTCTGAAAAGCGCAATATTCGGGTGGGAGTGACCCGATTTTCCAGGCTGCTATCCATGTCCAGGGCCAAACATGAATCCT 160
1 0
161 ATTGCTCTTGGGAGCCGCTGGCTTGCTTATGCAGAAAACAAGTTGATTCGATGTCATCAGTCCCGTGGTGGAGCCTGTGG 240
1 0
241 AGACAACATTCAGTCTTATACTGCCACAGTCATTAGTGCTGCTAAAACATTGAAAAGTGGCCTGACAATGGTAGGGAAAG 320
1 0
321 TGGTGACTCAGCTGACAGGCACACTGCCTTCAGGTGTGACAGAAGATGATGTTGCCATCCACAGTAATTCACGGCGGAGT 400
1 0
401 CCTTTGGTCCCAGGCATCATCACAGTTATTGACACCGAAACCGTTGGAGAGGGCCAGGTGCTTGTGAGTGAGGATTCTGA 480
1 0
481 CAGTGATGGCATTGTGGCCCACTTCCCTGCCATGAGAAGCCAGTGTGCTGCATGGCTTTTAATACAAGTGGAATGCTTC 560
1 0
561 TAGTCACAACAGACACCCTTGGCCATGACTTTCATGTCTTCCAAATTCTGACTCATCCTTGGTCCTCATCACAATGTGCT 640
1 0
641 GTCCACCATCTGTATACTCTTCACAGGGAGAAACTGAAGCCAAAGTACAGGACATCTGCTTCAGCCATGACTGTCGCTG 720
1 0
721 GGTTGTGGTCAGTACTCTCCCGGGTACTTCCCCATCAACCCTTATGGTGGCCAGCCTTGTGTTCGTACAC 800
1 0
801 ATATGTCACCACGAGTAGTGAATCGCATGAGCCGTTTCCAGAAAAGTGCTGGACTGGAAGAGATTGAACAAGAACTGACG 880
1 0
881 TCTAAGCAAGGAGGTCGCTGTAGCCCTGTTCCAGGTCTATCAAGCAGCCCTTCTGGGTCACCCTTGCATGGGAAACTGAA 960
1 0
961 CAGCCAAGACTCCTATAACAATTTTACCAACAACAACCCTGGCAACCCTCGGCTCTCTCCTCTTCCCAGCTTGATGGTAG 1040
1 0
1041 TGATGCCTCTTTGCACAAATCAAGCAGCCAATGACATTGGGGACCATCACCAAACGAACCGGGCCTTATCTCTTTGGAGCG 1120
1 0
1121 GGGTGTTTTTCCATAAAAGCCCCATGCAAAGTTAAACCTCCTCCACAAATTTCACCCAGCAAATTGATGGGCGGAGAATT 1200
1 0
1201 TTGTGTGGCTGCTATCTTCGGAACATCCAGGTCATGGTTTGCAAATAATGCAGGTCTGAAAAGAGAAAAGATCAGTCCA 1280

FIG. 1A

```
                                                                      0
1281 AACAAGTTGTAGTTGAGTCCCTGTACATTATCAGTTGCTATGGCACCTTAGTGGAACACATGATGGAGCCGCGACCCCTC 1360
   1                                                                  0
1361 AGCACTGCACCCAAGATTAGTGACGACACACCACTGGAAATGATGACATCGCCTCGAGCCAGCTGGACTCTGGTTAGAAC 1440
   1                                                                  0
1441 CCCTCAATGGAATGAATTGCAGCCACCGTTTAATGCAAACCACCCTCTGCTCCTCGCTGCAGATGCAGTACAGTATTATC 1520
   1                                                                  0
1521 AGTTCCTGCTTGCTGGCCTGGTTCCCCCTGGAAGTCCTGGGCCCATTACTCGACATGGGTCTTACGACAGTTTAGCTTCT 1600
   1                                                                  0
1601 GACCATAGTGGACAGGAAGATGAAGAATGGCTTTCCCAGGTTGAAATTGTAACACACACTGGACCCCATAGACGTCTGTG 1680
   1                                                                  0
1681 GATGGGTCCACAGTTCCAGTTCAAAACCATCCATCCCTCAGGCCAAACCACACAGTTATCTCATCCAGTTCATCTGTGTTGC 1760
   1                                                                  0
1761 AGTCTCATGGTCCGAGTGACACGCCACAGCCTCTCTTTGGATTTTGATACAGATGATCTTGATCTCAACAGTCTCAGGATC 1840
                                                                      0
                                TCGGAGCCCATGCGCAGCGGGGCGCGTTAGCTCGCGCTCTTCCTGACCCC   50
   1                                                                  0
1841 CAGCCAGTCCCGCTCTGACCCCGTCAGCATGCCAGGGTCATCCCCGTCCAGTCTCTGATCGAAGGGAGTTTCCACAGTGAT 1920
                                * * * *   **    *   *   *    * * *
  51 CGATCCTGGGGCCGAGGTACCTTTGACAGGAGCGTGACCCTGCTGGAGGTGTGCGGGAGCTGGCCTGAGGCTTCGGGCT  130
1921 TGATGCTG--CCTCAGGTACCTTTGACAGGAGCGTGACCCTGCTGGAGGTGTGCGGGAGCTGGCCTGAGGCTTCGGGCT 1998
   *** ***   *  ********************************************************************
 131 GCGGCACATGTCCTCCATGGAGCACACGGAGGAGGGCCTCCGGGAGCGACTTGCCGACGCCATGGCCGAGTCACCTAGCC  210
1999 GCGGCACATGTCCTCCATGGAGCACACGGAGGAGGGCTCCGGGAGCGACTTGCCGACGCCATGGCCGAGTCACCTAGCC 2078
     ********************************** ********************************************
 211 GGGACGTCGTGGGATCCGGAACAGAACTTCAGCGAGAGGGAAGCATCGAGACTCTGAGTAACAGCTCAGGCTCCACCAGC  290
2079 GG-ACGTCGTGGGATCCGGACAGGAAAAAAAAAAAAAAAAAGG     SEQ. ID NO:317                2124
     ********************  ***   *   *   **   *
 291 GGCAGCATACCAAGAAACTTTGATGGCTACCGATCTCCGCTGCCCACCAATGAGAGCCAGCCCCTCAGCCTCTTCCCGAC  370
2125                                                                               2124

 371 TGGCTTCCCGTAGGTACCAGCAACCTGCTTCTGACTGGCCAG 412    SEQ. ID NO:315
2125                                              2124
```

FIG. 1B

FIG. 2

```
1     CGAGAACTCTGAGTAACAGCTCAGGCTCCACCAGCGGCAGCATACCAAGAAACTTTGATGGCTACCGATCTCCGCTGCCC   80
1                                                                                        0

1                GCCAGCCCCTCAGCCTCTTCCCGACTGGCTTCCGTAGGTACCAGCAACCTGCTTCTGACTGGCCAGCCC   70
81    ACCAATGAGAGCCAGCCCCTCAGCCTCTTCCCGACTGGCTTCCGTAGGTACCAGCAACCTGCTTCTGACTGGCCAGCCC  160
      ************************************************************************

71    CCTCCCCCTGCTGGAGGAGGGGAGAAGCCCCGCTCTGGTCCTACCCTTCAGTCTCTGCTCTTCCTTCATCAACCACCTTCC  150
161   CCTCCCCCTGCTGGAGGAGGGGAGAAGCCCCGCTCTGGTCCTACCCTTCAGTCTCTGCTCTTCCTTCATCAACCACCTTCC  240
      ************************************************************************

151   CCAAGCTTAGTGACAGCAGCCGCCCATCCTACCTGGATGGAGAAGACCCTTCTCCAAGCACCTCAGCGCACTTGCCCCT  230
241   CCAAGCTTAGTGACAGCAGCCGCCCATCCTACCTGGATGGAGAAGACCCTTCTCCAAGCACCTCAGCGCACTTGCCCCT  320
      ************************************************************************

231   CTGCCACACCTGTCGGTGGAGGCTGTGGCCAGGAGAGACTGTAGAAGCTCGGTCCCTGTGTATGTTTGCA SEQ.ID NO:316  300
321   CTGCCACACCTGTCGGTGGAGGCTGTGGCCAGGAGAGACTGTAGAAGCTCGGTCCCTGTGTATGTTTGCATATGACATCC  400
      ************************************************************

301   TGCATTGGATCCGCTTTTGTATTTTTTAACCATACCCACGGTGGGGCGGGTGGGGCAGCCTGGAACAGTGACCAGATCT  480
401

301   GGGGGCCTGAGTGGGGACAGAGTTGATCGTCCACCTGGCCATTTTGACCCTGAGTGGACAGTCACAGCCTCAGCTCATGT  560
481

301   CTGGCTGTGACACACACTGCCCCCAGCTTCCCTTGGTCAGCCCCACTCCAGCACGGGGTGAACGGAGGCCCAGAGTACTA  640
561

301   GGGAAGGAGGAAGGGAGGACATGCCTCTCTTCTCCTCTTTCTTTCCCCATCTGTTCCTGGGAAGAGTTTGTCTTTCTTAT  720
641

301   CTTTAAGCCCCCTTTACCCTGGTCCTGTACTGATCAGTGAAGGAAACCGTGGTTACTGAGGCCCTGTTGAAAAGTGCACGT  800
721

301   CTTGTCCAATAAATCACGCTGCAGTTGGAAAAAAAAAAAAAAAAAAAAGGATCTTTAATTAAGCGGCCGCAAGCTTATT  880
801

301   CCCTTTAGTGAGGGTTAATTTTAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGTAAACCCTGGCGTTACCCA  960
881

301   ACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAAC 1040
961

301   AGTTGCGCAGCCTGAATGGCGAATGGGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAG 1120
1041

301   CGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCCACGTTCGCCGGC 1200
1121

301   TTTCCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAA 1280
1201

301   AACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCAC 1360
1281

301   GTTCT 1365    SEQ.ID NO:318
1361
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