FIG. 1A

```
         1                                                  50
  42_2   .......... .......... .......... .......... ..........
  42_8   .......... .......... .......... .......... ..........
 42_15   .......... .......... .......... .......... ..........
 42_5b   .......... .......... .......... .......... ..........
 42_1b   .......... .......... .......... .......... ..........
 42_13   .......... .......... .......... .......... ..........
 42_3a   .......... .......... .......... .......... ..........
  42_4   .......... .......... .......... .......... ..........
 42_5a   .......... .......... .......... .......... ..........
 42_10   .......... .......... .......... .......... ..........
 42_3b   .......... .......... .......... .......... ..........
 42_11   .......... .......... .......... .......... ..........
 42_6b   .......... .......... .......... .......... ..........
  43_1   .......... .......... .......... .......... ..........
  43_5   .......... .......... .......... .......... ..........
 43_12   .......... .......... .......... .......... ..........
 43_20   .......... .......... .......... .......... ..........
 43_21   .......... .......... .......... .......... ..........
 43_23   .......... .......... .......... .......... ..........
 43_25   .......... .......... .......... .......... ..........
  44_1   .......... .......... .......... .......... ..........
  44_5   .......... .......... .......... .......... ..........
223_10   .......... .......... .......... .......... ..........
 223_2   .......... .......... .......... .......... ..........
 223_4   .......... .......... .......... .......... ..........
 223_5   .......... .......... .......... .......... ..........
 223_6   .......... .......... .......... .......... ..........
 223_7   .......... .......... .......... .......... ..........
  A3_4   .......... .......... .......... .......... ..........
  A3_5   .......... .......... .......... .......... ..........
  A3_7   .......... .......... .......... .......... ..........
  A3_3   .......... .......... .......... .......... ..........
 42_12   .......... .......... .......... .......... ..........
  AAV1   TTGCCCACTC CCTCTCTGCG CGCTCGCTCG CTCGGTGGGG CCTGCGGACC
  AAV2   TTGGCCACTC CCTCTCTGCG CGCTCGCTCG CTCACTGAGG CCGGGCGACC
  AAV3   TTGGCCACTC CCTCTATGCG CACTCGCTCG CTCGGTGGGG CCTGGCGACC
  AAV8   .......... .......... .......... .......... ..........
  AAV9   .......... .......... .......... .......... ..........
  AAV7   TTGGCCACTC CCTCTATGCG CGCTCGCTCG CTCGGTGGGG CCTGCGGACC
  44_2   .......... .......... .......... .......... ..........
```

Fig. 1B

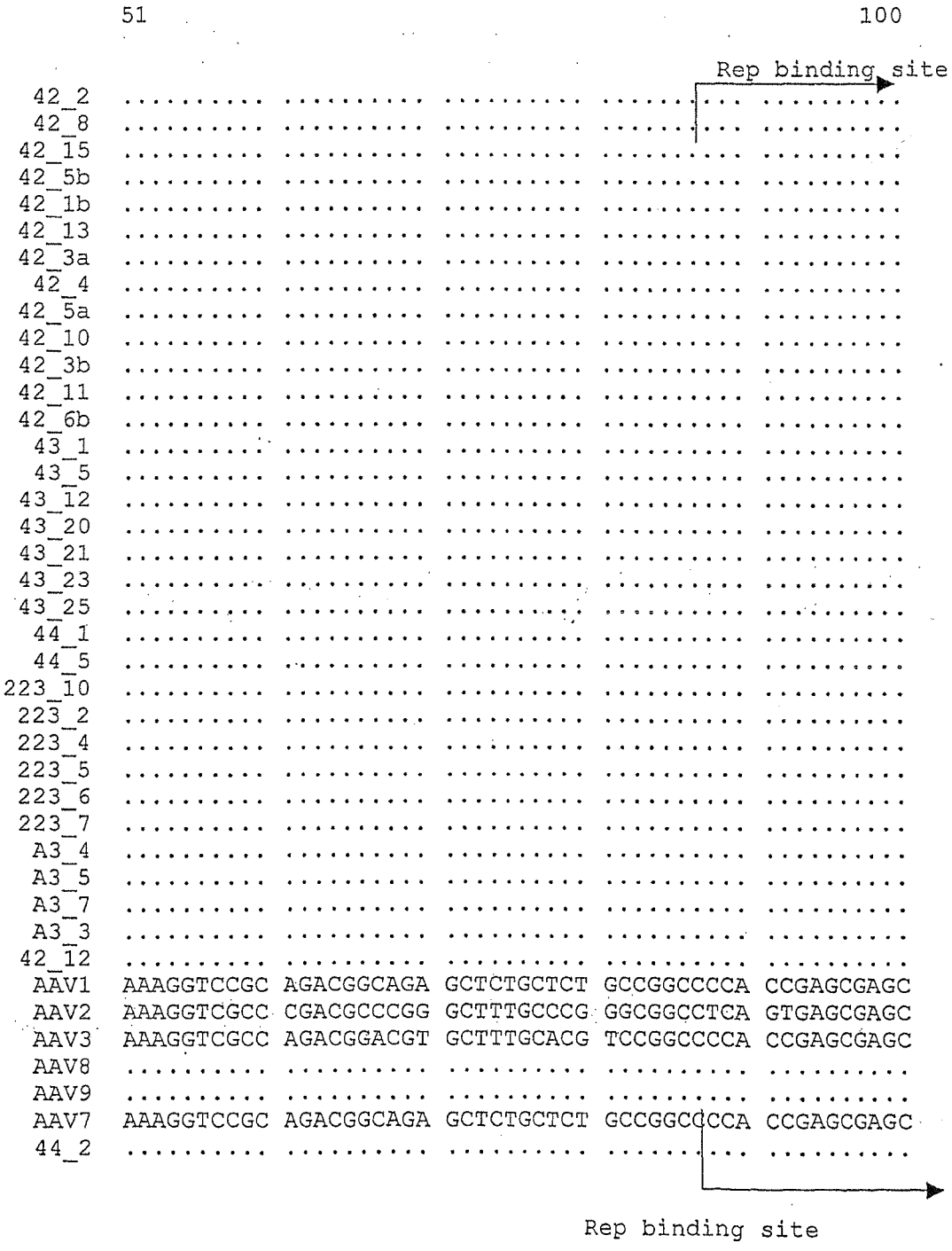

51
100
Rep binding site
42_2 ....
42_8 ....
42_15 ....
42_5b ....
42_1b ....
42_13 ....
42_3a ....
42_4 ....
42_5a ....
42_10 ....
42_3b ....
42_11 ....
42_6b ....
43_1 ....
43_5 ....
43_12 ....
43_20 ....
43_21 ....
43_23 ....
43_25 ....
44_1 ....
44_5 ....
223_10 ....
223_2 ....
223_4 ....
223_5 ....
223_6 ....
223_7 ....
A3_4 ....
A3_5 ....
A3_7 ....
A3_3 ....
42_12 ....
AAV1 AAAGGTCCGC AGACGGCAGA GCTCTGCTCT GCCGGCCCCA CCGAGCGAGC
AAV2 AAAGGTCGCC CGACGCCCGG GCTTTGCCCG GGCGGCCTCA GTGAGCGAGC
AAV3 AAAGGTCGCC AGACGGACGT GCTTTGCACG TCCGGCCCCA CCGAGCGAGC
AAV8 ....
AAV9 ....
AAV7 AAAGGTCCGC AGACGGCAGA GCTCTGCTCT GCCGGCCCCA CCGAGCGAGC
44_2 ....
Rep binding site

Fig. 1C

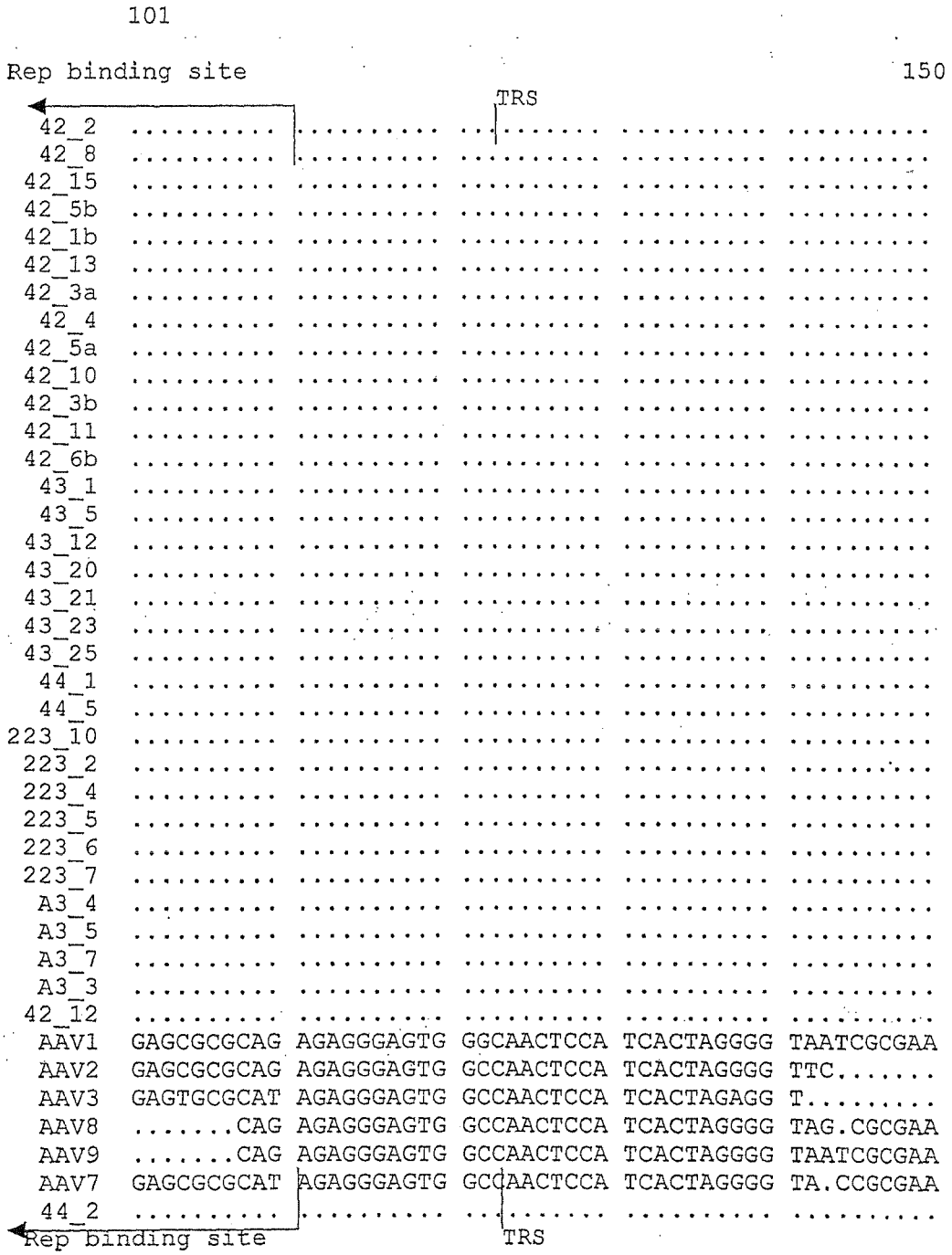

101
Rep binding site
150
TRS
42_2 ....
42_8 ....
42_15 ....
42_5b ....
42_1b ....
42_13 ....
42_3a ....
42_4 ....
42_5a ....
42_10 ....
42_3b ....
42_11 ....
42_6b ....
43_1 ....
43_5 ....
43_12 ....
43_20 ....
43_21 ....
43_23 ....
43_25 ....
44_1 ....
44_5 ....
223_10 ....
223_2 ....
223_4 ....
223_5 ....
223_6 ....
223_7 ....
A3_4 ....
A3_5 ....
A3_7 ....
A3_3 ....
42_12 ....
AAV1 GAGCGCGCAG AGAGGGAGTG GGCAACTCCA TCACTAGGGG TAATCGCGAA
AAV2 GAGCGCGCAG AGAGGGAGTG GCCAACTCCA TCACTAGGGG TTC.....
AAV3 GAGTGCGCAT AGAGGGAGTG GCCAACTCCA TCACTAGAGG T.....
AAV8 .....CAG AGAGGGAGTG GCCAACTCCA TCACTAGGGG TAG.CGCGAA
AAV9 .....CAG AGAGGGAGTG GCCAACTCCA TCACTAGGGG TAATCGCGAA
AAV7 GAGCGCGCAT AGAGGGAGTG GCCAACTCCA TCACTAGGGG TA.CCGCGAA
44_2 ....
Rep binding site
TRS

Fig. 1D

```
          151                                                  200
  42_2    .......... .......... .......... .......... ..........
  42_8    .......... .......... .......... .......... ..........
 42_15    .......... .......... .......... .......... ..........
 42_5b    .......... .......... .......... .......... ..........
 42_1b    .......... .......... .......... .......... ..........
 42_13    .......... .......... .......... .......... ..........
 42_3a    .......... .......... .......... .......... ..........
  42_4    .......... .......... .......... .......... ..........
 42_5a    .......... .......... .......... .......... ..........
 42_10    .......... .......... .......... .......... ..........
 42_3b    .......... .......... .......... .......... ..........
 42_11    .......... .......... .......... .......... ..........
 42_6b    .......... .......... .......... .......... ..........
  43_1    .......... .......... .......... .......... ..........
  43_5    .......... .......... .......... .......... ..........
 43_12    .......... .......... .......... .......... ..........
 43_20    .......... .......... .......... .......... ..........
 43_21    .......... .......... .......... .......... ..........
 43_23    .......... .......... .......... .......... ..........
 43_25    .......... .......... .......... .......... ..........
  44_1    .......... .......... .......... .......... ..........
  44_5    .......... .......... .......... .......... ..........
223_10    .......... .......... .......... .......... ..........
 223_2    .......... .......... .......... .......... ..........
 223_4    .......... .......... .......... .......... ..........
 223_5    .......... .......... .......... .......... ..........
 223_6    .......... .......... .......... .......... ..........
 223_7    .......... .......... .......... .......... ..........
  A3_4    .......... .......... .......... .......... ..........
  A3_5    .......... .......... .......... .......... ..........
  A3_7    .......... .......... .......... .......... ..........
  A3_3    .......... .......... .......... .......... ..........
 42_12    .......... .......... .......... .......... ..........
  AAV1    GCGCCTCCCA CGCTGCCGCG TCAGCGCTGA CGTAAATTAC GTCATAGGGG
  AAV2    .......CTG GAGGGGTGGA GTCGTGACGT GAATTACGTC ATAGGGTTAG
  AAV3    .......ATG GCAGTGACGT AACGCGAAGC GCGCGAAGCG AGACCACGCC
  AAV8    GCGCCTCCCA CGCTGCCGCG TCAGCGCTGA CGTAAATTAC GTCATAGGGG
  AAV9    GCGCCTCCCA CGCTGCCGCG TCAGCGCTGA CGTAGATTAC GTCATAGGGG
  AAV7    GCGCCTCCCA CGCTGCCGCG TCAGCGCTGA CGTAAATCAC GTCATAGGGG
  44_2    .......... .......... .......... .......... ..........
```

Fig. 1E

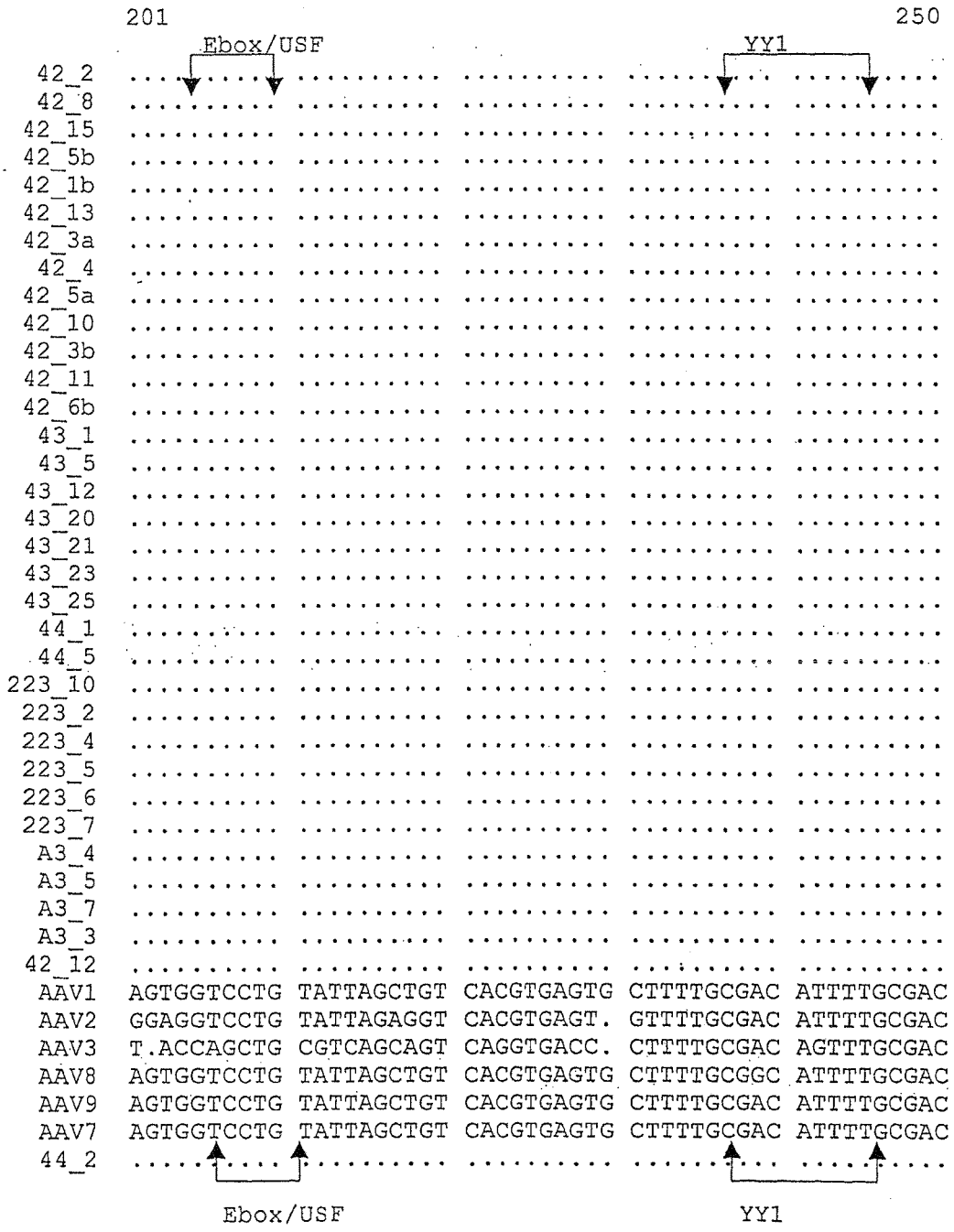

201
250
Ebox/USF
YY1
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 AGTGGTCCTG TATTAGCTGT CACGTGAGTG CTTTTGCGAC ATTTTGCGAC
AAV2 GGAGGTCCTG TATTAGAGGT CACGTGAGT. GTTTTGCGAC ATTTTGCGAC
AAV3 T.ACCAGCTG CGTCAGCAGT CAGGTGACC. CTTTTGCGAC AGTTTGCGAC
AAV8 AGTGGTCCTG TATTAGCTGT CACGTGAGTG CTTTTGCGGC ATTTTGCGAC
AAV9 AGTGGTCCTG TATTAGCTGT CACGTGAGTG CTTTTGCGAC ATTTTGCGAC
AAV7 AGTGGTCCTG TATTAGCTGT CACGTGAGTG CTTTTGCGAC ATTTTGCGAC
44_2
Ebox/USF
YY1

Fig. 1F

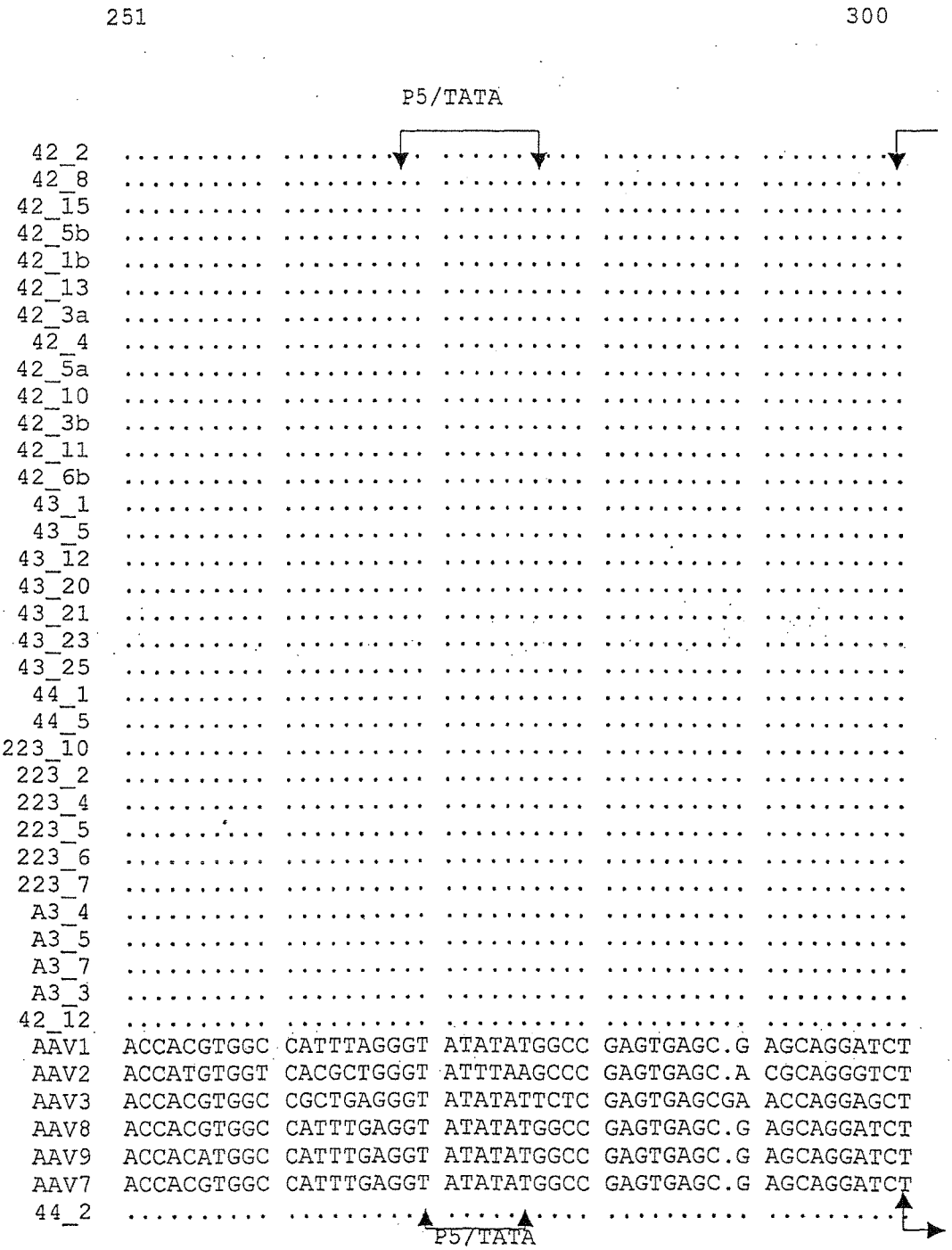

251
300
P5/TATA
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 ACCACGTGGC CATTTAGGGT ATATATGGCC GAGTGAGC.G AGCAGGATCT
AAV2 ACCATGTGGT CACGCTGGGT ATTTAAGCCC GAGTGAGC.A CGCAGGGTCT
AAV3 ACCACGTGGC CGCTGAGGGT ATATATTCTC GAGTGAGCGA ACCAGGAGCT
AAV8 ACCACGTGGC CATTTGAGGT ATATATGGCC GAGTGAGC.G AGCAGGATCT
AAV9 ACCACATGGC CATTTGAGGT ATATATGGCC GAGTGAGC.G AGCAGGATCT
AAV7 ACCACGTGGC CATTTGAGGT ATATATGGCC GAGTGAGC.G AGCAGGATCT
44_2
P5/TATA

Fig. 1G

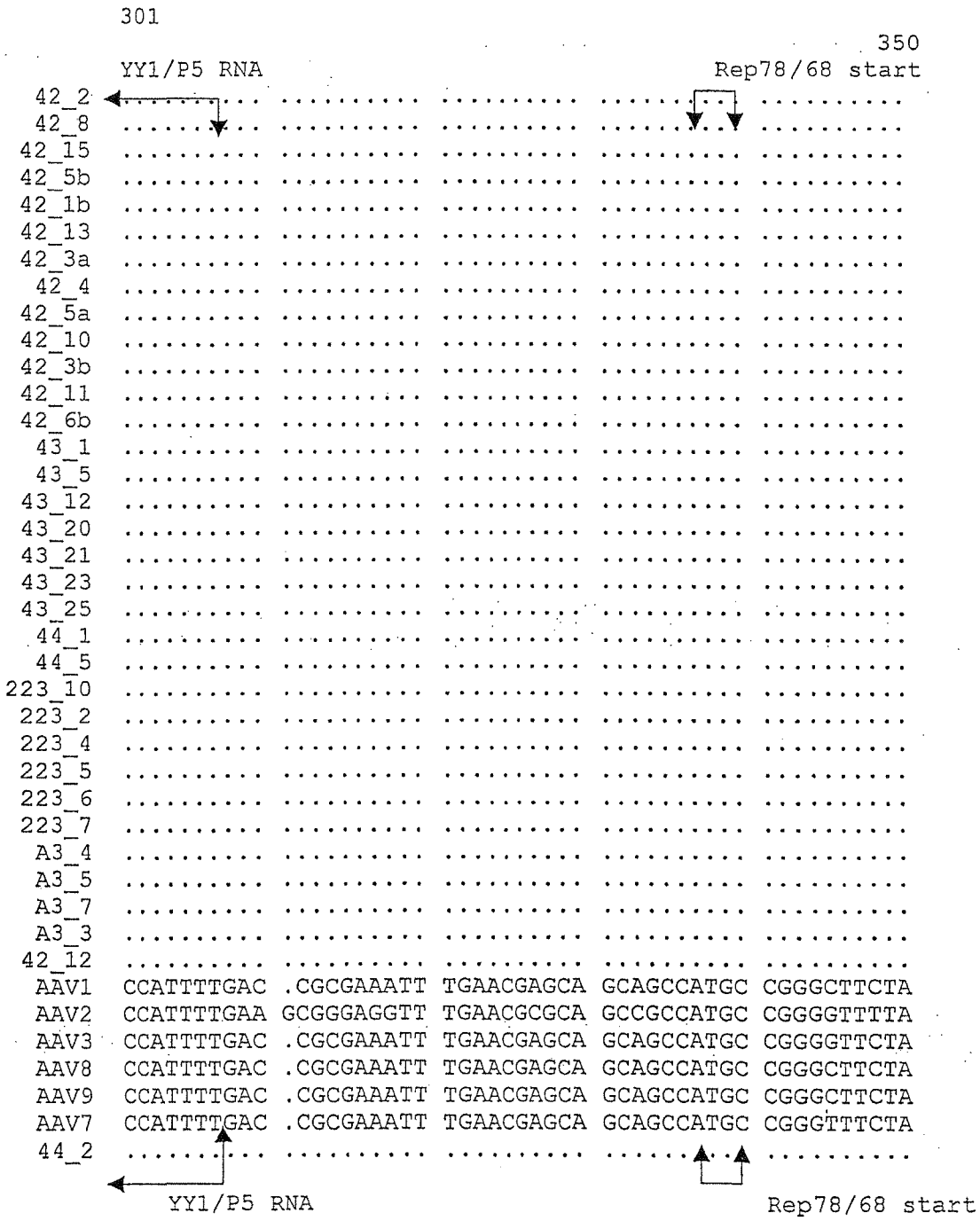

301
350
YY1/P5 RNA
Rep78/68 start
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 CCATTTTGAC .CGCGAAATT TGAACGAGCA GCAGCCATGC CGGGCTTCTA
AAV2 CCATTTTGAA GCGGGAGGTT TGAACGCGCA GCCGCCATGC CGGGGTTTTA
AAV3 CCATTTTGAC .CGCGAAATT TGAACGAGCA GCAGCCATGC CGGGGTTCTA
AAV8 CCATTTTGAC .CGCGAAATT TGAACGAGCA GCAGCCATGC CGGGCTTCTA
AAV9 CCATTTTGAC .CGCGAAATT TGAACGAGCA GCAGCCATGC CGGGCTTCTA
AAV7 CCATTTTGAC .CGCGAAATT TGAACGAGCA GCAGCCATGC CGGGTTTCTA
44_2
YY1/P5 RNA
Rep78/68 start

Fig. 1H

```
        351                                                  400
  42_2  .......... .......... .......... .......... ..........
  42_8  .......... .......... .......... .......... ..........
 42_15  .......... .......... .......... .......... ..........
 42_5b  .......... .......... .......... .......... ..........
 42_1b  .......... .......... .......... .......... ..........
 42_13  .......... .......... .......... .......... ..........
 42_3a  .......... .......... .......... .......... ..........
  42_4  .......... .......... .......... .......... ..........
 42_5a  .......... .......... .......... .......... ..........
 42_10  .......... .......... .......... .......... ..........
 42_3b  .......... .......... .......... .......... ..........
 42_11  .......... .......... .......... .......... ..........
 42_6b  .......... .......... .......... .......... ..........
  43_1  .......... .......... .......... .......... ..........
  43_5  .......... .......... .......... .......... ..........
 43_12  .......... .......... .......... .......... ..........
 43_20  .......... .......... .......... .......... ..........
 43_21  .......... .......... .......... .......... ..........
 43_23  .......... .......... .......... .......... ..........
 43_25  .......... .......... .......... .......... ..........
  44_1  .......... .......... .......... .......... ..........
  44_5  .......... .......... .......... .......... ..........
223_10  .......... .......... .......... .......... ..........
 223_2  .......... .......... .......... .......... ..........
 223_4  .......... .......... .......... .......... ..........
 223_5  .......... .......... .......... .......... ..........
 223_6  .......... .......... .......... .......... ..........
 223_7  .......... .......... .......... .......... ..........
  A3_4  .......... .......... .......... .......... ..........
  A3_5  .......... .......... .......... .......... ..........
  A3_7  .......... .......... .......... .......... ..........
  A3_3  .......... .......... .......... .......... ..........
 42_12  .......... .......... .......... .......... ..........
  AAV1  CGAGATCGTG ATCAAGGTGC CGAGCGACCT GGACGAGCAC CTGCCGGGCA
  AAV2  CGAGATTGTG ATTAAGGTCC CCAGCGACCT TGACGGGCAT CTGCCCGGCA
  AAV3  CGAGATTGTC CTGAAGGTCC CGAGTGACCT GGACGAGCGC CTGCCGGGCA
  AAV8  CGAGATCGTG ATCAAGGTGC CGAGCGACCT GGACGAGCAC CTGCCGGGCA
  AAV9  CGAGATTGTG ATCAAGGTGC CGAGCGACCT GGACGAGCAC CTGCCGGGCA
  AAV7  CGAGATCGTG ATCAAGGTGC CGAGCGACCT GGACGAGCAC CTGCCGGGCA
  44_2  .......... .......... .......... .......... ..........
```

Fig. 1I

```
          401                                                  450
  42_2    .......... .......... .......... .......... ..........
  42_8    .......... .......... .......... .......... ..........
 42_15    .......... .......... .......... .......... ..........
 42_5b    .......... .......... .......... .......... ..........
 42_1b    .......... .......... .......... .......... ..........
 42_13    .......... .......... .......... .......... ..........
 42_3a    .......... .......... .......... .......... ..........
  42_4    .......... .......... .......... .......... ..........
 42_5a    .......... .......... .......... .......... ..........
 42_10    .......... .......... .......... .......... ..........
 42_3b    .......... .......... .......... .......... ..........
 42_11    .......... .......... .......... .......... ..........
 42_6b    .......... .......... .......... .......... ..........
  43_1    .......... .......... .......... .......... ..........
  43_5    .......... .......... .......... .......... ..........
 43_12    .......... .......... .......... .......... ..........
 43_20    .......... .......... .......... .......... ..........
 43_21    .......... .......... .......... .......... ..........
 43_23    .......... .......... .......... .......... ..........
 43_25    .......... .......... .......... .......... ..........
  44_1    .......... .......... .......... .......... ..........
  44_5    .......... .......... .......... .......... ..........
223_10    .......... .......... .......... .......... ..........
 223_2    .......... .......... .......... .......... ..........
 223_4    .......... .......... .......... .......... ..........
 223_5    .......... .......... .......... .......... ..........
 223_6    .......... .......... .......... .......... ..........
 223_7    .......... .......... .......... .......... ..........
  A3_4    .......... .......... .......... .......... ..........
  A3_5    .......... .......... .......... .......... ..........
  A3_7    .......... .......... .......... .......... ..........
  A3_3    .......... .......... .......... .......... ..........
 42_12    .......... .......... .......... .......... ..........
  AAV1    TTTCTGACTC GTTTGTGAGC TGGGTGGCCG AGAAGGAATG GGAGCTGCCC
  AAV2    TTTCTGACAG CTTTGTGAAC TGGGTGGCCG AGAAGGAATG GGAGTTGCCG
  AAV3    TTTCTAACTC GTTTGTTAAC TGGGTGGCCG AGAAGGAATG GGACGTGCCG
  AAV8    TTTCTGACTC GTTTGTGAAC TGGGTGGCCG AGAAGGAATG GGAGCTGCCC
  AAV9    TTTCTGACTC TTTTGTGAAC TGGGTGGCCG AGAAGGAATG GGAGCTGCCC
  AAV7    TTTCTGACTC GTTTGTGAAC TGGGTGGCCG AGAAGGAATG GGAGCTGCCC
  44_2    .......... .......... .......... .......... ..........
```

Fig. 1J

```
          451                                                  500
   42_2   .......... .......... .......... .......... ..........
   42_8   .......... .......... .......... .......... ..........
  42_15   .......... .......... .......... .......... ..........
  42_5b   .......... .......... .......... .......... ..........
  42_1b   .......... .......... .......... .......... ..........
  42_13   .......... .......... .......... .......... ..........
  42_3a   .......... .......... .......... .......... ..........
   42_4   .......... .......... .......... .......... ..........
  42_5a   .......... .......... .......... .......... ..........
  42_10   .......... .......... .......... .......... ..........
  42_3b   .......... .......... .......... .......... ..........
  42_11   .......... .......... .......... .......... ..........
  42_6b   .......... .......... .......... .......... ..........
   43_1   .......... .......... .......... .......... ..........
   43_5   .......... .......... .......... .......... ..........
  43_12   .......... .......... .......... .......... ..........
  43_20   .......... .......... .......... .......... ..........
  43_21   .......... .......... .......... .......... ..........
  43_23   .......... .......... .......... .......... ..........
  43_25   .......... .......... .......... .......... ..........
   44_1   .......... .......... .......... .......... ..........
   44_5   .......... .......... .......... .......... ..........
 223_10   .......... .......... .......... .......... ..........
  223_2   .......... .......... .......... .......... ..........
  223_4   .......... .......... .......... .......... ..........
  223_5   .......... .......... .......... .......... ..........
  223_6   .......... .......... .......... .......... ..........
  223_7   .......... .......... .......... .......... ..........
   A3_4   .......... .......... .......... .......... ..........
   A3_5   .......... .......... .......... .......... ..........
   A3_7   .......... .......... .......... .......... ..........
   A3_3   .......... .......... .......... .......... ..........
  42_12   .......... .......... .......... .......... ..........
   AAV1   CCGGATTCTG ACATGGATCT GAATCTGATT GAGCAGGCAC CCCTGACCGT
   AAV2   CCAGATTCTG ACATGGATCT GAATCTGATT GAGCAGGCAC CCCTGACCGT
   AAV3   CCGGATTCTG ACATGGATCC GAATCTGATT GAGCAGGCAC CCCTGACCGT
   AAV8   CCGGATTCTG ACATGGATCG GAATCTGATC GAGCAGGCAC CCCTGACCGT
   AAV9   CCGGATTCTG ACATGGATCG GAATCTGATC GAGCAGGCAC CCCTGACCGT
   AAV7   CCGGATTCTG ACATGGATCT GAATCTGATC GAGCAGGCAC CCCTGACCGT
   44_2   .......... .......... .......... .......... ..........
```

Fig. 1K

```
          501                                                       550
  42_2    .......... .......... .......... .......... ..........
  42_8    .......... .......... .......... .......... ..........
 42_15    .......... .......... .......... .......... ..........
 42_5b    .......... .......... .......... .......... ..........
 42_1b    .......... .......... .......... .......... ..........
 42_13    .......... .......... .......... .......... ..........
 42_3a    .......... .......... .......... .......... ..........
  42_4    .......... .......... .......... .......... ..........
 42_5a    .......... .......... .......... .......... ..........
 42_10    .......... .......... .......... .......... ..........
 42_3b    .......... .......... .......... .......... ..........
 42_11    .......... .......... .......... .......... ..........
 42_6b    .......... .......... .......... .......... ..........
  43_1    .......... .......... .......... .......... ..........
  43_5    .......... .......... .......... .......... ..........
 43_12    .......... .......... .......... .......... ..........
 43_20    .......... .......... .......... .......... ..........
 43_21    .......... .......... .......... .......... ..........
 43_23    .......... .......... .......... .......... ..........
 43_25    .......... .......... .......... .......... ..........
  44_1    .......... .......... .......... .......... ..........
  44_5    .......... .......... .......... .......... ..........
223_10    .......... .......... .......... .......... ..........
 223_2    .......... .......... .......... .......... ..........
 223_4    .......... .......... .......... .......... ..........
 223_5    .......... .......... .......... .......... ..........
 223_6    .......... .......... .......... .......... ..........
 223_7    .......... .......... .......... .......... ..........
  A3_4    .......... .......... .......... .......... ..........
  A3_5    .......... .......... .......... .......... ..........
  A3_7    .......... .......... .......... .......... ..........
  A3_3    .......... .......... .......... .......... ..........
 42_12    .......... .......... .......... .......... ..........
  AAV1    GGCCGAGAAG CTGCAGCGCG ACTTCCTGGT CCAATGGCGC CGCGTGAGTA
  AAV2    GGCCGAGAAG CTGCAGCGCG ACTTTCTGAC GGAATGGCGC CGTGTGAGTA
  AAV3    GGCCGAAAAG CTTCAGCGCG AGTTCCTGGT GGAGTGGCGC CGCGTGAGTA
  AAV8    GGCCGAGAAG CTGCAGCGCG ACTTCCTGGT CCAATGGCGC CGCGTGAGTA
  AAV9    GGCCGAGAAG CTGTAGCGCG ACTTCCTGGT CCAATGGCGC CGCGTGAGTA
  AAV7    GGCCGAGAAG CTGCAGCGCG ACTTCCTGGT CCAATGGCGC CGCGTGAGTA
  44_2    .......... .......... .......... .......... ..........
```

Fig. 1L

```
          551                                                  600
   42_2   .......... .......... .......... .......... ..........
   42_8   .......... .......... .......... .......... ..........
  42_15   .......... .......... .......... .......... ..........
  42_5b   .......... .......... .......... .......... ..........
  42_1b   .......... .......... .......... .......... ..........
  42_13   .......... .......... .......... .......... ..........
  42_3a   .......... .......... .......... .......... ..........
   42_4   .......... .......... .......... .......... ..........
  42_5a   .......... .......... .......... .......... ..........
  42_10   .......... .......... .......... .......... ..........
  42_3b   .......... .......... .......... .......... ..........
  42_11   .......... .......... .......... .......... ..........
  42_6b   .......... .......... .......... .......... ..........
   43_1   .......... .......... .......... .......... ..........
   43_5   .......... .......... .......... .......... ..........
  43_12   .......... .......... .......... .......... ..........
  43_20   .......... .......... .......... .......... ..........
  43_21   .......... .......... .......... .......... ..........
  43_23   .......... .......... .......... .......... ..........
  43_25   .......... .......... .......... .......... ..........
   44_1   .......... .......... .......... .......... ..........
   44_5   .......... .......... .......... .......... ..........
 223_10   .......... .......... .......... .......... ..........
  223_2   .......... .......... .......... .......... ..........
  223_4   .......... .......... .......... .......... ..........
  223_5   .......... .......... .......... .......... ..........
  223_6   .......... .......... .......... .......... ..........
  223_7   .......... .......... .......... .......... ..........
   A3_4   .......... .......... .......... .......... ..........
   A3_5   .......... .......... .......... .......... ..........
   A3_7   .......... .......... .......... .......... ..........
   A3_3   .......... .......... .......... .......... ..........
  42_12   .......... .......... .......... .......... ..........
   AAV1   AGGCCCCGGA GGCCCTCTTC TTTGTTCAGT TCGAGAAGGG CGAGTCCTAC
   AAV2   AGGCCCCGGA GGCCCTTTTC TTTGTGCAAT TTGAGAAGGG AGAGAGCTAC
   AAV3   AGGCCCCGGA GGCCCTCTTT TTTGTCCAGT TCGAAAAGGG GGAGACCTAC
   AAV8   AGGCCCCGGA GGCCCTCTTC TTTGTTCAGT TCGAGAAGGG CGAGAGCTAC
   AAV9   AGGCCCCGGA GGCCCTCTTC TTTGTTCAGT TCGAGAAGGG CGAGAGCTAC
   AAV7   AGGCCCCGGA GGCCCTGTTC TTTGTTCAGT TCGAGAAGGG CGAGAGCTAC
   44_2   .......... .......... .......... .......... ..........
```

Fig. 1M

```
          601                                                       650
  42_2    .......... .......... .......... .......... ..........
  42_8    .......... .......... .......... .......... ..........
 42_15    .......... .......... .......... .......... ..........
 42_5b    .......... .......... .......... .......... ..........
 42_1b    .......... .......... .......... .......... ..........
 42_13    .......... .......... .......... .......... ..........
 42_3a    .......... .......... .......... .......... ..........
  42_4    .......... .......... .......... .......... ..........
 42_5a    .......... .......... .......... .......... ..........
 42_10    .......... .......... .......... .......... ..........
 42_3b    .......... .......... .......... .......... ..........
 42_11    .......... .......... .......... .......... ..........
 42_6b    .......... .......... .......... .......... ..........
  43_1    .......... .......... .......... .......... ..........
  43_5    .......... .......... .......... .......... ..........
 43_12    .......... .......... .......... .......... ..........
 43_20    .......... .......... .......... .......... ..........
 43_21    .......... .......... .......... .......... ..........
 43_23    .......... .......... .......... .......... ..........
 43_25    .......... .......... .......... .......... ..........
  44_1    .......... .......... .......... .......... ..........
  44_5    .......... .......... .......... .......... ..........
223_10    .......... .......... .......... .......... ..........
 223_2    .......... .......... .......... .......... ..........
 223_4    .......... .......... .......... .......... ..........
 223_5    .......... .......... .......... .......... ..........
 223_6    .......... .......... .......... .......... ..........
 223_7    .......... .......... .......... .......... ..........
  A3_4    .......... .......... .......... .......... ..........
  A3_5    .......... .......... .......... .......... ..........
  A3_7    .......... .......... .......... .......... ..........
  A3_3    .......... .......... .......... .......... ..........
 42_12    .......... .......... .......... .......... ..........
  AAV1    TTCCACCTCC ATATTCTGGT GGAGACCACG GGGGTCAAAT CCATGGTGCT
  AAV2    TTCCACATGC ACGTGCTCGT GGAAACCACC GGGGTGAAAT CCATGGTTTT
  AAV3    TTCCACCTGC ACGTGCTGAT TGAGACCATC GGGGTCAAAT CCATGGTGGT
  AAV8    TTTCACCTGC ACGTTCTGGT CGAGACCACG GGGGTCAAGT CCATGGTGCT
  AAV9    TTTCACCTGC ACGTTCTGGT CGAGACCACG GGGGTCAAGT CCATGGTGCT
  AAV7    TTCCACCTTC ACGTTCTGGT GGAGACCACG GGGGTCAAGT CCATGGTGCT
  44_2    .......... .......... .......... .......... ..........
```

Fig. 1N

```
        651                                                  700
  42_2  .......... .......... .......... .......... ..........
  42_8  .......... .......... .......... .......... ..........
 42_15  .......... .......... .......... .......... ..........
 42_5b  .......... .......... .......... .......... ..........
 42_1b  .......... .......... .......... .......... ..........
 42_13  .......... .......... .......... .......... ..........
 42_3a  .......... .......... .......... .......... ..........
  42_4  .......... .......... .......... .......... ..........
 42_5a  .......... .......... .......... .......... ..........
 42_10  .......... .......... .......... .......... ..........
 42_3b  .......... .......... .......... .......... ..........
 42_11  .......... .......... .......... .......... ..........
 42_6b  .......... .......... .......... .......... ..........
  43_1  .......... .......... .......... .......... ..........
  43_5  .......... .......... .......... .......... ..........
 43_12  .......... .......... .......... .......... ..........
 43_20  .......... .......... .......... .......... ..........
 43_21  .......... .......... .......... .......... ..........
 43_23  .......... .......... .......... .......... ..........
 43_25  .......... .......... .......... .......... ..........
  44_1  .......... .......... .......... .......... ..........
  44_5  .......... .......... .......... .......... ..........
223_10  .......... .......... .......... .......... ..........
 223_2  .......... .......... .......... .......... ..........
 223_4  .......... .......... .......... .......... ..........
 223_5  .......... .......... .......... .......... ..........
 223_6  .......... .......... .......... .......... ..........
 223_7  .......... .......... .......... .......... ..........
  A3_4  .......... .......... .......... .......... ..........
  A3_5  .......... .......... .......... .......... ..........
  A3_7  .......... .......... .......... .......... ..........
  A3_3  .......... .......... .......... .......... ..........
 42_12  .......... .......... .......... .......... ..........
  AAV1  GGGCCGCTTC CTGAGTCAGA TTAGGGACAA GCT.GGTGCA GACCATCTAC
  AAV2  GGGACGTTTC CTGAGTCAGA TTCGCGAAAA ACT..GATTC AGAGAATTTA
  AAV3  CGGCCGCTAC GTGAGCCAGA TTAAAGAGAA GCT..GGTGA CCCGCATCTA
  AAV8  AGGCCGCTTC CTGAGTCAGA TTCGGGAAAA GCTTGGTCCA GACCATCTAC
  AAV9  AGGCCGCTTC CTGAGTCAGA TTCGGGAGAA GCT.GGTCCA GACCATCTAC
  AAV7  AGGCCGCTTC CTGAGTCAGA TTCGGGAGAA GCT....G.. GTCCAGACCA
  44_2  .......... .......... .......... .......... ..........
```

Fig. 10

```
          701                                                  750
  42_2    .......... .......... .......... .......... ..........
  42_8    .......... .......... .......... .......... ..........
 42_15    .......... .......... .......... .......... ..........
 42_5b    .......... .......... .......... .......... ..........
 42_1b    .......... .......... .......... .......... ..........
 42_13    .......... .......... .......... .......... ..........
 42_3a    .......... .......... .......... .......... ..........
  42_4    .......... .......... .......... .......... ..........
 42_5a    .......... .......... .......... .......... ..........
 42_10    .......... .......... .......... .......... ..........
 42_3b    .......... .......... .......... .......... ..........
 42_11    .......... .......... .......... .......... ..........
 42_6b    .......... .......... .......... .......... ..........
  43_1    .......... .......... .......... .......... ..........
  43_5    .......... .......... .......... .......... ..........
 43_12    .......... .......... .......... .......... ..........
 43_20    .......... .......... .......... .......... ..........
 43_21    .......... .......... .......... .......... ..........
 43_23    .......... .......... .......... .......... ..........
 43_25    .......... .......... .......... .......... ..........
  44_1    .......... .......... .......... .......... ..........
  44_5    .......... .......... .......... .......... ..........
223_10    .......... .......... .......... .......... ..........
 223_2    .......... .......... .......... .......... ..........
 223_4    .......... .......... .......... .......... ..........
 223_5    .......... .......... .......... .......... ..........
 223_6    .......... .......... .......... .......... ..........
 223_7    .......... .......... .......... .......... ..........
  A3_4    .......... .......... .......... .......... ..........
  A3_5    .......... .......... .......... .......... ..........
  A3_7    .......... .......... .......... .......... ..........
  A3_3    .......... .......... .......... .......... ..........
 42_12    .......... .......... .......... .......... ..........
  AAV1    C.GCGGGATC GAGCCG.ACC CTGCCCAACT GGTTCGCGGT GACCAA.GAC
  AAV2    CCGCGGGATC GAGCCG.ACT TTGCCAAACT GGTTCGCGGT CACAAA...G
  AAV3    CCGCGGGGTC GAGCCG.CAG CTTCCGAACT GGTTCGCGGT GACCAA...A
  AAV8    CCGCGGGGTC GAGCCCCACC TTGCCCAACT GGTTCGCGGT GACCAAAGAC
  AAV9    C.GCGGGATC GAGCCG.ACC CTGCCCAACT GGTTCGCGGT GACCAA.GAC
  AAV7    TCTACCGCGG GGTCGAGCCC ACGCTGCCCA ACTGGTTCGC GGTGACCAAG
  44_2    .......... .......... .......... .......... ..........
```

Fig. 1P

```
          751                                                       800
  42_2    .......... .......... .......... .......... ..........
  42_8    .......... .......... .......... .......... ..........
 42_15    .......... .......... .......... .......... ..........
 42_5b    .......... .......... .......... .......... ..........
 42_1b    .......... .......... .......... .......... ..........
 42_13    .......... .......... .......... .......... ..........
 42_3a    .......... .......... .......... .......... ..........
  42_4    .......... .......... .......... .......... ..........
 42_5a    .......... .......... .......... .......... ..........
 42_10    .......... .......... .......... .......... ..........
 42_3b    .......... .......... .......... .......... ..........
 42_11    .......... .......... .......... .......... ..........
 42_6b    .......... .......... .......... .......... ..........
  43_1    .......... .......... .......... .......... ..........
  43_5    .......... .......... .......... .......... ..........
 43_12    .......... .......... .......... .......... ..........
 43_20    .......... .......... .......... .......... ..........
 43_21    .......... .......... .......... .......... ..........
 43_23    .......... .......... .......... .......... ..........
 43_25    .......... .......... .......... .......... ..........
  44_1    .......... .......... .......... .......... ..........
  44_5    .......... .......... .......... .......... ..........
223_10    .......... .......... .......... .......... ..........
223_2     .......... .......... .......... .......... ..........
223_4     .......... .......... .......... .......... ..........
223_5     .......... .......... .......... .......... ..........
223_6     .......... .......... .......... .......... ..........
223_7     .......... .......... .......... .......... ..........
 A3_4     .......... .......... .......... .......... ..........
 A3_5     .......... .......... .......... .......... ..........
 A3_7     .......... .......... .......... .......... ..........
 A3_3     .......... .......... .......... .......... ..........
42_12     .......... .......... .......... .......... ..........
 AAV1     GCG.TAATGG CGCCGGAGGG GGG.AACAAG GTGGTGGACG AGTGCTACAT
 AAV2     ACCAGAAATG GCGCCGGAGG CGGGAACAAG GTGGTGGATG AGTGCTACAT
 AAV3     ACGCGAAATG GCGCCGGGGG CGGGAACAAG GTGGTGGACG ACTGCTACAT
 AAV8     GCGGTAATGG CGCCGGCGGG GGGGAACAAG GTGGTGGACG AGTGCTACAT
 AAV9     GCG.TAATGG CGCCGGCGGG GGG.AACAAG GTGGTGGACG AGTGCTACAT
 AAV7     ACGCGTAATG GCGCCGGCGG GGGGAACAAG GTGGTGGACG AGTGCTACAT
 44_2     .......... .......... .......... .......... ..........
```

Fig. 1Q

```
         801                                                       850
 42_2    .......... .......... .......... .......... ..........
 42_8    .......... .......... .......... .......... ..........
42_15    .......... .......... .......... .......... ..........
42_5b    .......... .......... .......... .......... ..........
42_1b    .......... .......... .......... .......... ..........
42_13    .......... .......... .......... .......... ..........
42_3a    .......... .......... .......... .......... ..........
 42_4    .......... .......... .......... .......... ..........
42_5a    .......... .......... .......... .......... ..........
42_10    .......... .......... .......... .......... ..........
42_3b    .......... .......... .......... .......... ..........
42_11    .......... .......... .......... .......... ..........
42_6b    .......... .......... .......... .......... ..........
 43_1    .......... .......... .......... .......... ..........
 43_5    .......... .......... .......... .......... ..........
43_12    .......... .......... .......... .......... ..........
43_20    .......... .......... .......... .......... ..........
43_21    .......... .......... .......... .......... ..........
43_23    .......... .......... .......... .......... ..........
43_25    .......... .......... .......... .......... ..........
 44_1    .......... .......... .......... .......... ..........
 44_5    .......... .......... .......... .......... ..........
223_10   .......... .......... .......... .......... ..........
223_2    .......... .......... .......... .......... ..........
223_4    .......... .......... .......... .......... ..........
223_5    .......... .......... .......... .......... ..........
223_6    .......... .......... .......... .......... ..........
223_7    .......... .......... .......... .......... ..........
 A3_4    .......... .......... .......... .......... ..........
 A3_5    .......... .......... .......... .......... ..........
 A3_7    .......... .......... .......... .......... ..........
 A3_3    .......... .......... .......... .......... ..........
42_12    .......... .......... .......... .......... ..........
 AAV1    CCCCAACTAC CTCCTGCCCA AGACTCAGCC CGAGCTGCAG TGGGCGTGGA
 AAV2    CCCCAATTAC TTGCTCCCCA AAACCCAGCC TGAGCTCCAG TGGGCGTGGA
 AAV3    CCCCAACTAC CTGCTCCCCA AGACCCAGCC CGAGCTCCAG TGGGCGTGGA
 AAV8    CCCCAACTAC CTCCTGCCCA AGACTCAGCC CGAGCTGCAG TGGGCGTGGA
 AAV9    CCCCAACTAC CTCCTGCCCA AGACTCAGCC CGAGCTGCAG TGGGCGTGGA
 AAV7    CCCCAACTAC CTCCTGCCCA AGACCCAGCC CGAGCTGCAG TGGGCGTGGA
 44_2    .......... .......... .......... .......... ..........
```

Fig. 1R

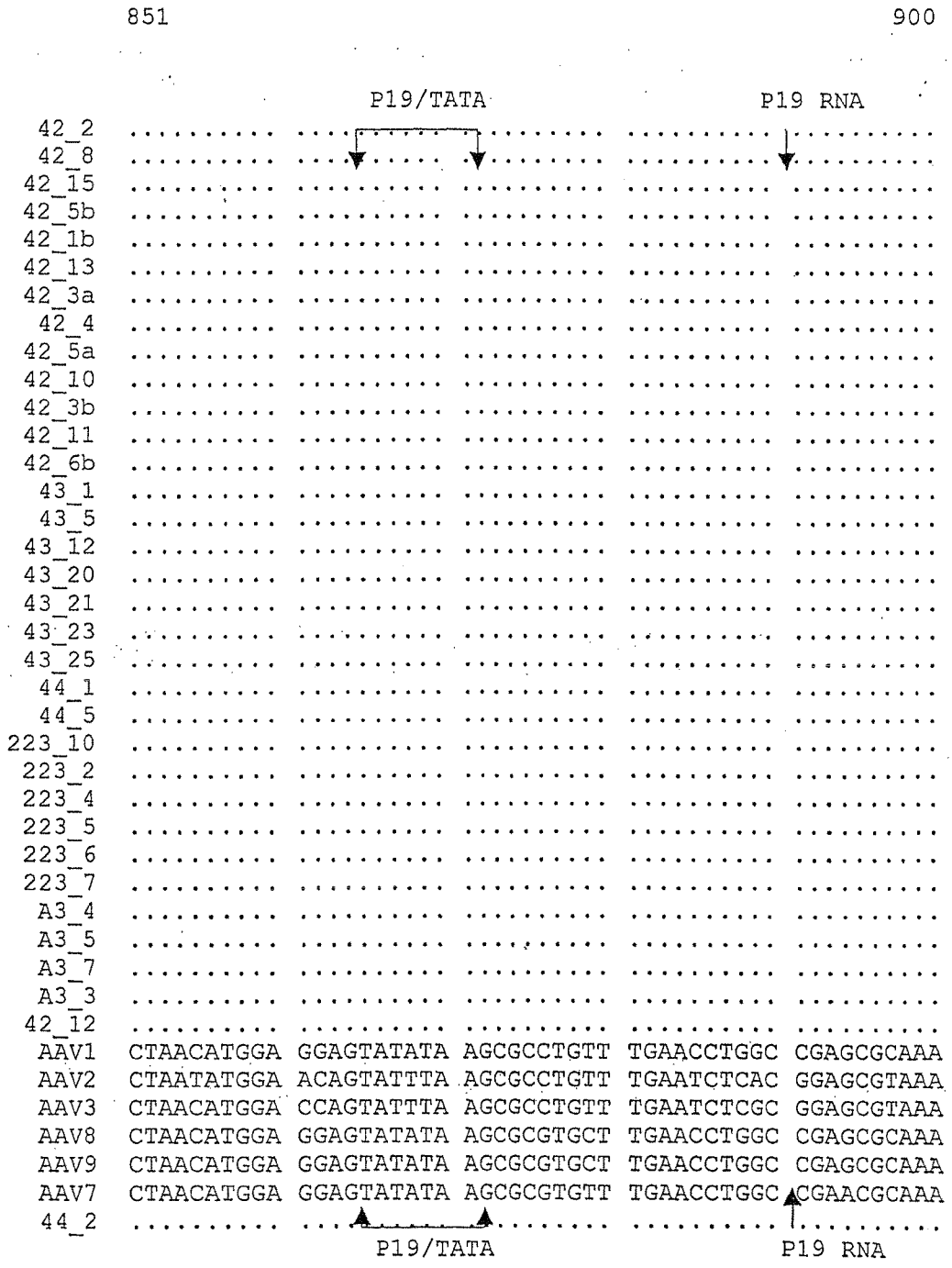

851
900
P19/TATA
P19 RNA
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 CTAACATGGA GGAGTATATA AGCGCCTGTT TGAACCTGGC CGAGCGCAAA
AAV2 CTAATATGGA ACAGTATTTA AGCGCCTGTT TGAATCTCAC GGAGCGTAAA
AAV3 CTAACATGGA CCAGTATTTA AGCGCCTGTT TGAATCTCGC GGAGCGTAAA
AAV8 CTAACATGGA GGAGTATATA AGCGCGTGCT TGAACCTGGC CGAGCGCAAA
AAV9 CTAACATGGA GGAGTATATA AGCGCGTGCT TGAACCTGGC CGAGCGCAAA
AAV7 CTAACATGGA GGAGTATATA AGCGCGTGTT TGAACCTGGC CGAACGCAAA
44_2
P19/TATA
P19 RNA

Fig. 1S

```
        901                                                  950
  42_2  .......... .......... .......... .......... ..........
  42_8  .......... .......... .......... .......... ..........
 42_15  .......... .......... .......... .......... ..........
 42_5b  .......... .......... .......... .......... ..........
 42_1b  .......... .......... .......... .......... ..........
 42_13  .......... .......... .......... .......... ..........
 42_3a  .......... .......... .......... .......... ..........
  42_4  .......... .......... .......... .......... ..........
 42_5a  .......... .......... .......... .......... ..........
 42_10  .......... .......... .......... .......... ..........
 42_3b  .......... .......... .......... .......... ..........
 42_11  .......... .......... .......... .......... ..........
 42_6b  .......... .......... .......... .......... ..........
  43_1  .......... .......... .......... .......... ..........
  43_5  .......... .......... .......... .......... ..........
 43_12  .......... .......... .......... .......... ..........
 43_20  .......... .......... .......... .......... ..........
 43_21  .......... .......... .......... .......... ..........
 43_23  .......... .......... .......... .......... ..........
 43_25  .......... .......... .......... .......... ..........
  44_1  .......... .......... .......... .......... ..........
  44_5  .......... .......... .......... .......... ..........
223_10  .......... .......... .......... .......... ..........
 223_2  .......... .......... .......... .......... ..........
 223_4  .......... .......... .......... .......... ..........
 223_5  .......... .......... .......... .......... ..........
 223_6  .......... .......... .......... .......... ..........
 223_7  .......... .......... .......... .......... ..........
  A3_4  .......... .......... .......... .......... ..........
  A3_5  .......... .......... .......... .......... ..........
  A3_7  .......... .......... .......... .......... ..........
  A3_3  .......... .......... .......... .......... ..........
 42_12  .......... .......... .......... .......... ..........
  AAV1  CGGCTCGTGG CGCAGCACCT GACCCACGTC AGCCAGACCC AGGAGCAGAA
  AAV2  CGGTTGGTGG CGCAGCATCT GACGCACGTG TCGCAGACGC AGGAGCAGAA
  AAV3  CGGCTGGTGG CGCAGCATCT GACGCACGTG TCGCAGACGC AGGAGCAGAA
  AAV8  CGGCTCGTGG CGCAGCACCT GACCCACGTC AGCCAGACGC AGGAGCAGAA
  AAV9  CGGCTCGTGG CGCAGCACCT GACCCACGTC AGCCAGACGC AGGAGCAGAA
  AAV7  CGGCTCGTGG CGCAGCACCT GACCCACGTC AGCCAGACGC AGGAGCAGAA
  44_2  .......... .......... .......... .......... ..........
```

Fig. 1T

```
        951                                                  1000
  42_2  .......... .......... .......... .......... ..........
  42_8  .......... .......... .......... .......... ..........
 42_15  .......... .......... .......... .......... ..........
 42_5b  .......... .......... .......... .......... ..........
 42_1b  .......... .......... .......... .......... ..........
 42_13  .......... .......... .......... .......... ..........
 42_3a  .......... .......... .......... .......... ..........
  42_4  .......... .......... .......... .......... ..........
 42_5a  .......... .......... .......... .......... ..........
 42_10  .......... .......... .......... .......... ..........
 42_3b  .......... .......... .......... .......... ..........
 42_11  .......... .......... .......... .......... ..........
 42_6b  .......... .......... .......... .......... ..........
  43_1  .......... .......... .......... .......... ..........
  43_5  .......... .......... .......... .......... ..........
 43_12  .......... .......... .......... .......... ..........
 43_20  .......... .......... .......... .......... ..........
 43_21  .......... .......... .......... .......... ..........
 43_23  .......... .......... .......... .......... ..........
 43_25  .......... .......... .......... .......... ..........
  44_1  .......... .......... .......... .......... ..........
  44_5  .......... .......... .......... .......... ..........
223_10  .......... .......... .......... .......... ..........
 223_2  .......... .......... .......... .......... ..........
 223_4  .......... .......... .......... .......... ..........
 223_5  .......... .......... .......... .......... ..........
 223_6  .......... .......... .......... .......... ..........
 223_7  .......... .......... .......... .......... ..........
  A3_4  .......... .......... .......... .......... ..........
  A3_5  .......... .......... .......... .......... ..........
  A3_7  .......... .......... .......... .......... ..........
  A3_3  .......... .......... .......... .......... ..........
 42_12  .......... .......... .......... .......... ..........
  AAV1  CAAGGAGAAT CTGAACCCCA ATTCTGACGC GCCTGTCATC CGGTCAAAAA
  AAV2  CAAAGAGAAT CAGAATCCCA ATTCTGATGC GCCGGTGATC AGATCAAAAA
  AAV3  CAAAGAGAAT CAGAACCCCA ATTCTGACGC GCCGGTCATC AGGTCAAAAA
  AAV8  CAAGGAGAAT CTGAACCCCA ATTCTGACGC GCCCGTGATC AGGTCAAAAA
  AAV9  CAAGGAGAAT CTGAACCCCA ATTCTGACGC GCCCGTGATC AGGTCAAAAA
  AAV7  CAAGGAGAAT CTGAACCCCA ATTCTGACGC GCCCGTGATC AGGTCAAAAA
  44_2  .......... .......... .......... .......... ..........
```

Fig. 1U

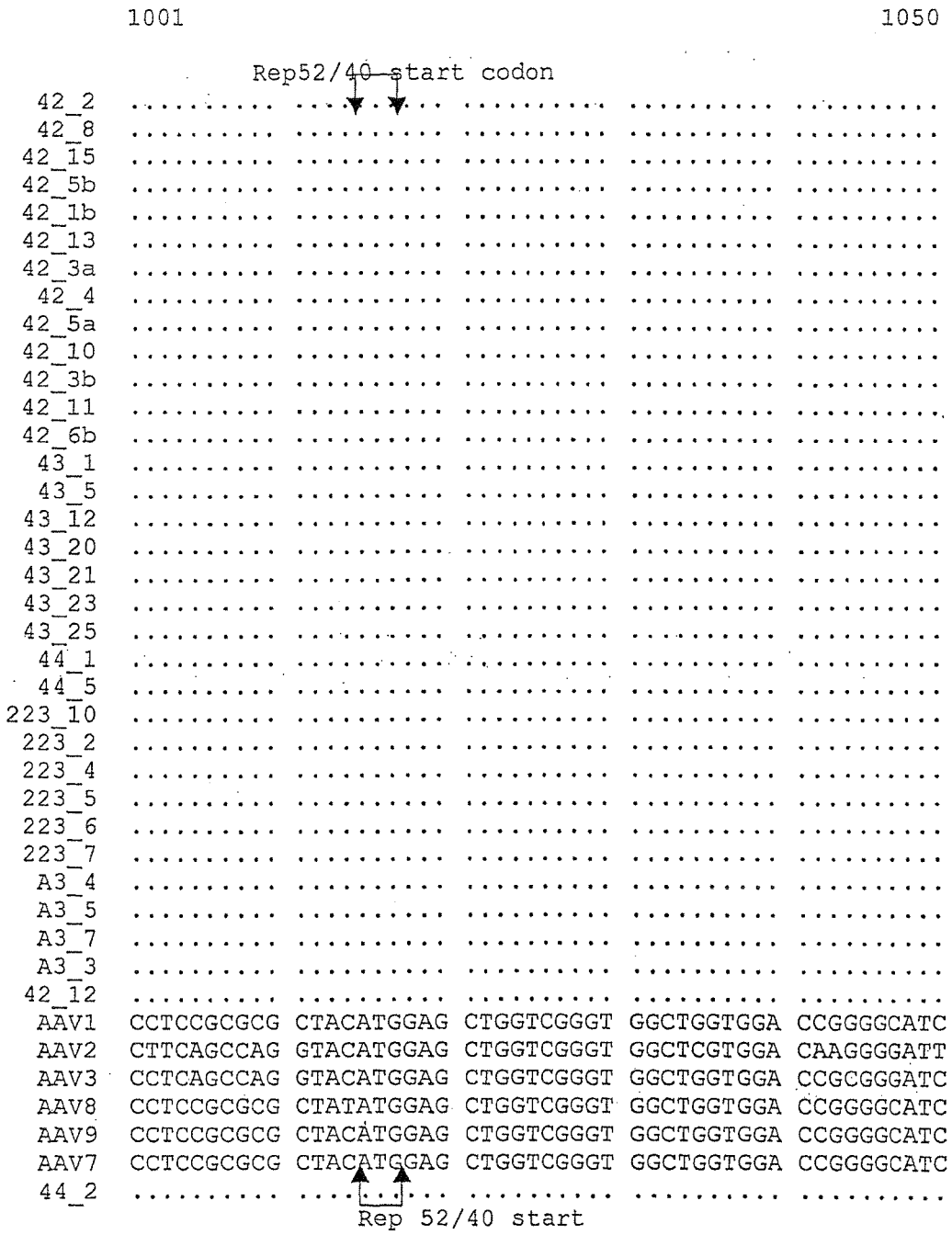

1001
1050
Rep52/40 start codon
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 CCTCCGCGCG CTACATGGAG CTGGTCGGGT GGCTGGTGGA CCGGGGCATC
AAV2 CTTCAGCCAG GTACATGGAG CTGGTCGGGT GGCTCGTGGA CAAGGGGATT
AAV3 CCTCAGCCAG GTACATGGAG CTGGTCGGGT GGCTGGTGGA CCGCGGGATC
AAV8 CCTCCGCGCG CTATATGGAG CTGGTCGGGT GGCTGGTGGA CCGGGGCATC
AAV9 CCTCCGCGCG CTACATGGAG CTGGTCGGGT GGCTGGTGGA CCGGGGCATC
AAV7 CCTCCGCGCG CTACATGGAG CTGGTCGGGT GGCTGGTGGA CCGGGGCATC
44_2
Rep 52/40 start

Fig. 1V

```
        1051                                                        1100
  42_2  .......... .......... .......... .......... ..........
  42_8  .......... .......... .......... .......... ..........
 42_15  .......... .......... .......... .......... ..........
 42_5b  .......... .......... .......... .......... ..........
 42_1b  .......... .......... .......... .......... ..........
 42_13  .......... .......... .......... .......... ..........
 42_3a  .......... .......... .......... .......... ..........
  42_4  .......... .......... .......... .......... ..........
 42_5a  .......... .......... .......... .......... ..........
 42_10  .......... .......... .......... .......... ..........
 42_3b  .......... .......... .......... .......... ..........
 42_11  .......... .......... .......... .......... ..........
 42_6b  .......... .......... .......... .......... ..........
  43_1  .......... .......... .......... .......... ..........
  43_5  .......... .......... .......... .......... ..........
 43_12  .......... .......... .......... .......... ..........
 43_20  .......... .......... .......... .......... ..........
 43_21  .......... .......... .......... .......... ..........
 43_23  .......... .......... .......... .......... ..........
 43_25  .......... .......... .......... .......... ..........
  44_1  .......... .......... .......... .......... ..........
  44_5  .......... .......... .......... .......... ..........
223_10  .......... .......... .......... .......... ..........
 223_2  .......... .......... .......... .......... ..........
 223_4  .......... .......... .......... .......... ..........
 223_5  .......... .......... .......... .......... ..........
 223_6  .......... .......... .......... .......... ..........
 223_7  .......... .......... .......... .......... ..........
  A3_4  .......... .......... .......... .......... ..........
  A3_5  .......... .......... .......... .......... ..........
  A3_7  .......... .......... .......... .......... ..........
  A3_3  .......... .......... .......... .......... ..........
 42_12  .......... .......... .......... .......... ..........
  AAV1  ACCTCCGAGA AGCAGTGGAT CCAGGAGGAC CAGGCCTCGT ACATCTCCTT
  AAV2  ACCTCGGAGA AGCAGTGGAT CCAGGAGGAC CAGGCCTCAT ACATCTCCTT
  AAV3  ACGTCAGAAA AGCAATGGAT TCAGGAGGAC CAGGCCTCGT ACATCTCCTT
  AAV8  ACCTCCGAGA AGCAGTGGAT CCAGGAGGAC CAGGCCTCGT ACATCTCCTT
  AAV9  ACCTCCGAGA AGCAGTGGAT CCAGGAGGAC CAGGCCTCGT ACATCTCCTT
  AAV7  ACCTCCGAGA AGCAGTGGAT CCAGGAGGAC CAGGCCTCGT ACATCTCCTT
  44_2  .......... .......... .......... .......... ..........
```

Fig. 1W

```
        1101                                                        1150
 42_2   .......... .......... .......... .......... ..........
 42_8   .......... .......... .......... .......... ..........
42_15   .......... .......... .......... .......... ..........
42_5b   .......... .......... .......... .......... ..........
42_1b   .......... .......... .......... .......... ..........
42_13   .......... .......... .......... .......... ..........
42_3a   .......... .......... .......... .......... ..........
 42_4   .......... .......... .......... .......... ..........
42_5a   .......... .......... .......... .......... ..........
42_10   .......... .......... .......... .......... ..........
42_3b   .......... .......... .......... .......... ..........
42_11   .......... .......... .......... .......... ..........
42_6b   .......... .......... .......... .......... ..........
 43_1   .......... .......... .......... .......... ..........
 43_5   .......... .......... .......... .......... ..........
43_12   .......... .......... .......... .......... ..........
43_20   .......... .......... .......... .......... ..........
43_21   .......... .......... .......... .......... ..........
43_23   .......... .......... .......... .......... ..........
43_25   .......... .......... .......... .......... ..........
 44_1   .......... .......... .......... .......... ..........
 44_5   .......... .......... .......... .......... ..........
223_10  .......... .......... .......... .......... ..........
223_2   .......... .......... .......... .......... ..........
223_4   .......... .......... .......... .......... ..........
223_5   .......... .......... .......... .......... ..........
223_6   .......... .......... .......... .......... ..........
223_7   .......... .......... .......... .......... ..........
 A3_4   .......... .......... .......... .......... ..........
 A3_5   .......... .......... .......... .......... ..........
 A3_7   .......... .......... .......... .......... ..........
 A3_3   .......... .......... .......... .......... ..........
42_12   .......... .......... .......... .......... ..........
 AAV1   CAACGCCGCT TCCAACTCGC GGTCCCAGAT CAAGGCCGCT CTGGACAATG
 AAV2   CAATGCGGCC TCCAACTCGC GGTCCCAAAT CAAGGCTGCC TTGGACAATG
 AAV3   CAACGCCGCC TCCAACTCGC GGTCCCAGAT CAAGGCCGCG CTGGACAATG
 AAV8   CAACGCCGCC TCCAACTCGC GGTCCCAGAT CAAGGCCGCG CTGGACAATG
 AAV9   CAACGCCGCC TCCAACTCGC GGTCCCAGAT CAAGGCCGCG CTGGACAATG
 AAV7   CAACGCCGCC TCCAACTCGC GGTCCCAGAT CAAGGCCGCG CTGGACAATG
 44_2   .......... .......... .......... .......... ..........
```

Fig. 1X

```
         1151                                                  1200
  42_2   .......... .......... .......... .......... ..........
  42_8   .......... .......... .......... .......... ..........
 42_15   .......... .......... .......... .......... ..........
 42_5b   .......... .......... .......... .......... ..........
 42_1b   .......... .......... .......... .......... ..........
 42_13   .......... .......... .......... .......... ..........
 42_3a   .......... .......... .......... .......... ..........
  42_4   .......... .......... .......... .......... ..........
 42_5a   .......... .......... .......... .......... ..........
 42_10   .......... .......... .......... .......... ..........
 42_3b   .......... .......... .......... .......... ..........
 42_11   .......... .......... .......... .......... ..........
 42_6b   .......... .......... .......... .......... ..........
  43_1   .......... .......... .......... .......... ..........
  43_5   .......... .......... .......... .......... ..........
 43_12   .......... .......... .......... .......... ..........
 43_20   .......... .......... .......... .......... ..........
 43_21   .......... .......... .......... .......... ..........
 43_23   .......... .......... .......... .......... ..........
 43_25   .......... .......... .......... .......... ..........
  44_1   .......... .......... .......... .......... ..........
  44_5   .......... .......... .......... .......... ..........
223_10   .......... .......... .......... .......... ..........
 223_2   .......... .......... .......... .......... ..........
 223_4   .......... .......... .......... .......... ..........
 223_5   .......... .......... .......... .......... ..........
 223_6   .......... .......... .......... .......... ..........
 223_7   .......... .......... .......... .......... ..........
  A3_4   .......... .......... .......... .......... ..........
  A3_5   .......... .......... .......... .......... ..........
  A3_7   .......... .......... .......... .......... ..........
  A3_3   .......... .......... .......... .......... ..........
 42_12   .......... .......... .......... .......... ..........
  AAV1   CCGGCAAGAT CATGGCGCTG ACCAAATCCG CGCCCGACTA CCTGGTAGGC
  AAV2   CGGGAAAGAT TATGAGCCTG ACTAAAACCG CCCCCGACTA CCTGGTGGGC
  AAV3   CCTCCAAGAT CATGAGCCTG ACAAAGACGG CTCCGGACTA CCTGGTGGGC
  AAV8   CCGGCAAGAT CATGGCGCTG ACCAAATCCG CGCCCGACTA CCTGGTGGGG
  AAV9   CCGGCAAGAT CATGGCGCTG ACCAAATCCG CGCCCGACTA CCTGGTAGGC
  AAV7   CCGGCAAGAT CATGGCGCTG ACCAAATCCG CGCCCGACTA CCTGGTGGGG
  44_2   .......... .......... .......... .......... ..........
```

Fig. 1Y

```
         1201                                                  1250
  42_2   .......... .......... .......... .......... ..........
  42_8   .......... .......... .......... .......... ..........
 42_15   .......... .......... .......... .......... ..........
 42_5b   .......... .......... .......... .......... ..........
 42_1b   .......... .......... .......... .......... ..........
 42_13   .......... .......... .......... .......... ..........
 42_3a   .......... .......... .......... .......... ..........
  42_4   .......... .......... .......... .......... ..........
 42_5a   .......... .......... .......... .......... ..........
 42_10   .......... .......... .......... .......... ..........
 42_3b   .......... .......... .......... .......... ..........
 42_11   .......... .......... .......... .......... ..........
 42_6b   .......... .......... ........GA ATTCGCCCTT TCTACGGCTG
  43_1   .......... .......... .......... .......... ..........
  43_5   .......... .......... .......... .......... ..........
 43_12   .......... .......... .......... .......... ..........
 43_20   .......... .......... .......... .......... ..........
 43_21   .......... .......... .......... .......... ..........
 43_23   .......... .......... .......... .......... ..........
 43_25   .......... .......... .......... .......... ..........
  44_1   .......... .......... .......... .......... ..........
  44_5   .......... .......... .......... .......... ..........
223_10   .......... .......... .......... .......... ..........
 223_2   .......... .......... .......... .......... ..........
 223_4   .......... .......... .......... .......... ..........
 223_5   .......... .......... .......... .......... ..........
 223_6   .......... .......... .......... .......... ..........
 223_7   .......... .......... .......... .......... ..........
  A3_4   .......... .......... .......... .......... ..........
  A3_5   .......... .......... .......... .......... ..........
  A3_7   .......... .......... .......... .......... ..........
  A3_3   .......... .......... .......... .......... ..........
 42_12   .......... .......... .......... .......... ..........
  AAV1   CCCGCTCCGC CCGCGGACAT TAAAACCAAC CGCATCTACC GCATCCTGGA
  AAV2   CAGCAGCCCG TGGAGGACAT TTCCAGCAAT CGGATTTATA AAATTTTGGA
  AAV3   AGCAACCCGC CGGAGGACAT TACCAAAAAT CGGATCTACC AAATCCTGGA
  AAV8   CCCTCGCTGC CCGCGGACAT TACCCAGAAC CGCATCTACC GCATCCTCGC
  AAV9   CCTTCACTTC CGGTGGACAT TACGCAGAAC CGCATCTACC GCATCCTGCA
  AAV7   CCCTCGCTGC CCGCGGACAT TAAAACCAAC CGCATCTACC GCATCCTGGA
  44_2   .......... .......... .......... .......... ..........
```

Fig. 1Z

```
        1251                                                        1300
  42_2  .......... .......... .......... .......... ..........
  42_8  .......... .......... .......... .......... ..........
 42_15  .......... .......... .......... .......... ..........
 42_5b  .......... .......... .......... .......... ..........
 42_1b  .......... .......... .......... .......... ..........
 42_13  .......... .......... .......... .......... ..........
 42_3a  .......... .......... .......... .......... ..........
  42_4  .......... .......... .......... .......... ..........
 42_5a  .......... .......... .......... .......... ..........
 42_10  .......... .......... .......... .......... ..........
 42_3b  .......... .......... .......... .......... ..........
 42_11  .......... .......... .......... .......... ..........
 42_6b  CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC GTCGACAAGA
  43_1  .......... .......... .......... .......... ..........
  43_5  .......... .......... .......... .......... ..........
 43_12  .......... .......... .......... .......... ..........
 43_20  .......... .......... .......... .......... ..........
 43_21  .......... .......... .......... .......... ..........
 43_23  .......... .......... .......... .......... ..........
 43_25  .......... .......... .......... .......... ..........
  44_1  .......... .......... .......... .......... ..........
  44_5  .......... .......... .......... .......... ..........
223_10  .......... .......... .......... .......... ..........
 223_2  .......... .......... .......... .......... ..........
 223_4  .......... .......... .......... .......... ..........
 223_5  .......... .......... .......... .......... ..........
 223_6  .......... .......... .......... .......... ..........
 223_7  .......... .......... .......... .......... ..........
  A3_4  .......... .......... .......... .......... ..........
  A3_5  .......... .......... .......... .......... ..........
  A3_7  .......... .......... .......... .......... ..........
  A3_3  .......... .......... .......... .......... ..........
 42_12  .......... .......... .......... .......... ..........
  AAV1  GCTGAACGGC TACGAACCTG CCTACGCCGG CTCCGTCTTT CTCGGCTGGG
  AAV2  ACTAAACGGG TACGATCCCC AATATGCGGC TTCCGTCTTT CTGGGATGGG
  AAV3  GCTGAACGGG TACGATCCGC AGTACGCGGC CTCCGTCTTC CTGGGCTGGG
  AAV8  TCTCAACGGC TACGACCCTG CCTACGCCGG CTCCGTCTTT CTCGGCTGGG
  AAV9  GCTCAACGGC TACGACCCTG CCTACGCCGG CTCCGTCTTT CTCGGCTGGG
  AAV7  GCTGAACGGG TACGATCCTG CCTACGCCGG CTCCGTCTTT CTCGGCTGGG
  44_2  .......... .......... .......... .......... ..........
```

Fig. 1AA

```
        1301                                                        1350
 42_2   .......... .......... .......... .......... ..........
 42_8   .......... .......... .......... .......... ..........
42_15   .......... .......... .......... .......... ..........
42_5b   .......... .......... .......... .......... ..........
42_1b   .......... .......... .......... .......... ..........
42_13   .......... .......... .......... .......... ..........
42_3a   .......... .......... .......... .......... ..........
 42_4   .......... .......... .......... .......... ..........
42_5a   .......... .......... .......... .......... ..........
42_10   .......... .......... .......... .......... ..........
42_3b   .......... .......... .......... .......... ..........
42_11   .......... .......... .......... .......... ..........
42_6b   TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT CGTGGAGTCC
 43_1   .......... .......... .......... .......... ..........
 43_5   .......... .......... .......... .......... ..........
43_12   .......... .......... .......... .......... ..........
43_20   .......... .......... .......... .......... ..........
43_21   .......... .......... .......... .......... ..........
43_23   .......... .......... .......... .......... ..........
43_25   .......... .......... .......... .......... ..........
 44_1   .......... .......... .......... .......... ..........
 44_5   .......... .......... .......... .......... ..........
223_10  .......... .......... .......... .......... ..........
223_2   .......... .......... .......... .......... ..........
223_4   .......... .......... .......... .......... ..........
223_5   .......... .......... .......... .......... ..........
223_6   .......... .......... .......... .......... ..........
223_7   .......... .......... .......... .......... ..........
 A3_4   .......... .......... .......... .......... ..........
 A3_5   .......... .......... .......... .......... ..........
 A3_7   .......... .......... .......... .......... ..........
 A3_3   .......... .......... .......... .......... ..........
42_12   .......... .......... .......... .......... ..........
 AAV1   CCCAGAAAAG GTTCGGGAAG CGCAACACCA TCTGGCTGTT TGGGCCGGCC
 AAV2   CCACGAAAAA GTTCGGCAAG AGGAACACCA TCTGGCTGTT TGGGCCTGCA
 AAV3   CGCAAAAGAA GTTCGGGAAG AGGAACACCA TCTGGCTCTT TGGGCCGGCC
 AAV8   CTCAGAAAAA GTTCGGGAAA CGCAACACCA TCTGGCTGTT TGGACCCGCC
 AAV9   CACAAAAGAA GTTCGGGAAA CGCAACACCA TCTGGCTGTT TGGGCCGGCC
 AAV7   CCCAGAAAAA GTTCGGGAAG CGCAACACCA TCTGGCTGTT TGGGCCCGCC
 44_2   .......... .......... .......... .......... ..........
```

Fig. 1AB

```
        1351                                                  1400

  42_2  .......... .......... .......... .......GAA TTCGCCCTTT
  42_8  .......... .......... .......... .......GAA TTCGCCCTTT
 42_15  .......... .......... .......... .......GAA TTCGCCCTTT
 42_5b  .......... .......... .......... .......GAA TTCGCCCTTT
 42_1b  .......... .......... .......... .......... ..........
 42_13  .......... .......... .......... .......GAA TTCGCCCTTT
 42_3a  .......... .......... .......... .......GAA TTCGCCCTTT
  42_4  .......... .......... .......... .......... ..........
 42_5a  .......... .......... .......... ........GA ATTCGCCCTT
 42_10  .......... .......... .......... .......... ..........
 42_3b  .......... .......... .......... .......... ..........
 42_11  .......... .......... .......... .......GAA TTCGCCCTTT
 42_6b  GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC AAAAGTGCAA
  43_1  .......... .......... .......... .......GAA TTCGCCCTTT
  43_5  .......... .......... .......... .......GAA TTCGCCCTTT
 43_12  .......... .......... .......... .......GAA TTCGCCCTT.
 43_20  .......... .......... .......... .......GAA TTCGCCCTTT
 43_21  .......... .......... .......... .......GAA TTCGCCCTT.
 43_23  .......... .......... .......... .......GAA TTCGCCCTT.
 43_25  .......... .......... .......... .......GAA TTCGCCCTTT
  44_1  .......... .......... .......... .......GAA TTCGCCCTTT
  44_5  .......... .......... .......... .......GAA TTCGCCCTTT
223_10  .......... .......... .......... .......... ..........
 223_2  .......... .......... .......... .......... ..........
 223_4  .......... .......... .......... .......... ..........
 223_5  .......... .......... .......... .......... ..........
 223_6  .......... .......... .......... .......... ..........
 223_7  .......... .......... .......... .......... ..........
  A3_4  .......... .......... .......... ........GA ATTCGCCCTT
  A3_5  .......... .......... .......... ........GA ATTCGCCCTT
  A3_7  .......... .......... .........A GCGGCCGCGA ATTCGCCCTT
  A3_3  .......... .......... .......... ........GA ATTCGCCCTT
 42_12  .......... .......... .......... .......GAA TTCGCCCTTT
  AAV1  ACCACGGGCA AGACCAACAT CGCGGAAGCC ATCGCCCACG CCGTGCCCTT
  AAV2  ACTACCGGGA AGACCAACAT CGCGGAGGCC ATAGCCCACA CTGTGCCCTT
  AAV3  ACGACGGGTA AAACCAACAT CGCGGAAGCC ATCGCCCACG CCGTGCCCTT
  AAV8  ACCACCGGCA AGACCAACAT TGCGGAAGCC ATCGCCCACG CCGTGCCCTT
  AAV9  ACCACGGGAA AGACCAACAT CGCAGAAGCC ATTGCCCACG CCGTGCCCTT
  AAV7  ACCACCGGCA AGACCAACAT TGCGGAAGCC ATCGCCCACG CCGTGCCCTT
  44_2  .......... .......... .......... ........GA ATTCGCCCTT
```

Fig. 1AC

```
        1401                                                  1450
  42_2  .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
  42_8  .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
 42_15  .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
 42_5b  .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
 42_1b  .......... .......... .......... .......... ..........
 42_13  .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
 42_3a  .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
  42_4  .......... .......... .......... .......... ..........
 42_5a  .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
 42_10  .......... .......... .......... .......... ..........
 42_3b  .......... .......... .......... .......... ..........
 42_11  .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
 42_6b  .GTCTTCCGC CCAGATCGAT CCCACCCCCG TGATCGTCAC TTCCAACACC
  43_1  .CTACGGCTG CATCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
  43_5  .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
 43_12  .....GGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
 43_20  .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
 43_21  .....GGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
 43_23  .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
 43_25  .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
  44_1  .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
  44_5  .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
223_10  .......... .......... .......... .......... ..........
 223_2  .......... .......... .......... .......... ..........
 223_4  .......... .......... .......... .......... ..........
 223_5  .......... .......... .......... .......... ..........
 223_6  .......... .......... .......... .......... ..........
 223_7  .......... .......... .......... .......... ..........
  A3_4  TCTACGGCTG CGTCAACTGG ACCAATGAAA ACTTTCCCTT CAACGATTGC
  A3_5  TCTACGGCTG CGTCAACTGG ACCAATGAAA ACTTTCCCTT CAACGATTGC
  A3_7  TCTACGGCTG CGTCAACTGG ACCAATGAAA ACTTTCCCTT CAACGATTGC
  A3_3  TCTACGGCTG CGTCAACTGG ACCAATGAAA ACTTTCCCTT CAACGATTGC
 42_12  .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
  AAV1  .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAATGATTGC
  AAV2  .CTACGGGTG CGTAAACTGG ACCAATGAGA ACTTTCCCTT CAACGACTGT
  AAV3  .CTACGGCTG CGTAAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
  AAV8  .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAATGATTGC
  AAV9  .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
  AAV7  .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
  44_2  TCTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
```

Fig. 1AD

```
          1451                                                        1500
  42_2    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
  42_8    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
 42_15    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
 42_5b    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
 42_1b    .......... .......... .......... .......... ..........
 42_13    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
 42_3a    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
  42_4    .......... .......... .......... .......... ..........
 42_5a    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
 42_10    .......... .......... .......... .......... ..........
 42_3b    .......... .......... .......... .......... ..........
 42_11    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
 42_6b    AACATGTGCG CCGTGATTGA CGGGAACAGC ACCACCTTCG AGCACCAGCA
  43_1    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
  43_5    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
 43_12    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
 43_20    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
 43_21    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
 43_23    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
 43_25    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
  44_1    GTCGACAAGA TGTTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
  44_5    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
223_10    .......... .......... .......... .......... ..........
 223_2    .......... .......... .......... .......... ..........
 223_4    .......... .......... .......... .......... ..........
 223_5    .......... .......... .......... .......... ..........
 223_6    .......... .......... .......... .......... ..........
 223_7    .......... .......... .......... .......... ..........
  A3_4    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGAAAGATGA CCGCCAAGGT
  A3_5    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGAAAGATGA CCGCCAAGGT
  A3_7    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGAAAGATGA CCGCCAAGGT
  A3_3    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGAAAGATGA CCGCCAAGGT
 42_12    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
  AAV1    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
  AAV2    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGGAAGATGA CCGCCAAGGT
  AAV3    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
  AAV8    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
  AAV9    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
  AAV7    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
  44_2    GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
```

Fig. 1AE

```
        1501                                                        1550
 42_2   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC
 42_8   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC
42_15   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC
42_5b   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC
42_1b   .......... .......... .......... .......... ..........
42_13   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC
42_3a   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC
 42_4   .......... .......... .......... .......... ..........
42_5a   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC
42_10   .......... .......... .......... .......... ..........
42_3b   .......... .......... .......... .......... ..........
42_11   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC
42_6b   GCCGTTGCAG GACCGGATGT TCAAATTTGA ACTCACCCGC CGTCTGGAGC
 43_1   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC
 43_5   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC
43_12   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC
43_20   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGTGTGGACC
43_21   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGTGTGGACC
43_23   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGTGTGGACC
43_25   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGTGTGGACC
 44_1   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAAGTG CGCGTGGACC
 44_5   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAAGTG CGCGTGGACC
223_10  .......... .......... .......... .......... ..........
223_2   .......... .......... .......... .......... ..........
223_4   .......... .......... .......... .......... ..........
223_5   .......... .......... .......... .......... ..........
223_6   .......... .......... .......... .......... ..........
223_7   .......... .......... .......... .......... ..........
 A3_4   CGTGGAATCT GCCAAAGCCA TTCTGGGTGG AAGCAAGGTT CGTGTGGACC
 A3_5   CGTGGAATCT GCCAAAGCCA TTCTGGGTGG AAGCAAGGTT CGTGTGGACC
 A3_7   CGTGGAATCT GCCAAAGCCA TTCTGGGTGG AAGCAAGGTT CGTGTGGACC
 A3_3   CGTGGAATCT GCCAAAGCCA TTCTGGGTGG AGGCAAGGTT CGTGTGGACC
42_12   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC
 AAV1   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC
 AAV2   CGTGGAGTCG GCCAAAGCCA TTCTCGGAGG AAGCAAGGTG CGCGTGGACC
 AAV3   CGTGGAGAGC GCCAAGGCCA TTCTGGGCGG AAGCAAGGTG CGCGTGGACC
 AAV8   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC
 AAV9   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC
 AAV7   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC
 44_2   CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAAGTG CGCGTGGACC
```

Fig. 1AF

```
        1551                                                  1600
  42_2  AAAAGTGCAA GTCTTCCGCC CAGATCGATC CCACCCCCGT GATCGTCACT
  42_8  AAAAGTGCAA GTCTTCCGCC CAGATCGATC CCACCCCCGT GATCGTCACT
 42_15  AAAAGTGCAA GTCGTCCGCC CAGATCGACC CCACCCCCGT GATCGTCACC
 42_5b  AAAAGTGCAA GTCGTCCGCC CAGATCGACC CCACCCCCGT GATCGTCACC
 42_1b  .......... .......... .......... .......... ..........
 42_13  AAAAGTGCAA GTCGTCCGCC CAGATCGATC CCACCCCCGT GATCGTCACT
 42_3a  AAAAGTGCAA GTCGTCCGCC CAGATCGATC CCACCCCCGT GATCGTCACT
  42_4  .......... .......... .......... .......... ..........
 42_5a  AAAAGTGCAA GTCGTCCGCC CAGATCGACC CCACCCCCGT GATCGTCACC
 42_10  .......... .......... .......... .......... ..........
 42_3b  .......... .......... .......... .......... ..........
 42_11  AAAAGTGCAA GTCTTCCGCC CAGATCGATC CCACCCCCGT GATCGTCACT
 42_6b  ATGACTTTGG CAAGGTGACA AAGCAGGAAG TCAAAGAGTT CTTCCGCTGG
  43_1  AAAAGTGCAA GTCGTCCGCC CAGATCGACC CCACCCCCGT GATCGTCACC
  43_5  AAAAGTGCAA GTCGTCCGCC CAGATCGACC CCACCCCCGT GATCGTCACC
 43_12  AAAAGTGCAA GTCGTCCGCC CAGATCGACC CCACCCCCGT GATCGTCACC
 43_20  AAAAGTGCAA GTCTTCCGCC CAGATCGATC CCACCCCCGT GATCGTCACC
 43_21  AAAAGTGCAA GTCTTCCGCC CAGATCGATC CCACCCCCGT GATCGTCACC
 43_23  AAAAGTGCAA GTCTTCCGCC CAGATCGATC CCACCCCCGT GATCGTCACC
 43_25  AAAAGTGCAA GTCTTCCGCC CAGATCGATC CCACCCCCGT GATCGTCACC
  44_1  AAAAGTGCAA GCCGTCCGCC CAGATCGACC CCACCCCCGT GATCGTCACC
  44_5  AAAAGTGCAA GTCGTCCGCC CAGATCGACC CCACCCCCGT GATCGTCACC
223_10  .......... .......... .......... .......... ..........
 223_2  .......... .......... .......... .......... ..........
 223_4  .......... .......... .......... .......... ..........
 223_5  .......... .......... .......... .......... ..........
 223_6  .......... .......... .......... .......... ..........
 223_7  .......... .......... .......... .......... ..........
  A3_4  AGAAATGCAA GTCTTCGGCC CAGATCGACC CGACTCCGGT GATTGTCACC
  A3_5  AGAAATGCAA GTCTTCGGCC CAGATCGACC CGACTCCGGT GATTGTCACC
  A3_7  AGAAATGCAG GTCTTCGGCC CAGATCGACC CGACTCCGGT GATTGTCACC
  A3_3  AGAAATGCAA GTCTTCGGCC CAGATCGACC CGACTCCGGT GATTGTCACC
 42_12  AAAAGTGCAA GTCGTCCGCC CAGATCGACC CCACCCCCGT GATCGTCACC
  AAV1  AAAAGTGCAA GTCGTCCGCC CAGATCGACC CCACCCCCGT GATCGTCACC
  AAV2  AGAAATGCAA GTCCTCGGCC CAGATAGACC CGACTCCCGT GATCGTCACC
  AAV3  AAAAGTGCAA GTCATCGGCC CAGATCGAAC CCACTCCCGT GATCGTCACC
  AAV8  AAAAGTGCAA GTCGTCCGCC CAGATCGACC CCACCCCCGT GATCGTCACC
  AAV9  AAAAGTGCAA GTCGTCCGCC CAGATCGACC CCACTCCCGT GATCGTCACC
  AAV7  AAAAGTGCAA GTCGTCCGCC CAGATCGACC CCACCCCCGT GATCGTCACC
  44_2  AAAAGTGCAA GTCGTCCGCC CAGATCGACC CCACCCCCGT GATCGTCACC
```

Fig. 1AG

```
        1601                                                  1650
  42_2  TCCAACACCA ACATGTGCGC TGTGATTGAC GGGAACAGCA CCACCTTCGA
  42_8  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
 42_15  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
 42_5b  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
 42_1b  .......... .......... .......... .......... ..........
 42_13  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
 42_3a  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
  42_4  .......... .......... .......... .......... ..........
 42_5a  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
 42_10  .......... .......... .......... .......... ..........
 42_3b  .......... .......... .......... .......... ..........
 42_11  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
 42_6b  GCGCAGGATC ACGTGACCGA GGTGGCGCAT GAGTTCTACG TCAGAAAGGG
  43_1  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
  43_5  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
 43_12  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
 43_20  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCG CCACCTTCGA
 43_21  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
 43_23  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
 43_25  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
  44_1  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
  44_5  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
223_10  .......... .......... .......... .......... ..........
 223_2  .......... .......... .......... .......... ..........
 223_4  .......... .......... .......... .......... ..........
 223_5  .......... .......... .......... .......... ..........
 223_6  .......... .......... .......... .......... ..........
 223_7  .......... .......... .......... .......... ..........
  A3_4  TCTAACACCA ACATGTGCGC CGTGATTGAC GGAAACTCGA CCACCTTCGA
  A3_5  TCTAACACCA ACATGTGCGC CGTGATTGAC GGAAACTCGA CCACCTTCGA
  A3_7  TCTAACACCA ACATGTGCGC CGTGATTGAC GGAAACTCGA CCACCTTCGA
  A3_3  TCTAACACCA ACATGTGCGC CGTGATTGAC GGAAACTCGA CCACCTTCGA
 42_12  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
  AAV1  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
  AAV2  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACTCAA CGACCTTCGA
  AAV3  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
  AAV8  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
  AAV9  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
  AAV7  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
  44_2  TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
```

Fig. 1AH

```
        1651                                                  1700
  42_2  GCACCAGCAG CCGTTACAAG ACCGGATGTT CAAATTTGAA CTCACCCGCC
  42_8  GCACCAGCAG CCGTTACAAG ACCGGATGTT CAAATTTGAA CTCACCCGCC
 42_15  GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAATTTGAA CTCACCCGCC
 42_5b  GCACCAGCAG CCGTTACAAG ACCGGATGTT CAAATTTGAA CTCACCCGCC
 42_1b  .......... .......... .......... .......... ..........
 42_13  GCACCAGCAG CCGTTACAAG ACCGGATGTT CAAATTTGAA CTCACCCGCC
 42_3a  GCACCAGCAG CCGTTACAAG ACCGGATGTT CAAATTTGAA CTCACCCGCC
  42_4  .......... .......... .......... .......... ..........
 42_5a  GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAATTTGAA CTCACCCGCC
 42_10  .......... .......... .......... .......... ..........
 42_3b  .......... .......... .......... .......... ..........
 42_11  GCACCAGCAG CCGTTACAAG ACCGGATGTT CAAATTTGAA CTCACCCGCC
 42_6b  TGGAGCCAAC AAGAGACCCG CCCCCGATGA CGCGGATAAA AGCGAGCCCA
  43_1  GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAGTTCGAA CTCACCCGCC
  43_5  GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAGTTCGAA CTCACCCGCC
 43_12  GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAGTTCGAA CTCACCCGCC
 43_20  GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAATTTGAA CTCACCCGCC
 43_21  GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAATTTGAA CTCACCCGCC
 43_23  GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAATTTGAA CTCACCCGCC
 43_25  GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAATTTGAA CTCACCCGCC
  44_1  GCACCAGCAG CCGTTGCGGG ACCGGATGTT CAAGTTTGAA CTCACCCGCC
  44_5  GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAGTTTGAA CTCACCCGCC
223_10  .......... .......... .......... .......... ..........
 223_2  .......... .......... .......... .......... ..........
 223_4  .......... .......... .......... .......... ..........
 223_5  .......... .......... .......... .......... ..........
 223_6  .......... .......... .......... .......... ..........
 223_7  .......... .......... .......... .......... ..........
  A3_4  GCACCAGCAG CCGTTGCAAG ACCGGATGTT CAAATTTGAA CTTACCCGCC
  A3_5  GCACCAGCAG CCGTTGCAAG ACCGGATGTT CAAATTTGAA CTTACCCGCC
  A3_7  GCACCAGCAG CCGTTGCAAG ACCGGATGTT CAAATTTGAA CTTACCCGCC
  A3_3  GCACCAGCAG CCGTTGCAAG ACCGGATGTT CAAATTTGAA CTTACCCGCC
 42_12  GCACCAGCAG CCGTTACAAG ACCGGATGTT CAAATTTGAA CTCACCCGCC
  AAV1  GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAATTTGAA CTCACCCGCC
  AAV2  ACACCAGCAG CCGTTGCAAG ACCGGATGTT CAAATTTGAA CTCACCCGCC
  AAV3  GCATCAGCAG CCGCTGCAGG ACCGGATGTT TGAATTTGAA CTTACCCGCC
  AAV8  GCACCAGCAG CCTCTCCAGG ACCGGATGTT TAAGTTCGAA CTCACCCGCC
  AAV9  GCACCAGCAG CCTCTCCAGG ACCGGATGTT TAAGTTCGAA CTCACCCGCC
  AAV7  GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAATTTGAA CTCACCCGCC
  44_2  GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAGTTTGAA CTCACCCGCC
```

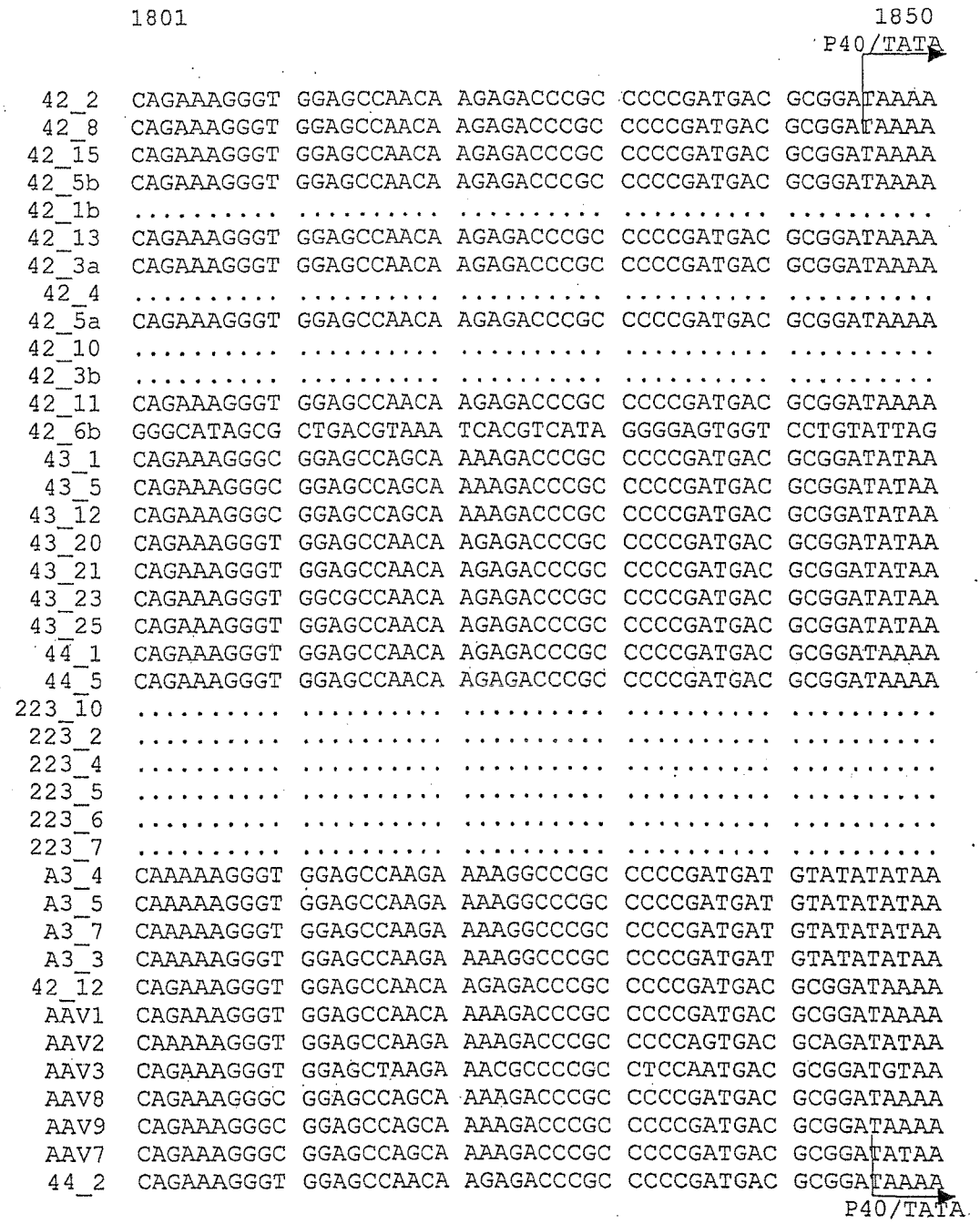
Fig. 1AI

```
        1701                                                  1750
  42_2  GTCTGGAGCA CGACTTTGGC AAGGTGACAA AGCAGGAAGT CAAAGAGTTC
  42_8  GTCTGGAGCA CGACTTTGGC AAGGTGACAA AGCAGGAAGT CAAAGAGTTC
 42_15  GTCTGGAGCA TGACTTTGGC AAGGTGACAA AGCAGGAAGT CAAAGAGTTC
 42_5b  GTCTGGAGCA CGACTTTGGC AAGGTGACAA AGCAGGAAGT CAAAGAGTTC
 42_1b  .......... .......... .......... .......... ..........
 42_13  GTCTGGAGCA TGACTTTGGC AAGGTGACAA AGCAGGAAGT CAAAGAGTTC
 42_3a  GTCTGGAGCA TGACTTTGGC AAGGTGACAA AGCAGGAAGT CAAAGAGTTC
  42_4  .......... .......... .......... .......... ..........
 42_5a  GTCTGGAGCA TGACTTTGGC AAGGCGACAA AGCAGGAAGT CAAAGAGTTC
 42_10  .......... .......... .......... .......... ..........
 42_3b  .......... .......... .......... .......... ..........
 42_11  GTCTGGAGCA CGACTTTGGC AAGGTGACAA AGCAGGAAGT CAAAGAGTTC
 42_6b  AGCGGGCCTG CCCCTCAGTC GCGGATCCAT CGACGTCAGA CGCGGAAGGA
  43_1  GTCTGGAGCA CGACTTTGGC AAGGTGACCA AGCAGGAAGT CAAAGAGTTC
  43_5  GTCTGGAGCA CGACTTTGGC AAGGTGACCA AGCAGGAAGT CAAAGAGTTC
 43_12  GTCTGGAGCA CGACTTTGGC AAGGTGACCA AGCAGGAAGT CAAAGAGTTC
 43_20  GTCTGGAGCA TGACTTTGGC AAGGTGACGA AGCAGGAAGT CAAAGAGTTC
 43_21  GTCTGGAGCA TGACTTTGGC AAGGTGACGA AGCAGGAAGT CAAAGAGTTC
 43_23  GTCTGGAGCA TGACTTTGGC AAGGTGACGA AGCAGGAAGT CAAAGAGTTC
 43_25  GTCTGGAGCA TGACTTTGGC AAGGTGACGA AGCAGGAAGT CAAAGGGTTC
  44_1  GTCTGGAGCA CGACTTTGGC AAGGTGACAA AGCAGGAAGT CAGAGAGTTC
  44_5  GTCTGGAGCA CGACTTTGGC AAGGTGACAA AGCAGGAAGT CAGAGAGTTC
223_10  .......... .......... .......... .......... ..........
 223_2  .......... .......... .......... .......... ..........
 223_4  .......... .......... .......... .......... ..........
 223_5  .......... .......... .......... .......... ..........
 223_6  .......... .......... .......... .......... ..........
 223_7  .......... .......... .......... .......... ..........
  A3_4  GTTTGGATCA TGACTTTGGG AAGGTCACCA AGCAGGAAGT CAAAGACTTT
  A3_5  GTTTGGATCA TGACTTTGGG AAGGTCACCA AGCAGGAAGT CAAAGACTTT
  A3_7  GTTTGGATCA TGACTTTGGG AAGGTCACCA AGCAGGAAGT CAAAGACTTT
  A3_3  GTTTGGATCA TGACTTTGGG AAGGTCACCA AGCAGGAAGT CAAAGACTTT
 42_12  GTCTGGAGCA CGACTTTGGC AAGGTGACAA AGCAGGAAGT CAAAGAGTTC
  AAV1  GTCTGGAGCA TGACTTTGGC AAGGTGACAA AGCAGGAAGT CAAAGAGTTC
  AAV2  GTCTGGATCA TGACTTTGGG AAGGTCACCA AGCAGGAAGT CAAAGACTTT
  AAV3  GTTTGGACCA TGACTTTGGG AAGGTCACCA AACAGGAAGT AAAGGACTTT
  AAV8  GTCTGGAGCA CGACTTTGGC AAGGTGACAA AGCAGGAAGT CAAAGAGTTC
  AAV9  GTCTGGAGCA CGACTTTGGC AAGGTGACAA AGCAGGAAGT CAAAGAGTTC
  AAV7  GTCTGGAGCA CGACTTTGGC AAGGTGACGA AGCAGGAAGT CAAAGAGTTC
  44_2  GTCTGGAGCA CGACTTTGGC AAGGTGACAA AGCAGGAAGT CAGAGAGTTC
```

Fig. 1AJ

```
         1751                                                      1800
 42_2    TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCTACGT
 42_8    TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCTACGT
42_15    TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCTACGT
42_5b    TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCTACGT
42_1b    .......... .......... .......... .......... ..........
42_13    TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCTACGT
42_3a    TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCTACGT
 42_4    .......... .......... .......... .......... ..........
42_5a    TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCTACGT
42_10    .......... .......... .......... .......... ..........
42_3b    .......... .......... .......... .......... ..........
42_11    TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCTACGT
42_6b    GCTCCGGTGG ACTTTGCCGA CAGGTACCAA AACAAATGTT CTCGTCACGC
 43_1    TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCTACGT
 43_5    TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCTACGT
43_12    TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCTACGT
43_20    TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCCACGT
43_21    TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCCACGT
43_23    TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCCACGT
43_25    TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCCACGT
 44_1    TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCACG AGTTCTACGT
 44_5    TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCACG AGTTCTACGT
223_10   .......... .......... .......... .......... ..........
223_2    .......... .......... .......... .......... ..........
223_4    .......... .......... .......... .......... ..........
223_5    .......... .......... .......... .......... ..........
223_6    .......... .......... .......... .......... ..........
223_7    .......... .......... .......... .......... ..........
 A3_4    TTCCGGTGGG CTCAAGATCA CGTGACTGAG GTGGAGCATG AGTTCTACGT
 A3_5    TTCCGGTGGG CTCAAGATCA CGTGACTGAG GTGGAGCATG AGTTCTACGT
 A3_7    TTCCGGTGGG CTCAAGATCA CGTGACTGAG GTGGAGCATG AGTTCTACGT
 A3_3    TTCCGGTGGG CTCAAGATCA CGTGACTGAG GTGGAGCATG AGTTCTACGT
42_12    TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCTACGT
 AAV1    TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCTACGT
 AAV2    TTCCGGTGGG CAAAGGATCA CGTGGTTGAG GTGGAGCATG AATTCTACGT
 AAV3    TTCCGGTGGG CTTCCGATCA CGTGACTGAC GTGGCTCATG AGTTCTACGT
 AAV8    TTCCGCTGGG CCAGTGATCA CGTGACCGAG GTGGCGCATG AGTTTTACGT
 AAV9    TTCCGCTGGG CCAGTGATCA CGTGACCGAG GTGGCGCATG AGTTTTACGT
 AAV7    TTCCGCTGGG CCAGTGATCA CGTGACCGAG GTGGCGCATG AGTTCTACGT
 44_2    TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCACG AGTTCTACGT
```

Fig. 1AK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1850
P40/TATA
42_2 CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATAAAA
42_8 CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATAAAA
42_15 CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATAAAA
42_5b CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATAAAA
42_1b ....
42_13 CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATAAAA
42_3a CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATAAAA
42_4 ....
42_5a CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATAAAA
42_10 ....
42_3b ....
42_11 CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATAAAA
42_6b GGGCATAGCG CTGACGTAAA TCACGTCATA GGGGAGTGGT CCTGTATTAG
43_1 CAGAAAGGGC GGAGCCAGCA AAAGACCCGC CCCCGATGAC GCGGATATAA
43_5 CAGAAAGGGC GGAGCCAGCA AAAGACCCGC CCCCGATGAC GCGGATATAA
43_12 CAGAAAGGGC GGAGCCAGCA AAAGACCCGC CCCCGATGAC GCGGATATAA
43_20 CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATATAA
43_21 CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATATAA
43_23 CAGAAAGGGT GGCGCCAACA AGAGACCCGC CCCCGATGAC GCGGATATAA
43_25 CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATATAA
44_1 CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATAAAA
44_5 CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATAAAA
223_10 ....
223_2 ....
223_4 ....
223_5 ....
223_6 ....
223_7 ....
A3_4 CAAAAAGGGT GGAGCCAAGA AAAGGCCCGC CCCCGATGAT GTATATATAA
A3_5 CAAAAAGGGT GGAGCCAAGA AAAGGCCCGC CCCCGATGAT GTATATATAA
A3_7 CAAAAAGGGT GGAGCCAAGA AAAGGCCCGC CCCCGATGAT GTATATATAA
A3_3 CAAAAAGGGT GGAGCCAAGA AAAGGCCCGC CCCCGATGAT GTATATATAA
42_12 CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATAAAA
AAV1 CAGAAAGGGT GGAGCCAACA AAAGACCCGC CCCCGATGAC GCGGATAAAA
AAV2 CAAAAAGGGT GGAGCCAAGA AAAGACCCGC CCCCAGTGAC GCAGATATAA
AAV3 CAGAAAGGGT GGAGCTAAGA AACGCCCCGC CTCCAATGAC GCGGATGTAA
AAV8 CAGAAAGGGC GGAGCCAGCA AAAGACCCGC CCCCGATGAC GCGGATAAAA
AAV9 CAGAAAGGGC GGAGCCAGCA AAAGACCCGC CCCCGATGAC GCGGATAAAA
AAV7 CAGAAAGGGC GGAGCCAGCA AAAGACCCGC CCCCGATGAC GCGGATATAA
44_2 CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATAAAA
P40/TATA

Fig. 1AL

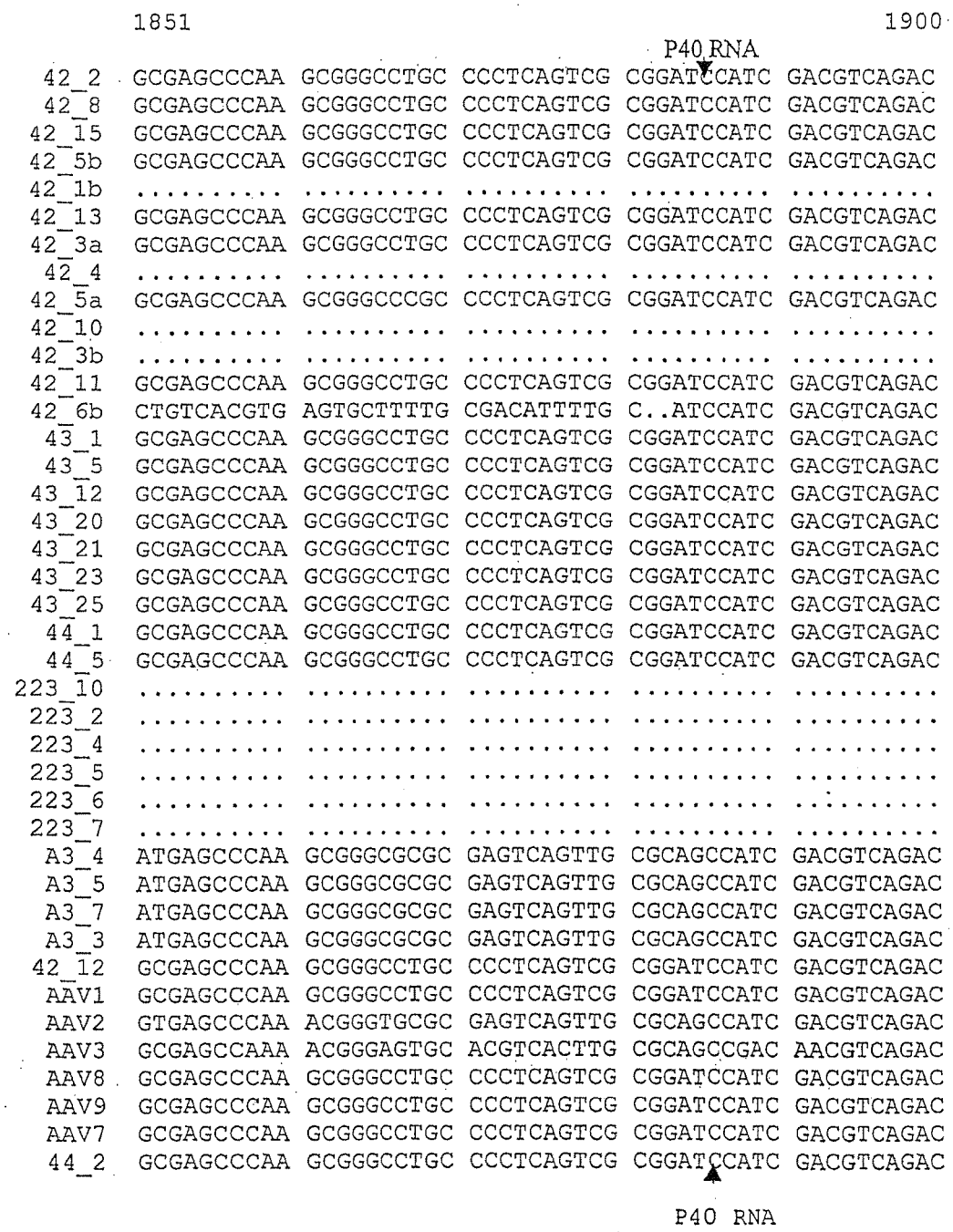
1851
1900
P40 RNA
42_2 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
42_8 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
42_15 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
42_5b GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
42_1b ....
42_13 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
42_3a GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
42_4 ....
42_5a GCGAGCCCAA GCGGGCCCGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
42_10 ....
42_3b ....
42_11 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
42_6b CTGTCACGTG AGTGCTTTTG CGACATTTTG C..ATCCATC GACGTCAGAC
43_1 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
43_5 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
43_12 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
43_20 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
43_21 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
43_23 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
43_25 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
44_1 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
44_5 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
223_10 ....
223_2 ....
223_4 ....
223_5 ....
223_6 ....
223_7 ....
A3_4 ATGAGCCCAA GCGGGCGCGC GAGTCAGTTG CGCAGCCATC GACGTCAGAC
A3_5 ATGAGCCCAA GCGGGCGCGC GAGTCAGTTG CGCAGCCATC GACGTCAGAC
A3_7 ATGAGCCCAA GCGGGCGCGC GAGTCAGTTG CGCAGCCATC GACGTCAGAC
A3_3 ATGAGCCCAA GCGGGCGCGC GAGTCAGTTG CGCAGCCATC GACGTCAGAC
42_12 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
AAV1 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
AAV2 GTGAGCCCAA ACGGGTGCGC GAGTCAGTTG CGCAGCCATC GACGTCAGAC
AAV3 GCGAGCCAAA ACGGGAGTGC ACGTCACTTG CGCAGCCGAC AACGTCAGAC
AAV8 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
AAV9 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
AAV7 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
44_2 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
P40 RNA

Fig. 1AM

```
        1901                                                  1950
  42_2  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
  42_8  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
 42_15  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
 42_5b  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
 42_1b  .......... .......... .......... .......... ..........
 42_13  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
 42_3a  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
  42_4  .......... .......... .......... .......... ..........
 42_5a  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
 42_10  .......... .......... .......... .......... ..........
 42_3b  .......... .......... .......... .......... ..........
 42_11  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
 42_6b  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAGTGTTC
  43_1  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
  43_5  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
 43_12  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
 43_20  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
 43_21  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
 43_23  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
 43_25  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
  44_1  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
  44_5  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
223_10  .......... .......... .......... .......... ..........
 223_2  .......... .......... .......... .......... ..........
 223_4  .......... .......... .......... .......... ..........
 223_5  .......... .......... .......... .......... ..........
 223_6  .......... .......... .......... .......... ..........
 223_7  .......... .......... .......... .......... ..........
  A3_4  GCGGA...AG CTTCGATAAA CTACGCGGGC AGGTACCAAA ACAAATGTTC
  A3_5  GCGGA...AG CTTCGATAAA CTACGCGGAC AGGTACCAAA ACAAATGTTC
  A3_7  GCGGA...AG CTTCGATAAA CTACGCGGAC AGGTACCAAA ACAAATGTTC
  A3_3  GCGGA...AG CTTCGATAAA CTACGCGGAC AGGTACCAAA ACAAATGTTC
 42_12  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
  AAV1  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
  AAV2  GCGGA...AG CTTCGATCAA CTACGCAGAC AGGTACCAAA ACAAATGTTC
  AAV3  GCGGA...AG CACCGGCGGA CTACGCGGAC AGGTACCAAA ACAAATGTTC
  AAV8  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
  AAV9  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
  AAV7  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
  44_2  GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
```

Fig. 1AN

```
        1951                                                  2000
  42_2  TCGTCACGCG GGCATGCTTC AGATGCTGTT TCCCTG.CAA GACATGCGAG
  42_8  TCGTCACGCG GGCATGCTTC AGATGCTGTT TCCCTG.CAA GACATGCGAG
 42_15  TCGTCACGCG GGCATGCTTC AGATGCTGTT TCCCTG.CAA GACATGCGAG
 42_5b  TCGTCACGCG GGCATGCTTC AGATGCTGTT TCCCTG.CAA GACATGCGAG
 42_1b  .......... .......... ....GAATTC GCCCTT.... .GGCTGCGTC
 42_13  TCGTCACGCG GGCATGCTTC AGATGCTGTT TCCCTG.CAA GACATGCGAG
 42_3a  TCGTCACGCG GGCATGCTTC AGATGCTGCT TCCCTG.CAA GACATGCGAG
  42_4  .......... .......... ....GAATTC GCCCTTTCTA CGGCTGCGTC
 42_5a  TCGTCACGCG GGCATGCTTC AGATGCTGTT TCCCTG.CAA AACATGCGAG
 42_10  .......... .......... ....GAATTC GCCCTTTCTA CGGCTGCGTC
 42_3b  .......... .......... ....GAATTC GCCCTTTCTA CGGCTGCGTC
 42_11  TCGTCACGCG GGCATGCTTC AGATGCTGTT TCCCTG.CAA GACATGCGAG
 42_6b  TCGTCACGCG GGCATGCTTC AGATGCTGTT TCCCTG.CAA GACATGCGAG
  43_1  TCGTCACGCG GGCATGCTTC AGATGCTGTT TCCCTG.CAA AACGTGCGAG
  43_5  TCGTCACGCG GGCATGCTTC AGACGCTGTT TCCCTG.CAA AACGTGCGAG
 43_12  TCGTCACGCG GGCATGCTCC AGATGCTGTT TCCCTG.CAA AACGTGCGAG
 43_20  TCGTCACGCG GGCATGCTTC AGATGCTGTT TCCCTG.CAA GACATGCGAG
 43_21  TCGTCACGCG GGCATGCTTC AGATGCTGTT TCCCTG.CAA GACATGCGAG
 43_23  TCGTCACGCG GGCATGCTTC AGATGCTGTT TCCCTG.CAA GACATGCGAG
 43_25  TCGTCACGCG GGCATGCTTC AGATGCTGTT TCCCTG.CAA GACATGCGAG
  44_1  TCGTCACGCG GGCATGCTTC AGATGCTGTT TCCCTG.CAA AACATGCGAG
  44_5  TCGTCACGCG GGCATGCTTC AGATGCTGTT TCCCTG.CAA AACATGCGAG
223_10  .......... .......... .......... .......... ..........
 223_2  .......... .......... .......... .......... ..........
 223_4  .......... .......... .......... .......... ..........
 223_5  .......... .......... .......... .......... ..........
 223_6  .......... .......... .......... .......... ..........
 223_7  .......... .......... .......... .......... ..........
  A3_4  TCGTCACGTG GGCATGAATC TGATGCTGTT TCCCTG.TCG ACAATGCGAA
  A3_5  TCGTCACGTG GGCATGAATC TGATGCTGTT TCCCTG.TCG ACAATGCGAA
  A3_7  TCGTCACGTG GGCATGAATC TGATGCTGTT TCCCTG.TCG ACAATGCGAA
  A3_3  TCGTCACGTG GGCATGAATC TGATGCTGTT TCCCTG.TCG ACAATGCGAA
 42_12  TCGTCACGCG GGCATGCTTC AGATGCTGTT TCCCTG.CAA GACATGCGAG
  AAV1  TCGTCACGCG GGCATGCTTC AGATGCTGTT TCCCTG.CAA GACATGCGAG
  AAV2  TCGTCACGTG GGCATGAATC TGATGCTGTT TCCCTG.CAG ACAATGCGAG
  AAV3  TCGTCACGTG GGCATGAATC TGATGCTTTT TCCCTG.TAA AACATGCGAG
  AAV8  TCGTCACGCG GGCATGCTTC AGATGCTGTT TCCCTG.CAA AACGTGCGAG
  AAV9  TCGTCACGCG GGCATGCTTC AGATGCTGCT TCCCTG.CAA AACGTGCGAG
  AAV7  TCGTCACGCG GGCATGATTC AGATGCTGTT TCCCTG.CAA AACGTGCGAG
  44_2  TCGTCACGCG GGCATGCTTC AGATGCTGTT TCCCTG.CAA AACATGCGAG
```

Fig. 1AO

```
          2001                                                      2050
  42_2    AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCACGGGA CCAGAGACTG
  42_8    AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCACGGGA CCAGAGACTG
 42_15    AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCGCGGGA CCAGAGACTG
 42_5b    AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCACGGGA CCAGAGACTG
 42_1b    A.ACTGGACC A..ATGAGAA CTTTCCCTTC A........A CGATTGCGTC
 42_13    AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCACGGGA CCAGAGACTG
 42_3a    AGAATGAATC AGAATTTCAG CATTTGCTTC ACGCACGGGA CCAGAGACTG
  42_4    A.ACTGGACC A..ATGAGAA CTTTCCCTTC A........A CGATTGCGTC
 42_5a    AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCACGGGA CCAGAGACTG
 42_10    A.ACTGGACC A..ATGAGAA CTTTCCCTTC A........A CGATTGCGTC
 42_3b    A.ACTAGACC A..ATGAGAA CTTTCCCTTC A........A CGATTGCGTC
 42_11    AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCACGGGA CCGGAGACTG
 42_6b    AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCACGGGA CCAGAGACTG
  43_1    AAAATGAATC AGAATTTCAA CATTTGCTTC ACGCACGGGG TCAGAGACTG
  43_5    AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCACGGGG TCAGAGACTG
 43_12    AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCACGGGG TCAGAGACTG
 43_20    AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCACGGGA CCAGAGACTG
 43_21    AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCACGGGA CCAGAGACTG
 43_23    AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCACGGGA CCAGAGACTG
 43_25    AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCACGGGA CCAGAGACTG
  44_1    AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCACGGGA CCAGAGACTG
  44_5    AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCACGGGA CCAGAGACTG
223_10    .......... .......... .......... .......... ..........
 223_2    .......... .......... .......... .......... ..........
 223_4    .......... .......... .......... .......... ..........
 223_5    .......... .......... .......... .......... ..........
 223_6    .......... .......... .......... .......... ..........
 223_7    .......... .......... .......... .......... ..........
  A3_4    AGAATGAATC AGAATTCAAA TATCTGCTTC ACACACGGGC AAAAAGACTG
  A3_5    AGAATGAATC AGAATTCAAA TATCTGCTTC ACACACGGGC AAAAAGACTG
  A3_7    AGAATGAATC AGAATTCAAA TATCTGCTTC ACACACGGGC AAAAAGACTG
  A3_3    AGAATGAATC AGAATTCAAA TATCTGCTTC ACACACGGGC AAAAAGACTG
 42_12    AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCACGGGA CCAGAGACTG
  AAV1    AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCACGGGA CGAGAGACTG
  AAV2    AGAATGAATC AGAATTCAAA TATCTGCTTC ACTCACGGAC AGAAAGACTG
  AAV3    AGAATGAATC AAATTTCCAA TGTCTGTTTT ACGCATGGTC AAAGAGACTG
  AAV8    AGAATGAATC AGAATTTCAA CATTTGCTTC ACACACGGGG TCAGAGACTG
  AAV9    AGAATGAATC AGAATTTCAA CATTTGCTTC ACACACGGGG TCAGAGACTG
  AAV7    AGAATGAATC AGAATTTCAA CATTTGCTTC ACACACGGGG TCAGAGACTG
  44_2    AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCACGGGA CCAGAGACTG
```

Fig. 1AP

```
        2051                                                        2100
 42_2   TTCAGAATGT TTCCCCGGCG TGTCAGAATC TCAACC.... ..GGTCGTCA

 42_8   TTCAGAATGT TTCCCCGGCG TGTCAGAATC TCAACC.... ..GGTCGTCA
42_15   TTCAGAATGT TTCCCGGGCG TGTCAGAATC TCAACC.... ..GGTCGTCA
42_5b   TTCAGAATGT TTCCCCGGCG TGTCAGAATC TCAACC.... ..GGTCGTCA
42_1b   GACAAGATGG TGATCTGGTG GG..AGGAGG GCAAGA.... ..TGACGGCC
42_13   TTCAGAATGT TTCCCCGGCG TGTCAGAATC TCAACC.... ..GGTCGTCA
42_3a   TTCAGAATGT TTCCCCGGCG TGTCAGAATC TCAACC.... ..GGTCGTCA
 42_4   GACAAGATGG TGATCTGGTG GG..AGGAGG GCAAGA.... ..TGACGGCC
42_5a   TTCAGAATGT TTCCCCGGCG TGTCAGAATC TCAACC.... ..GGTCGTCA
42_10   GACAAGATGG TGATCTGGTG GG..AGGAGG GCAAGA.... ..TGACGGCC
42_3b   GACAAGATGG TGATCTGGTG GG..AGGAGG GCAAGA.... ..TGACGGCC
42_11   TTCAGAATGT TTCCCCGGCG TGTCAGAATC TCAACC.... ..GGTCGTCA
42_6b   TTCAGAATGT TTCCCCGGCG TGTCAGAATC TCAACC.... ..GGTCGTCA
 43_1   CTCAGAATGT TTCCCCGGTG CATCAGAATC TCAACC.... ..GGTCGTCA
 43_5   CTCAGAATGT TTCCCCGGTG CATCAGAATC TCAACC.... ..GGTCGTCA
43_12   CTCAGAATGT TTCCCCGGTG CATCAGAATC TCAACC.... ..GGTCGTCA
43_20   TTCAGAATGT TTCCCCGGCG TGTCAGAATC TCAACC.... ..GGTCGTCA
43_21   TTCAGAATGT TTCCCCGGCG TGTCAGAATC TCAACC.... ..GGTCGTCA
43_23   TTCAGAATGT TTCCCCGGCG TGTCAGAATC TCAACC.... ..GGTCGTCA
43_25   TTCAGAATGT TTCCCCGGCG TGTCAGAATC TCAACC.... ..GGTCGTCA
 44_1   TTCAGAATGT TTCCCCGGCG TGTCAGAATC TCAACC.... ..GGTCGTCA
 44_5   TTCAGAATGT TTCCCCGGCG TGTCAGAATC TCAACC.... ..GGTTGTCA
223_10  .......... .......... .......... .......... ..........
223_2   .......... .......... .......... .......... ..........
223_4   .......... .......... .......... .......... ..........
223_5   .......... .......... .......... .......... ..........
223_6   .......... .......... .......... .......... ..........
223_7   .......... .......... .......... .......... ..........
 A3_4   TTTGGAATGC TTTCCCG... TGTCAGAATC TCAACCCGTT TCTGTCGTCA
 A3_5   TTTGGAATGC TTTCCCG... TGTCAGAATC TCAACCCGTT CCTGTCGTCA
 A3_7   TTTGGAATGC TTTCCCG... TGTCAGAATC TCAACCCGTT TCTGTCGTCA
 A3_3   TTTGGAATGC TTTCCCG... TGTCAGAATC TCAACCCGTT TCTGTCGTCA
42_12   TTCAGAATGT TTCCCCGGCG TGTCAGAATC TCAACC.... ..GGTCGTCA
 AAV1   TTCAGAGTGC TTCCCCGGCG TGTCAGAATC TCAACC.... ..GGTCGTCA
 AAV2   TTTAGAGTGC TTTCCCG... TGTCAGAATC TCAACCCGTT TCTGTCGTCA
 AAV3   TGGGGAATGC TTCCCTGGAA TGTCAGAATC TCAACCCGTT TCTGTCGTCA
 AAV8   CTCAGAGTGT TTCCCCGGCG TGTCAGAATC TCAACC.... ..GGTCGTCA
 AAV9   CTCAGAGTGT TTCCCCGGCG TGTCAGAATC TCAACC.... ..GGTCGTCA
 AAV7   TTTAGAGTGT TTCCCCGGCG TGTCAGAATC TCAACC.... ..GGTCGTCA
 44_2   TTCAGAATGT TTCCCCGGCG TGTCAGAATC TCAACC.... ..GGTCGTCA
```

Fig. 1AQ

```
        2101                                                        2150
 42_2   GAAAGAGGAC GTATCGGAAA CTCTGTGCCA TTCATCATCT GCTGGGG.CG

 42_8   GAAAGAGGAC GTATCGGAAA CTCTGTGCCA TTCATCATCT GCTAGGG.CG
42_15   GAAAGAGGAC GTATCGGAAA CTCTGTGCCA TTCATCATCT GCTGGGG.CG
42_5b   GAAAGAGGAC GTATCGGAAA CTCTGTGCCA TTCATCATCT GCTGGGG.CG
42_1b   .AAGGTCGTG GAGTCCGCCA AG....GCCA TTCATCATCT GCTGGGG.CG
42_13   GAAAGAGGAC GTATCGGAAA CTCTGTGCCA TTCATCATCT GCTGGGG.CG
42_3a   GAAAGAGGAC GTATCGGAAA CTCTGTGCCA TTCATCATCT GCTGGGG.CG
 42_4   .AAGGTCGTG GAGTCCGCCA AG....GCCA TTCATCATCT GCTGGGG.CG
42_5a   GAAAGAGGAC GTATCGGAAA CTCTGTGCCA TTCATCATCT GCTGGGG.CG
42_10   AA....GGTC GTGAAGTCCG CCAAG.GCCA TTCATCATCT GCTGGGG.CG
42_3b   AA....GGTC GTGGAGTCCG CCAAG.GCCA TTCATCATCT GCTGGGG.CG
42_11   GAAAGAGGAC GTATCGGAAA CTCTGTGCCA TTCATCATCT GCTGGGG.CG
42_6b   GAAAGAGGAC GTATCGGAAA CTCTGTGCCA TTCATCATCT GCTGGGG.CG
 43_1   GAAAAAAAAC GTATCAGAAA CTGTGTGCCA TTCATCATCT GCTGGGG.CG
 43_5   GAAAAAAAAC GTATCAGAAA CTGTGTGCCA TTCATCATCT GCTGGGG.CG
43_12   GAAAAAAAAC GTATCAGAAA CTGTGTGCCA TTCATCATCT GCTGGGG.CG
43_20   GAAAGAGGAC GTATCGGAAA CTCTGTGCGA TTCATCATCT GCTGGGG.CG
43_21   GAAAGAGGAC GTATCGGAAA CTCTGTGCGA TTCATCATCT GCTGGGG.CG
43_23   GAAAGAGGAC GTATCGGAAA CTCTGTGCGA TTCATCATCT GCTGGGG.CG
43_25   GAAAGAGGAC GTATCGGAAA CTCTGTGCGA TTCATCATCT GCTGGGG.CG
 44_1   GAAAAAAGAC GTATCGGAAA CTCTGTGCGA TTCATCATCT GCTGGGG.CG
 44_5   GAAAAAAGAC GTATCGGAAA CTCTGTGCGA TTCATCATCT GCTGGGG.CG
223_10  .......... .......... .......... .......... ..........
223_2   .......... .......... .......... .......... ..........
223_4   .......... .......... .......... .......... ..........
223_5   .......... .......... .......... .......... ..........
223_6   .......... .......... .......... .......... ..........
223_7   .......... .......... .......... .......... ..........
 A3_4   GAAAAACG.. .TATCAGAAA CTTTGTTACA TTCATCATAT CATGGGA.AA
 A3_5   GAAAAACG.. .TATCAGAAA CTTTGTTACA TTCATCATAT CATGGGA.AA
 A3_7   GAAAAACG.. .TATCAGAAA CTTTGTTACA TTCATCATAT CATGGGA.AA
 A3_3   GAAAAACG.. .TATCAGAAA CTTTGTTACA TTCATCATAT CATGGGA.AA
42_12   GAAAGAGGAC GTATCGGAAA CTCTGTGCCA TTCATCATCT GCTGGGG.CG
 AAV1   GAAAGAGGAC GTATCGGAAA CTCTGTGCCA TTCATCATCT GCTGGGG.CG
 AAV2   AAAAGGCG.. .TATCAGAAA CTGTGCTACA TTCATCATAT CATGGGA.AA
 AAV3   AAAAGAAGAC TTATCAGAAA CTGTGTCCAA TTCATCATAT CCTGGGA.AG
 AAV8   GAAAGAGGAC GTATCGGAAA CTCTGTGCGA TTCATCATCT GCTGGGG.CG
 AAV9   GAAAGAGGAC GTATCGGAAA CTCTGTGCGA TTCATCATCT GCTGGGG.CG
 AAV7   GAAAAAAGAC GTATCGGAAA CTCTGCGCGA TTCATCATCT GCTGGGG.CG
 44_2   GAAAAAAGAC GTATCGGAAA CTCTGTGCGA TTCATCATCT GCTGGGGGCG
```

Fig. 1AR

```
         2151                                                        2200
  42_2   GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
  42_8   GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
 42_15   GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
 42_5b   GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
 42_1b   GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
 42_13   GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
 42_3a   GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
  42_4   GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
 42_5a   GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
 42_10   GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
 42_3b   GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
 42_11   GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
 42_6b   GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
  43_1   GGCACCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
  43_5   GGCACCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
 43_12   GGCACCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
 43_20   GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
 43_21   GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
 43_23   GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
 43_25   GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
  44_1   GGCACCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTAG
  44_5   GGCACCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTAG
223_10   .......... .......... .......... .......... ..........
 223_2   .......... .......... .......... .......... ..........
 223_4   .......... .......... .......... .......... ..........
 223_5   .......... .......... .......... .......... ..........
 223_6   .......... .......... .......... .......... ..........
 223_7   .......... .......... .......... .......... ..........
  A3_4   AGAACCAGAC ...GCCTGCA CTGCCTGCGA CCTGGTAAAT GTGGACTTGG
  A3_5   AGTACCAGAC ...GCCTGCA CTGCCTGCGA CCTGGTAAAT GTGGACTTGG
  A3_7   AGTACCAGAC ...GCCTGCA CTGCCTGCGA CCTGGTAAAT GTGGACTTGG
  A3_3   AGTACCAGAC ...GCCTGCA CTGCCTGCGA CCTGGTAAAT GTGGACTTGG
 42_12   GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
   AAV1  GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
   AAV2  GGTGCCAGAC ...GCTTGCA CTGCCTGCGA TCTGGTCAAT GTGGATTTGG
   AAV3  GGCACCCGAG ATTGCCTGTT CGGCCTGCGA TTTGGCCAAT GTGGACTTGG
   AAV8  GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
   AAV9  GGCTCCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTGG
   AAV7  GGCGCCCGAG ATTGCTTGCT CGGCCTGCGA CCTGGTCAAC GTGGACCTGG
  44_2   GGCACCCGAG ATTGCTTGCT CGGCCTGCGA TCTGGTCAAC GTGGACCTAG
```

Fig. 1AS

```
          2201                                                    2250

                                  Rep 78 stop          vp1 start
  42_2    ATGACCGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
  42_8    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
 42_15    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
 42_5b    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
 42_1b    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
 42_13    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
 42_3a    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
  42_4    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
 42_5a    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
 42_10    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
 42_3b    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
 42_11    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
 42_6b    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
  43_1    ACGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
  43_5    ACGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
 43_12    ACGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
 43_20    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
 43_21    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
 43_23    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
 43_25    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
  44_1    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
  44_5    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
223_10    .......... .......... .......... .......... ..........
 223_2    .......... .......... .......... .......... ..........
 223_4    .......... .......... .......... .......... ..........
 223_5    .......... .......... .......... .......... ..........
 223_6    .......... .......... .......... .......... ..........
 223_7    .......... .......... .......... .......... ..........
  A3_4    ATGACTGTAT TTCTGAGCAA TAAATGACTT AAATCAGGTA TGGCTGCTGA
  A3_5    ATGACTGTAT TTCTGAGCAA TAAATGACTT AAATCAGGTA TGGCTGCTGA
  A3_7    ATGACTGTAT TTCTGAGCAA TAAATGACTT AAATCAGGTA TGGCTGCTGA
  A3_3    ATGACTGTAT TTCTGAGCAA TAAATGACTT AAATCAGGTA TGGCTGCTGA
 42_12    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
  AAV1    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
  AAV2    ATGACTGCAT CTTTGAACAA TAAATGATTT AAATCAGGTA TGGCTGCCGA
  AAV3    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCTGA
  AAV8    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
  AAV9    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
  AAV7    ACGACTGCGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
  44_2    ATGACTGTGT TTCTGAGCAA TAAATGACTT AAACCAGGTA TGGCTGCCGA
                              Rep78 stop           vp1 start
```

Fig. 1AT

```
        2251                                                  2300
                                                   Rep68 stop
  42_2  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
  42_8  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
 42_15  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
 42_5b  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
 42_1b  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
 42_13  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
 42_3a  TGGTCATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
  42_4  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
 42_5a  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
 42_10  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
 42_3b  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
 42_11  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
 42_6b  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
  43_1  TGGTTATCTT CCAGATTGGC TTGAGGACAA CCTCTCTGAG GGCATTCGCG
  43_5  TGGTTATCTT CCAGATTGGC TTGAGGACAA CCTCTCTGAG GGCATTCGCG
 43_12  TGGTTATCTT CCAGATTGGC TTGAGGACAA CCTCTCTGAG GGCATTCGCG
 43_20  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
 43_21  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
 43_23  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
 43_25  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
  44_1  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
  44_5  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
223_10  .......... .......... .......... .......... ..........
 223_2  .......... .......... .......... .......... ..........
 223_4  .......... .......... .......... .......... ..........
 223_5  .......... .......... .......... .......... ..........
 223_6  .......... .......... .......... .......... ..........
 223_7  .......... .......... .......... .......... ..........
  A3_4  CGGTTATCTT CCAGATTGGC TCGAGGACAC TCTCTCTGAA GGAATCAGAC
  A3_5  CGGTTATCTT CCAGATTGGC TCGAGGACAC TCTCTCTGAA GGAATCAGAC
  A3_7  CGGTTATCTT CCAGATTGGC TCGAGGACAC TCTCTCTGAA GGAATCAGAC
  A3_3  CGGTTATCTT CCAGATTGGC TCGAGGACAC TCTCTCTGAA GGAATCAGAC
 42_12  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATCCGCG
  AAV1  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
  AAV2  TGGTTATCTT CCAGATTGGC TCGAGGACAC TCTCTCTGAA GGAATAAGAC
  AAV3  CGGTTATCTT CCAGATTGGC TCGAGGACAA CCTTTCTGAA GGCATTCGTG
  AAV8  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
  AAV9  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
  AAV7  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
  44_2  TGGTTATCTT CCAGATTGGC TCGAGGACAA CCTCTCTGAG GGCATTCGCG
                                                   Rep 68 stop
```

Fig. 1AU

```
          2301                                                      2350
 42_2     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA

 42_8     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
42_15     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
42_5b     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
42_1b     AGTGGTGGGA CTTGAGACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
42_13     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
42_3a     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
 42_4     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
42_5a     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
42_10     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
42_3b     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
42_11     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
42_6b     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
 43_1     AGTGGTGGGA CCTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
 43_5     AGTGGTGGGA CCTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
43_12     AGTGGTGGGA CCTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
43_20     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
43_21     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
43_23     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
43_25     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
 44_1     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
 44_5     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
223_10    .......... .......... .......... .......... ..........
223_2     .......... .......... .......... .......... ..........
223_4     .......... .......... .......... .......... ..........
223_5     .......... .......... .......... .......... ..........
223_6     .......... .......... .......... .......... ..........
223_7     .......... .......... .......... .......... ..........
 A3_4     AGTGGTGGAA GCTCAAACCT GGCCCACCAC CGCCGAAACC TAACCAACAA
 A3_5     AGTGGTGGAA GCTCAAACCT GGCCCACCAC CGCCGAAACC TAACCAACAA
 A3_7     AGTGGTGGAA GCTCAAACCT GGCCCACCAC CGCCGAAACC TAACCAACAA
 A3_3     AGTGGTGGAA GCTCAAACCT GGCCCACCAC CGCCGAAACC TAACCAACAA
42_12     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
 AAV1     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AGCCCAAAGC CAACCAGCAA
 AAV2     AGTGGTGGAA GCTCAAACCT GGCCCACCAC CACCAAAGCC CGCAGAGCGG
 AAV3     AGTGGTGGGC TCTGAAACCT GGAGTCCCTC AACCCAAAGC GAACCAACAA
 AAV8     AGTGGTGGGC GCTGAAACCT GGAGCCCCGA AGCCCAAAGC CAACCAGCAA
 AAV9     AGTGGTGGGC GCTGAAACCT GGAGCCCCGA AGCCCAAAGC CAACCAGCAA
 AAV7     AGTGGTGGGA CCTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
 44_2     AGTGGTGGGA CTTGAAACCT GGAGCCCCGA AACCCAAAGC CAACCAGCAA
```

Fig. 1AV

```
        2351                                                        2400
 42_2   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 42_8   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
42_15   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
42_5b   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
42_1b   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
42_13   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
42_3a   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 42_4   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
42_5a   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
42_10   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
42_3b   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
42_11   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
42_6b   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 43_1   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 43_5   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
43_12   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
43_20   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
43_21   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
43_23   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
43_25   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 44_1   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 44_5   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
223_10  .......... .......... .......... .......... ..........
223_2   .......... .......... .......... .......... ..........
223_4   .......... .......... .......... .......... ..........
223_5   .......... .......... .......... .......... ..........
223_6   .......... .......... .......... .......... ..........
223_7   .......... .......... .......... .......... ..........
 A3_4   CACCGGGACG ACAGTAGGGG TCTTGTGCTT CCTGGGTACA AGTACCTCGG
 A3_5   CACCGGGACG ACAGTAGGGG TCTTGTGCTT CCTGGGTACA AGTACCTCGG
 A3_7   CACCGGGACG ACAGTAGGGG TCTTGTGCTT CCTGGGTACA AGTACCTCGG
 A3_3   CACCGGGACG ACAGTAGGGG TCTTGTGCTT CCTGGGTACA AGTACCTCGG
42_12   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 AAV1   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 AAV2   CATAAGGACG ACAGCAGGGG TCTTGTGCTT CCTGGGTACA AGTACCTCGG
 AAV3   CACCAGGACA ACCGTCGGGG TCTTGTGCTT CCGGGTTACA AATACCTCGG
 AAV8   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 AAV9   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 AAV7   AAGCAGGACA ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 44_2   AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
```

Fig. 1AW

```
          2401                                                        2450
 42_2     ACCCTTCAAC GGACTCGACA AGGGAGAGCC GGTCAACGAG GCAGACGCCG
 42_8     ACCCTTCAAC GGACTCGACA AGGGGGAGCC CGTCAACGCG GCGGACGCAG
42_15     ACCCTTCAAC GGACTCGACA AGGGGGAGCC CGTCAACGCG GCGGACGCAG
42_5b     ACCCTTCAAC GGACTCGACA AGGGAGAGCC GGTCAACGAG GCAGACGCCG
42_1b     ACCCTTCAAC GGACTCGACA AGGGAGAGCC GGTCAACGAG GCAGACGCCG
42_13     ACCCTTCAAC GGACTCGACA AGGGGGAGCC CGTCAACGCG GCGGACGCAG
42_3a     ACCCTTCAAC GGACTCGACA AGGGGGAGCC CGTCAACGCG GCGGACGCAG
 42_4     ACCCTTCAAC GGACTCGACA AGGGAGAGCC GGTCAACGAG GCAGACGCCG
42_5a     ACCCTTCAAC GGACTCGACA AGGGAGAGCC GGTCAACGAG GCAGACGCCG
42_10     ACCCTTCAAC GGACTCGACA AGGGAGAGCC GGTCAACGAG GCAGACGCCG
42_3b     ACCCTTCAAC GGACTCGACA AGGGAGAGCC GGTCAACGAG GCAGACGCCG
42_11     ACCCTTCAAC GGACTCGACA AGGGAGAGCC GGTCAACGCG GCGGACGCAG
42_6b     ACCCTTCAAC GGACTCGACA AGGGAGAGCC GGTCAACGAG GCAGACGCCG
 43_1     ACCCTTCAAC GGACTCGACA AGGGGGAGCC CGTCAACGCG GCGGACGCAG
 43_5     ACCCTTCAAC GGACTCGACA AGGGGGAGCC CGTCAACGCG GCGGACGCAG
43_12     ACCCTTCAAC GGACTCGACA AGGGGGAGCC CGTCAACGCG GCGGACGCAG
43_20     ACCCTTCAAC GGACTCGACA AGGGGGAGCC CGTCAACGCG GCGGACGCAG
43_21     ACCCTTCAAC GGACTCGACA AGGGGGAGCC CGTCAACGCG GCGGACGCAG
43_23     ACCCTTCAAC GGACTCGACA AGGGGGAGCC CGTCAACGCG GCGGACGCAG
43_25     ACCCTTCAAC GGACTCGACA AGGGGGAGCC CGTCAACGCG GCGGACGCAG
 44_1     ACCCTTCAAC GGACTCGACA AGGGGGAGCC CGTCAACGCG GCGGACGCAG
 44_5     ACCCTTCAAC GGACTCGACA AGGGGGAGCC CGTCAACGCG GCGGACGCAG
223_10    .......... .......... .......... .......... ..........
223_2     .......... .......... .......... .......... ..........
223_4     .......... .......... .......... .......... ..........
223_5     .......... .......... .......... .......... ..........
223_6     .......... .......... .......... .......... ..........
223_7     .......... .......... .......... .......... ..........
 A3_4     ACCCTTCAAC GGACTCGACA AAGGAGAGCC GGTCAACGAG GCAGACGCCG
 A3_5     ACCCTTCAAC GGACTCGACA AAGGAGAGCC GGTCAACGAG GCAGACGCCG
 A3_7     ACCCTTCAAC GGACTCGACA AAGGAGAGCC GGTCAACGAG GCAGACGCCG
 A3_3     ACCCTTCAAC GGACTCGACA AAGGAGAGCC GGTCAACGAG GCAGACGCCG
42_12     ACCCTTCAAC GGACTCGACA AGGGAGAGCC GGTCAACGAG GCAGACGCCG
 AAV1     ACCCTTCAAC GGACTCGACA AGGGGGAGCC CGTCAACGCG GCGGACGCAG
 AAV2     ACCCTTCAAC GGACTCGACA AGGGAGAGCC GGTCAACGAG GCAGACGCCG
 AAV3     ACCCGGTAAC GGACTCGACA AAGGAGAGCC GGTCAACGAG GCGGACGCGG
 AAV8     ACCCTTCAAC GGACTCGACA AGGGGGAGCC CGTCAACGCG GCGGACGCAG
 AAV9     ACCCTTCAAC GGACTCGACA AGGGGGAGCC CGTCAACGCG GCGGACGCAG
 AAV7     ACCCTTCAAC GGACTCGACA AGGGGGAGCC CGTCAACGCG GCGGACGCAG
 44_2     ACCCTTCAAC GGACTCGACA AGGGGGAGCC CGTCAACGCG GCGGACGCAG
```

Fig. 1AX

```
         2451                                                  2500
  42_2   CGGCCCTCGA GCACG.ACAA GGCCTACGAC AAGCAGCTCG AGCAGGGGGA
  42_8   CGGCCCTCGA GCACG.ACAA GGCCTACGAC CAGCAGCTCA AAGCGGGTGA
 42_15   CGGCCCTCGA GCACG.ACAA GGCCTACGAC CAGCAGCTCA AAGCGGGTGA
 42_5b   CGGCCCTCGA GCACG.ACAA GGCCTACGAC AAGCAGCTCG AGCAGGGGGA
 42_1b   CGGCCCTCGA GCACG.ACAA GGCCTACGAC AAGCAGCTCG AGCAGGGGGA
 42_13   CGGCCCTCGA GCACG.ACAA GGCCTACGAC CAGCAGCTCA AAGCGGGTGA
 42_3a   CGGCCCTCGA GCACG.ACAA GGCCTACGAC CAGCAGCTCA AAGCGGGTGA
  42_4   CGGCCCTCGA GCACG.ACAA GGCCTACGAC AAGCAGCTCG AGCAGGGGGA
 42_5a   CGGCCCTCGA GCACG.ACAA GGCCTACGAC AAGCAGCTCG AGCAGGGGGA
 42_10   CGGCCCTCGA GCACG.ACAA GGCCTACGAC AAGCAGCTCG AGCAGGGGGA
 42_3b   CGGCCCTCGA GCACG.ACAA GGCCTACGAC AAGCAGCTCG AGCAGGGGGA
 42_11   CGGCCCTCGA GCACG.ACAA GGCCTACGAC CAGCAGCTCA AAGCGGGTGA
 42_6b   CGGCCCTCGA GCACG.ACAA GGCCTACGAC AAGCAGCTCG AGCAGGGGGA
  43_1   CGGCCCTCGA GCACG.ACAA GGCCTACGAC CAGCAGCTCA AAGCGGGTGA
  43_5   CGGCCCTCGA GCACG.ACAA GGCCTACGAC CAGCAGCTCA AAGCGGGTGA
 43_12   CGGCCCTCGA GCACG.ACAA GGCCTACGAC CAGCAGCTCA AAGCGGGTGA
 43_20   CGGCCCTCGA GCACG.ACAA AGCCTACGAC CAGCAGCTCA AAGCGGGTGA
 43_21   CGGCCCTCGA GCACG.ACAA AGCCTACGAC CAGCAGCTCA AAGCGGGTGA
 43_23   CGGCCCTCGA GCACG.ACAA AGCCTACGAC CAGCAGCTCA AAGCGGGTGA
 43_25   CGGCCCTCGA GCACG.ACAA AGCCTACGAC CAGCAGCTCA AAGCGGGTGA
  44_1   CGGCCCTCGA GCACG.ACAA GGCCTACGAC CAGCAGCTCA AAGCGGGTGA
  44_5   CGGCCCTCGA GCACG.ACAA GGCCTACGAC CAGCAGCTCA AAGCGGGTGA
223_10   .......... .......CAA GGCCTACGAC CAGCAGCTCA AAGCGGGTGA
 223_2   .......... .......CAA GGCCTACGAC CAGCAGCTCA AAGCGGGTGA
 223_4   .......... .......CAA GGCCTACGAC CAGCAGCTCA AAGCGGGTGA
 223_5   .......... .......CAA GGCCTACGAC CAGCAGCTCA AAGCGGGTGA
 223_6   .......... .......CAA GGCCTACGAC CAGCAGCTCA AAGCGGGTGA
 223_7   .......... .......CAA GGCCTACGAC CAGCAGCTCA AAGCGGGTGA
  A3_4   CGGCCCTCGA GCACG.ACAA AGCCTACGAC CACCAGCTCA AGCAAGGGGA
  A3_5   CGGCCCTCGA GCACG.ACAA AGCCTACGAC CACCAGCTCA AGCAAGGGGA
  A3_7   CGGCCCTCGA GCACG.ACAA AGCCTACGAC CACCAGCTCA AGCAAGGGGA
  A3_3   CGGCCCTCGA GCACG.ACAA AGCCTACGAC CACCAGCTCA AGCAAGGGGA
 42_12   CGGCCCTCGA GCACG.ACAA GGCCTACGAC AAGCAGCTCG AGCAGGGGGA
  AAV1   CGGCCCTCGA GCACG.ACAA GGCCTACGAC CAGCAGCTCA AAGCGGGTGA
  AAV2   CGGCCCTCGA GCACGTACAA AGCCTACGAC CGGCAGCTCG ACAGCGGAGA
  AAV3   CAGCCCTCGA ACACG.ACAA AGCTTACGAC CAGCAGCTCA AGGCCGGTGA
  AAV8   CGGCCCTCGA GCACG.ACAA GGCCTACGAC CAGCAGCTGC AGGCGGGTGA
  AAV9   CGGCCCTCGA GCACG.GCAA GGCCTACGAC CAGCAGCTGC AGGCGGGTGA
  AAV7   CGGCCCTCGA GCACG.ACAA GGCCTACGAC CAGCAGCTCA AAGCGGGTGA
  44_2   CGGCCCTCGA GCACG.ACAA GGCCTACGAC CAGCAGCTCA AAGCGGGTGA
```

Fig. 1AY

	2501				2550
42_2	CAACCCGTAC	CTCAAGTACA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
42_8	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
42_15	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
42_5b	CAACCCGTAC	CTCAAGTACA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
42_1b	CAACCCGTAC	CTCAAGTACA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
42_13	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
42_3a	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
42_4	CAACCCGTAC	CTCAAGTACA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
42_5a	CAACCCGTAC	CTCAAGTACA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
42_10	CAACCCGTAC	CTCAAGTACA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
42_3b	CAACCCGTAC	CTCAAGTACA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
42_11	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
42_6b	CAACCCGTAC	CTCAAGTACA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
43_1	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
43_5	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
43_12	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
43_20	CAATCCGTAC	CTGCGGTATA	ATCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
43_21	CAATCCGTAC	CTGCGGTATA	ATCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
43_23	CAATCCGTAC	CTGCGGTATA	ATCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
43_25	CAATCCGTAC	CTGCGGTATA	ATCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
44_1	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
44_5	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
223_10	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
223_2	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGTGTC
223_4	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
223_5	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
223_6	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
223_7	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
A3_4	CAACCCGTAC	CTCAAATACA	ACCACGCGGA	CGCTGAATTT	CAGGAGCGTC
A3_5	CAACCCGTAC	CTCAAATACA	ACCACGCGGA	CGCTGAATTT	CAGGAGCGTC
A3_7	CAACCCGTAC	CTCAAATACA	ACCACGCGGA	CGCTGAATTT	CAGGAGCGTC
A3_3	CAACCCGTAC	CTCAAATACA	ACCACGCGGA	CGCTGAATTT	CAGGAGCGTC
42_12	CAACCCGTAC	CTCAAGTACA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
AAV1	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
AAV2	CAACCCGTAC	CTCAAGTACA	ACCACGCCGA	CGCGGAGTTT	CAGGAGCGCC
AAV3	CAACCCGTAC	CTCAAGTACA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
AAV8	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
AAV9	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
AAV7	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC
44_2	CAATCCGTAC	CTGCGGTATA	ACCACGCCGA	CGCCGAGTTT	CAGGAGCGTC

Fig. 1AZ

	2551				2600
42_2	TTCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
42_8	TGCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
42_15	TGCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
42_5b	TTCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
42_1b	TTCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
42_13	TTCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
42_3a	TTCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
42_4	TTCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
42_5a	TTCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCGG
42_10	TTCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
42_3b	TTCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
42_11	TTCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
42_6b	TTCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
43_1	TGCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
43_5	TGCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
43_12	TGCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
43_20	TGCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
43_21	TGCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
43_23	TGCAAGAAGA	TACGTCCTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
43_25	TGCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
44_1	TGCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
44_5	TGCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
223_10	TTCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
223_2	TTCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
223_4	TTCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
223_5	TTCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
223_6	TTCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
223_7	TTCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
A3_4	TTCAAGAAGA	TACGTCTTTC	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
A3_5	TTCAAGAAGA	TACGTCTTTC	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
A3_7	TTCAAGAAGA	TACGTCTTTC	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
A3_3	TTCAAGAAGA	TACGTCTTTC	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
42_12	TTCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
AAV1	TGCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
AAV2	TTAAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGACGAGC	AGTCTTCCAG
AAV3	TTCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TTGGCAGAGC	AGTCTTCCAG
AAV8	TGCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
AAV9	TGCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
AAV7	TGCAAGAAGA	TACGTCATTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG
44_2	TGCAAGAAGA	TACGTCTTTT	GGGGGCAACC	TCGGGCGAGC	AGTCTTCCAG

Fig. 1AAA

```
         2601                                                  2650
  42_2   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
  42_8   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
 42_15   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
 42_5b   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
 42_1b   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
 42_13   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
 42_3a   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
  42_4   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
 42_5a   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
 42_10   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
 42_3b   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
 42_11   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
 42_6b   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
  43_1   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
  43_5   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
 43_12   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
 43_20   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
 43_21   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
 43_23   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
 43_25   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
  44_1   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
  44_5   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
223_10   GCCAAAAAGC GGGTTCTCGA ACCTCTTGGT CTGGTTGAGA CGCCAGCTAA
 223_2   GCCAAAAAGC GGGTTCTCGA ACCTCTTGGT CTGGTTGAGA CGCCAGCTAA
 223_4   GCCAAAAAGC GGGTTCTCGA ACCTCTTGGT CTGGTTGAGA CGCCAGCTAA
 223_5   GCCAAAAAGC GGGTTCTCGA ACCTCTTGGT CTGGTTGAGA CGCCAGCTAA
 223_6   GCCAAAAAGC GGGTTCTCGA ACCTCTTGGT CTGGTTGAGA CGCCAGCTAA
 223_7   GCCAAAAAGC GGGTTCTCGA ACCTCTTGGT CTGGTTGAGA CGCCAGCTAA
  A3_4   GCCAAAAAGA GGGTACTCGA GCCTCTTGGT CTGGTTGAGG AAGCTGTTAA
  A3_5   GCCAAAAAGA GGGTACTCGA GCCTCTTGGT CTGGTTGAGG AAGCTGTTAA
  A3_7   GCCAAAAAGA GGGTACTCGA GCCTCTTGGT CTGGTTGAGG AAGCTGTTAA
  A3_3   GCCAAAAAGA GGGTACTCGA GCCTCTTGGT CTGGTTGAGG AAGCTGTTAA
 42_12   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
  AAV1   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
  AAV2   GCGAAAAAGA GGGTTCTTGA ACCTCTGGGC CTGGTTGAGG AACCTGTTAA
  AAV3   GCCAAAAAGA GGATCCTTGA GCCTCTTGGT CTGGTTGAGG AAGCAGCTAA
  AAV8   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
  AAV9   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
  AAV7   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
  44_2   GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
```

Fig. 1AAB

```
        2651                                                  2700

         vp2 start
  42_2  GACGGCTCCT GGAAAGAAGA GACCCATAGA ...ATCCCCC ..........
  42_8  GACGGCTCCT GGAAAGAAGA GACCGGTAGA GCCATCACCC CAGCGTTCTC
 42_15  GACGGCTCCT GGAAAGAAGA GACCGGTAGA GCCATCACCC CAGCGTTCTC
 42_5b  GACGGCTCCT GGAAAGAAGA GACCGGTAGA GCCATCACCC CAGCGTTCTC
 42_1b  GACGGCTCCT GGAAAGAAGA GACCCATAGA ...ATCCCCC ..........
 42_13  GACGGCTCCT GGAAAGAAGA GACCCATAGA ...ATCCCCC ..........
 42_3a  GACGGCTCCT GGAAAGAAGA GACCCATAGA ...ATCCCCC ..........
  42_4  GACGGCTCCT GGAAAGAAGA GACCCATAGA ...ATCCCCC ..........
 42_5a  GACGGCTCCT GGAAAGAAGA GACCCATAGA ...ATCCCCC ..........
 42_10  GACGGCTCCT GGAAAGAAGA GACCCATAGA ...ATCCCCC ..........
 42_3b  GACGGCTCCT GGAAAGAAGA GACCCATAGA ...ATCCCCC ..........
 42_11  GACGGCTCCT GGAAAGAAGA GACCCATAGA ...ATCCCCC ..........
 42_6b  GACGGCTCCT GGAAAGAAGA GACCGGTAGA GCCATCACCC CAGCGTTCTC
  43_1  GACGGCTCCT GGAAAGAAGA GACCGGTAGA GCCATCACCT CAGCGTTCCC
  43_5  GACGGCTCCT GGAAAGAAGA GACCGGTAGA GCCATCACCT CAGCGTTCCC
 43_12  GACGGCTCCT GGAAAGAAGA GACCGGTAGA GCCATCACCT CAGCGTTCCC
 43_20  GACGGCTCCT GGAAAGAAGA GACTGGTAGA GCAGTCGCCA CAAGAG...C
 43_21  GACGGCTCCT GGAAAGAAGA GACCGGTAGA GCAGTCGCCA CAAGAG...C
 43_23  GACGGCTCCT GGAAAGAAGA GACCGGTAGA GCAGTCGCCA CAAGAG...C
 43_25  GACGGCTCCT GGAAAGAAGA GACCGGTAGA GCAGTCGCCA CAAGAG...C
  44_1  GACGGCTCCT GGAAAGAAGA GACCGGTAGA GCCATCACCC CAGCGTTCTC
  44_5  GACGGCTCCT GGAAAGAAGA GACCGGTAGA GCCATCACCC CAGCGTTCTC
223_10  GACGGCACCT GGAAAGAAGC GACCGGTAGA CTCGCCA... ..........
 223_2  GACGGCACCT GGAAAGAAGC GACCGGTAGA CTCGCCA... ..........
 223_4  GACGGCACCT GGAAAGAAGC GACCGGTAGA CTCGCCA... ..........
 223_5  GACGGCACCT GGAAAGAAGC GACCGGTAGA CTCGCCA... ..........
 223_6  GACGGCACCT GGAAAGAAGC GACCGGTAGA CTCGCCA... ..........
 223_7  GACGGCACCT GGAAAGAAGC GACCGGTAGA CTCGCCA... ..........
  A3_4  GACGGCTCCT GGAAAAAAGA GACCTATAGA GCAGTCTCCT GCAGAA...C
  A3_5  GACGGCTCCT GGAAAAAAGA GACCTATAGA GCAGTCTCCT GCAGAA...C
  A3_7  GACGGCTCCT GGAAAAAAGA GACCTATAGA GCAGTCTCCT GCAGAA...C
  A3_3  GACGGCTCCT GGAAAAAAGA GACCTATAGA GCAGTCTCCT GCAGAA...C
 42_12  GACGGCTCCT GGAAAGAAGA GACCGGTAGA GCCATCACCC CAGCGTTCTC
  AAV1  GACGGCTCCT GGAAAGAAAC GTCCGGTAGA GCAGTCGCCA CAAGAG...C
  AAV2  GACGGCTCCG GGAAAAAAGA GGCCGGTAGA GCACTCTCCT GTGGAG...C
  AAV3  AACGGCTCCT GGAAAGAAGG GGGCTGTAGA TCAGTCTCCT CAGGAA...C
  AAV8  GACGGCTCCT GGAAAGAAGA GACCGGTAGA GCCATCACCC CAGCGTTCTC
  AAV9  GACGGCTCCT GGAAAGAAGA GACCGGTAGA GCCATCACCC CAGCGTTCTC
  AAV7  GACGGCTCCT GCAAAGAAGA GACCGGTAGA GCCGTCACCT CAGCGTTCCC
  44_2  GACGGCTCCT GGAAAGAAGA GACCGGTAGA GCCATCACCC CAGCGTTCTC
         vp2 start
```

Fig. 1AAC

```
        2701                                                  2750
  42_2  ..GACTCCTC CACGGGCATC GGCAAGAAAG GCCAGCAGCC CGCTAAAAAG
  42_8  CAGACTCCTC TACGGGCATC GGCAAGACAG GCCAGCAGCC CGCGAAAAAG
 42_15  CAGACTCCTC TACGGGCATC GGCAAGACAG GCCAGCAGCC CGCGAAAAAG
 42_5b  CAGACTCCTC TACGGGCATC GGCAAGACAG GCCAGCAGCC CGCGAAAAAG
 42_1b  ..GACTCCTC CACGGGCATC GGCAAGAAAG GCCAGCAGCC CGCTAAAAAG
 42_13  ..GACTCCTC CACGGGCATC GGCAAGAAAG GCCAGCAGCC CGCTAAAAAG
 42_3a  ..GACTCCTC CACGGGCATC GGCAAGAAAG GCCAGCAGCC CGCTAAAAAG
  42_4  ..GACTCCTC CACGGGCATC GGCAAGAAAG GCCAGCAGCC CGCTAAAAAG
 42_5a  ..GACTCCTC CACGGGCATC GGCAAGAAAG GCCAGCAGCC CGCTAAAAAG
 42_10  ..GACTCCTC CACGGGCATC GGCAGGAAAG GCCAGCAGCC CGCTAAAAAG
 42_3b  ..GACTCCTC CACGGGCATC GGCAAGAAAG GCCAGCAGCC CGCTAAAAAG
 42_11  ..GACTCCTC CACGGGCATC GGCAAGAAAG GCCAGCAGCC CGCTAAAAAG
 42_6b  CAGACTCCTC TACGGGCATC GGCAAGACAG GCCAGCAGCC CGCGAAAAAG
  43_1  CCGACTCCTC CACGGGCATC GGCAAGAAAG GCCACCAGCC CGCGAGAAAG
  43_5  CCGACTCCTC CACGGGCATC GGCAAGAAAG GCCACCAGCC CGCGAGAAAG
 43_12  CCGACTCCTC CACGGGCATC GGCAAGAAAG GCCACCAGCC CGCGAGAAAG
 43_20  CAGACTCCTC CTCGGGCATC GGCAAGACAG GCCAGCAGCC CGCTAAAAAG
 43_21  CAGACTCCTC CTCGGGCATC GGCAAGACAG GCCAGCAGCC CGCTAAAAAG
 43_23  CAGACTCCTC CTCGGGCATC GGCAAGACAG GCCAGCAGCC CGCTAAAAAG
 43_25  CAGACTCCTC CTCGGGCATC GGCAAGACAG GCCAGCAGCC CGCTAAAAAG
  44_1  CAGACTCCTC TACGGGCATC GGCAAGAAAG GCCAGCAGCC CGCGAAAAAG
  44_5  CAGACTCCTC TACGGGCATC GGCAAGAAAG GCCAGCAGCC CGCGAAAAAG
223_10  ..GACTCCAC CTCGGGCATC GGCAAGAAAG GCCAGCAGCC CGCGAAAAAG
 223_2  ..GACTCCAC CTCGGGCATC GGCAAGAAAG GCCAGCAGCC CGCGAAAAAG
 223_4  ..GACTCCAC CTCGGGCATC GGCAAGAAAG GCCAGCAGCC CGCGAAAAAG
 223_5  ..GACTCCAC CTCGGGCATC GGCAAGAAAG GCCAGCAGCC CGCGAAAAAG
 223_6  ..GACTCCAC CTCGGGCATC GGCAAGAAAG GCCAGCAGCC CGCGAAAAAG
 223_7  ..GACTCCAC CTCGGGCATC GGCAAGAAAG GCCAGCAGCC CGCGAAAAAG
  A3_4  CGGACTCTTC CTCGGGCATC GGCGAATCAG GCCAGCAGCC CGCTAAGAAA
  A3_5  CGGACTCTTC CTCGGGCATC GGCAAATCAG GCCAGCAGCC CGCTAAGAAA
  A3_7  CGGACTCTTC CTCGGGCATC GGCAAATCAG GCCAGCAGCC CGCTAAGAAA
  A3_3  CGGACTCTTC CTCGGGCATC GGCAAATCAG GCCAGCAGCC CGCTAAGAAA
 42_12  CAGACTCCTC TACGGGCATC GGCAAGACAG GCCAGCAGCC CGCGAAAAAG
  AAV1  CAGACTCCTC CTCGGGCATC GGCAAGACAG GCCAGCAGCC CGCTAAAAAG
  AAV2  CAGACTCCTC CTCGGGAACC GGAAAGGCGG GCCAGCAGCC TGCAAGAAAA
  AAV3  CGGACTCATC ATCTGGTGTT GGCAAATCGG GCAAACAGCC TGCCAGAAAA
  AAV8  CAGACTCCTC TACGGGCATC GGCAAGAAAG GCCAACAGCC CGCCAGAAAA
  AAV9  CAGACTCCTC TACGGGCATC GGCAAGAAAG GCCAACAGCC CGCCAGAAAA
  AAV7  CCGACTCCTC CACGGGCATC GGCAAGAAAG GCCAGCAGCC CGCCAGAAAG
  44_2  CAGACTCCTC TACGGGCATC GGCAAGAAAG GCCAGCAGCC CGCGAAAAAG
```

Fig. 1AAD

```
        2751                                                        2800
 42_2   AAGCTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTGC CCGACCCCCA
 42_8   AGACTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTGC CCGACCCTCA
42_15   AGACTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTGC CCGACCCTCA
42_5b   AGACTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTGC CCGACCCTCA
42_1b   AGACTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTGC CCGACCCTCA
42_13   AAGCTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTGC CCGACCCTCA
42_3a   AAGCTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTGC CCGACCCTCA
 42_4   AAGCTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTGC CCGACCCTCA
42_5a   AAGCTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTGC CCGACCCCCA
42_10   AAGCTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTGC CCGACCCTCA
42_3b   AAGCTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTGC CCGACCCTCA
42_11   AAGCTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTGC CCGACCCTCA
42_6b   AGACTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTGC CCGACCCTCA
 43_1   AGACTGAACT TTGGGCAGAC TGGCGACTCG GAGTCAGTCC CCGACCCTCA
 43_5   AGACTGAACT TTGGGCAGAC TGGCGACTCG GAGTCAGTCC CCGACCCTCA
43_12   AGACTGAACT TTGGGCAGAC TGGCGACTCG GAGTCAGTCC CCGACCCTCA
43_20   AGACTCAATT TTGGTCAGAC TGGCGACTCA GAGTCAGTCC CCGACCCACA
43_21   AGACTCAATT TTGGTCAGAC TGGCGACTCA GAGTCAGTCC CCGACCCACA
43_23   AGACTCAATT TTGGTCAGAC TGGCGACTCA GAGTCAGTCC CCGACCCACA
43_25   AGACTCAATT TTGGTCAGAC TGGCGACTCA GAGTCAGTCC CCGACCCACA
 44_1   AGACTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTGC CCGACCCTCA
 44_5   AGACTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTGC CCGACCCTCA
223_10  AGACTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTCC CCGACCCTCA
223_2   AGACTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTCC CCGACCCTCA
223_4   AGACTCAACT TTGGGCAGAC TGGCGACTCA GAGCCAGTCC CCGACCCTCA
223_5   AGACTCAACT TTGGGCAGAC TGGCGACTCA GAGCCAGTCC CCGACCCTCA
223_6   AGACTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTCC CCGACCCTCA
223_7   AGACTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTCC CCGACCCTCA
 A3_4   AGACTCAATT TTGGTCAGAC TGGCGACACA GAGTCAGTCC CAGACCCTCA
 A3_5   AGACTCAATT TTGGTCAGAC TGGCGACACA GAGTCAGTCC CAGACCCTCA
 A3_7   AGACTCAATT TTGGTCAGAC TGGCGACACA GAGTCAGTCC CAGACCCTCA
 A3_3   AGACTCAATT TTGGTCAGAC TGGCGACACA GAGTCAGTCC CAGGCCCTCA
42_12   AGACTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTGC CCGACCCTCA
 AAV1   AGACTCAATT TTGGTCAGAC TGGCGACTCA GAGTCAGTCC CCGATCCACA
 AAV2   AGATTGAATT TTGGTCAGAC TGGAGACGCA GACTCAGTAC CTGACCCCCA
 AAV3   AGACTAAATT TCGGTCAGAC TGGAGACTCA GAGTCAGTCC CAGACCCTCA
 AAV8   AGACTCAATT TTGGTCAGAC TGGCGACTCA GAGTCAGTTC CAGACCCTCA
 AAV9   AGACTCAATT TTGGTCAGAC TGGCGACTCA GAGTCAGTTC CAGACCCTCA
 AAV7   AGACTCAATT TCGGTCAGAC TGGCGACTCA GAGTCAGTCC CCGACCCTCA
 44_2   AGACTCAACT TTGGGCAGAC TGGCGACTCA GAGTCAGTGC CCGACCCTCA
```

Fig. 1AAE

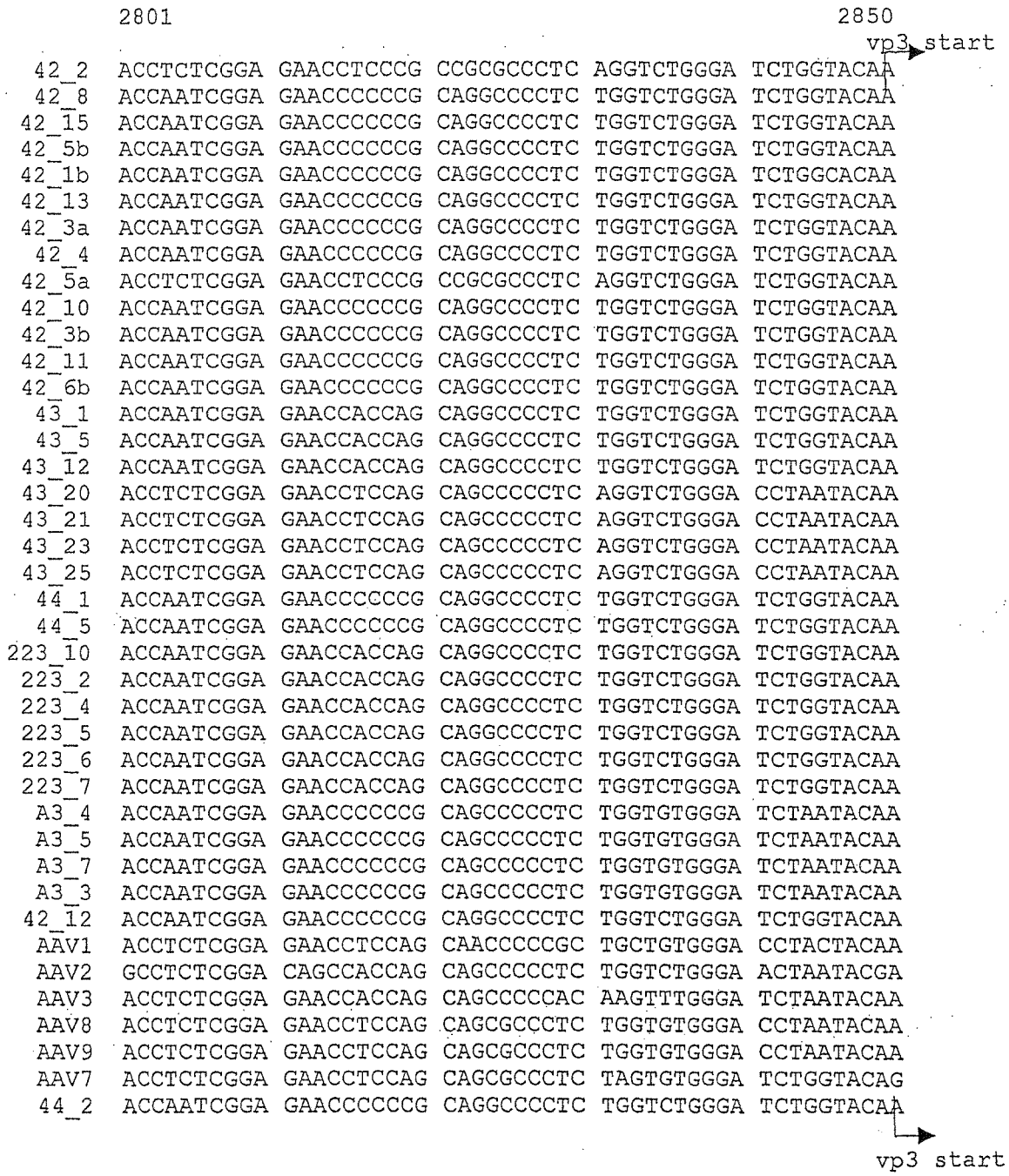
2801
2850
vp3 start
42_2 ACCTCTCGGA GAACCTCCCG CCGCGCCCTC AGGTCTGGGA TCTGGTACAA
42_8 ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
42_15 ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
42_5b ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
42_1b ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGCACAA
42_13 ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
42_3a ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
42_4 ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
42_5a ACCTCTCGGA GAACCTCCCG CCGCGCCCTC AGGTCTGGGA TCTGGTACAA
42_10 ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
42_3b ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
42_11 ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
42_6b ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
43_1 ACCAATCGGA GAACCACCAG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
43_5 ACCAATCGGA GAACCACCAG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
43_12 ACCAATCGGA GAACCACCAG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
43_20 ACCTCTCGGA GAACCTCCAG CAGCCCCCTC AGGTCTGGGA CCTAATACAA
43_21 ACCTCTCGGA GAACCTCCAG CAGCCCCCTC AGGTCTGGGA CCTAATACAA
43_23 ACCTCTCGGA GAACCTCCAG CAGCCCCCTC AGGTCTGGGA CCTAATACAA
43_25 ACCTCTCGGA GAACCTCCAG CAGCCCCCTC AGGTCTGGGA CCTAATACAA
44_1 ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
44_5 ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
223_10 ACCAATCGGA GAACCACCAG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
223_2 ACCAATCGGA GAACCACCAG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
223_4 ACCAATCGGA GAACCACCAG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
223_5 ACCAATCGGA GAACCACCAG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
223_6 ACCAATCGGA GAACCACCAG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
223_7 ACCAATCGGA GAACCACCAG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
A3_4 ACCAATCGGA GAACCCCCCG CAGCCCCCTC TGGTGTGGGA TCTAATACAA
A3_5 ACCAATCGGA GAACCCCCCG CAGCCCCCTC TGGTGTGGGA TCTAATACAA
A3_7 ACCAATCGGA GAACCCCCCG CAGCCCCCTC TGGTGTGGGA TCTAATACAA
A3_3 ACCAATCGGA GAACCCCCCG CAGCCCCCTC TGGTGTGGGA TCTAATACAA
42_12 ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
AAV1 ACCTCTCGGA GAACCTCCAG CAACCCCCGC TGCTGTGGGA CCTACTACAA
AAV2 GCCTCTCGGA CAGCCACCAG CAGCCCCCTC TGGTCTGGGA ACTAATACGA
AAV3 ACCTCTCGGA GAACCACCAG CAGCCCCCAC AAGTTTGGGA TCTAATACAA
AAV8 ACCTCTCGGA GAACCTCCAG CAGCGCCCTC TGGTGTGGGA CCTAATACAA
AAV9 ACCTCTCGGA GAACCTCCAG CAGCGCCCTC TGGTGTGGGA CCTAATACAA
AAV7 ACCTCTCGGA GAACCTCCAG CAGCGCCCTC TAGTGTGGGA TCTGGTACAG
44_2 ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
vp3 start

Fig. 1AAF

```
        2851                                                  2900
      vp3 start codon
  42_2  TGGCTGCAGG CGGTGGCGCA CCAATGGCAG ACAATAACGA AGGCGCCGAC
  42_8  TGGCTGCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
 42_15  TGGCTGCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
 42_5b  TGGCTGCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
 42_1b  TGGCTGCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
 42_13  TGGCTGCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
 42_3a  TGGCTGCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
  42_4  TGGCTGCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
 42_5a  TGGCTGCAGG CGGTGGCGCA CCAATGGCAG ACAATAACGA AGGCGCCGAC
 42_10  TGGCTGCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
 42_3b  TGGCTGCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
 42_11  TGGCTGCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
 42_6b  TGGCTGCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
  43_1  TGGCTGCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
  43_5  TGGCTGCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
 43_12  TGGCTGCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
 43_20  TGGCTTCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
 43_21  TGGCTTCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
 43_23  TGGCTTCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
 43_25  TGGCTTCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
  44_1  TGGCTGCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
  44_5  TGGCTGCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
223_10  TGGCTGCAGG CGGTGGCGCA CCAATGGCTG ACAATAACGA GGGCGCCGAC
 223_2  TGGTTGCAGG CGGTGGCGCA CCAATGGCTG ACAATAACGA GGGCGCCGAC
 223_4  TGGCTGCAGG CGGTGGCGCA CCAATGGCTG ACAATAACGA GGGCGCCGAC
 223_5  TGGCTGCAGG CGGTGGCGCA CCAATGGCTG ACAATAACGA GGGCGCCGAC
 223_6  TGGCTGCAGG CGGTGGCGCA CCAATGGCTG ACAATAGCGA GGGCGCCGAC
 223_7  TGGCTGCAGG CGGTGGCGCA CCAATGGCTG ACAATAACGA GGGCGCCGAC
  A3_4  TGGCTTCAGG CGGTGGGGCA CCAATGGCAG ACGATAACGA AGGCGCCGAC
  A3_5  TGGCTTCAGG CGGTGGGGCA CCAATGGCAG ACAATAACGA AGGCGCCGAC
  A3_7  TGGCTTCAGG CGGTGGGGCA CCAATGGCAG ACAATAACGA AGGCGCCGAC
  A3_3  TGGCTTCAGG CGGTGGGGCA CCAATGGCAG ACAATAACGA AGGCGCCGAC
 42_12  TGGCTGCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
  AAV1  TGGCTTCAGG CGGTGGCGCA CCAATGGCAG ACAATAACGA AGGCGCCGAC
  AAV2  TGGCTACAGG CAGTGGCGCA CCAATGGCAG ACAATAACGA GGGCGCCGAC
  AAV3  TGGCTTCAGG CGGTGGCGCA CCAATGGCAG ACAATAACGA GGGTGCCGAT
  AAV8  TGGCTGCAGG CGGTGGCGCA CCAATGGCAG ACAATAACGA AGGCGCCGAC
  AAV9  TGGCTGCAGG CGGTGGCGCA CCAATGGCAG ACAATAACGA AGGCGCCGAC
  AAV7  TGGCTGCAGG CGGTGGCGCA CCAATGGCAG ACAATAACGA AGGTGCCGAC
  44_2  TGGCTGCAGG CGGTGGCGCT CCAATGGCAG ACAATAACGA AGGCGCCGAC
      vp3 start codon (cont'd)
```

Fig. 1AAG

```
          2901                                                    2950
  42_2    GGAGTGGGTA ATGCCTCCGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
  42_8    GGAGTGGGTA GTTCCTCAGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
 42_15    GGAGTGGGTA GTTCCTCAGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
 42_5b    GGAGTGGGTA GTTCCTCAGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
 42_1b    GGAGTGGGTA GTTCCTCAGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
 42_13    GGAGTGGGTA GTTCCTCAGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
 42_3a    GGAGTGGGTA GTTCCTCAGG AAATTGGCAT TGCGATTCCA CATAGCTGGG
  42_4    GGAGTGGGTA ATGCCTCCGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
 42_5a    GGAGTGGGTA ATGCCTCCGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
 42_10    GGAGTGGGTA ATGCCTCCGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
 42_3b    GGAGTGGGTA ATGCCTCCGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
 42_11    GGAGTGGGTA ATGCCTCCGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
 42_6b    GGAGTGGGTA GTTCCTCAGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
  43_1    GGAGTGGGTA GTTCCTCAGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
  43_5    GGAGTGGGTA GTTCCTCAGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
 43_12    GGAGTGGGTA GTTCCTCAGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
 43_20    GGAGTGGGTA ATTCCTCGGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
 43_21    GGAGTGGGTA ATTCCTCGGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
 43_23    GGAGTGGGTA ATTCCTCGGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
 43_25    GGAGTGGGTA ATTCCTCGGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
  44_1    GGAGTGGGTA GTTCCTCAGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
  44_5    GGAGTGGGTA GTTCCTCAGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
223_10    GGAGTGGGTA ATGCCTCAGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
223_2     GGAGTGGGTA ATGCCTCAGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
223_4     GGAGTGGGTA ATGCCTCAGG AAATTGGCAT TGCGATTCCA CACGGCTGGG
223_5     GGAGTGGGTA ATGCCTCAGG AAATTGGCAT TGCGATTCCA CACGGCTGGG
223_6     GGAGTGGGTA ATGCCTCAGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
223_7     GGAGTGGGTA ATGCCTCAGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
  A3_4    GGAGTGGGTA ATTCCTCGGG AAATTGGCAT TGCGATTCCA CATGGATGGG
  A3_5    GGAGTGGGTA ATTCCTCGGG AAATTGGCAT TGCGATTCCA CATGGATGGG
  A3_7    GGAGTGGGTA ATTCCTCGGG AAATTGGCAT TGCGATTCCA CATGGATGGG
  A3_3    GGAGTGGGTA ATTCCTCGGG AAATTGGCAT TGCGATTCCA CATGGATGGG
 42_12    GGAGTGGGTA GTTCCTCAGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
  AAV1    GGAGTGGGTA ATGCCTCAGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
  AAV2    GGAGTGGGTA ATTCCTCCGG AAATTGGCAT TGCGATTCCA CATGGATGGG
  AAV3    GGAGTGGGTA ATTCCTCAGG AAATTGGCAT TGCGATTCCC AATGGCTGGG
  AAV8    GGAGTGGGTA GTTCCTCGGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
  AAV9    GGAGTGGGTA ATTCCTCGGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
  AAV7    GGAGTGGGTA ATGCCTCAGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
 AAV10          GGTA ATTCCTCCGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
 AAV11          GGTA ATTCCTCCGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
 AAV12          GGTA ATTCCTCCGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
  44_2    GGAGTGGGTA GTTCCTCAGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
```

FIG. 1AAH

```
        2951                                                  3000
  42_2  CGACAGAGTC ATCACCACCA GCACCCGCAC CTGGGCCCTG CCCACCTACA
  42_8  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTC CCCACCTACA
 42_15  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTC CCCACCTACA
 42_5b  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTC CCCACCTACA
 42_1b  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTC CCCACCTACA
 42_13  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTC CCCACCTACA
 42_3a  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTC CCCACCTACA
  42_4  CGACAGAGTC ATCACCACCA GCACCCGCAC CTGGGCCCTG CCCACCTACA
 42_5a  CGACAGAGTC ATCACCACCA GCACCCGCAC CTGGGCCCTG CCCACCTACA
 42_10  CGACAGAGTC ATCACCACCA GCACCCGCAC CTGGGCCCTG CCCACCTACA
 42_3b  CGACAGAGTC ATCACCACCA GCACCCGCAC CTGGGCCCTG CCCACCTACA
 42_11  CGACAGAGTC ATCACCACCA GCACCCGCAC CTGGGCCCTG CCCACCTACA
 42_6b  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTC CCCACCTACA
  43_1  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTG CCCACCTACA
  43_5  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTG CCCACCTACA
 43_12  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTG CCCACCTACA
 43_20  GGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTG CCCACCTACA
 43_21  GGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTG CCCACCTACA
 43_23  GGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTG CCCACCTACA
 43_25  GGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTG CCCACCTACA
  44_1  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTC CCCACCTACA
  44_5  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTC CCCACCTACA
223_10  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTG CCCACCTACA
 223_2  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTG CCCACCTACA
 223_4  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTG CCCACCTACA
 223_5  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTG CCCACCTACA
 223_6  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTG CCCACCTACA
 223_7  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTG CCCACCTACA
  A3_4  CGACAGAGTT ATCACCACCA GCACAAGAAC CTGGGCCCTC CCCACCTACA
  A3_5  CGACAGAGTT ATCACCACCA GCACAAGAAC CTGGGCCCTC CCCACCTACA
  A3_7  CGACAGAGTT ATCACCACCA GCACAAGAAC CTGGGCCCTC CCCACCTACA
  A3_3  CGACAGAGTT ATCACCACCA GCACAAGAAC CTGGGCCCTC CCCACCTACA
 42_12  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTC CCCACCTACA
  AAV1  CGACAGAGTC ATCACCACCA GCACCCGCAC CTGGGCCTTG CCCACCTACA
  AAV2  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTG CCCACCTACA
  AAV3  CGACAGAGTC ATCACCACCA GCACCAGAAC CTGGGCCCTG CCCACTTACA
  AAV8  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTG CCCACCTACA
  AAV9  GGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCATTG CCCACCTACA
  AAV7  CGACAGAGTC ATTACCACCA GCACCCGAAC CTGGGCCCTG CCCACCTACA
 AAV10  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGTCCTG CCCACCTACA
 AAV11  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTG CCAACCTACA
 AAV12  CGACCGAGTC ATTACCACCA GCACCCGGAC TTGGGCCCTG CCCACCTACA
  44_2  CGACAGAGTC ATCACCACCA GCACCCGAAC CTGGGCCCTC CCCACCTACA
```

Fig. 1AAI

```
        3001                                                  3050
  42_2  ACAACCACCT CTACAAGCAG ATATCAA..G TCAGAGCGGG GCT....ACC
  42_8  ACAACCACCT CTACAAGCAA ATCTCCAACG GGACATCGGG AGGAAGCACC
 42_15  ACAACCACCT CTACAAGCAA ATCTCCAACG GGACATCGGG AGGAAGCACC
 42_5b  ACAACCACCT CTACAAGCAA ATCTCCAACG GGACATCGGG AGGAAGCACC
 42_1b  ACAACCACCT CTACAAGCAA ATCTCCAACG GGACATCGGG AGGAAGCACC
 42_13  ACAACCACCT CTACAAGCAA ATCTCCAACG GGACATCGGG AGGAAGCACC
 42_3a  ACAACCACCT CTACAAGCAA ATCTCCAACG GGACATCGGG AGGAAGCACC
  42_4  ACAACCACCT CTACAAGCAG ATATCAA... .GTCAGAGCG GGGC..TACC
 42_5a  ACAACCACCT CTACAAGCAG ATATCAA... .GTCAGAGCG GGGC..TACC
 42_10  ACAACCACCT CTACAAGCAG ATATCAA..G TCAGAGCGGG GCTA....CC
 42_3b  ACAACCACCT CTACAAGCAG ATATCAA..G TCAGAGCGGG GCTA....CC
 42_11  ACAACCACCT CTACAAGCAG ATATCAA..G TCAGAGCGGG GCTA....CC
 42_6b  ACAACCACCT CTACAAGCAA ATCTCCAACG GGACATCGGG AGGAAGCACC
  43_1  ACAACCATCT CTACAAGCAA ATCTCCAACG GGACATCGGG AGGAAGCACT
  43_5  ACAACCATCT CTACAAGCAA ATCTCCAACG GGACATCGGG AGGAAGCACT
 43_12  ACAACCATCT CTACAAGCAA ATCTCCAACG GGACATCGGG AGGAAGCACT
 43_20  ACAACCACCT CTACAAGCAA ATCTCCAACG GCACCTCGGG AGGAAGCACC
 43_21  ACAACCACCT CTACAAGCAA ATCTCCAACG GCACCTCGGG AGGAAGCACC
 43_23  ACAACCACCT CTACAAGCAA ATCTCCAACG GCACCTCGGG AGGAAGCACC
 43_25  ACAACCACCT CTACAAGCAA ATCTCCAACG GCACCTCGGG AGGAAGCACC
  44_1  ACAACCACCT CTACAAGCAA ATCTCCAACG GGACTTCGGG AGGAAGCACC
  44_5  ACAACCACCT CTACAAGCAA ATCTCCAACG GGACTTCGGG AGGAAGCACC
223_10  ACAACCACCT CTACAAGCAA ATCTCCAGTC AGTCAGCAGG GAG...CACC
 223_2  ACAACCACCT CTACAAGCAA ATCTCCAGTC AGTCAGCAGG GAG...CACC
 223_4  ACAACCACCT CTACAAGCAA ATCTCCAGTC AGTCAGCAGG GAG...CACC
 223_5  ACAACCACCT CTACAAGCAA ATCTCCAGTC AGTCAGCAGG GAG...CACC
 223_6  ACAACCACCT CTACAAGCAA ATCTCCAGTC AGTCAGCAGG GAG...CACC
 223_7  ACAACCACCT CTACAAGCAA ATCTCCAGTC AGTCAGCAGG GAG...CACC
  A3_4  ATAATCACCT CTACAAGCAA ATCTCCA... GCGAATCGGG AGC...CACC
  A3_5  ATAATCACCT CTACAAGCAA ATCTCCA... GCGAATCGGG AGC...CACC
  A3_7  ATAATCGCCT CTACAAGCAA ATCTCCA... GCGAATCGGG AGC...CACC
  A3_3  ATAATCACCT CTACAAGCAA ATCTCCA... GCGAATCGGG AGC...CACC
 42_12  ACAACCACCT CTACAAGCAA ATCTCCAACG GGACATCGGG AGGAAGCACC
  AAV1  ATAACCACCT CTACAAGCAA ATCTCCAGTG CTTCAACGGG .GG..CCAGC
  AAV2  ACAACCACCT CTACAAACAA ATTTCCA... GCCAATCAGG AGC...CTCG
  AAV3  ACAACCATCT CTACAAGCAA ATCTCCA... GCCAATCAGG AGC...TTCA
  AAV8  ACAACCACCT CTACAAGCAA ATCTCCAACG GGACATCGGG AGGAGCCACC
  AAV9  ACAACCACCT CTACAAGCAA ATCTCCAATG GAACATCGGG AGGAAGCACC
  AAV7  ACAACCACCT CTACAAGCAA ATCTCCAGTG AAACTGCAGG TAG...TACC
 AAV10  ACAACCACAT CTACAAGCAA ATCTCCAGCG AGACAGGAGC CACCAACGAC
 AAV11  ACAACCACCT CTACAAACAA ATCTCCAGCG CTTCAACGGG GGCCAGCAAC
 AAV12  ACAACCACCT CTACAAGCAA ATCTCCAGCC AATCGGGTGC CACCAACGAC
  44_2  ACAACCACCT CTACAAGCAA ATCTCCAACG GGACTTCGGG AGGAAGCACC
```

Fig. 1AAJ

```
        3051                                                  3100
  42_2  AACGACAACC ACTTCTTCGG CTACAGCACC CCCTGGGGCT ATTTTGACTT
  42_8  AACGACAACA CCTACTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
 42_15  AACGACAACA CCTACTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
 42_5b  AACGACAACA CCTACTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
 42_1b  AACGACAACA CCTACTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
 42_13  AACGACAACA CCTACTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
 42_3a  AACGACAACA CCTACTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
  42_4  AACGACAACC ACTTCTTCGG CTACAGCACC CCCTGGGGCT ATTTTGACTT
 42_5a  AACGACAACC ACTTCTTCGG CTACAGCACC CCCTGGGGCT ATTTTGACTT
 42_10  AACGACAACC ACTTCTTCGG CTACAGCACC CCCTGGGGCT ATTTTGACTT
 42_3b  AACGACAACC ACTTCTTCGG CTACAGCACC CCCTGGGGCT ATTTTGACTT
 42_11  AACGACAACC ACTTCTTCGG CTACAGCACC CCCTGGGGCT ATTTTGACTT
 42_6b  AACGACAACA CCTACTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
  43_1  AACGACAACA CCTACTTTGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
  43_5  AACGACAACA CCTACTTTGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
 43_12  AACGACAACA CCTACTTTGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
 43_20  AACGACAACA CCTATTTTGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
 43_21  AACGACAACA CCTATTTTGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
 43_23  AACGACAACA CCTATTTTGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
 43_25  AACGACAACA CCTATTTTGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
  44_1  AACGACAACA CCTACTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
  44_5  AACGACAACA CCTACTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
223_10  AACGATAACG TCTATTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
 223_2  AACGATAACG TCTATTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
 223_4  AACGATAACG TCTATTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
 223_5  AACGATAACG TCTATTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
 223_6  AACGATAACG TCTATTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
 223_7  AACGATAACG TCTATTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
  A3_4  AACGACAACC ACTACTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
  A3_5  AACGACAACC ACTACTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
  A3_7  AACGACAACC ACTACTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
  A3_3  AACGACAACC ACTACTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
 42_12  AACGACAACA CCTACTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
  AAV1  AACGACAACC ACTACTTCGG CTACAGCACC CCCTGGGGGT ATTTTGATTT
  AAV2  AACGACAATC ACTACTTTGG CTACAGCACC CCTTGGGGGT ATTTTGACTT
  AAV3  AACGACAACC ACTACTTTGG CTACAGCACC CCTTGGGGGT ATTTTGACTT
  AAV8  AACGACAACA CCTACTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
  AAV9  AACGACAACA CCTACTTTGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
  AAV7  AACGACAACA CCTACTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
 AAV10  AACCACTACT TCGGCTACAG C......ACC CCCTGGGGGT ATTTTGACTT
 AAV11  ...GACAACC ACTACTTTGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
 AAV12  AACCACTACT TCGGCTA... ...CAGCACC CCTTGGGGGT ATTTTGATTT
 44_2   AACGACAACA CCTACTTCGG CTACAGCACC CCCTGGGGGT ATTTTGACTT
```

Fig. 1AAK

```
        3101                                                        3150
 42_2   TAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
 42_8   TAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
42_15   TAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
42_5b   TAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
42_1b   TAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
42_13   TAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
42_3a   TAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
 42_4   CAACAGATTC CACTGCCACT TCTCATCACG TGACTGGCAG CGACTCATCA
42_5a   CAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
42_10   CAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
42_3b   CAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
42_11   CAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
42_6b   TAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
 43_1   CAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
 43_5   CAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
43_12   CAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
43_20   CAACAGATTC CACTGTCACT TTTCACCACG TGACTGGCAA CGACTCATCA
43_21   CAACAGATTC CACTGTCACT TTTCACCACG TGACTGGCAA CGACTCATCA
43_23   CAACAGATTC CACTGTCACT TTTCACCACG TGACTGGCAA CGACTCATCA
43_25   CAACAGATTC CACTGTCACT TTTCACCACG TGACTGGCAA CGACTCATCA
 44_1   TAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
 44_5   TAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
223_10  CAACAGATTC CATTGCCACT TCTCACCACG TGACTGGCAG CGACTTATCA
223_2   CAACAGATTC CATTGCCACT TCTCACCACG TGACTGGCAG CGACTTATCA
223_4   CAACAGATTC CATTGCCACT TCTCACCACG TGACTGGCAG CGACTTATCA
223_5   CAACAGATTC CATTGCCACT TCTCACCACG TGACTGGCAG CGACTTATCA
223_6   CAACAGATTC CATTGCCACT TCTCACCACG TGACTGGCAG CGACTTATCA
223_7   CAACAGATTC CATTGCCACT TCTCACCACG TGACTGGCAG CGACTTATCA
 A3_4   TAACAGATTC CACTGTCACT TCTCACCACG TGACTGGCAG CGACTCATCA
 A3_5   TAACAGATTC CACTGTCACT TCTCACCACG TGACTGGCAG CGACTCATCA
 A3_7   TAACAGATTC CACTGTCACT TCTCACCACG TGACTGGCAG CGACTCATCA
 A3_3   TAACAGATTC CACTGTCACT TCTCACCACG TGACTGGCAG CGACTCATCA
42_12   TAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
 AAV1   CAACAGATTC CACTGCCACT TTTCACCACG TGACTGGCAG CGACTCATCA
 AAV2   CAACAGATTC CACTGCCACT TTTCACCACG TGACTGGCAA AGACTCATCA
 AAV3   TAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATTA
 AAV8   TAACAGATTC CACTGCCACT TTTCACCACG TGACTGGCAG CGACTCATCA
 AAV9   CAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
 AAV7   TAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
AAV10   TAACAGATTC CACTGCCACT TTTCACCACG TGACTGGCAG CGACTCATCA
AAV11   TAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
AAV12   CAACAGATTC CACTGCCATT TCTCACCACG TGACTGGCAG CGACTCATCA
 44_2   TAACAGATTC CACTGCCACT TCTCACCACG TGACTGGCAG CGACTCATCA
```

Fig. 1AAL

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        3151                                                        3200
 42_2   ACAACAACTG GGGATTCCGG CCCAGAAAGC TGCGGTTCAA GTTGTTCAAC
 42_8   ACAACAACTG GGGATTCCGG CCCAAGAGAC TCAACTTCAA GCTCTTCAAC
42_15   ACAACAACTG GGGATTCCGG CCCAAGAGAC TCAACTTCAA GCTCTTCAAC
42_5b   ACAACAACTG GGGATTCCGG CCCAAGAGAC TCAACTTCAA GCTCTTCAAC
42_1b   ACAACAACTG GGGATTCCGG CCCAAGAGAC TCAACTTCAA GCTCTTCAAC
42_13   ACAACAACTG GGGATTCCGG CCCAAGAGAC TCAACTTCAA GCTCTTCAAC
42_3a   ACAACAGCTG GGGATTCCGG CCCAAGAGAC TCAACTTCAA GCTCTTCAAC
 42_4   ACAACAACTG GGGATTCCGG CCCAAGAGAC TCAACTTCAA GCTCTTCAAC
42_5a   ACAACAACCG GGGATTCCGG CCCAGAAAGC TGCGGTTCAA GTTGTTCAAC
42_10   ACAACAACTG GGGATTCCGG CCCAGAAAGC TGCGGTTCAA GTTGTTCAAC
42_3b   ACAACAACTG GGGATTCCGG CCCAGAAAGC TGCGGTTCAA GTTGTTCAAC
42_11   ACAACAACTG GGGATTCCGG CCCAGAAAGC TGCGGTTCAA GTTGTTCAAC
42_6b   ACAACAACTG GGGATTCCGG CCCAGAAAGC TGCGGTTCAA GTTGTTCAAC
 43_1   ACAATAACTG GGGATTCCGG CCCAAGAGAC TCAACTTCAA GCTCTTCAAC
 43_5   ACAATAACTG GGGATTCCGG CCCAAGAGAC TCAACTTCAA GCTCTTCAAC
43_12   ACAATAACTG GGGATTCCGG CCCAAGAGAC TCAACTTCAA GCTCTTCAAC
43_20   ACAACAATTG GGGATTCCGG CCCAAAAGAC TCAACTTCAA GCTGTTCAAC
43_21   ACAACAATTG GGGATTCCGG CCCAAAAGAC TCAACTTCAA GCTGTTCAAC
43_23   ACAACAATTG GGGATTCCGG CCCAAAAGAC TCAACTTCAA GCTGTTCAAC
43_25   ACAACAATTG GGGATTCCGG CCCAAAAGAC TCAACTTCAA GCTGTTCAAC
 44_1   ACAACAACTG GGGATTCCGG CCCAAGAGAC TCAACTTCAA GCTCTTCAAC
 44_5   ACAACAACTG GGGATTCCGG CCCAAGAGAC CCAACTTCAA GCTCTTCAAC
223_10  ACAACAACTG GGGATTCCGG CCCAAGAAGC TCAACTTCAA GCTCTTCAAC
223_2   ACAACAACTG GGGATTCCGG CCCAAGAAGC TCAACTTCAA GCTCTTCAAC
223_4   ACAACAACTG GGGATTCCGG CCCAAGAAGC TCAACTTCAA GCTCTTCAAC
223_5   ACAACAACTG GGGATTCCGG CCCAAGAAGC TCAACTTCAA GCTCTTCAAC
223_6   ACAACAACTG GGGATTCCGG CCCAAGAAGC TCAACTTCAA GCTCTTCAAC
223_7   ACAACAACTG GGGATTCCGG CCCAAGAAGC TCAACTTCAA GCTCTTCAAC
 A3_4   ACAACAACTG GGGATTTAGA CCCAAGAAAC TCAATTTCAA GCTCTTCAAC
 A3_5   ATAACAACTG GGGATTTAGA CCCAAGAAAC TCAATTTCAA GCTCTTCAAC
 A3_7   ACAACAACTG GGGATTTAGA CCCAAGAAAC TCAATTTCAA GCTCTTCAAC
 A3_3   ACAACAACTG GGGATTTAGA CCCAAGAAAC TCAATTTCAA GCTCTTCAAC
42_12   ACAACAACTG GGGATTCCGG CCCAAGAGAC TCAACTTCAA GCTCTTCAAC
 AAV1   ACAACAATTG GGGATTCCGG CCCAAGAGAC TCAACTTCAA ACTCTTCAAC
 AAV2   ACAACAACTG GGGATTCCGA CCCAAGAGAC TCAACTTCAA GCTCTTTAAC
 AAV3   ACAACAACTG GGGATTCCGG CCCAAGAAAC TCAGCTTCAA GCTCTTCAAC
 AAV8   ACAACAACTG GGGATTCCGG CCCAAGAGAC TCAGCTTCAA GCTCTTCAAC
 AAV9   ACAACAACTG GGGATTCCGG CCAAAGAGAC TCAACTTCAA GCTGTTCAAC
 AAV7   ACAACAACTG GGGATTCCGG CCCAAGAAGC TGCGGTTCAA GCTCTTCAAC
AAV10   ACAACAACTG GGGATTC
AAV11   ACAACAACTG GGGATTC
AAV12   ACAACAACTG GGGATTC
 44_2   ACAACAACTG GGGATTCCGG CCCAAGAGAC TCAACTTCAA GCTCTTCAAC
```

Fig. 1AAM

```
        3201                                                        3250
 42_2   ATCCAGGTCA AGGAGGTCAC GACGAACGAC GGCGTTACGA CCATCGCTAA
 42_8   ATCCAGGTCA AGGAGGTCAC GCAGAATGAA GGCACCAAGA CCATCGCCAA
42_15   ATCCAGGTCA AGGAGGTCAC GCAGAATGAA GGCACCAAGA CCATCGCCAA
42_5b   ATCCAGGTCA AGGAGGTCAC GCAGAATGAA GGCACCAAGA CCATCGCCAA
42_1b   ATCCAGGTCA AGGAGGTCAC GCAGAATGAA GGCACCAAGA CCATCGCCAA
42_13   ATCCAGGTCA AGGAGGTCAC GCAGAATGAA GGCACCAAGA CCATCGCCAA
42_3a   ATCCAGGTCA AGGAGGTCAC GCAGAATGAA GGCACCAAGA CCATCGCCAA
 42_4   ATCCAGGTCA AGGAGGTCAC GCAGAATGAA GGCACCAAGA CCATCGCCAA
42_5a   ATCCAGGTCA AGGAGGTCAC GACGAACGAC GGCGTTACGA CCATCGCTAA
42_10   ATCCAGGTCA AGGAGGTCAC GACGAACGAC GGCGTTACGA CCATCGCCAA
42_3b   ATCCAGGTCA AGGAGGTCAC GACGAACGAC GGCGTTACGA CCATCGCTAA
42_11   ATCCAGGTCA AGGAGGTCAC GACGAACGAC GGCGTTACGA CCATCGCTAA
42_6b   ATCCAGGTCA AGGAGGTCAC GACGGACGAC GGCGTTACGA CCATCGCTAA
 43_1   ATCCAGGTCA AGGAGGTCAC GCAGAATGAA GGCACCAAGA CCATCGCCAA
 43_5   ATCCAGGTCA AGGAGGTCAC GCAGAATGAA GGCACCAAGA CCATCGCCAA
43_12   ATCCAGGTCA AGGAGGTCAC GCAGAATGAA GGCACCAAGA CCATCGCCAA
43_20   ATCCAGGTCA AGGAAGTCAC GACGAACGAA GGCACCAAGA CCATCGCCAA
43_21   ATCCAGGTCA AGGAAGTCAC GACGAACGAA GGCACCAAGA CCATCGCCAA
43_23   ATCCAGGTCA AGGAAGTCAC GACGAACGAA GGCACCAAGA CCATCGCCAA
43_25   ATCCAGGTCA AGGAAGTCAC GACGAACGAA GGCACCAAGA CCATCGCCAA
 44_1   ATCCAGGTCA AGGAGGTCAC GCAGAATGAA GGCACCAAGA CCATCGCCAA
 44_5   ATCCAGGTCA AGGAGGTCAC GCAGAATGAA GGCACCAAGA CCATCGCCAA
223_10  ATCCAGGTCA AGGAGGTCAC GACGAATGAC GGTGTCACAA CCATCGCTAA
223_2   ATCCAGGTCA AGGAGGTCAC GACGAATGAC GGTGTCACAA CCATCGCTAA
223_4   ATCCAGGTCA AGGAGGTCAC GACGAATGAC GGCGTCACAA CCATCGCTAA
223_5   ATCCAGGTCA AGGAGGTCAC GACGAATGAC GGCGTCACAA CCATCGCTAA
223_6   ATCCAGGTCA AGGAGGTCAC GACGAATGAC GGTGTCACAA CCATCGCTAA
223_7   ATCCAGGTCA AGGAGGTCAC GACGAATGAC GGCGTCACAA CCATCGCTAA
 A3_4   ATCCAAGTCA AGGAGGTCAC GCAGAATGAT GGAACCACGA CCATCGCCAA
 A3_5   ATCCAAGTCA AGGAGGTCAC GCAGAATGAT GGAACCACGA CCATCGCCAA
 A3_7   ATCCAAGTCA AGGAGGTCAC GCAGAATGAT GGAACCACGA CCATCGCCAA
 A3_3   ATCCAAGTCA AGGAGGTCAC GCAGAATGAT GGAACCACGA CCATCGCCAA
42_12   ATCCAGGTCA AGGAGGTCAC GCAGAATGAA GGCACCAAGA CCATCGCCAA
 AAV1   ATCCAAGTCA AGGAGGTCAC GACGAATGAT GGCGTCACAA CCATCGCTAA
 AAV2   ATTCAAGTCA AAGAGGTCAC GCAGAATGAC GGTACGACGA CGATTGCCAA
 AAV3   ATCCAAGTTA GAGGGGTCAC GCAGAACGAT GGCACGACGA CTATTGCCAA
 AAV8   ATCCAGGTCA AGGAGGTCAC GCAGAATGAA GGCACCAAGA CCATCGCCAA
 AAV9   ATCCAGGTCA AGGAGGTTAC GACGAACGAA GGCACCAAGA CCATCGCCAA
 AAV7   ATCCAGGTCA AGGAGGTCAC GACGAATGAC GGCGTTACGA CCATCGCTAA
 44_2   ATCCAGGTCA AGGAGGTCAC GCAGAATGAA GGCACCAAGA CCATCGCCAA
```

Fig. 1AAN

```
        3251                                                        3300
 42_2   TAACCTTACC AGCACGATTC AGGTCTTCTC GGACTCGGAG TACCAACTGC
 42_8   TAACCTTACC AGCACGATTC AGGTCTTTAC GGACTCGGAA TACCAGCTCC
42_15   TAACCTTACC AGCACGATTC AGGTCTTTAC GGACTCGGAA TACCAGCTCC
42_5b   TAACCTTACC AGCACGATTC AGGTCTTTAC GGACTCGGAA TACCAGCTCC
42_1b   TAACCTTACC AGCACGATTC AGGTCTTTAC GGACTCGGAA TACCAGCTCC
42_13   TAACCTTACC AGCACGATTC AGGTCTTTAC GGACTCGGAA TACCAGCTCC
42_3a   TAACCTTACC AGCACGATTC AGGTCTTTAC GGACTCGGAA TACCAGCTCC
 42_4   TAACCTTACC AGCACGATTC AGGTCTTTAC GGACTCGGAA TACCGGCTCC
42_5a   TAACCTTACC AGCACGATTC AGGTCTTCTC GGACTCGGAG TACCAACTGC
42_10   TAACCTTACC AGCACGATTC AGGTCTTCTC GGACTCGGAG TACCAACTGC
42_3b   TAACCTTACC AGCACGATTC AGGTCTTCTC GGACTCGGAG TACCAACTGC
42_11   TAACCTTACC AGCACGATTC AGGTCTTCTC GGACTCGGAG TACCAACTGC
42_6b   TAACCTTACC AGCACGATTC AGGTCTTCTC GGACTCGGAG TACCAACTGC
 43_1   TAACCTTACC AGCACGATTC AGGTGTTTAC GGACTCGGAA TACCAGCTCC
 43_5   TAACCTTACC AGCACGATTC AGGTGTTTAC GGACTCGGAA TACCAGCTCC
43_12   TAACCTTACC AGCACGATTC AGGTGTTTAC GGACTCGGAA TACCAGCTCC
43_20   TAATCTCACC AGCACCGTGC AGGTCTTTAC GGACTCGGAG TACCAGTTAC
43_21   TAATCTCACC AGCACCGTGC GGGTCTTTAC GGACTCGGAG TACCAGTTAC
43_23   TAATCTCACC AGCACCGTGC AGGTCTTTAC GGACTTGGAG TACCAGTTAC
43_25   TAATCTCACC AGCACCGTGC AGGTCTTTAC GGACTCGGAG TACCAGTTAC
 44_1   TAACCTTACC AGCACGATTC AGGTCTTTAC GGACTCGGAA TACCAGCTCC
 44_5   TAACCTTACC AGCACGATTC AGGTCTTTAC GGACTCGGAA TACCAGCTCC
223_10  TAACCTTACC AGCACGGTTC AGGTCTTTTC GGACTCGGAA TATCAACTGC
223_2   TAACCTTACC AGCACGGTTC AGGTCTTTTC GGACTCGGAA TATCAACTGC
223_4   TAACCTTACC AGCACGGTTC AGGTCTTTTC GGACTCGGAA TATCAACTGC
223_5   TAACCTTACC AGCACGGTTC AGGTCTTTTC GGACTCGGAA TATCAACTGC
223_6   TAACCTTACC AGCACGGTTC AGGTCTTTTC GGACTCGGAA TATCAACTGC
223_7   TAACCTTACC AGCACGGTTC AGGTCTTTTC GGACCCGGAA TATCAACTGC
 A3_4   TAACCTTACC AGCACGGTGC AGGTCTTCAC AGACTCTGAG TACCAGCTGC
 A3_5   TAACCTTACC AGCACGGTGC AGGTCTTCAC AGACTCTGAG TACCAGCTGC
 A3_7   TAACCTTACC AGCACGGTGC AGGTCTTCAC AGACTCTGAG TACCAGCTGC
 A3_3   TAACCTTACC AGCGCGGTGC AGGTCTTCAC AGACTCTGAG TACCAGCTGC
42_12   TAACCTTACC AGCACGATTC AGGTCTTTAC GGACTCGGAA TACCAGCTCC
 AAV1   TAACCTTACC AGCACGGTTC AAGTCTTCTC GGACTCGGAG TACCAGCTTC
 AAV2   TAACCTTACC AGCACGGTTC AGGTGTTTAC TGACTCGGAG TACCAGCTCC
 AAV3   TAACCTTACC AGCACGGTTC AAGTGTTTAC GGACTCGGAG TATCAGCTCC
 AAV8   TAACCTCACC AGCACCATCC AGGTGTTTAC GGACTCGGAG TACCAGCTGC
 AAV9   TAACCTTACC AGCACCGTCC AGGTCTTTAC GGACTCGGAG TACCAGCTAC
 AAV7   TAACCTTACC AGCACGATTC AGGTATTCTC GGACTCGGAA TACCAGCTGC
 44_2   TAACCTTACC AGCACGATTC AGGTCTTTAC GGACTCGGAA TACCAGCTCC
```

Fig. 1AAO

```
        3301                                                        3350
 42_2   CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCTCCCTCC GTTCCCTGCG
 42_8   CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCTGCCTCC GTTCCCGGCG
42_15   CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCCGCCTCC GTTCCCGGCG
42_5b   CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCTGCCTCC GTTCCCGGCG
42_1b   CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCTGCCTCC GTTCCCGGCG
42_13   CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCTGCCTCC GTTCCCGGCG
42_3a   CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCTGCCTCC GTTCCCGGCG
 42_4   CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCTGCCTCC GTTCCCGGCG
42_5a   CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCTCCCTCC GTTCCCTGCG
42_10   CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCTCCCTCC GTTCCCTGCG
42_3b   CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCTCCCTCC GTTCCCTGCG
42_1    CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCTCCCTCC GTTCCCTGCG
42_6b   CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCTCCCTCC GTTCCCTGCG
 43_1   CGTACGTCCC CGGCTCTGCG CACCAGGGCT GCCTCCCTCC GTTCCCGGCG
 43_5   CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCTCCCTCC GTTCCCGGCG
43_12   CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCTCCCTCC GTTCCCGGCG
43_20   CGTACGTGCT AGGATCCGCT CACCAGGGAT GTCTGCCTCC GTTCCCGGCG
43_21   CGTACGTGCT AGGATCCGCT CACCAGGGAT GTCTGCCTCC GTTCCCGGCG
43_23   CGTACGTGCT AGGATCCGCT CACCAGGGAT GTCTGCCTCC GTTCCCGGCG
43_25   CGTACGTGCT AGGATCCGCT CACCAGGGAT GTCTGCCTCC GTTCCCGGCG
 44_1   CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCTGCCTCC GTTCCCGGCG
 44_5   CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCTGCCTCC GTTCCCGGCG
223_10  CGTACGTCCT CGGCTCCGCG CACCAGGGCT GCCTGCCTCC GTTCCCGGCA
223_2   CGTACGTCCT CGGCTCCGCG CACCAGGGCT GCCTGCCTCC GTTCCCGGCA
223_4   CGTACGTCCT CGGCTCCGCG CACCAGGGCT GCCTGCCTCC GTTCCCGGCA
223_5   CGTACGTCCT CGGCTCCGCG CACCAGGGCT GCCTGCCTCC GTTCCCGGCA
223_6   CGTACGTCCT CGGCTCCGCG CACCAGGGCT GCCTGCCTCC GTTCCCGGCA
223_7   CGTACGTCCT CGGCTCCGCG CACCAGGGCT GCCTGCCTCC GTTCCCGGCA
 A3_4   CCTACGTCCT CGGTTCGGCT CACCAGGGCT GCCTTCCGCC GTTCCCAGCA
 A3_5   CCTACGTCCT CGGTTCGGCT CACCAGGGCT GCCTTCCGCC GTTCCCAGCA
 A3_7   CCTACGTCCT CGGTTCGGCT CACCAGGGCT GCCTTCCGCC GTTCCCAGCA
 A3_3   CCTACGTCCT CGGTTCGGCT CACCAGGGCT GCCTTCCGCC GTTCCCAGCA
42_12   CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCTGCCTCC GTTCCCGGCG
 AAV1   CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCTCCCTCC GTTCCCGGCG
 AAV2   CGTACGTCCT CGGCTCGGCG CATCAAGGAT GCCTCCCGCC GTTCCCAGCA
 AAV3   CGTACGTGCT CGGGTCGGCG CACCAAGGCT GTCTCCCGCC GTTTCCAGCG
 AAV8   CGTACGTTCT CGGCTCTGCC CACCAGGGCT GCCTGCCTCC GTTCCCGGCG
 AAV9   CGTACGTCCT AGGCTCTGCC CACCAAGGAT GCCTGCCACC GTTTCCTGCA
 AAV7   CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCTGCCTCC GTTCCCGGCG
 44_2   CGTACGTCCT CGGCTCTGCG CACCAGGGCT GCCTGCCTCC GTTCCCGGCG
```

Fig. 1AAP

```
        3351                                                  3400
  42_2  GACGTGTTCA TGATTCCTCA GTACGGATAT CTGACTCTAA ACAACGGCAG
  42_8  GACGTCTTCA TGATTCCTCA GTACGGGTAC CTGACTCTGA ACAACGGCAG
 42_15  GACGTCTTCA TGATTCCTCA GTACGGGTAC CTGACTCTGA ACAACGGCAG
 42_5b  GACGTCTTCA TGATTCCTCA GTACGGGTAC CTGACTCTGA ACAACGGCAG
 42_1b  GACGTCTTCA TGATTCCTCA GTACGGGTAC CTGACTCTGA ACAACGGCAG
 42_13  GACGTCTTCA TGATTCCTCA GTACGGGTAC CTGACTCTGA ACAACGGCAG
 42_3a  GACGTCTTCA TGATTCCTCA GTACGGGTAC CTGACTCTGA ACAACGGCAG
  42_4  GACGTCTTCA TGATTCCTCA GTACGGGTAC CTGACTCTGA ACAACGGCAG
 42_5a  GACGTGTTCA TGATTCCTCA GTACGGATAT CTGACTCTAA ACAACGGCAG
 42_10  GACGTGTTCA TGATTCCTCA GTACGGATAT CTGACTCTAA ACAACGGCAG
 42_3b  GACGTGTTCA TGATTCCTCA GTACGGATAT CTGACTCTAA ACAACGGCAG
 42_1   GACGTGTTCA TGATTCCTCA GTACGGATAT CTGACTCTAA ACAACGGCAG
 42_6b  GACGTGTTCA TGATTCCTCA GTACGGATAT CTGACTCTAA ACAACGGCAG
  43_1  GACGTCTTCA TGATTCCTCA GTACGGGTAT CTGACCCTAA ACAATGGCAG
  43_5  GACGTCTTCA TGATTCCTCA GTACGGGTAT CTGACCCTAA ACAATGGCAG
 43_12  GACGTCTTCA TGATTCCTCA GTACGGGTAT CTGACCCTAA ACAATGGCAG
 43_20  GACGTCTTCA CGGTTCCTCA GTACGGCTAT TTAACTTTAA ACAATGGAAG
 43_21  GACGTCTTCA TGGTTCCTCA GTACGGCTAT TTAACTTTAA ACAATGGAAG
 43_23  GACGTCTTCA TGGTTCCTCA GTACGGCTAT TTAACTTTAA ACAATGGAAG
 43_25  GACGTCTTCA TGGTTCCTCA GTACGGCTAT TTAACTTTAA ACAATGGAAG
  44_1  GACGTCTTCA TGATTCCTCA GTACGGGTAC CTGACTCTGA ACAATGGCAG
  44_5  GACGTCTTCA TGATTCCTCA GTACGGGTAC CTGACTCTGA ACAATGGCAG
223_10  GACGTGTTCA TGATTCCGCA GTACGGATAC CTGACTCTGA ACAATGGCAG
 223_2  GACGTGTTCA TGATTCCGCA GTACGGATAC CTGACTCTGA ACAATGGCAG
 223_4  GACGTGTTCA TGATTCCGCA GTACGGATAC CTGACTCTGA ACAATGGCAG
 223_5  GACGTGTTCA TGATTCCGCA GTACGGATAC CTGACTCTGA ACAATGGCAG
 223_6  GACGTGTTCA TGATTCCGCA GTACGGATAC CTGACTCTGA ACAATGGCAG
 223_7  GACGTGTTCA TGATTCCGCA GTACGGATAC CTGACTCTGA ACAATGGCAG
  A3_4  GACGTCTTCA TGATTCCTCA GTACGGCTAC TTGACTCTGA ACAATGGCAG
  A3_5  GACGTCTTCA TGATTCCTCA GTACGGCTAC TTGACTCTGA ACAATGGCAG
  A3_7  GACGTCTTCA TGATTCCTCA GTACGGCTAC TTGACTCTGA ACAATGGCAG
  A3_3  GACGTCTTCA TGATTCCTCA GTACGGCTAC TTGACTCTGA ACAATGGCAG
 42_12  GACGTCTTCA TGATTCCTCA GTACGGGTAC CTGACTCTGA ACAACGGCAG
  AAV1  GACGTGTTCA TGATTCCGCA ATACGGCTAC CTGACGCTCA ACAATGGCAG
  AAV2  GACGTCTTCA TGGTGCCACA GTATGGATAC CTCACCCTGA ACAACGGGAG
  AAV3  GACGTCTTCA TGGTCCCTCA GTATGGATAC CTCACCCTGA ACAACGGAAG
  AAV8  GACGTGTTCA TGATTCCCCA GTACGGCTAC CTAACACTCA ACAACGGTAG
  AAV9  GACGTCTTCA TGGTTCCTCA GTACGGCTAC CTGACGCTCA ACAATGGAAG
  AAV7  GACGTCTTCA TGATTCCTCA GTACGGCTAC CTGACTCTCA ACAATGGCAG
  44_2  GACGTCTTCA TGATTCCTCA GTACGGGTAC CTGACTCTGA ACAATGGCAG
```

Fig. 1AAQ

	3401				3450
42_2	TCAGTCTGTG	GGACGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
42_8	TCAGGCCGTG	GGCCGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
42_15	TCAGGCCGTG	GGCCGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
42_5b	TCAGGCCGTG	GGCCGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
42_1b	TCAGGCCGTG	GGCCGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
42_13	TCAGGCCGTG	GGCCGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
42_3a	TCAGGCCGTG	GGCCGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
42_4	TCAGGCCGTG	GGCCGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
42_5a	TCAGTCTGTG	GGACGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
42_10	TCAGTCTGTG	GGACGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
42_3b	TCAGTCTGTG	GGACGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
42_11	TCAGTCTGTG	GGACGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
42_6b	TCAGTCTGTG	GGACGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
43_1	TCAGGCTGTG	GGCCGTTCCT	CCTTCTACTG	CCTGGAATAC	TTCCCTTCTC
43_5	TCAGGCTGTG	GGCCGTTCCT	CCTTCTACTG	CCTGGAATAC	TTCCCTTCTC
43_12	TCAGGCTGTG	GGCCGTTCCT	CCTTCTACTG	CCTGGAATAC	TTCCCTTCTC
43_20	CCAAGCCCTG	GGACGTTCCT	CCTTCTACTG	TCTGGAGTAT	TTCCCATCGC
43_21	CCAAGCCCTG	GGACGTTCCT	CCTTCTACTG	TCTGGAGTAT	TTCCCATCGC
43_23	CCAAGCCCTG	GGACGTTCCT	CCTTCTACTG	TCTGGAGTAT	TTCCCATCGC
43_25	CCAAGCCCTG	GGACGTTCCT	CCTTCTACTG	TCTGGAGTAT	TTCCCATCGC
44_1	TCAGGCCGTG	GGCCGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
44_5	TCAGGCCGTG	GGCCGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
223_10	CCAATCGGTA	GGCCGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
223_2	CCAATCGGTA	GGCCGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
223_4	CCAATCGGTA	GGCCGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
223_5	CCAATCGGTA	GGCCGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
223_6	CCAATCGGTA	GGCCGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
223_7	CCAATCGGTA	GGCCGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
A3_4	CCAAGCGGTA	GGACGTTCTT	CATTCTACTG	TCTAGAGTAT	TTTCCCTCTC
A3_5	CCAAGCGGTA	GGACGTTCTT	CATTCTACTG	TCTAGAGTAT	TTTCCCTCTC
A3_7	CCAAGCGGTA	GGACGTTCTT	CATTCTACTG	TCTAGAGTAT	TTTCCCTCTC
A3_3	CCAAGCGGTA	GGACGTTCTT	CATTCTACTG	TCTAGAGTAT	TTTCCCTCTC
42_12	TCAGGCCGTG	GGCCGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC
AAV1	CCAAGCCGTG	GGACGTTCAT	CCTTTTACTG	CCTGGAATAT	TTCCCTTCTC
AAV2	TCAGGCAGTA	GGACGCTCTT	CATTTTACTG	CCTGGAGTAC	TTTCCTTCTC
AAV3	TCAAGCGGTG	GGACGCTCAT	CCTTTTACTG	CCTGGAGTAC	TTCCCTTCGC
AAV8	TCAGGCCGTG	GGACGCTCCT	CCTTCTACTG	CCTGGAATAC	TTTCCTTCGC
AAV9	TCAAGCGTTA	GGACGTTCTT	CTTTCTACTG	TCTGGAATAC	TTCCCTTCTC
AAV7	TCAGTCTGTG	GGACGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTCCCCTCTC
44_2	TCAGGCCGTG	GGCCGTTCCT	CCTTCTACTG	CCTGGAGTAC	TTTCCTTCTC

Fig. 1AAR

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         3451                                                        3500
  42_2   AGATGCTGAG AACGGGCAAT AACTTTGAAT TCAGCTACAC CTTTGAGGAA
  42_8   AAATGCTGAG AACGGGCAAC AACTTTGAGT TCAGCTACCA GTTTGAGGAC
 42_15   AAATGCGGAG AACGGGCAAC AACTTTGAGT TCAGCTACCA GTTTGAGGAC
 42_5b   AAATGCTGAG AACGGGCAAC AACTTTGAGT TCAGCTACCA GTTTGAGGAC
 42_1b   AAATGCTGAG AACGGGCAAC AACTTTGAGT TCAGCTACCA GTTTGAGGAC
 42_13   AAATGCTGAG AACGGGCAAC AACTTTGAGT TCAGCTACCA GTTTGAGGAC
 42_3a   AAATGCTGAG AACGGGCAAC AACTTTGAGT TCAGCTACCA GTTTGAGGAC
  42_4   AAATGCTGAG AACGGGCAAC AACTTTGAGT TCAGCTACCA GTTTGAGGAC
 42_5a   AGATGCTGAG AACGGGCAAT AACTTTGAAT TCAGCTACCA GTTTGAGGAC
 42_10   AGATGCTGAG AACGGGCAAT AACTTTGAAT TCAGCTACAC CTTTGAGGAA
 42_3b   AGATGCTGAG AACGGGCAAT AACTTTGAAT TCAGCTACAC CTTTGAGGAA
 42_11   AGATGCTGAG AACGGGCAAT AACTTTGAAT TCAGCTACAC CTTTGAGGAA
 42_6b   AGATGCTGAG AACGGGCAAT AACTTTGAAT TCAGCTACAC CTTTGAGGAA
  43_1   AAATGCTGAG GACGGGCAAC AACTTTGAAT TCAGCTACAC CTTCGAGGAC
  43_5   AAATGCTGAG GACGGGCAAC AACTTTGAAT TCAGCTACAC CTTCGAGGAC
 43_12   AAATGCTGAG GACGGGCAAC AACTTTGAAT TCAGCTACAC CTTCGAGGAC
 43_20   AGATGCTGAG AACCGGCAAC AACTTTCAGT TCAGCTACAC CTTCGAGGAC
 43_21   AGATGCTGAG AACCGGCAAC AACTTTCAGT TCAGCTACAC CTTCGAGGAC
 43_23   AGATGCCGAG AACCGGCAAC AACTTTCAGT TCAGCTACAC CTTCGAGGAC
 43_25   AGATGCTGAG AACCGGCAAC AACTTTCAGT TCAGCTACAC CTTCGAGGAC
  44_1   AAATGCTGAG AACGGGCAAC AACTTTGAGT TCAGCTACCA GTTTGAGGAC
  44_5   AAATGCTGAG AACGGGCAAC AACTTTGAGT TCAGCTACCA GTTTGAGGAC
223_10   AGATGCTGAG AACGGGCAAC AACTTCACCT TTAGCTACAC CTTCGAGGAC
 223_2   AGATGCTGAG AACGGGCAAC AACTTCACCT TTAGCTACAC CTTCGAGGAC
 223_4   AGATGCTGAG AACGGGCAAC AACTTCACCT TTAGCTACAC CTTCGAGGAC
 223_5   AGATGCTGAG AACGGGCAAC AACTTCACCT TTAGCTACAC CTTCGAGGAC
 223_6   AGATGCTGAG AACGGGCAAC AACTTCACCT TTAGCTACAC CTTCGAGGAC
 223_7   AGATGCTGAG AACGGGCAAC AACTTCACCT TTAGCTACAC CTTCGAGGAC
  A3_4   AGATGCTGAG GACGGGAAAC AACTTCACCT TCAGCTACAC TTTTGAAGAC
  A3_5   AGATGCTGAG GACGGGAAAC AACTTCACCT TCAGCTACAC TTTTGAAGAC
  A3_7   AGATGCTGAG GACGGGAAAC AACTTCACCT TCAGCTACAC TTTTGAAGAC
  A3_3   AGATGCTGAG GACGGGAAAC AACTTCACCT TCAGCTACAC TTTTGAAGAC
 42_12   AAATGCTGAG AACGGGCAAC AACTTTGAGT TCAGCTACCA GTTTGAGGAC
   AAV1  AGATGCTGAG AACGGGCAAC AACTTTACCT TCAGCTACAC CTTTGAGGAA
   AAV2  AGATGCTGCG TACCGGAAAC AACTTTACCT TCAGCTACAC TTTTGAGGAC
   AAV3  AGATGCTAAG GACTGGAAAT AACTTCCAAT TCAGCTATAC CTTCGAGGAT
   AAV8  AGATGCTGAG AACCGGCAAC AACTTCCAGT TTACTTACAC CTTCGAGGAC
   AAV9  AGATGCTGAG AACCGGCAAC AACTTTCAGT TCAGCTACAC TTTCGAGGAC
   AAV7  AGATGCTGAG AACGGGCAAC AACTTTGAGT TCAGCTACAG CTTCGAGGAC
  44_2   AAATGCTGAG AACGGGCAAC AACTTTGAGT TCAGCTACCA GTTTGAGGAC
```

Fig. 1AAS

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        3501                                                  3550
  42_2  GTGCCTTTCC ACAGCAGCTA TGCGCACAGC CAGAGCCTGG ACCGGCTGAT
  42_8  GTGCCTTTTC ACAGCAGCTA CGCGCACAGC CAAAGCCTGG ACCGGCTGAT
 42_15  GTGCCTTTTC ACAGCAGCTA CGCGCATAGC CAAAGCCTGG ACCGGCTGAT
 42_5b  GTGCCTTTTC ACAGCAGCTA CGCGCACAGC CAAAGCCTGG ACCGGCTGAT
 42_1b  GTGCCTTTTC ACAGCAGCTA TGCGCACAGC CAAAGCCTGG ACCGGCTGAT
 42_13  GTGCCTTTTC ACAGCAGCTA TGCGCACAGC CAAAGCCTGG ACCGGCTGAT
 42_3a  GTGCCTTTTC ACAGCAGCTA CGCGCACAGC CAAAGCCTGG ACCGGCTGAT
  42_4  GTGCCTTTTC ACAGCAGCTA CGCGCACAGC CAAAGCCTGG ACCGGCTGAT
 42_5a  GTGCCCTTTC ACAGCAGCTA CGCGCACAGC CAAAGCCTGG ACCGGCTGAT
 42_10  GTGCCTTTCC ACAGCAGCTA TGCGCACAGC CAGAGCCTGG ACCGGCTGAT
 42_3b  GTGCCTTTCC ACAGCAGCTA TGCGCACAGC CAGAGCCTGG ACCGGCTGAT
 42_11  GTGCCTTTCC ACAGCAGCTA TGCGCACAGC CAGAGCCTGG ACCGGCTGAT
 42_6b  GTGCCTTTCC ACAGCAGCTA TGCGCATAGC CAGAGCCTGG ACCGGCTGAT
  43_1  GTGCCTTTCC ACAGCAGCTA CGCGCACAGC CAGAGCCTGG ACCGGCTGAT
  43_5  GTGCCTTTCC ACAGCAGCTA CGCGCACAGC CAGAGCCTGG ACCGGCTGAT
 43_12  GTGCCTTTCC ACAGCAGCTA CGCGCACAGC CAGAGCCTGG ACCGGCTGAT
 43_20  GTGCCTTTCC ACAGCAGCTA CGCGCACAGC CAGAGCCTGG ACAGGCTGAT
 43_21  GTGCCTTTCC ACAGCAGCTA CGCGCACAGC CAGAGCCTGG ACAGGCTGAT
 43_23  GTGCCTTTCC ACAGCAGCTA CGCGCACAGC CAGAGCCTGG ACAGGCTGAT
 43_25  GTGCCTTTCC ACAGCAGCTA CGCGCACAGC CAGAGCCTGG ACAGGCTGAT
  44_1  GTGCCTTTTC ACAGCAGCTA CGCGCACAGC CAAAGCCTGG ACCGGCTGAT
  44_5  GTGCCTTTTC ACAGCAGCTA CGCGCACAGC CAAAGCCTGG ACCGGCTGAT
223_10  GTGCCTTTCC ACAGCAGCTA CGCGCACAGC CAGAGTCTGG ACCGGCTGAT
 223_2  GTGCCTTTCC ACAGCAGCTA CGCGCACAGC CAGAGTCTGG ACCGGCTGAT
 223_4  GTGCCTTTCC ACAGCAGCTA CGCGCACAGC CAGAGTCTGG GCCGGCTGAT
 223_5  GTGCCTTTCC ACAGCAGCTA CGCGCACAGC CAGAGTCTGG GCCGGCTGAT
 223_6  GTGCCTTTCC ACAGCAGCTA CGCGCACAGC CAGAGTCTGG ACCGGCTGAT
 223_7  GTGCCTTTCC ACAGCAGCTA CGCGCACAGC CAGAGTCTGG ACCGGCTGAT
  A3_4  GTGCCTTTCC ACAGCAGCTA CGCGCACAGC CAGAGTCTGG ATCGGCTGAT
  A3_5  GTGCCTTTCC ACAGCAGCTA CGCGCACAGC CAGAGTCTGG ATCGGCTGAT
  A3_7  GTGCCTTTCC ACAGCAGCTA CGCGCACAGC CAGAGTCTGG ATCGGCTGAT
  A3_3  GTGCCTTTCC ACAGCAGCTA CGCGCACAGC CAGAGTCTGG ATCGGCTGAT
 42_12  GTGCCTTTTC ACAGCAGCTA CGCGCACAGC CAAAGCCTGG ACCGGCTGAC
  AAV1  GTGCCTTTCC ACAGCAGCTA CGCGCACAGC CAGAGCCTGG ACCGGCTGAT
  AAV2  GTTCCTTTCC ACAGCAGCTA CGCTCACAGC CAGAGTCTGG ACCGTCTCAT
  AAV3  GTACCTTTTC ACAGCAGCTA CGCTCACAGC CAGAGTTTGG ATCGCTTGAT
  AAV8  GTGCCTTTCC ACAGCAGCTA CGCCCACAGC CAGAGCTTGG ACCGGCTGAT
  AAV9  GTGCCTTTCC ACAGCAGCTA CGCACACAGC CAGAGTCTAG ATCGACTGAT
  AAV7  GTGCCTTTCC ACAGCAGCTA CGCACACAGC CAGAGCCTGG ACCGGCTGAT
  44_2  GTGCCTTTTC ACAGCAGCTA CGCGCACAGC CAAAGCCTGG ACCGGCTGAT
```

Fig. 1AAT

```
        3551                                                  3600
  42_2  GAATCCCCTC ATCGACCAGT ACCTGTACTA CCTGGCCCGG ACCCAGAGCA
  42_8  GAACCCCCTC ATCGACCAGT ACCTGTACTA CCTGTCTCGG ACTCAGTCCA
 42_15  GAACCCCCTC ATCGACCAGT ACCTGTACTA CCTGTCTCGG ACTCAGTCCA
 42_5b  GAACCCCCTC ATCGACCAGT ACCTGTACTA CCTGTCTCGG ACTCAGTCCA
 42_1b  GAACCCCCTC ATCGACCAGT ACCTGTACTA CCTGTCTCGG ACTCAGTCCA
 42_13  GAACCCCCTC ATCGACCAGT ACCTGTACTA CCTGTCTCGG ACTCAGTCCA
 42_3a  GAACCCCCTC ATCGACCAGT ACCTGTACTA CCTGTCTCGG ACTCAGTCCA
  42_4  GAACCCCCTC ATCGACCAGT ACCTGTACTA CCTGTCTCGG ACTCAGTCCA
 42_5a  GAACCCCCTC ATCGACCAGT ACCTGTACTA CCTGTCTCGG ACTCAGTCCA
 42_10  GAATCCCCTC ATCGACCAGT ACCTGTACTA CCTGGCCCGG ACCCAGAGCA
 42_3b  GAATCCCCTC ATCGACCAGT ACCTGTACTA CCTGGCCCGG ACCCAGAGCA
 42_11  GAATCCCCTC ATCGACCAGT ACCTGTACTA CCTGGCCCGG ACCCAGAGCA
 42_6b  GAATCCCCTC ATCGACCAGT ACCTGTACTA CCTGGCCCGG ACCCAGAGCA
  43_1  GAACCCTCTC ATCGACCAGT ACCTGTATTA CTTATCCAGA ACTCAGTCCA
  43_5  GAACCCTCTC ATCGACCAGT ACCTGTATTA CTTATCCAGA ACTCAGTCCA
 43_12  GAACCCTCTC ATCGACCAGT ACCTGTATTA CTTATCCAGA ACTCAGTCCA
 43_20  GAATCCCCTC ATCGACCAGT ACCTGTACTA CCTGGTCAGA ACGCAAACGA
 43_21  GAATCCCCTC ATCGACCAGT ACCTGTACTA CCTGGTCAGA ACGCAAACGA
 43_23  GAATCCCCTC ATCGACCAGT ACCTGTACTA CCTGGTCAGA ACGCAAACGA
 43_25  GAATCCCCTC ATCGACCAGT ACCTGTACTA CCTGGTCAGA ACGCAAACGA
  44_1  GAACCCCCTC ATCGACCAGT ACCTGTACTA CCTGTCTCGG ACTCAGTCCA
  44_5  GAACCCCCTC ATCGACCAGT ACCTGTACTA CCTGTCTCGG ACTCAGTCCA
223_10  GAATCCCCTC ATCGACCAGT ACCTGTACTA CTTGGCCAGA ACACAGAGCA
 223_2  GAATCCCCTC ATCGACCAGT ACCTGTACTA CTTGGCCAGA ACACAGAGCA
 223_4  GAATCCCCTC ATCGACCAGT ACCTGTACTA CTTGGCCAGA ACACAGAGCA
 223_5  GAATCCCCTC ATCGACCAGT ACCTGTACTA CTTGGCCAGA ACACAGAGCA
 223_6  GAATCCCCTC ATCGACCAGT ACCTGTACTA CTTGGCCAGA ACACAGAGCA
 223_7  GAATCCCCTC ATCGACCAGT ACCTGTACTA CTTGGCCAGA ACACAGAGCA
  A3_4  GAATCCTCTC ATTGACCAGT ACCTGTATTA CCTGAGCAAA ACTCAGGGTA
  A3_5  GAATCCTCTC ATTGACCAGT ACCTGTATTA CCTGAGCAAA ACTCAGGGTA
  A3_7  GAATCCTCTC ATTGACCAGT ACCTGTATTA CCTGAGCAAA ACTCAGGGTA
  A3_3  GAATCCTCTC ATTGACCAGT ACCTGTATTA CCTGAGCAAA ACTCAGGGTA
 42_12  GAACCCCCTC ATCGACCAGT ACCTGTACTA CCTGGCCCGG ACCCAGAGCA
  AAV1  GAATCCTCTC ATCGACCAAT ACCTGTATTA CCTGAACAGA ACTCAAA.AT
  AAV2  GAATCCTCTC ATCGACCAGT ACCTGTATTA CTTGAGCAGA ACAAACACTC
  AAV3  GAATCCTCTT ATTGATCAGT ATCTGTACTA CCTGAACAGA ACGCAAGGAA
  AAV8  GAATCCTCTG ATTGACCAGT ACCTGTACTA CTTGTCTCGG ACTCAAACAA
  AAV9  GAACCCCCTC ATCGACCAGT ACCTATACTA CCTGGTCAGA ACACAGACAA
  AAV7  GAATCCCCTC ATCGACCAGT ACTTGTACTA CCTGGCCAGA ACACAGAGTA
  44_2  GAACCCCCTC ATCGACCAGT ACCTGTACTA CCTGTCTCGG ACTCAGTCCA
```

Fig. 1AAU

```
        3601                                                  3650
  42_2  CTACGG..GG TCCACAAGGG AGCTGCA.GT TCCA...... TCAGGCTGGG
  42_8  CGGGA...GG TACCGCAGGA ACTCAGCAGT TGCTATTTTC TCAGGCCGGG
 42_15  CGGGA...GG TACCGCAGGA ACTCAGCAGT TGCTATTTTC TCAGGCCGGG
 42_5b  CGGGA...GG TACCGCAGGA ACTCAGCAGT TGCTATTTTC TCAGGCCGGG
 42_1b  CGGGA...GG TACCGCAGGA ACTCAGCAGT TGCTATTTTC TCAGGCCGGG
 42_13  CGGGA...GG TACCGCAGGA ACTCAGCAGT TGCTATTTTC TCAGGCCGGG
 42_3a  CGGGA...GG TACCGCAGGA ACTCAGCAGT TGCTATTTTC TCAGGCCGGG
  42_4  CGGGA...GG TACCGCAGGA ACTCAGCAGT TGCTATTTTC TCAGGCCGGG
 42_5a  CGGGA...GG TACCGCAGGA ACTCAGCAGT TGCTATTTTC TCAGGCCGGG
 42_10  CTACG...GG GTCCACAAGG GAGCTGCAGT TCCA...... TCAGGCTGGG
 42_3b  CTACG...GG GTCCACAAGG GAGCTGCAGT TCCA...... TCAGGCTGGG
 42_11  CTACG...GG GTCCACAAGG GAGCTGCAGT TCCA...... TCAGGCTGGG
 42_6b  CTACG...GG GTCCACAAGG GAGCTGCAGT TCCA...... TCAGGCTGGG
  43_1  CAGGA...GG AACTCAAGGT ACTCAGCAAT TGTTATTTTC TCAAGCCGGG
  43_5  CAGGA...GG AACTCAAGGT ACTCAGCAAT TGTTATTTTC TCAAGCCGGG
 43_12  CAGGA...GG AACTCAAGGT ACTCAGCAAT TGTTATTTTC TCAAGCCGGG
 43_20  CT......GG AACTGGAGGG ACGCAGACTC TGGCATTCAG CCAAGCGGGT
 43_21  CT......GG AACTGGAGGG ACGCAGACTC TGGCATTCAG CCAAGCGGGT
 43_23  CT......GG AACTGGAGGG ACGCAGACTC TGGCATTCAG CCAAGCGGGT
 43_25  CT......GG AACTGGAGGG ACGCAGACTC TGGCATTCAG CCAAGCGGGT
  44_1  CGGGA...GG TACCGCAGGA ACTCAGCAGT TGCTATTTTC TCAGGCCGGG
  44_5  CGGGA...GG TACCGCAGGA ACTCAGCAGT TGCTATTTTC TCAGGCCGGG
223_10  ACGCAGGAGG TACTGCTGGC AATCGGGAAC TGCAGTTTTA TCAGGGCGGA
 223_2  ACGCAGGAGG TACTGCTGGC AATCGGGAAC TGCAGTTTTA TCAGGGCGGA
 223_4  ACGCAGGAGG TACTGCTGGC AATCGGGAAC TGCAGTTTTA TCAGGGCGGA
 223_5  ACGCAGGAGG TACTGCTGGC AATCGGGAAC TGCAGTTTTA TCAGGGCGGA
 223_6  ACGCAGGAGG TACTGCTGGC AATCGGGAAC TGCAGTTTTA TCAGGGCGGA
 223_7  ACGCAGGAGG TACTGCTGGC AATCGGGAAC TGCAGTTTTA TCAGGGCGGA
  A3_4  CAAG...TGG AACAACGCAG CAATCGAGAC TGCAGTTCAG CCAAGCTGGG
  A3_5  CAAG...TGG AACAACGCAG CAATCGAGAC TGCAGTTCAA CCAAGCTGGG
  A3_7  CAAG...TGG AACAACGCAG CAATCGAGAC TGCAGTTCAG CCAAGCTGGG
  A3_3  CAAG...TGG AACAACGCAG CAATCGAGAC TGCAGTTCAG CCAAGCTGGG
 42_12  CTACG...GG GTCCACAAGG GGGCTGCAGT TCCA...... TCAGGCTGGG
  AAV1  CAGTCC..GG AAGTGCCCAA AACAAGGACT TGCTGTTTAG CCGTGGGTCT
  AAV2  CAAG...TGG AACCACCACG CAGTCAAGGC TTCAGTTTTC TCAGGCCGGA
  AAV3  CAACCTCTGG AACAACCAAC CAATCACGGC TGCTTTTTAG CCAGGCTGGG
  AAV8  CAGGAG..GC .ACGGCAAAT ACGCAGACTC TGGGCTTCAG CCAAGGTGGG
  AAV9  CTGGA..... .ACTGGGGGA ACTCAAACTT TGGCATTCAG CCAAGCAGGC
  AAV7  ACCCAGGAGG CACAGCTGGC AATCGGGAAC TGCAGTTTTA CCAGGGCGGG
  44_2  CGGGA...GG TACCGCAGGA ACTCAGCAGT TGCTATTTTC TCAGGCCGGG
```

Fig. 1AAV

	3651				3700
42_2	CCCAACACCA	TGGCCGAGCA	ATCAAAGAAC	TGGCTGCCCG	GACCCTGTTA
42_8	CCTAATAACA	TGTCGGCTCA	GGCCAAAAAC	TGGCTACCCG	GGCCCTGCTA
42_15	CCTAATAACA	TGTCGGCTCA	GGCCAAAAAC	TGGCTACCCG	GGCCCTGCTA
42_5b	CCTAATAACA	TGTCGGCTCA	GGCCAAAAAC	TGGCTACCCG	GGCCCTGCTA
42_1b	CCTAATAACA	TGTCGGCTCA	GGCCAAAAAC	TGGCTACCCG	GGCCCTGCTA
42_13	CCTAATAACA	TGTCGGCTCA	GGCCAAAAAC	TGGCTACCCG	GGCCCTGCTA
42_3a	CCTAATAACA	TGTCGGCTCA	GGCCAAAAAC	TGGCTACCCG	GGCCCTGCTA
42_4	CCTAATAACA	TGTCGGCTCA	GGCCAAAAAC	TGGCTACCCG	GGCCCTGCTA
42_5a	CCTAATAACA	TGTCGGCTCA	GGCCAAAAAC	TGGCTACCCG	GGCCCTGCTA
42_10	CCCAACACCA	TGGCCGAGCA	ATCAAAGAAC	TGGCTGCCCG	GACCCTGTTA
42_3b	CCCAACACCA	TGGCCGAGCA	ATCAAAGAAC	TGGCTGCCCG	GACCCTGTTA
42_11	CCCAACACCA	TGGCCGAGCA	ATCAAAGAAC	TGGCTGCCCG	GACCCTGTTA
42_6b	CCCAACACCA	TGGCCGAGCA	ATCAAAGAAC	TGGCTGCCCG	GACCCTGTTA
43_1	CCCGCAAACA	TGTCGGCTCA	GGCCAAGAAC	TGGCTACCTG	GACCGTGTTA
43_5	CCCGCAAACA	TGTCGGCTCA	GGCCAAGAAC	TGGCTACCTG	GACCGTGTTA
43_12	CCCGCAAACA	TGTCGGCTCA	GGCCAAGAAC	TGGCTACCTG	GACCGTGTTA
43_20	CCTAGCTCAA	TGGCCAACCA	GGCTAGAAAT	TGGGTGCCCG	GACCTTGCTA
43_21	CCTAGCTCAA	TGGCCAACCA	GGCTAGAAAT	TGGGTGCCCG	GACCTTGCTA
43_23	CCTAGCTCAA	TGGCCAACCA	GGCTAGAAAT	TGGGTGCCCG	GACCTTGCTA
43_25	CCTAGCTCAA	TGGCCAACCA	GGCTAGAAAT	TGGGTGCCCG	GACCTTGCTA
44_1	CCTAATAACA	TGTCGGCTCA	GGCCAAAAAC	TGGCTACCCG	GGCCCTGCTA
44_5	CCTAATAACA	TGTCGGCTCA	GGCCAAAAAC	TGGCTACCCG	GGCCCTGCTA
223_10	CCTACCACCA	TGGCCGAACA	AGCAAAGAAC	TGGCTGCCCG	GACCTTGCTT
223_2	CCTACCACCA	TGGCCGAACA	AGCAAAGAAC	TGGCTGCCCG	GACCTTGCTT
223_4	CCTACCACCA	TGGCCGAACA	AGCAAAGAAC	TGGCTGCCCG	GACCTTGCTT
223_5	CCTACCACCA	TGGCCGAACA	AGCAAAGAAC	TGGCTGCCCG	GACCTTGCTT
223_6	CCTACCACCA	TGGCCGAACA	AGCAAAGAAC	TGGCTGCCCG	GACCTTGCTT
223_7	CCTACCACCA	TGGCCGAACA	AGCAAAGAAC	TGGCTGCCCG	GACCTTGCTT
A3_4	CCTAGCTCCA	TGGCTCAGCA	GGCCAAAAAC	TGGCTACCGG	GACCCAGCTA
A3_5	CCTAGCTCCA	TGGCTCAGCA	GGCCAAAAAC	TGGCTACCGG	GACCCAGCTA
A3_7	CCTAGCTCCA	TGGCTCAGCA	GGCCAAAAAC	TGGCTACCGG	GACCCAGCTA
A3_3	CCTAGCTCCA	TGGCTCAGCA	GGCCAAAAAC	TGGCTACCGG	GACCCAGCTA
42_12	CCCAACACCA	TGGCCGAGCA	ATCAAAGAAC	TGGCTGCCCG	GACCCTGTTA
AAV1	CCAGCTGGCA	TGTCTGTTCA	GCCCAAAAAC	TGGCTACCTG	GACCCTGTTA
AAV2	GCGAGTGACA	TTCGGGACCA	GTCTAGGAAC	TGGCTTCCTG	GACCCTGTTA
AAV3	CCTCAGTCTA	TGTCTTTGCA	GGCCAGAAAT	TGGCTACCTG	GGCCCTGCTA
AAV8	CCTAATACAA	TGGCCAATCA	GGCAAAGAAC	TGGCTGCCAG	GACCCTGTTA
AAV9	CCTAGCTCAA	TGGCCAATCA	GGCTAGAAAC	TGGGTACCCG	GGCCTTGCTA
AAV7	CCTTCAACTA	TGGCCGAACA	AGCCAAGAAT	TGGTTACCTG	GACCTTGCTT
44_2	CCTAATAACA	TGTCGGCTCA	GGCCAAAAAC	TGGCTACCCG	GGCCCTGCTA

Fig. 1AAW

	3701				3750
42_2	TCGGCAGCAG	AGACTGTCAA	AAAACATAGA	CAGCAACAAC	AACAGTAACT
42_8	CCGGCAGCAA	CGCGTCTCCA	CGACACTGTC	GCAAAATAAC	AACAGCAACT
42_15	CCGGCAGCAA	CGCGTCTCCA	CGACACTGTC	GCAAAATAAC	AACAGCAACT
42_5b	CCGGCAGCAA	CGCGTCTCCA	CGACACTGTC	GCAAAATAAC	AACAGCAACT
42_1b	CCGGCAGCAA	CGCGTCTCCA	CGACAGTGTC	GCAAAATAAC	AACAGCAACT
42_13	CCGGCAGCAA	CGCGTCTCCA	CGACAGTGTC	GCAAAATAAC	AACAGCAACT
42_3a	CCGGCAGCAA	CGCGTCTCCA	CGACACTGTC	GCAAAATAAC	AACAGCAACT
42_4	CCGGCAGCAA	CGCGTCTCCA	CGACACTGTC	GCAAAATAAC	AACAGCAACT
42_5a	CCGGCAGCAA	CGCGTCTCCA	CGACACTGTC	GCAAAATAAC	AACAGCAACT
42_10	TCGGCAGCAG	AGACTGTCAA	AAAACATAGA	CAGCAACAAC	AACAGTAACT
42_3b	TCGGCAGCAG	AGACTGTCAA	AAAACATAGA	CAGCAACAAC	ACCAGTAACT
42_11	TCGGCGGCAG	AGACTGTCAA	AAGACATAGA	CAGCAACAAC	AACAGTAACT
42_6b	TCGGCAGCAG	AGACTGTCAA	AAAACATAGA	CAGCAACAAC	AACAGTAACT
43_1	CCGTCAGCAA	CGAGTTTCCA	CGACACTGTC	GCAAAACAAC	AACAGCAATT
43_5	CCGTCAGCAA	CGAGTTTCCA	CGACACTGTC	GCAAAACAAC	AACAGCAATT
43_12	CCGTCAGCAA	CGAGTTTCCA	CGACACTGTC	GCAAAACAAC	AACAGCAATT
43_20	CCGGCAGCAG	CGCGTCTCCA	CGACAACCAA	CCAGAACAAC	AACAGCAACT
43_21	CCGGCAGCAG	CGCGTCTCCA	CGACAACCAA	CCAGAGCAAC	AACAGCAACT
43_23	CCGGCAGCAG	CGCGTCTCCA	CGACAACCAA	CCAGAACAAC	AACAGCAACT
43_25	CCGGCAGCAG	CGCGTCTCCA	CGACAACCAA	CCAGAACAAC	AACAGCAACT
44_1	CCGGCAGCAA	CGCGTCTCCA	CGACACTGTC	GCAAAATAAC	AACAGCAACT
44_5	CCGGCAGCAA	CGCGTCTCCA	CGACACTGTC	GCAAAATAAC	AACAGCAACT
223_10	CCGGCAACAG	AGAGTATCCA	AGACGCTGGA	TCAAAATAAC	AACAGCAACT
223_2	CCGGCAACAG	AGAGTATCCA	AGACGCTGGA	TCAAAATAAC	AACAGCAACT
223_4	CCGGCAACAG	AGAGTATCCA	AGACGCTGGA	TCAAAATAAC	AACAGCAACT
223_5	CCGGCAACAG	AGAGTATCCA	AGACGCTGGA	TCAAAATAAC	AACAGCAACT
223_6	CCGGCAACAG	AGAGTATCCA	AGACGCTGGA	TCAAAATAAC	AACAGCAACT
223_7	CCGGCAACAG	AGAGTATCCA	AGACGCTGGA	TCAAAATAAC	AACAGCAACT
A3_4	CCGACAGCAG	CGAATGTCTA	AGACGGCTAA	TGACAACAAC	AACAGTGAAT
A3_5	CCGACAGCAG	CGAATGTCTA	AGACGGCTAA	TGACAACAAC	AACAGTGAAT
A3_7	CCGACAGCAG	CGAATGTCTA	AGACGGCTAA	TGACAACAAC	AACAGTGAAT
A3_3	CCGACAGCAG	CGAATGTCTA	AGACGGCTAA	TGACAACAAC	AACAGTGAAT
42_12	TCGGCAGCAG	AGACTGTCAA	AAAACATAGA	CAGCAACAAC	AACAGTAACT
AAV1	TCGGCAGCAG	CGCGTTTCTA	AAACAAAAAC	AGACAACAAC	AACAGCAATT
AAV2	CCGCCAGCAG	CGAGTATCAA	AGACATCTGC	GGATAACAAC	AACAGTGAAT
AAV3	CCGGCAACAG	AGACTTTCAA	AGACTGCTAA	CGACAACAAC	AACAGTAACT
AAV8	CCGCCAACAA	CGCGTCTCAA	CGACAACCGG	GCAAAACAAC	AATAGCAACT
AAV9	CCGTCAGCAG	CGCGTCTCCA	CAACCACCAA	CCAAAATAAC	AACAGCAACT
AAV7	CCGGCAACAA	AGAGTCTCCA	AAACGCTGGA	TCAAAACAAC	AACAGCAACT
44_2	CCGGCAGCAA	CGCGTCTCCA	CGACACTGTC	GCAAAATAAC	AACAGCAACT

Fig. 1AAX

```
        3751                                                        3800
 42_2   TTGCCTGGAC CGGGGCCACT AAATACCATC TGAATGGTAG AAATTCATTA
 42_8   TTGCTTGGAC CGGTGCCACC AAGTATCATC TGAATGGCAG AGACTCTCTG
42_15   TTGCTTGGAC CGGTGCCACC AAGTATCATC TGAATGGCAG AGACTCTCTG
42_5b   TTGCTTGGAC CGGTGCCACC AAGTATCATC TGAATGGCAG AGACTCTCTG
42_1b   TTGCTTGGAC CGGTGCCACC AAGTATCATC TGAATGGCAG AGACTCTCTG
42_13   TTGCTTGGAC CGGTGCCACC AAGTATCATC TGAATGGCAG AGACTCTCTG
42_3a   TTGCTTGGAC CGGTGCCACC AAGTATCATC TGAATGGCAG AGACTCTCTG
 42_4   TTGCTTGGAC CGGTGCCACC AAGTATCATC TGAATGGCAG AGACTCTCTG
42_5a   TTGCTTGGAC CGGTGCCACC AAGTATCATC TGAATGGCAG AGACTCTCTG
42_10   TTGCCTGGAC CGGGGCCACT AAATACCATC TGAATGGTAG AAATTCATTA
42_3b   TTGCCTGGAC CGGGGCCACT AAATACCATC TGAATGGTAG AAATTCATTA
42_11   TTGCCTGGAC CGGGGCCACT AAATACCATC TGAATGGTAG AAATTCATTA
42_6b   TTGCCTGGAC CGGGGCCACT AAATACCATC TGAATGGTAG AAATTCATTA
 43_1   TTGCTTGGAC CGGTGCCACC AAGTATCACC TGAATGGCAG AGACTCCCTG
 43_5   TTGCTTGGAC CGGTGCCACC AAGTATCACC TGAATGGCAG AGACTCCCTG
43_12   TTGCTTGGAC CGGTGCCACC AAGTATCACC TGAATGGCAG AGACTCCCTG
43_20   TTGCCTGGAC GGGAGCTGCC AAGTTTAAGC TGAACGGCCG AGACTCTCTA
43_21   TTGCCTGGAC GGGAGCTGCC AAGTTTAAGC TGAACGGCCG AGACTCTCTA
43_23   TTGCCTGGAC GGGAGCTGCC AAGTTTAAGC TGAACGGCCG AGACTCTCTA
43_25   TTGCCTGGAC GGGAGCTGCC AAGTTTAAGC TGAACGGCCG AGACTCTCTA
 44_1   TTGCCTGGAC CGGTGCCACC AAGTATCATC TGAATGGCAG AGACTCTCTG
 44_5   TTGCCTGGAC CGGTGCCACC AAGTATCATC TGAATGGCAG AGACTCTCTG
223_10  TTGCCTGGAC TGGTGCCACA AAATACCATT TAAATGNAAG AAATTCATTG
223_2   TTGCCTGGAC TGGTGCCACA AAATACCATT TAAATGGAAG AAATTCATTG
223_4   TTGCCTGGAC TGGTGCCACA AAATACCATT TAAATGGAAG AAATTCATTG
223_5   TTGCCTGGAC TGGTGCCACA AAATACCATT TAAATGGAAG AAATTCATTG
223_6   TTGCCTGGAC TGGTGCCACA AAATACCATT TAAATGGAAG AAATTCATTG
223_7   TTGCCTGGAC TGGTGCCACA AAATACCATT TAAATGGAAG AAATTCATTG
 A3_4   TTGCTTGGAC TGCAGCCACC AAATATTACC TGAATGGAAG AAATTCTCTG
 A3_5   TTGCTTGGAC TGCAGCCACC AAATATTACC CGAATGGAAG AAATTCTCTG
 A3_7   TTGCTTGGAC TGCAGCCACC AAATATTACC TGAATGGAAG AAATTCTCTG
 A3_3   TTGCTTGGAC TGCAGCCACC AAATATTACC TGAATGGAAG AAATTCTCTG
42_12   TTGCCTGGAC CGGGGCCACT AAATACCATC TGAATGGTAG AAATTCATTA
 AAV1   TTACCTGGAC TGGTGCTTCA AAATATAACC TCAATGGGCG TGAATCCATC
 AAV2   ACTCGTGGAC TGGAGCTACC AAGTACCACC TCAATGGCAG AGACTCTCTG
 AAV3   TTCCTTGGAC AGCGGCCAGC AAATATCATC TCAATGGCCG CGACTCGCTG
 AAV8   TTGCCTGGAC TGCTGGGACC AAATACCATC TGAATGGAAG AAATTCATTG
 AAV9   TTGCGTGGAC GGGAGCTGCT AAATTCAAGC TGAACGGGAG AGACTCGCTA
 AAV7   TTGCTTGGAC TGGTGCCACC AAATATCACC TGAACGGCAG AAACTCGTTG
 44_2   TTGCCTGGAC CGGTGCCACC AAGTATCATC TGAATGGCAG AGACTCTCTG
```

Fig. 1AAY

```
        3801                                                  3850
  42_2  ACCAACCCGG GCGTAGCCAT GGCCACCAAC AAGGACGACG AGGACCAGTT
  42_8  GTAAATCCCG GTGTCGCTAT GGCAACGCAC AAGGACGACG AAGAGCGATT
 42_15  GTAAATCCCG GTGTCGCTAT GGCAACGCAC AAGGACGACG AAGAGCGATT
 42_5b  GTAAATCCCG GTGTCGCTAT GGCAACGCAC AAGGACGACG AAGAGCGATT
 42_1b  GTAAATCCCG GTGTCGCTAT GGCAACGCAC AAGGGCGACG AAGAGCGATT
 42_13  GTAAATCCCG GTGTCGCTAT GGCAACGCAC AAGGGCGACG AAGAGCGATT
 42_3a  GTAAATCCCG GTGTCGCTAT GGCAACGCAC AAGGACGACG AAGAGCGATT
  42_4  GTAAATCCCG GTGTCGCTAT GGCAACGCAC AAGGACGACG AAGAGCGATT
 42_5a  GTAAATCCCG GTGTCGCTAT GGCAACGCAC AAGGACGACG AAGAGCGATT
 42_10  ACCAACCCGG GCGTAGCCAT GGCCACCAAC AAGGACGACG AGGACCAGTT
 42_3b  ACCAACCCGG GCGTAGCCAT GGCCACCAAC AAGGACGACG AGGACCAGTT
 42_11  ACCAACCCGG GCGTAGCCAT GGCCACCAAC AAGGACGACG AGGACCAGTT
 42_6b  ACCAACCCGG GCGTAGCCAT GGCCACCAAC AAGGACGACG AGGACCAGTT
  43_1  GTTAATCCCG GCGTTGCCAT GGCTACCCAC AAGGACGACG AGGAGCGCTT
  43_5  GTTAATCCCG GCGTTGCCAT GGCTACCCAC AAGGACGACG AGGAGCGCTT
 43_12  GTTAATCCCG GCGTTGCCAT GGCTACCCAC AAGGACGACG AGGAGCGCTT
 43_20  ATGAATCCGG GCGTGGCAAT GGCTTCCCAC AAGGATGACG ACGACCGCTT
 43_21  ATGAATCCGG GCGTGGCAAT GGCTTCCCAC AAGGATGACG ACGACCGCTT
 43_23  ATGAATCCGG GCGTGGCAAT GGCTTCCCAC AAGGATGACG ACGACCGCTT
 43_25  ATGAATCCGG GCGTGGCAAT GGCTTCCCAC AAGGATGACG ACGACCGCTT
  44_1  GTAAATCCCG GTGTCGCTAT GGCAACCCAC AAGGACGACG AAGAGCGATT
  44_5  GTAAATCCCG GTGTCGCTAT GGCAACCCAC AAGGACGACG AAGAGCGATT
223_10  GTTAATCCCG GTGTCGCCAT GGCAACCCAC AAGGACGACG AGGAACGCTT
 223_2  GTTAATCCCG GTGTCGCCAT GGCAACCCAC AAGGACGACG AGGAACGCTT
 223_4  GTTAATCCCG GTGTCGCCAT GGCAACCCAC AAGGACGACG AGGAACGCTT
 223_5  GTTAATCCCG GTGTCGCCAT GGCAACCCAC AAGGACGACG AGGAACGCTT
 223_6  GTTAATCCCG GTGTCGCCAT GGCAACCCAC AAGGACGACG AGGAACGCTT
 223_7  GTTAATCCCG GTGTCGCCAT GGCAACCCAC AAGGACGACG AGGAACGCTT
  A3_4  GTCAATCCCG GGCCCCCAAT GGCCAGTCAC AAGGACGATG AGGAAAAGTA
  A3_5  GTCAATCCCG GGCCCCCAAT GGCCAGTCAC AAGGACGATG AGGAAAAGTA
  A3_7  GTCAATCCCG GGCCCCCAAT GGCCAGTCAC AAGGACGATG AGGAAAAGTA
  A3_3  GTCAATCCCG GGCCCCCAGT GGCCAGTCAC AAGGACGATG AGGAAAAGTA
 42_12  ACCAACCCGG GCGTAGCCAT GGCCACCAAC AAGGACGACG AGGACCAGTT
  AAV1  ATCAACCCTG GCACTGCTAT GGCCTCACAC AAAGACGACG AAGACAAGTT
  AAV2  GTGAATCC.. GGCC....AT GGCAAGCCAC AAGGACGATG AAGAAAAGTT
  AAV3  GTGAATCCAG GACCAGCTAT GGCCAGTCAC AAGGACGATG AAGAAAAATT
  AAV8  GCTAATCCTG GCATCGCTAT GGCAACACAC AAAGACGACG AGGAGCGTTT
  AAV9  ATGAATCCTG GCGTGGCTAT GGCATCGCAC AAAGACGACG AGGACCGCTT
  AAV7  GTTAATCCCG GCGTCGCCAT GGCAACTCAC AAGGACGACG AGGACCGCTT
  44_2  GTAAATCCCG GTGTCGCTAT GGCAACCCAC AAGGACGACG AAGAGCGATT
```

Fig. 1AAZ

```
        3851                                                  3900
 42_2   CTTTCCCATC AACGGAGTGC TGGTTTTTGG CGAAACGGGG GCTGCCAACA
 42_8   TTTTCCATCC AGCGGAGTCT TGATGTTTGG GAAACAGGGA GCTGGAAA..
42_15   TTTTCCATCC AGCGGAGTCT TGATGTTTGG GAAACAGGGA GCTGGAAA..
42_5b   TTTTCCATCC AGCGGAGTCT TGATGTTTGG GAAACAGGGA GCTGGAAA..
42_1b   TTTTCCATCC AGCGGAGTCT TGATGTTTGG GAAACAGGGA GCTGGAAA..
42_13   TTTTCCATCC AGCGGAGTCT TGATGTTTGG GAAACAGGGA GCTGGAAA..
42_3a   TTTTCCATCC AGCGGAGTCT TGATGTTTGG GAAACAGGGA GCTGGAAA..
 42_4   TTTTCCATCC AGCGGAGTCT TGATGTTTGG GAAACAGGGA GCTGGAAA..
42_5a   TTTTCCATCC AGCGGAGTCT TGATGTTTGG GAAACAGGGA GCTGGAAA..
42_10   CTTTCCCATC AACGGAGTGC TGGTTTTTGG CAAAACGGGG GCTGCCAACA
42_3b   CTTTCCCATC AACGGAGTGC TGGTTTTTGG CAAAACGGGG GCTGCCAACA
42_11   CTTTCCCATC AACGGAGTGC TGGTTTTTGG CAAAACGGGG GCTGCCAACA
42_6b   CTTTCCCATC AACGGAGTGC TGGTTTTTGG CAAAACGGGG GCTGCCAACA
 43_1   CTTCCCGTCA AGCGGAGTTC TAATGTTTGG CAAGCAGGGG GCTGGAAA..
 43_5   CTTCCCGTCA AGCGGAGTTC TAATGTTTGG CAAGCAGGGG GCTGGAAA..
43_12   CTTCCCGTCA AGCGGAGTTC TAATGTTTGG CAAGCAGGGG GCTGGAAA..
43_20   CTTCCCTTCG AGCGGGGTCC TGATTTTTGG CAAGCAAGGA GCCGGGAA..
43_21   CTTCCCTTCG AGCGGGGTCC TGATTTTTGG CAAGCAAGGA GCCGGGAA..
43_23   CTTCCCTTCG AGCGGGGTCC TGATTTTTGG CAAGCAAGGA GCCGGGAA..
43_25   CTTCCCTTCG AGCGGGGTCC TGATTTTTGG CAAGCAAGGA GCCGGGAA..
 44_1   TTTTCCGTCC AGCGGAGTCT TAATGTTTGG GAAACAGGGA GCTGGAAA..
 44_5   TTTTCCGTCC AGCGGAGTCT TAATGTTTGG GAAACAGGGA GCTGGAAA..
223_10  CTTCCCTTCG AGCGGAGTTC TAATTTTTGG CAAAACTGGA GCAGCTAATA
223_2   CTCCCCTTCG AGCGGAGTTC TAATTTTTGG CAAAACTGGA GCAGCTAATA
223_4   CTTCCCTTCG AGCGGAGTTC TAATTTTTGG CAAAACTGGA GCAGCTAATA
223_5   CTTCCCTTCG AGCGGAGTTC TAATTTTTGG CAAAACTGGA GCAGCTAATA
223_6   CTTCCCTTCG AGCGGAGTTC TAATTTTTGG CAAAACTGGA GCAGCTAATA
223_7   CTTCCCTTCG AGCGGAGTTC TAATTTTTGG CAAAACTGGA GCAGCTAATA
 A3_4   TTTCCCCATG CACGGAAATC TCATCTTTGG AAAACAAGGC ACAGGAAC..
 A3_5   TTTCCCCATG CACGGAAATC TCATCTTTGG AAAACAAGGC ACAGGAAC..
 A3_7   TTTCCCCATG CACGGAAATC TCATCTTTGG AAAACAAGGC ACAGGAAC..
 A3_3   TTTCCCCATG CACGGAAATC TCATCTTTGG AAAACAAGGC ACAGGAAC..
42_12   CTTTCCCATC AACGGAGTGC TGGTTTTTGG CAAAACGGGG GCTGCCAACA
 AAV1   CTTTCCCATG AGCGGTGTCA TGATTTTTGG AAAAGAGAGC GCCGGAGC..
 AAV2   TTTTCCTCAG AGCGGGGTTC TCATCTTTGG GAAGCAAGGC TCAGAGAA..
 AAV3   TTTCCCTATG CACGGCAATC TAATATTTGG CAAAGAAGGG ACAACGGC..
 AAV8   TTTTCCCAGT AACGGGATCC TGATTTTTGG CAAACAAAAT GCTGCCAG..
 AAV9   CTTTCCATCA AGTGGCGTTC TCATATTTGG CAAGCAAGGA GCCGGGAA..
 AAV7   TTTCCCATCC AGCGGAGTCC TGATTTTTGG AAAAACTGGA GCAACTAACA
 44_2   TTTTCCGTCC AGCGGAGTCT TAATGTTTGG GAAACAGGGA GCTGGAAA..
```

Fig. 1AAAA

```
        3901                                                  3950
  42_2  AGACAACGCT GGAA...... AACGTGCTAA TGACCAGCGA GGAGGAGATC
  42_8  AGACAACG.T GGACTATAGC AGCGTTATGC TAACCAGTGA GGAAGAAATC
 42_15  AGACAACG.T GGACTATAGC AGCGTTATGC TAACCAGTGA GGAAGAAATC
 42_5b  AGACAACG.T GGACTATAGC AGCGTTATGC TAACCAGTGA GGAAGAAATC
 42_1b  AGACAACG.T AGACTATAGC AGCGTTATGC TAACCAGTGA GGAAGAAATC
 42_13  AGACAACG.T GGACTATAGC AGCGTTATGC TAACCAGTGA GGAAGAAATC
 42_3a  AGACAACG.T GGACTATAGC AGCGTTATGC TAACCAGTGA GGAAGAAATC
  42_4  AGACAACG.T GGACTATAGC AGCGTTATGC TAACCAGTGA GGAAGAAATC
 42_5a  AGACAACG.T GGACTATAGC AGCGTTATGC TAACCAGTGA GGAAGAAATC
 42_10  AGACAACGCT GGAA...... AACGTGCTAA TGACCAGCGA GGAGGAGATC
 42_3b  AGACAACGCT GGAA...... AACGTGCTAA TGACCAGCGA GGAGGAGATC
 42_11  AGACAACGCT GGAA...... AACGTGCTAA TGACCAGCGA GGAGGAGATC
 42_6b  AGACAACGCT GGAA...... AACGTGCTAA TGACCAGCGA GGAGGAGATC
  43_1  AGACAATG.T GGACTACAGC AGCGTGATGC TCACCAGCGA AGAAGAAATT
  43_5  AGACAATG.T GGACTACAGC AGCGTGATGC TCACCAGCGA AGAAGAAATT
 43_12  AGACAATG.T GGACTACAGC AGCGTGATGC TCACCAGCGA AGAAGAAATT
 43_20  CGATGGAG.T GGATTACAGC CAAGTGCTGA TTACAGATGA GGAAGAAATC
 43_21  CGATGGAG.T GGATTACAGC CAAGTGCTGA TTACAGATGA GGAAGAAATC
 43_23  CGATGGAG.T GGATTACAGC CAAGTGCTGA TTACAGATGA GGAAGAAATC
 43_25  CGATGGAG.T GGATTACAGC CAAGTGCTGA TTACAGATGA GGAAGAAATC
  44_1  AGACAACG.T GGACTATAGC AGCGTTATGC TAACCAGTGA GGAAGAAATT
  44_5  AGACAACG.T GGACTATAGC AGCGTTATGC TAACCAGTGA GGAAGAAATT
223_10  AAACTACATT AGAA...... AACGTGCTCA TGACAAATGA AGAAGAAATT
 223_2  AAACTACATT AGAA...... AACGTGCTCA TGACAAATGA AGAAGAAATT
 223_4  AAACTACATT AGAA...... AACGTGCTCA TGACAAATGA AGAAGAAATT
 223_5  AAACTACATT AGAA...... AACGTGCTCA TGACAAATGA AGAAGAAATT
 223_6  AAACTACATT AGAA...... AACGTGCTCA TGACAAATGA AGAAGAAATT
 223_7  AAACTACATT AGAA...... AACGTGCTCA TGACAAATGA AGAAGAAATT
  A3_4  TACCAATG.T GGACATTGAA TCAGTGCTTA TTACAGACGA AGAAGAAATC
  A3_5  TACCAATG.T GGACATTGAA TCAGTGCTTA TTACAGACGA AGAAGAAATC
  A3_7  TACCAATG.T GGACATTGAA TCAGTGCTTA TTACAGACGA AGAAGAAATC
  A3_3  TACCAATG.T GGACATTGAA TCAGTGCTTA TTACAGACGA AGAAGAAATC
 42_12  AGACAACGCT GGAA...... AACGTGCTAA TGACCAGCGA GGAGGAGATC
  AAV1  TTCAAACA.C TGCATTGGAC AATGTCATGA TTACAGACGA AGAGGAAATT
  AAV2  AACAAATG.T GAACATTGAA AAGGTCATGA TTACAGACGA AGAGGAAATC
  AAV3  AAGTAACG.C AGAATTAGAT AATGTAATGA TTACGGATGA AGAAGAGATT
  AAV8  AGACAATG.C GGATTACAGC GATGTCATGC TCACCAGCGA GGAAGAAATC
  AAV9  CGATGGAG.T CGACTACAGC CAGGTGCTGA TTACAGATGA GGAAGAAATT
  AAV7  AAACTACATT GGAA...... AATGTGTTAA TGACAAATGA AGAAGAAATT
  44_2  AGACAACG.T GGACTATAGC AGCGTTATGC TAACCAGTGA GGAAGAAATT
```

Fig. 1AAAB

	3951				4000
42_2	AAAACCACCA	ATCCCGTGGC	TACAGAAGAA	TACGGTGTGG	TCTCCAGCAA
42_8	AAAACCACCA	ACCCAGTGGC	CACAGAACAG	TACGGCGTGG	TGGCCGATAA
42_15	AAAACCACCA	ACCCAGTGGC	CACAGAACAG	TACGGCGTGG	TGGCCGATAA
42_5b	AAAACCACCA	ACCCAGTGGC	CACAGAACAG	TACGGCGTGG	TGGCCGATAA
42_1b	AAAACCACCA	ACCCAGTGGC	CACAGAACAG	TACGGCGTGG	TGGCCGATAA
42_13	AAAACCACCA	ACCCAGTGGC	CACAGAACAG	TACGGCGTGG	TGGCCGATAA
42_3a	AAAACCACCA	ACCCAGTGGC	CACAGAACAG	TACGGCGTGG	TGGCCGATAA
42_4	AAAACCACCA	ACCCAGTGGC	CACAGAACAG	TACGGCGTGG	TGGCCGATAA
42_5a	AAAACCACCA	ACCCAGTGGC	CACAGAACAG	TACGGCGTGG	TGGCCGATAA
42_10	AAAACCACCA	ATCCCGTGGC	TACAGAAGAA	TACGGTGTGG	TCTCCAGCAA
42_3b	AAAACCACCA	ATCCCGTGGC	TACAGAACAG	TACGGTGTGG	TCTCCAGCAA
42_11	AAAACCACCA	ATCCCGTGGC	TACAGAAGAA	TACGGTGTGG	TCTCCAGCAA
42_6b	AAAACCACCA	ATCCCGTGGC	TACAGAAGAA	TACGGTGTGG	TCTCCAGCAA
43_1	AAAACTACTA	ACCCAGTGGC	TACAGAGCAG	TATGGTGTGG	TGGCAGACAA
43_5	AAAACTACTA	ACCCAGTGGC	TACAGAGCAG	TATGGTGTGG	TGGCAGACAA
43_12	AAAACTACTA	ACCCAGTGGC	TACAGAGCAG	TATGGTGTGG	TGGCAGACAA
43_20	AAGGCTACCA	ACCCCGTGGC	CACAGAAGAA	TATGGAGCAG	TGGCCATCAA
43_21	AAGGCTACCA	ACCCCGTGGC	CACAGAAGAA	TATGGAGCAG	TGGCCATCAA
43_23	AAGGCTACCA	ACCCCGTGGC	CACAGAAGAA	TATGGAGCAG	TGGCCATCAA
43_25	AAGGCTACCA	ACCCCGTGGC	CACAGAAGAA	TATGGAGCAG	TGGCCATCAA
44_1	AAAACCACCA	ACCCAGTGGC	CACGGAACAG	TACGGCGTGG	TGGCCGATAA
44_5	AAAACCACCA	ACCCAGTGGC	CACAGAACAG	TACGGCGTGG	TGGCCGATAA
223_10	CGTCCTACCA	ACCCGGTAGC	TACCGAGGAA	TACGGGATTG	TAAGCAGCAA
223_2	CGTCCTACCA	ACCCGGTAGC	TACCGAGGAA	TACGGGATTG	TAAGCAGCAA
223_4	CGTCCTACCA	ACCCGGTAGC	TACCGAGGAA	TACGGGATTG	TAAGCAGCAA
223_5	CGTCCTACCA	ACCCGGTAGC	TACCGAGGAA	TACGGGATTG	TAAGCAGCAA
223_6	CGTCCTACCA	ACCCGGTAGC	TACCGAGGAA	TACGGGATTG	TAAGCAGCAA
223_7	CGTCCTACCA	ACCCGGTAGC	TACCGAGGAA	TACGGGATTG	TAAGCAGCAA
A3_4	AGAACAACTA	ATCCTGTGGC	TACAGAACAA	TACGGACAGG	TTGCCACCAA
A3_5	AGAACGACTA	ATCCTGTGGC	TACAGAACAA	TACGGACAGG	TTGCCACCAA
A3_7	AGAACAACTA	ATCCTGTGGC	TACAGAACAA	TACGGACAGG	TTGCCACCAA
A3_3	AGAACAACTA	ATCCTGTGGC	TACAGAACAA	TACGGACAGG	TTGCCACCAA
42_12	AAAACCACCA	ATCCCGTGGC	TACAGAAGAA	TACGGTGTGG	TCTCCAGCAA
AAV1	AAAGCCACTA	ACCCTGTGGC	CACCGAAAGA	TTTGGGACCG	TGGCAGTCAA
AAV2	GGAACAACCA	ATCCCGTGGC	TACGGAGCAG	TATGGTTCTG	TATCTACCAA
AAV3	CGTACCACCA	ATCCTGTGGC	AACAGAGCAG	TATGGAACTG	TGGCAAATAA
AAV8	AAAACCACTA	ACCCTGTGGC	TACAGAGGAA	TACGGTATCG	TGGCAGATAA
AAV9	AAAGCCACCA	ACCCTGTAGC	CACAGAGGAA	TACGGAGCAG	TGGCCATCAA
AAV7	CGTCCTACTA	ATCCTGTAGC	CACGGAAGAA	TACGGGATAG	TCAGCAGCAA
44_2	AAAACCACCA	ACCCAGTGGC	CACAGAACAG	TACGGCGTGG	TGGCCGATAA

Fig. 1AAAC

```
        4001                                                        4050
 42_2   CCTGCAATCG TCTACGGCCG GACCCCAGAC ACAGACTGTC AACAGCCAGG
 42_8   CCTGCAACAG CAAAACGCCG CTCCTATTGT AGGGGCCGTC AACAGTCAAG
42_15   CCTGCAACAG CAAAACGCCG CTCCTATTGT AGGGGCCGTC AACAGTCAAG
42_5b   CCTGCAACAG CAAAACGCCG CTCCTATTGT AGGGGCCGTC AACAGTCAAG
42_1b   CCTGCAACAG CAAAACGCCG CTCCTATTGT AGGGGCCGTC AACAGTCAAG
42_13   CCTGCAACAG CAAAACGCCG CTCCTATTGT AGGGGCCGTC AACAGTCAAG
42_3a   CCTGCAACAG CAAAACGCCG CTCCTATTGT AGGGGCCGTC AACAGTCAAG
 42_4   CCTGCAACAG CAAAACGCCG CTCCTATTGT AGGGGCCGTC AACAGTCAAG
42_5a   CCTGCAACAG CAAAACGCCG CTCCTATTGT AGGGGCCGTC AACAGTCAAG
42_10   CCTGCAATCG TCTACGGCCG GACCCCAGAC ACAGACTGTC AACAGCCAGG
42_3b   CCTGCAATCG TCTACGGCCG GACCCCAGAC ACAGACTGTC AACAGCCAGG
42_11   CCTGCAATCG TCTACGGCCG GACCCCAGAC ACAGACTGTC AACAGCCAGG
42_6b   CCTGCAATCG TCTACGGCCG GACCCCAGAC ACAGACTGTC AACAGCCAGG
 43_1   CCTGCAGCAG ACCAACGGAG CTCCCATTGT GGGAACTGTC AACAGCCAGG
 43_5   CCTGCAGCAG ACCAACGGAG CTCCCATTGT GGGAACTGTC AACAGCCAGG
43_12   CCTGCAGCAG ACCAACGGAG CTCCCATTGT GGGAACTGTC AACAGCCAGG
43_20   CAACCAGGCC GCCAATACGC AGGCGCAGAC CGGACTCGTG CACAACCAGG
43_21   CAACCAGGCC GCCAATACGC AGGCGCAGAC CGGACTCGTG CACAACCAGG
43_23   CAACCAGGCC GCCAATACGC AGGCGCAGAC CGGACTCGTG CACAACCAGG
43_25   CAACCAGGCC GCCAATACGC AGGCGCAGAC CGGACTCGTG CACAACCAGG
 44_1   CCTGCAACAG CAAAACGCCG CTCCTATTGT AGGGGCCGTC AACAGTCAAG
 44_5   CCTGCAACAG CAAAACGCCG CTCCTATTGT AGGGGCCGTC AACAGTCAAG
223_10  CTTGCAGGCG GCTAGCACCG CAGCCCAGAC ACAAGTTGTT AACAACCAGG
223_2   CTTGCAGGCG GCTAGCACCG CAGCCCAGAC ACAAGTTGTT AACAACCAGG
223_4   CTTGCAGGCG GCTAGCACCG CAGCCCAGAC ACAAGTTGTT AACAACCAGG
223_5   CTTGCAGGCG GCTAGCACCG CAGCCCAGAC ACAAGTTGTT AACAACCAGG
223_6   CTTGCAGGCG GCTAGCACCG CAGCCCAGAC ACAAGTTGTT AACAACCAGG
223_7   CTTGCAGGCG GCTAGCACCG CAGCCCAGAC ACAAGTTGTT AACAACCAGG
 A3_4   CCATCAGAGT CAGGACACCA CAGCTTCCTA TGGAAGTGTG GACAGCCAGG
 A3_5   CCGTCAGAGT CAGAACACCA CAGCTTCCTA TGGAAGTGTG GACAGCCAGG
 A3_7   CCATCAGAGT CAGAACACCA CAGCTTCCTA TGGAAGTGTG GACAGCCAGG
 A3_3   CCATCAGAGT CAGAACACCA CAGCTTCCTA TGGAAGTGTG GACAGCCAGG
42_12   CCTGCAATCG TCTACGGCCG GACCCCAGAC ACAGACTGTC AACAGCCAGG
 AAV1   TTTCCAGAGC AGCAGCACAG ACCCTGCGAC CGGAGATGTG CATGCTATGG
 AAV2   CCTCCAGAGA GGCAACAGAC AAGCAGCTAC CGCAGATGTC AACACACAAG
 AAV3   CTTGCAGAGC TCAAATACAG CTCCCACGAC TGGAACTGTC AATCATCAGG
 AAV8   CTTGCAGCAG CAAAACACGG CTCCTCAAAT TGGAACTGTC AACAGCCAGG
 AAV9   CAACCAGGCC GCTAACACGC AGGCGCAAAC TGGACTTGTG CATAACCAGG
 AAV7   CTTACAAGCG GCTAATACTG CAGCCCAGAC ACAAGTTGTC AACAACCAGG
 44_2   CCTGCAACAG CAAAACGCCG CTCCTATTGT AGGGGCCGTC AACAGTCAAG
```

Fig. 1AAAD

```
        4051                                                        4100
 42_2   GGGCTCTGCC CGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAGGGT
 42_8   GAGCCTTACC TGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAGGGT
42_15   GAGCCTTACC TGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAGGGT
42_5b   GAGCCTTACC TGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAGGGT
42_1b   GAGCCTTACC TGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAGGGT
42_13   GAGCCTTACC TGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAGGGT
42_3a   GAGCCTTACC TGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAGGGT
 42_4   GAGCCTTACC TGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAGGGT
42_5a   GAGCCTTACC TGGCATGGCC TGGCAGAACC GGGACGTGTA CCTGCAGGGT
42_10   GGGCTCTGCC CGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAGGGT
42_3b   GGGCTCTGCC CGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAGGGT
42_11   GGGCTCTGCC CGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAGGGT
42_6b   GGGCTCTGCC CGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAGGGT
 43_1   GGGCCTTACC TGGTATGGTC TGGCAAAACC GGGACGTGTA CCTGCAGGGC
 43_5   GGGCCTTACC TGGTATGGTC TGGCAAAACC GGGACGTGTA CCTGCAGGGC
43_12   GGGCCTTACC TGGTATGGTC TGGCAAAACC GGGACGTGTA CCTGCAGGGC
43_20   GGGTGATTCC CGGCATGGTG TGGCAGAATA GAGACGTGTA CCTGCAGGGT
43_21   GGGTGATTCC CGGCATGGTG TGGCAGAATA GAGACGTGTA CCTGCAGGGT
43_23   GGGTGATTCC CGGCATGGTG TGGCAGAATA GAGACGTGTA CCTGCAGGGT
43_25   GGGTGATTCC CGGCATGGTG TGGCAGAATA GAGACGTGTA CCTGCAGGGT
 44_1   GAGCCTTACC TGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAGGGT
 44_5   GAGCCTTACC TGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAGGGT
223_10  GAGCCTTACC TGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAAGGT
223_2   GAGCCTTACC TGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAAGGT
223_4   GAGCCTTACC TGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAAGGT
223_5   GAGCCTTACC TGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAAGGT
223_6   GAGCCTTACC TGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAAGGT
223_7   GAGCCTTACC TGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAAGGT
 A3_4   GAATCTTACC TGGAATGGTG TGGCAGGACC GCGATGTCTA TCTTCAAGGT
 A3_5   GAATCTTACC TGGAATGGTG TGGCAGGACC GCGATGTCTA TCTTCAAGGT
 A3_7   GAATCTTACC TGGAATGGTG TGGCAGGACC GCGATGTCTA TCTTCAAGGT
 A3_3   GAATCTTACC TGGAATGGTG TGGCAGGACC GCGATGTCTA TCTTCAAGGT
42_12   GGGCTCTGCC CGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAGGGT
 AAV1   GAGCATTACC TGGCATGGTG TGGCAAGATA GAGACGTGTA CCTGCAGGGT
 AAV2   GCGTTCTTCC AGGCATGGTC TGGCAGGACA GAGATGTGTA CCTTCAGGGG
 AAV3   GGGCCTTACC TGGCATGGTG TGGCAAGATC GTGACGTGTA CCTTCAAGGA
 AAV8   GGGCCTTACC CGGTATGGTC TGGCAGAACC GGGACGTGTA CCTGCAGGGT
 AAV9   GAGTTATTCC TGGTATGGTC TGGCAGAACC GGGACGTGTA CCTGCAGGGC
 AAV7   GAGCCTTACC TGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAGGGT
 44_2   GAGCCTTACC TGGCATGGTC TGGCAGAACC GGGACGTGTA CCTGCAGGGT
```

Fig. 1AAAE

```
        4101                                                        4150
  42_2  CCC.ATCTGG GCCAAAATTC CTCACACGGA CGGCAACTTT CACCCGTCTC
  42_8  CCT.ATCTGG GCCAAGATTC CTCACACGGA CGGCAACTTT CATCCTTCGC
 42_15  CCT.ATCTGG GCCAAGATTC CTCACACGGA CGGCAACTTT CATCCTTCGC
 42_5b  CCT.ATCTGG GCCAAGATTC CTCACACGGA CGGCAACTTT CATCCTTCGC
 42_1b  CCT.ATCTGG GCCAAGATTC CTCACACGGA CGGCAACTTT CATCCTTCGC
 42_13  CCT.ATCTGG GCCAAGATTC CTCACACGGA CGGCAACTTT CATCCTTCGC
 42_3a  CCT.ATCTGG GCCAAGATTC CTCACACGGA CGGCAACTTT CATCCTTCGC
  42_4  CCT.ATCTGG GCCAAGATTC CTCACACGGA CGGCAACTTT CATCCTTCGC
 42_5a  CCT.ATCTGG GCCAAGATTC CTCACACGGA CGGCAACTTT CATCCTTCGC
 42_10  CCC.ATCTGG GCCAAAATTC CTCACACGGA CGGCAACTTT CACCCGTCTC
 42_3b  CCC.ATCTGG GCCAAAATTC CTCACACGGA CGGCAACTTT CACCCGTCTC
 42_11  CCC.ATCTGG GCCAAAATTC CTCACACGGA CGGCAACTTT CACCCGTCTC
 42_6b  CCC.ATCTGG GCCAAAATTC CTCACACGGA CGGCAACTTT CACCCGTCTC
  43_1  CCC.ATCTGG GCCAAAATTC CTCACACGGA CGGCAACTTT CATCCTTCGC
  43_5  CCC.ATCTGG GCCAAAATTC CTCACACGGA CGGCAACTTT CATCCTTCGC
 43_12  CCC.ATCTGG GCCAAAATTC CTCACACGGA CGGCAACTTT CATCCTTCGC
 43_20  CCC.ATCTGG GCCAAAATTC CTCACACGGA CGGCAACTTT CACCCGTCTC
 43_21  CCC.ATCTGG GCCAAAATTC CTCACACGGA CGGCAACTTT CACCCGTCTC
 43_23  CCC.ATCTGG GCCAAAATTC CTCACACGGA CGGCAACTTT CACCCGTCTC
 43_25  CCC.ATCTGG GCCAAAATTC CTCACACGGA CGGCAACTTT CACCCGTCTC
  44_1  CCT.ATCTGG GCCAAGATTC CTCACACGGA CGGAAACTTT CATCCCTCGC
  44_5  CCT.ATCTGG GCCAAGATTC CTCACACGGA CGGAAACTTT CATCCCTCGC
223_10  CCC.ATTTGG GCCAAGATTC CTCACACGGA CGGCAACTTT CACCCGTCTC
 223_2  CCC.ATTTGG GCCAAGATTC CTCACACGGA CGGCAACTTT CACCCGTCTC
 223_4  CCC.ATTTGG GCCAAGATTC CTCACACGGA CGGCAACTTT CACCCGTCTC
 223_5  CCC.ATTTGG GCCAAGATTC CTCACACGGA CGGCAACTTT CACCCGTCTC
 223_6  CCC.ATTTGG GCCAAGATTC CTCACACGGA CGGCAACTTT CACCCGTCTC
 223_7  CCC.ATTTGG GCCAAGATTC CTCACACGGA CGGCAACTTT CACCCGTCTC
  A3_4  CCC.ATTTGG GCCAAAACTC CTCACACGGA CGGACACTTT CATCCTTCTC
  A3_5  CCC.ATTTGG GCCAAAACTC CTCACACGGA CGGACACTTT CATCCTTCTC
  A3_7  CCC.ATTTGG GCCAAAACTC CTCACACGGA CGGACACTTT CATCCTTCTC
  A3_3  CCC.ATTTGG GCCAAAACTC CTCACACGGA CGGACACTTT CATCCTTCTC
 42_12  CCC.ATCTGG GCCAAAATTC CTCACACGGA CGGCAACTTT CACCCGTCTC
  AAV1  CCC.ATTTGG GCCAAAATTC CTCACACAGA TGGACACTTT CACCCGTCTC
  AAV2  CCC.ATCTGG GCAAAGATTC CACACACGGA CGGACATTTT CACCCCTCTC
  AAV3  CCT.ATCTGG GCAAAGATTC CTCACACGGA TGGACACTTT CATCCTTCTC
  AAV8  CCC.ATCTGG GCCAAGATTC CTCACACGGA CGGCAACTTC CACCCGTCTC
  AAV9  CCCTATTTGG GCTAAAATAC CTCACACAGA TGGCAACTTT CACCCGTCTC
  AAV7  CCC.ATCTGG GCCAAGATTC CTCACACGGA TGGCAACTTT CACCCGTCTC
  44_2  CCT.ATCTGG GCCAAGATTC CTCACACGGA CGGAAACTTT CATCCCTCGC
```

Fig. 1AAAF

```
        4151                                                        4200
  42_2  CCCTGATGGG CGGATTTGGA CTCAAACACC CGCCTCCTCA AATTCTCATC
  42_8  CGCTGATGGG AGGCTTTGGA CTGAAACACC CGCCTCCTCA GATCCTGATT
 42_15  CGCTGATGGG AGGCTTTGGA CTGAAACACC CGCCTCCTCA GATCCTGATT
 42_5b  CGCTGATGGG AGGCTTTGGA CTGAAACACC CGCCTCCTCA GATCCTGATT
 42_1b  CGCTGATGGG AGGCTTTGGA CTGAAACACC CGCCTCCTCA GATCCTGATT
 42_13  CGCTGATGGG AGGCTTTGGA CTGAAACACC CGCCTCCTCA GATCCTGATT
 42_3a  CGCTGATGGG AGGCTTTGGA CTGAAACACC CGCCTCCTCA GATCCTGATT
  42_4  CGCTGATGGG AGGCTTTGGA CTGAAACACC CGCCTCCTCA GATCCTGATT
 42_5a  CGCTGATGGG AGGCTTTGGA CTGAAACACC CGCCTCCTCA GATCCTGATT
 42_10  CCCTGATGGG CGGATTTGGA CTCAAACACC CGCCTCCTCA AATTCTCATC
 42_3b  CCCTGATGGG CGGATTTGGA CTCAAACACC CGCCTCCTCA AATTCTCATC
 42_11  CCCTGATGGG CGGATTTGGA CTCAAACACC CGCCTCCTCA AATTCTCATC
 42_6b  CCCTGATGGA CGGATTTGGA CTCAAACACC CGCCTCCTCA AATTCTCATC
  43_1  CGCTGATGGG AGGCTTTGGA CTGAAACACC CGCCTCCTCA GATCCTGGTG
  43_5  CGCTGATGGG AGGCTTTGGA CTGAAACACC CGCCTCCTCA GATCCTGGTG
 43_12  CGCTGATGGG AGGCTTTGGA CTGAAACACC CGCCTCCTCA GATCCTGGTG
 43_20  CCCTGATGGG CGGCTTTGGA CTGAAGCACC CGCCTCCTCA AATTCTCATC
 43_21  CCCTGATGGG CGGCTTTGGA CTGAAGCACC CGCCTCCTCA AATTCTCATC
 43_23  CCCTGATGGG CGGCTTTGGA CTGAAGCACC CGCCTCCTCA AATTCTCATC
 43_25  CCCTGATGGG CGGCTTTGGA CTGAAGCACC CGCCTCCTCA AATTCTCATC
  44_1  CGCTGATGGG AGGCTTTGGA CTGAAACACC CGCCTCCTCA GATCCTGATT
  44_5  CGCTGATGGG AGGCTTTGGA CTGAAACACC CGCCTCCTCA GATCCTGATT
223_10  CTCTAATGGG TGGCTTTGGA CTGAAACACC CGCCTCCCCA GATCCTGATC
 223_2  CTCTAATGGG TGGCTTTGGA CTGAAACACC CGCCTCCCCA GATCCTGATC
 223_4  CTCTAATGGG TGGCTTTGGA CTGAAACACC CGCCTCCCCA GATCCTGATC
 223_5  CTCTAATGGG TGGCTTTGGA CTGAAACACC CGCCTCCCCA GATCCTGATC
 223_6  CTCTAATGGG TGGCTTTGGA CTGAAACACC CGCCTCCCCA GATCCTGATC
 223_7  CTCTAATGGG TGGCTTTGGA CTGAAACACC CGCCTCCCCA GATCCTGATC
  A3_4  CGCTCATGGG AGGCTTTGGA CTGAAACACC CTCCTCCCCA GATCCTGATC
  A3_5  CGCTCATGGG AGGCTTTGGA CTGAAACACC CTCCTCCCCA GATCCTGATC
  A3_7  CGCTCATGGG AGGCTTTGGA CTGAAACACC CTCCTCCCCA GATCCTGATC
  A3_3  CGCTCATGGG AGGCTTTGGA CTGAAACACC CTCCTCCCCA GATCCTGATC
 42_12  CCCTGATGGG CGGATTTGGA CTCAAACACC CGCCTCCTCA AATTCTCATC
  AAV1  CTCTTATGGG CGGCTTTGGA CTCAAGAACC CGCCTCCTCA GATCCTCATC
  AAV2  CCCTCATGGG TGGATTCGGA CTTAAACACC CTCCTCCACA GATTCTCATC
  AAV3  CTCTGATGGG AGGCTTTGGA CTGAAACATC CGCCTCCTCA AATCATGATC
  AAV8  CGCTGATGGG CGGCTTTGGC CTGAAACATC CTCCGCCTCA GATCCTGATC
  AAV9  CTCTGATGGG TGGATTTGGA CTGAAACACC CACCTCCACA GATTCTAATT
  AAV7  CTTTGATGGG CGGCTTTGGA CTTAAACATC CGCCTCCTCA GATCCTGATC
  44_2  CGCTGATGGG AGGCTTTGGA CTGAAACACC CGCCTCCTCA GATCCTGATT
```

Fig. 1AAAG

```
          4201                                                      4250
  42_2    AAAAACACCC CGGTACCTGC TAATCCTCCA GAGGTGTTTA CTCCTGCCAA
  42_8    AAGAATACAC CTGTTCCCGC GGATCCTCCA ACTACCTTCA GTCAAGCCAA
 42_15    AAGAATACAC CTGTTCCCGC GGATCCTCCA ACTACCTTCA GTCAAGCCAA
 42_5b    AAGAATACAC CTGTTCCCGC GGATCCTCCA ACTACCTTCA GTCAAGCCAA
 42_1b    AAGAATACAC CTGTTCCCGC GGATCCTCCA ACTACCTTCA GTCAAGCCAA
 42_13    AAGAATACAC CTGTTCCCGC GGATCCTCCA ACTACCTTCA GTCAAGCCAA
 42_3a    AAGAATACAC CTGTTCCCGC GGATCCTCCA ACTACCTTCA GTCAAGCCAA
  42_4    AAGAATACAC CTGTTCCCGC GGATCCTCCA ACTACCTTCA GTCAAGCCAA
 42_5a    AAGAATACAC CTGTTCCCGC GGATCCTCCA ACTACCTTCA GTCAAGCCAA
 42_10    AAAAACACCC CGGTACCTGC TAATCCTCCA GAGGTGTTTA CTCCTGCCAA
 42_3b    AAAAACACCC CGGTACCTGC TAATCCTCCA GAGGTGTTTA CTCCTGCCAA
 42_11    AAAAACACCC CGGTACCTGC TAATCCTCCA GAGGTGTTTA CTCCTGCCAA
 42_6b    AAAAACACCC CGGTACCTGC TAATCCTCCA GAGGTGTTTA CTCCTGCCAA
  43_1    AAAAACACTC CTGTTCCTGC GGATCCTCCG ACCACCTTCA GCCAGGCCAA
  43_5    AAAAACACTC CTGTTCCTGC GGATCCTCCG ACCACCTTCA GCCAGGCCAA
 43_12    AAAAACACTC CTGTTCCTGC GGATCCTCCG ACCACCTTCA GCCAGGCCAA
 43_20    AAGAACACAC CGGTTCCAGC GGACCCGCCG CTTACCTTCA ACCAGGCCAA
 43_21    AAGAACACAC CGGTTCCAGC GGACCCGCCG CTTACCTTCA ACCAGGCCAA
 43_23    AAGAACACAC CGGTTCCAGC GGACCCGCCG CTTACCTTCA ACCAGGCCAA
 43_25    AAGAACACAC CGGTTCCAGC GGACCCGCCG CTTACCTTCA ACCAGGCCAA
  44_1    AAGAATACAC CTGTTCCCGC GGATCCTCCA ACTACCTTCA GTCAAGCTAA
  44_5    AAGAATACAC CTGTTCCCGC GGATCCTCCA ACTACCTTCA GTCAAGCTAA
223_10    AAAAACACAC CGGTACCTGC TAATCCTCCA GAAGTGTTTA CTCCTGCCAA
 223_2    AAAAACACGC CGGTACCTGC TAATCCTCCA GAAGTGTTTA CTCCTGCCAA
 223_4    AAAAACACAC CGGTACCTGC TAATCCTCCA GAAGTGTTTA CTCCTGCCAA
 223_5    AAAAACACAC CGGTACCTGC TAATCCTCCA GAAGTGTTTA CTCCTGCCAA
 223_6    AAAAACACAC CGGTACCTGC TAATCCTCCA GAAGTGTTTA CTCCTGCCAA
 223_7    AAAAACACAC CGGTACCTGC TAATCCTCCA GAAGTGTTTA CTCCTGCCAA
  A3_4    AAAAACACAC CTGTGCCAGC GAATCCCGCG ACCACTTTCA CTCCTGGAAA
  A3_5    AAAAACACAC CTGTGCCAGC GAATCCCGCG ACCACTTTCA CTCCTGGAAA
  A3_7    AAAAACACAC CTGTGCCAGC GAATCCCGCG ACCACTTTCA CTCCTGGAAA
  A3_3    AAAAACACAC CTGTGCCAGC GAATCCCGCG ACCACTTTCA CTCCTGGAAA
 42_12    A...A..... .......... .......... .......... ..........
  AAV1    AAAAACACGC CTGTTCCTGC GAATCCTCCG GCGGAGTTTT CAGCTACAAA
  AAV2    AAGAACACCC CGGTACCTGC GAATCCTTCG ACCACCTTCA GTGCGGCAAA
  AAV3    AAAAATACTC CGGTACCGGC AAATCCTCCG ACGACTTTCA GCCCGGCCAA
  AAV8    AAGAACACGC CTGTACCTGC GGATCCTCCG ACCACCTTCA ACCAGTCAAA
  AAV9    AAAAATACAC CAGTGCCGGC AGATCCTCCT CTTACCTTCA ATCAAGCCAA
  AAV7    AAGAACACTC CCGTTCCCGC TAATCCTCCG GAGGTGTTTA CTCCTGCCAA
  44_2    AAGAATACAC CTGTTCCCGC GGATCCTCCA ACTACCTTCA GTCAAGCTAA
```

Fig. 1AAAH

```
        4251                                                        4300
 42_2   GTTTGCCTCA TTTATCACGC AGTACAGCAC CGGCCA.GGT CAGCGTGGAG
 42_8   GCTGGCGTCG TTCATCACGC AGTACAGCAC CGGACA.GGT CAGCGTGGAA
42_15   GCTGGCGTCG TTCATCACGC AGTACAGCAC CGGACA.GGT CAGCGTGGAA
42_5b   GCTGGCGTCG TTCATCACGC AGTACAGCAC CGGACA.GGT CAGCGTGGAA
42_1b   GCTGGCGTCG TTCATCACGC AGTACAGCAC CGGACA.GGT CAGCGTGGAA
42_13   GCTGGCGTCG TTCATCACGC AGTACAGCAC CGGACA.GGT CAGCGTGGAA
42_3a   GCTGGCGTCG TTCATCACGC AGTACAGCAC CGGACA.GGT CAGCGTGGAA
 42_4   GCCGGCGTCG TTCATCACGC AGTACAGCAC CGGACA.GGT CAGCGTGGAA
42_5a   GCTGGCGTCG TTCATCACGC AGTACAGCAC CGGACA.GGT CAGCGTGGAA
42_10   GTTTGCCTCA TTTATCACGC AGTACAGCAC CGGCCA.GGT CAGCGTGGAG
42_3b   GTTTGCCTCA TTTATCACGC AGTACAGCAC CGGCCA.GGT CAGCGTGGAG
42_11   GTTTGCCTCA TTTATCACGC AGTACAGCAC CGGCCA.GGT CAGCGTGGAG
42_6b   GTTTGCCTCA TTTATCACGC AGTACAGCAC CGGCCA.GGT CAGCGTGGAG
 43_1   GCTGGCTTCT TTTATCACGC AGTACAGCAC CGGACA.GGT CAGCGTGGAA
 43_5   GCTGGCTTCT TTTATCACGC AGTACAGCAC CGGACA.GGT CAGCGTGGAA
43_12   GCTGGCTTCT TTTATCACGC AGTACAGCAC CGGACA.GGT CAGCGTGGAA
43_20   GCTGAACTCT TTCATCACGC AGTACAGCAC CGGACA.GGT CAGCGTGGAA
43_21   GCTGAACTCT TTCATCACGC AGTACAGCAC CGGACA.GGT CAGCGTGGAA
43_23   GCTGAACTCT TTCATCACGC AGTACAGCAC CGGACA.GGT CAGCGTGGAA
43_25   GCTGAACTCT TTCATCACGC AGTACAGCAC CGGACA.GGT CAGCGTGGAA
 44_1   GCTGGCGTCG TTCATCACGC AGTACAGCAC CGGACA.GGT CAGCGTGGAA
 44_5   GCTGGCGTCG TTCATCACGC AGTACAGCAC CGGACA.GGT CAGCGTGGAA
223_10  GTTTGCTTCC TTCATCACGC AGTACAGCAC CGGGCA.AGT CAGCGTTGAG
223_2   GTTTGCTTCC TTCATCACGC AGTACAGCAC CGGGCA.AGT CAGCGTTGAG
223_4   GTTTGCTTCC TTCATCACGC AGTACAGCAC CGGGCA.AGT CAGCGTTGAG
223_5   GTTTGCTTCC TTCATCACGC AGTACAGCAC CGGGCA.AGT CAGCGTTGAG
223_6   GCTTGCTTCC TTCATCACGC AGTACAGCAC CGGGCA.AGT CAGCGTTGAG
223_7   GATTGCTTCC TTCATCACGC AGTACAGCAC CGGGCA.AGT CAGCGTTGAG
 A3_4   GTTTGCTTCG TTCATTACCC AGTATTCCAC CGGACA.GGT CAGCGTGGAA
 A3_5   GTTTGCTTCG TTCATTACCC AGTATTCCAC CGGACA.GGT CAGCGTGGAA
 A3_7   GTTTGCTTCG TTCATTACCC AGTATTCCAC CGGACA.GGT CAGCGTGGAA
 A3_3   GTTTGCTTCG TTCATTACCC AGTATTCCAC CGGACA.GGT CAGCGTGGAA
42_12   .......... .......... .......... .......... ..........
 AAV1   GTTTGCTTCA TTCATCACCC AATACTCCAC AGGACA.AGT GAGTGTGGAA
 AAV2   GTTTGCTTCC TTCATCACAC AGTACTCCAC GGGACACGGT CAGCGTGGAG
 AAV3   GTTTGCTTCA TTTATCACTC AGTACTCCAC TGGACA.GGT CAGCGTGGAA
 AAV8   GCTGAACTCT TTCATCACGC AATACAGCAC CGGACA.GGT CAGCGTGGAA
 AAV9   GCTGAACTCT TTCATCACGC AGTACAGCAC GGGACA.AGT CAGCGTGGAA
 AAV7   GTTTGCTTCG TTCATCACAC AGTACAGCAC CGGACA.AGT CAGCGTGGAA
 44_2   GCTGGCGTCG TTCATCACGC AGTACAGCAC CGGACA.GGT CAGCGTGGAA
```

Fig. 1AAAI

```
        4301                                                  4350
  42_2  ATCGAGTGGG AACTGCAGAA AGAAAACAGC AAACGCTGGA ATCCAGAGAT
  42_8  ATTGAATGGG AGCTGCAGAA AGAGAACAGC AAGCGCTGGA ACCCAGAGAT
 42_15  ATTGAATGGG AGCTGCAGAA AGAGAACAGC AAGCGCTGGA ACCCAGAGAT
 42_5b  ATTGAATGGG AGCTGCAGAA AGAGAACAGC AAGCGCTGGA ACCCAGAGAT
 42_1b  ATTGAATGGG AGCTGCAGAA AGAGAACAGC AAGCGCTGGA ACCCAGAGAT
 42_13  ATTGAATGGG AGCTGCAGAA AGAGAACAGC AAGCGCTGGA ACCCAGAGAT
 42_3a  ATTGAATGGG AGCTGCAGAA AGAGAACAGC AAGCGCTGGA ACCCAGAGAT
  42_4  ATTGAATGGG AGCTGCAGAA AGAGAACAGC AAGCGCTGGA ACCCAGAGAT
 42_5a  ATTGAATGGG AGCTGCAGAA AGAGAACAGC AAGCGCTGGA ACCCAGAGAT
 42_10  ATCGAGTGGG AACTGCAGAA AGAAAACAGC AAACGCTGGA ATCCAGAGAT
 42_3b  ATCGAGTGGG AACTGCAGAA AGAAAACAGC AAACGCTGGA ATCCAGAGAT
 42_11  ATCGAGTGGG AACTGCAGAA AGAGAACAGC AAACGCTGGA ATCCAGAGAT
 42_6b  ATCGAGTGGG AACTGCAGAA AGAAAACAGC AAACGCTGGA ATCCAGAGAT
  43_1  ATCGAATGGG AGCTGCAGAA AGAAAACAGC AAGCGCTGGA ACCCAGAGAT
  43_5  ATCGAATGGG AGCTGCAGAA AGAAAACAGC AAGCGCTGGA ACCCAGAGAT
 43_12  ATCGAATGGG AGCTGCAGAA AGAAAACAGC AAGCGCTGGA ACCCAGAGAT
 43_20  ATCGAGTGGG AGCTGCAGAA AGAAAACAGC AAACGCTGGA ATCCAGAGAT
 43_21  ATCGAGTGGG AGCTGCAGAA AGAAAACAGC AAACGCTGGA ATCCAGAGAT
 43_23  ATCGAGTGGG AGCTGCAGAA AGAAAACAGC AAACGCTGGA ATCCAGAGAT
 43_25  ATCGAGTGGG AGCTGCAGAA AGAAAACAGC AAACGCTGGA ATCCAGAGAT
  44_1  ATTGAATGGG AGCTGCAGAA AGAAAACAGC AAACGCTGGA ACCCAGAGAT
  44_5  ATTGAATGGG AGCTGCAGAA AGAAAACAGC AAACGCTGGA ACCCAGAGAT
223_10  ATCGAGTGGG AGCTGCAGAA AGAGAACAGC AAGCGCTGGA ACCCAGAGAT
 223_2  ATCGAGTGGG AGCTGCAGAA AGAGAACAGC AAGCGCTGGA ACCCAGAGAT
 223_4  ATCGAATGGG AGCTGCAGAA AGAGAACAGC AAGCGCTGGA ACCCAGAGAT
 223_5  ATCGAATGGG AGCTGCAGAA AGAGAACAGC AAGCGCTGGA ACCCAGAGAT
 223_6  ATCGAGTGGG AGCTGCAGAA AGAGAACAGC AAGCGCTGGA ACCCAGAGAT
 223_7  ATCGAGTGGG AGCTGCAGAA AGAGAACAGC AAGCGCTGGA ACCCAGAGAT
  A3_4  ATAGAGTGGG AGCTGCAGAA AGAAAACAGC AAACGCTGGA ACCCAGAAAT
  A3_5  ATAGAGTGGG AGCTGCAGAA AGAAAACAGC AAACGCTGGA ACCCGGAAAT
  A3_7  ATAGAGTGGG AGCTGCAGAA AGAAAACAGC AAACGCTGGA ACCCAGAAAT
  A3_3  ATAGAGTGGG AGCTGCAGAA AGAAAACAGC AAACGCTGGA ACCCAGAAAT
 42_12  .......... .......... .......... .......... ..........
  AAV1  ATTGAATGGG AGCTGCAGAA AGAAAACAGC AAGCGCTGGA ATCCCGAAGT
  AAV2  ATCGAGTGGG AGCTGCAGAA GGAAAACAGC AAACGCTGGA ATCCCGAAAT
  AAV3  ATTGAGTGGG AGCTACAGAA AGAAAACAGC AAACGTTGGA ATCCAGAGAT
  AAV8  ATTGAATGGG AGCTGCAGAA GGAAAACAGC AAGCGCTGGA ACCCCGAGAT
  AAV9  ATCGAGTGGG AGCTGCAGAA AGAAAACAGC AAGCGCTGGA ATCCAGAGAT
  AAV7  ATCGAGTGGG AGCTGCAGAA GGAAAACAGC AAGCGCTGGA ACCCGGAGAT
  44_2  ATTGAATGGG AGCTGCAGAA AGAAAACAGC AAACGCTGGA ACCCAGAGAT
```

Fig. 1AAAJ

```
          4351                                                    4400
  42_2    TCAGTACACC TCAAATTATG CCAAGTCTAA TAAT.GTGGA ATTTGCTGTC
  42_8    TCAGTATACT TCCAACTACT ACAAATCTAC AAAT.GTGGA CTTTGCTGTC
 42_15    TCAGTATACT TCCAACTACT ACAAATCTAC AAAT.GTGGA CTTTGCTGTC
 42_5b    TCAGTATACT TCCAACTACT ACAAATCTAC AAAT.GTGGA CTTTGCTGTC
 42_1b    TCAGTATACT TCCAACTACT ACAAATCTAC AAAT.GTGGA CTTTGCTGTC
 42_13    TCAGTATACT TCCAACTACT ACAAATCTAC AAAT.GTGGA CTTTGCTGTC
 42_3a    TCAGTATACT TCCAACTACT ACAAATCTAC AAAT.GTGGA CTTTGCTGTC
  42_4    TCAGTATACT TCCAACTACT ACAAATCTAC AAAT.GTGGA CTTTGCTGTC
 42_5a    TCAGTATACT TCCAACTACT ACAAATCTAC AAAT.GTGGA CTTTGCTGTC
 42_10    TCAGTACACC TCAAATTATG CCAAGTCTAA TAAT.GTGGA ATTTGCTGTC
 42_3b    TCAGTACACC TCAAATTATG CCAAGTCTAA TAAT.GTGGA ATTTGCTGTC
 42_11    TCAGTACACC TCAAATTATG CCAAGTCTAA TAAT.GTGGA ATTTGCTGTC
 42_6b    TCAGTACACC TCAAATTATG CCAAGTCTAA TAAT.GTGGA ATTTGCTGTC
  43_1    TCAGTATACT TCCAACTACT ACAAATCTAC AAAT.GTGGA CTTTGCTGTC
  43_5    TCAGTATACT TCCAACTACT ACAAATCTAC AAAT.GTGGA CTTTGCTGTC
 43_12    TCAGTATACT TCCAACTACT ACAAATCTAC AAAT.GTGGA CTTTGCTGTC
 43_20    TCAATACACT TCCAACTACT ACAAATCTAC AAAT.GTGGA CTTTGCTGTC
 43_21    TCAATACACT TCCAACTACT ACAAATCTAC AAAT.GTGGA CTTTGCTGTC
 43_23    TCAATACACT TCCAACTACT ACAAATCTAC AAAT.GTGGA CTTTGCTGTC
 43_25    TCAATACACT TCCAACTACT ACAAATCTAC AAAT.GTGGA CTTTGCTGTC
  44_1    TCAATACACT TCCAACTACT ACAAATCTAC AAAT.GTGGA CTTCGCTGTT
  44_5    TCAATACACT TCCAACTACT ACAAATCTAC AAAT.GTGGA CTTTGCTGTT
223_10    TCAGTACACC TCCAACTTTG ACAAACAGAC TGGA.GTGGA CTTTGCTGTT
 223_2    TCAGTACACC TCCAACTTTG ACAAACAGAC TGGA.GTGGA CTTTGCTGTT
 223_4    TCAGTACACC TCCAACTTTG ACAAACAGAC TGGA.GTGGA CTTTGCTGTT
 223_5    TCAGTACACC TCCAACTTTG ACAAACAGAC TGGA.GTGGA CTTTGCTGTT
 223_6    TCAGTACACC TCCAACTTTG ACAAACAGAC TGGA.GTGGA CTTTGCTGTT
 223_7    TCAGTACACC TCCAACTTTG ACAAACAGAC TGGA.GTGGA CTTTGCTGTT
  A3_4    TCAGTACACC TCCAACTACA ACAAGTCGGT GAAT.GTGGA GTTTACCGTG
  A3_5    TCAGTACACC TCCAACTACA ACAAGTCGGT GAAT.GTGGA GTTTACCGTG
  A3_7    TCAGTACACC TCCAACTACA ACAAGTCGGT GAAT.GTGGA GTTTACCGTG
  A3_3    TCAGTACACC TCCAACTACA ACAAGTCGGT GAAT.GTGGA GTTTACCGTG
 42_12    ...GTATACT TCCAACTACT ACAAATCTAC AAAT.GTGGA CTTTGCTGTC
  AAV1    GCAGTACACA TCCAATTATG CAAAATCTGC CAAC.GTTGA TTTTACTGTG
  AAV2    TCAGTACACT TCCAACTACA ACAAGTCTGT TAATCGTGGA CTT.ACCGTG
  AAV3    TCAGTACACT TCCAACTACA ACAAGTCTGT TAAT.GTGGA CTTTACTGTA
  AAV8    CCAGTACACC TCCAACTACT ACAAATCTAC AAGT.GTGGA CTTTGCTGTT
  AAV9    CCAGTATACT TCAAACTACT ACAAATCTAC AAAT.GTGGA CTTTGCTGTC
  AAV7    TCAGTACACC TCCAACTTTG AAAAGCAGAC TGGT.GTGGA CTTTGCCGTT
  44_2    TCAATACACT TCCAACTACT ACAAATCTAC AAAT.GTGGA CTTTGCTGTT
```

Fig. 1AAAK

```
          4401                                                  4450
  42_2    AACAACGAAG GGGTTTATAC TGAGCCTCGC CCCATTGGCA CCCGTTACCT
  42_8    AATACTGAGG GTACTTATTC AGAGCCTCGC CCCATTGGCA CCCGTTACCT
 42_15    AATACTGAGG GTACTTATTC AGAGCCTCGC CCCATTGGCA CCCGTTACCT
 42_5b    AATACTGAGG GTACTTATTC AGAGCCTCGC CCCATTGGCA CCCGTTACCT
 42_1b    AATACTGAGG GTACTTATTC AGAGCCTCGC CCCATTGGCA CCCGTTACCT
 42_13    AATACTGAGG GTACTTATTC AGAGCCTCGC CCCATTGGCA CCCGTTACCT
 42_3a    AATACTGAGG GTACTTATTC AGAGCCTCGC CCCATTGGCA CCCGTTACCT
  42_4    AATACTGAGG GTACTTATTC AGAGCCTCGC CCCATTGGCA CCCGTTACCT
 42_5a    AATACTGAGG GTACTTATTC AGAGCCTCGC CCCATTGGCA CCCGTTACCT
 42_10    AACAACGAAG GGGTTTATAC TGAGCCTCGC CCCATTGGCA CCCGTTACCT
 42_3b    AACAACGAAG GGGTTTATAC TGAGCCTCGC CCCATTGGCA CCCGTTACCT
 42_11    AACAACGAAG GGGTTTATAC TGAGCCTCGC CCCATTGGCA CCCGTTACCT
 42_6b    AACAACGAAG GGGTTTATAC TGAGCCTCGC CCCATTGGCA CCCGTTACCT
  43_1    AATACTGAGG GTACTTATTC AGAGCCTCGC CCCATTGGCA CTCGTTATCT
  43_5    AATACCGAGG GTACTTATTC AGAGCCTCGC CCCATTGGCA CTCGTTATCT
 43_12    AATACTGAGG GTACTTATTC AGAGCCTCGC CCCATTGGCA CTCGTTATCT
 43_20    AACACGGAAG GAGTTTATAG CGAGCCTCGC CCCATTGGCA CCCGTTACCT
 43_21    AACACGGAAG GAGTTTATAG CGAGCCTCGC CCCATTGGCA CCCGTTACCT
 43_23    AACACGGAAG GAGTTTATAG CGAGCCTCGC CCCATTGGCA CCCGTTACCT
 43_25    AACACGGAGG GGGTTTATAG CGAGCCTCGC CCCATTGGCA CCCGTTACCT
  44_1    AACACAGATG GCACTTATTC TGAGCCTCGC CCCATTGGCA CCCGTTACCT
  44_5    AACACAGATG GCACTTATTC TGAGCCTCGC CCCATTGGCA CCCGTTACCT
223_10    GACAGCCAGG GTGTTTACTC TGAGCCT... .......... ..........
 223_2    GACAGCCAGG GTGTTTACTC TGAGCCT... .......... ..........
 223_4    GACAGCCAGG GTGTTTACTC TGAGCCT... .......... ..........
 223_5    GACAGCCAGG GTGTTTACTC TGAGCCT... .......... ..........
 223_6    GACAGCCAGG GTGTTTACTC TGAGCCT... .......... ..........
 223_7    GACAGCCAGG GTGTTTACTC TGAGCCT... .......... ..........
  A3_4    GACGCAAACG GTGTTTATTC TGAACCCCGC CCTATTGGCA CTCGTTACCT
  A3_5    GACGCAAACG GTGTTTATTC TGAACCCCGC CCTATTGGCA CTCGTTACCT
  A3_7    GACGCAAACG GTGTTTATTC TGAACCCCGC CCTATTGGCA CTCGTTACCT
  A3_3    GACGCAAACG GTGTTTATTC TGAACCCCGC CCTATTGGCA CTCGTTACCT
 42_12    AATACTGAGG GTACTTATTC AGAGCCTCGC CCCATTGGCA CCCGTTACCT
  AAV1    GACAACAATG GACTTTATAC TGAGCCTCGC CCCATTGGCA CCCGTTACCT
  AAV2    GATACTAATG GCGTGTATTC AGAGCCTCGC CCCATTGGCA CCAGATACCT
  AAV3    GACACTAATG GTGTTTATAG TGAACCTCGC CCTATTGGAA CCCGGTATCT
  AAV8    AATACAGAAG GCGTGTACTC TGAACCCCGC CCCATTGGCA CCCGTTACCT
  AAV9    AATACCGAAG GTGTTTACTC TGAGCCTCGC CCCATTGGTA CTCGTTACCT
  AAV7    GACAGCCAGG GTGTTTACTC TGAGCCTCGC CCTATTGGCA CTCGTTACCT
  44_2    AACACAGATG GCACTTATTC TGAGCCTCGC CCCATCGGCA CCCGTTACCT
```

Fig. 1AAAL

```
          4451                                                    4500
                          VP1-3 stop.      Poly A signal
  42_2    CACCCGTAAC CTGTAATTGC CTGTTAATCA ATAAACCGGT TAATTCGTTT
  42_8    CACCCGTAAC CTGTAATTGC CTGTTAATCA ATAAACCGGC TAATTCGTTT
 42_15    CACCCGTAAC CTGTAATTGC CTGTTAATCA ATAAACCGGT TAATTCGTTT
 42_5b    CACCCGTAAC CTGTAATTGC CTGTTAATCA ATAAACCGGT TAATTCGTTT
 42_1b    CACCCGTAAC CTGTAATTGC CTGTTAATCA ATAAACCGGT TGATTCGTTT
 42_13    CACCCGTAGC CTGTAATTGC CTGTTAATCA ATAAACCGGT TGATTCGTTT
 42_3a    CACCCGTAAC CTGTAATTGC CTGTTAATCA ATAAACCGGT TAATTCGTTT
  42_4    CACCCGTAAC CTGTAATTGC CTGTTAATCA ATAAACCGGT TAATTCGTTT
 42_5a    CACCCGTAAC CTGTAATTGC CTGTTAATCA ATAAACCGGT TAATTCGTTT
 42_10    CACCCGTAAC CTGTAATTGC CTGTTAATCA ATAAACCGGT TAATTCGTTT
 42_3b    CACCCGTAAC CTGTAATTGC CTGTTAATCA ATAAACCGGT TAATTCGTTT
 42_11    CACCCGTAAC CTGTAATTAC TTGTTAATCA ATAAACCGGT TGATTCGTTT
 42_6b    CACCCGTAAC CTGTAATTGC CTGTTAATCA ATAAACCGGT TAATTCGTTT
  43_1    CACCCGTAAT CTGTAATTGC TTGTTAATCA ATAAACCGGT ..........
  43_5    CACCCGTAAT CTGTAATTGC TTGTTAATCA ATAAACCGGT TAATTCGTTT
 43_12    CACCCGTAAT CTGTAATTGC TTGTTAATCA ATAAACCGGT TAATTCGTTT
 43_20    CACCCGCAAC CTGTAATTAC ATGTTAATCA ATAAACCGGT TAATTCGTTT
 43_21    CACCCGCAAC CTGTAATTAC ATGTTAATCA ATAAACCGGT TAATTCGTTT
 43_23    CACCCGCAAC CTGTAATTAC ATGTTAATCA ATAAACCGGT TAATTCGTTT
 43_25    CACCCGCAAC CTGTAATTAC ATGTTAATCA ATAAACCGGT TAATTCGTTT
  44_1    CACCCGTAAT CTGTAATTGC TCGTTAATCA ATAAACCGGT TGATTCGTTT
  44_5    CACCCGTAAT CTGTAATTGC TTGTTAATCA ATAAACCGGT TGATTCGTTT
223_10    .......... .......... .......... .......... ..........
 223_2    .......... .......... .......... .......... ..........
 223_4    .......... .......... .......... .......... ..........
 223_5    .......... .......... .......... .......... ..........
 223_6    .......... .......... .......... .......... ..........
 223_7    .......... .......... .......... .......... ..........
  A3_4    TACCCGGAAC TTGTAATTTC CTGTTAATGA ATAAACCGAT TTATGCGTTT
  A3_5    TACCCGGAAC TTGTAATTTC CTGTTAATGA ATAAACCGAT TTATGCGTTT
  A3_7    TACCCGGAAC TTGTAATTTC CTGTTAATGA ATAAACCGAT TTATGCGTTT
  A3_3    TACCCGGAAC TTGTAATTTC CTGTTAATGA ATAAGCCGAT TTATGCGTTT
 42_12    CACCCGTAAC CTGTAATTGC CTGTTAATCA ATAAACCGGT TAATTCGTTT
  AAV1    TACCCGTCCC CTGTAATTAC GTGTTAATCA ATAAACCGGT TGATTCGTTT
  AAV2    GACTCGTAAT CTGTAATTGC TTGTTAATCA ATAAACCGTT TAATTCGTTT
  AAV3    CACACGAAAC TTGTGAATCC TGGTTAATCA ATAAACCGTT TAATTCGTTT
  AAV8    CACCCGTAAT CTGTAATTGC CTGTTAATCA ATAAACCGGT TGATTCGTTT
  AAV9    CACCCGTAAT TTGTAATTGC CTGTTAATCA ATAAACCGGT TAATTCGTTT
  AAV7    CACCCGTAAT CTGTAATTGC ATGTTAATCA ATAAACCGGT TGATTCGTTT
  44_2    CACCCGTAAT CTGTAATTGC TTGTTAATCA ATAAACCGGT TGATTCGTTT
                          vp1-3 stop       PolyA signal
```

Fig. 1AAAM

```
        4501                                                  4550

  42_2  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
  42_8  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
 42_15  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
 42_5b  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTCGTTTA AACCTGCAGG
 42_1b  CAGTTGAACT TTGGTCTC.. ...AAGGGCG AATTC..... ..........
 42_13  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
 42_3a  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
  42_4  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
 42_5a  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
 42_10  CAGTTGAACT TTGGTC.... ...AAGGGCG AATTC..... ..........
 42_3b  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
 42_11  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
 42_6b  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
  43_1  .......... .......... .......... .......... ..........
  43_5  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTCGTTTA AACCTGCAGG
 43_12  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
 43_20  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
 43_21  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
 43_23  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
 43_25  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
  44_1  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
  44_5  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
223_10  .......... .......... .......... .......... ..........
 223_2  .......... .......... .......... .......... ..........
 223_4  .......... .......... .......... .......... ..........
 223_5  .......... .......... .......... .......... ..........
 223_6  .......... .......... .......... .......... ..........
 223_7  .......... .......... .......... .......... ..........
  A3_4  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTCGC.GG CCGCTA....
  A3_5  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
  A3_7  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
  A3_3  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTCGT.TT AAACCT....
 42_12  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
  AAV1  CAGTTGAACT TTGGTCTCCT GTCCTTCTTA TCTTATCGGT TACCATGGTT
  AAV2  CAGTTGAACT TTGGTCTC.T GCGTATTTCT ..TTCTT.AT CTAGTTTCCA
  AAV3  CAGTTGAACT TTGGCTCT.T GTGCACTTCT TTATCTTTAT CTTGTTTCCA
  AAV8  CAGTTGAACT TTGGTCTC.T GCG....... .......... ..........
  AAV9  CAGTTGAACT TTGGTCTC.T GCG....... .......... ..........
  AAV7  CAGTTGAACT TTGGTCTCCT GTGCTTCTTA TCTTATCGGT TTCCATAGCA
  44_2  CAGTTGAACT TTGGTCTC.T GCGAAGGGCG AATTC..... ..........
```

Fig. 1AAAN

```
        4551                                                  4600
  42_2  .......... .......... .......... .......... ..........
  42_8  .......... .......... .......... .......... ..........
 42_15  .......... .......... .......... .......... ..........
 42_5b  ACTAGTCCCT TTAGTGAGGG TTAATTCTGA G......... ..........
 42_1b  .......... .......... .......... .......... ..........
 42_13  .......... .......... .......... .......... ..........
 42_3a  .......... .......... .......... .......... ..........
  42_4  .......... .......... .......... .......... ..........
 42_5a  .......... .......... .......... .......... ..........
 42_10  .......... .......... .......... .......... ..........
 42_3b  .......... .......... .......... .......... ..........
 42_11  .......... .......... .......... .......... ..........
 42_6b  .......... .......... .......... .......... ..........
  43_1  .......... .......... .......... .......... ..........
  43_5  AC........ .......... .......... .......... ..........
 43_12  .......... .......... .......... .......... ..........
 43_20  .......... .......... .......... .......... ..........
 43_21  .......... .......... .......... .......... ..........
 43_23  .......... .......... .......... .......... ..........
 43_25  .......... .......... .......... .......... ..........
  44_1  .......... .......... .......... .......... ..........
  44_5  .......... .......... .......... .......... ..........
223_10  .......... .......... .......... .......... ..........
 223_2  .......... .......... .......... .......... ..........
 223_4  .......... .......... .......... .......... ..........
 223_5  .......... .......... .......... .......... ..........
 223_6  .......... .......... .......... .......... ..........
 223_7  .......... .......... .......... .......... ..........
  A3_4  .......... .......... .......... .......... ..........
  A3_5  .......... .......... .......... .......... ..........
  A3_7  .......... .......... .......... .......... ..........
  A3_3  .......... .......... .......... .......... ..........
 42_12  .......... .......... .......... .......... ..........
  AAV1  ATAGCTTACA CATTAACTGC TTGGTTGCGC T......... ..........
  AAV2  TGGCTAC... GTAGATAAGT AGC....... .......... ..........
  AAV3  TGGCTACTGC GTAGATAAGC AGCGGCCTGC GGCGCTTGCG CTTCGCGGTT
  AAV8  .......... .......... .......... .......... ..........
  AAV9  .......... .......... .......... .......... ..........
  AAV7  ACTGGTTACA CATTAACTGC TTGGGTGCGC TTCACGATAA GAACACTGAC
  44_2  .......... .......... .......... .......... ..........
```

Fig. 1AAAO

```
         4601                                                  4650
  42_2   .......... .......... .......... .......... ..........
  42_8   .......... .......... .......... .......... ..........
 42_15   .......... .......... .......... .......... ..........
 42_5b   ....CTTGGC GTAATCATGG GTCATAG... .......... ..........
 42_1b   .......... .......... .......... .......... ..........
 42_13   .......... .......... .......... .......... ..........
 42_3a   .......... .......... .......... .......... ..........
  42_4   .......... .......... .......... .......... ..........
 42_5a   .......... .......... .......... .......... ..........
 42_10   .......... .......... .......... .......... ..........
 42_3b   .......... .......... .......... .......... ..........
 42_11   .......... .......... .......... .......... ..........
 42_6b   .......... .......... .......... .......... ..........
  43_1   .......... .......... .......... .......... ..........
  43_5   .......... .......... .......... .......... ..........
 43_12   .......... .......... .......... .......... ..........
 43_20   .......... .......... .......... .......... ..........
 43_21   .......... .......... .......... .......... ..........
 43_23   .......... .......... .......... .......... ..........
 43_25   .......... .......... .......... .......... ..........
  44_1   .......... .......... .......... .......... ..........
  44_5   .......... .......... .......... .......... ..........
223_10   .......... .......... .......... .......... ..........
 223_2   .......... .......... .......... .......... ..........
 223_4   .......... .......... .......... .......... ..........
 223_5   .......... .......... .......... .......... ..........
 223_6   .......... .......... .......... .......... ..........
 223_7   .......... .......... .......... .......... ..........
  A3_4   .......... .......... .......... .......... ..........
  A3_5   .......... .......... .......... .......... ..........
  A3_7   .......... .......... .......... .......... ..........
  A3_3   .......... .......... .......... .......... ..........
 42_12   .......... .......... .......... .......... ..........
  AAV1   ....TCGCGA TAAAAGACTT ACGTCATCGG GTTACCCCTA GTGATGGAGT
  AAV2   ....ATGGCG GGTTAATCAT TAACTACAAG GA.ACCCCTA GTGATGGAGT
  AAV3   TACAACTGCT GGTTAATATT TAACTCTCGC CATACCTCTA GTGATGGAGT
  AAV8   .......... .......... .......... .......... ..........
  AAV9   .......... .......... .......... .......... ..........
  AAV7   .......... .......... ..GTCACCGC GGTACCCCTA GTGATGGAGT
  44_2   .......... .......... .......... .......... ..........
```

Fig. 1AAAP

```
         4651                                                  4700
  42_2   .......... .......... .......... .......... ..........
  42_8   .......... .......... .......... .......... ..........
 42_15   .......... .......... .......... .......... ..........
 42_5b   .......... .......... .......... .......... ..........
 42_1b   .......... .......... .......... .......... ..........
 42_13   .......... .......... .......... .......... ..........
 42_3a   .......... .......... .......... .......... ..........
  42_4   .......... .......... .......... .......... ..........
 42_5a   .......... .......... .......... .......... ..........
 42_10   .......... .......... .......... .......... ..........
 42_3b   .......... .......... .......... .......... ..........
 42_11   .......... .......... .......... .......... ..........
 42_6b   .......... .......... .......... .......... ..........
  43_1   .......... .......... .......... .......... ..........
  43_5   .......... .......... .......... .......... ..........
 43_12   .......... .......... .......... .......... ..........
 43_20   .......... .......... .......... .......... ..........
 43_21   .......... .......... .......... .......... ..........
 43_23   .......... .......... .......... .......... ..........
 43_25   .......... .......... .......... .......... ..........
  44_1   .......... .......... .......... .......... ..........
  44_5   .......... .......... .......... .......... ..........
223_10   .......... .......... .......... .......... ..........
 223_2   .......... .......... .......... .......... ..........
 223_4   .......... .......... .......... .......... ..........
 223_5   .......... .......... .......... .......... ..........
 223_6   .......... .......... .......... .......... ..........
 223_7   .......... .......... .......... .......... ..........
  A3_4   .......... .......... .......... .......... ..........
  A3_5   .......... .......... .......... .......... ..........
  A3_7   .......... .......... .......... .......... ..........
  A3_3   .......... .......... .......... .......... ..........
 42_12   .......... .......... .......... .......... ..........
  AAV1   TGCCCACTCC CTCTCTGCGC GCTCGCTCGC TCGGTGGGGC CTGCGGACCA
  AAV2   TGGCCACTCC CTCTCTGCGC GCTCGCTCGC TCACTGAGGC CGGGCGACCA
  AAV3   TGGCCACTCC CTCTATGCGC ACTCGCTCGC TCGGTGGGGC CTGGCGACCA
  AAV8   .......... .......... .......... .......... ..........
  AAV9   .......... .......... .......... .......... ..........
  AAV7   TGGCCACTCC CTCTATGCGC GCTCGCTCGC TCGGTGGGGC CTGCGGACCA
  44_2   .......... .......... .......... .......... ..........
```

Fig. 1AAAQ

```
        4701                                                  4750
  42_2  .......... .......... .......... .......... ..........
  42_8  .......... .......... .......... .......... ..........
 42_15  .......... .......... .......... .......... ..........
 42_5b  .......... .......... .......... .......... ..........
 42_1b  .......... .......... .......... .......... ..........
 42_13  .......... .......... .......... .......... ..........
 42_3a  .......... .......... .......... .......... ..........
  42_4  .......... .......... .......... .......... ..........
 42_5a  .......... .......... .......... .......... ..........
 42_10  .......... .......... .......... .......... ..........
 42_3b  .......... .......... .......... .......... ..........
 42_11  .......... .......... .......... .......... ..........
 42_6b  .......... .......... .......... .......... ..........
  43_1  .......... .......... .......... .......... ..........
  43_5  .......... .......... .......... .......... ..........
 43_12  .......... .......... .......... .......... ..........
 43_20  .......... .......... .......... .......... ..........
 43_21  .......... .......... .......... .......... ..........
 43_23  .......... .......... .......... .......... ..........
 43_25  .......... .......... .......... .......... ..........
  44_1  .......... .......... .......... .......... ..........
  44_5  .......... .......... .......... .......... ..........
223_10  .......... .......... .......... .......... ..........
 223_2  .......... .......... .......... .......... ..........
 223_4  .......... .......... .......... .......... ..........
 223_5  .......... .......... .......... .......... ..........
 223_6  .......... .......... .......... .......... ..........
 223_7  .......... .......... .......... .......... ..........
  A3_4  .......... .......... .......... .......... ..........
  A3_5  .......... .......... .......... .......... ..........
  A3_7  .......... .......... .......... .......... ..........
  A3_3  .......... .......... .......... .......... ..........
 42_12  .......... .......... .......... .......... ..........
  AAV1  AAGGTCCGCA GACGGCAGAG CTCTGCTCTG CCGGCCCCAC CGAGCGAGCG
  AAV2  AAGGTCGCCC GACGCCCGGG CTTTGCCCGG GCGGCCTCAG TGAGCGAGCG
  AAV3  AAGGTCGCCA GACGGACGTG CTTTGCACGT CCGGCCCCAC CGAGCGAGCG
  AAV8  .......... .......... .......... .......... ..........
  AAV9  .......... .......... .......... .......... ..........
  AAV7  AAGGTCCGCA GACGGCAGAG CTCTGCTCTG CCGGCCCCAC CGAGCGAGCG
  44_2  .......... .......... .......... .......... ..........
```

Fig. 1AAAR

```
         4751                    4774
  42_2   .......... .......... ....
  42_8   .......... .......... ....
 42_15   .......... .......... ....
 42_5b   .......... .......... ....
 42_1b   .......... .......... ....
 42_13   .......... .......... ....
 42_3a   .......... .......... ....
  42_4   .......... .......... ....
 42_5a   .......... .......... ....
 42_10   .......... .......... ....
 42_3b   .......... .......... ....
 42_11   .......... .......... ....
 42_6b   .......... .......... ....
  43_1   .......... .......... ....
  43_5   .......... .......... ....
 43_12   .......... .......... ....
 43_20   .......... .......... ....
 43_21   .......... .......... ....
 43_23   .......... .......... ....
 43_25   .......... .......... ....
  44_1   .......... .......... ....
  44_5   .......... .......... ....
223_10   .......... .......... ....
 223_2   .......... .......... ....
 223_4   .......... .......... ....
 223_5   .......... .......... ....
 223_6   .......... .......... ....
 223_7   .......... .......... ....
  A3_4   .......... .......... ....
  A3_5   .......... .......... ....
  A3_7   .......... .......... ....
  A3_3   .......... .......... ....
 42_12   .......... .......... ....
  AAV1   AGCGCGCAGA GAGGGAGTGG GCAA
  AAV2   AGCGCGCAGA GAGGGAGTGG CCAA
  AAV3   AGTGCGCATA GAGGGAGTGG CCAA
  AAV8   .......... .......... ....
  AAV9   .......... .......... ....
  AAV7   AGCGCGCATA GAGGGAGTGG CCAA
  44_2   .......... .......... ....
```

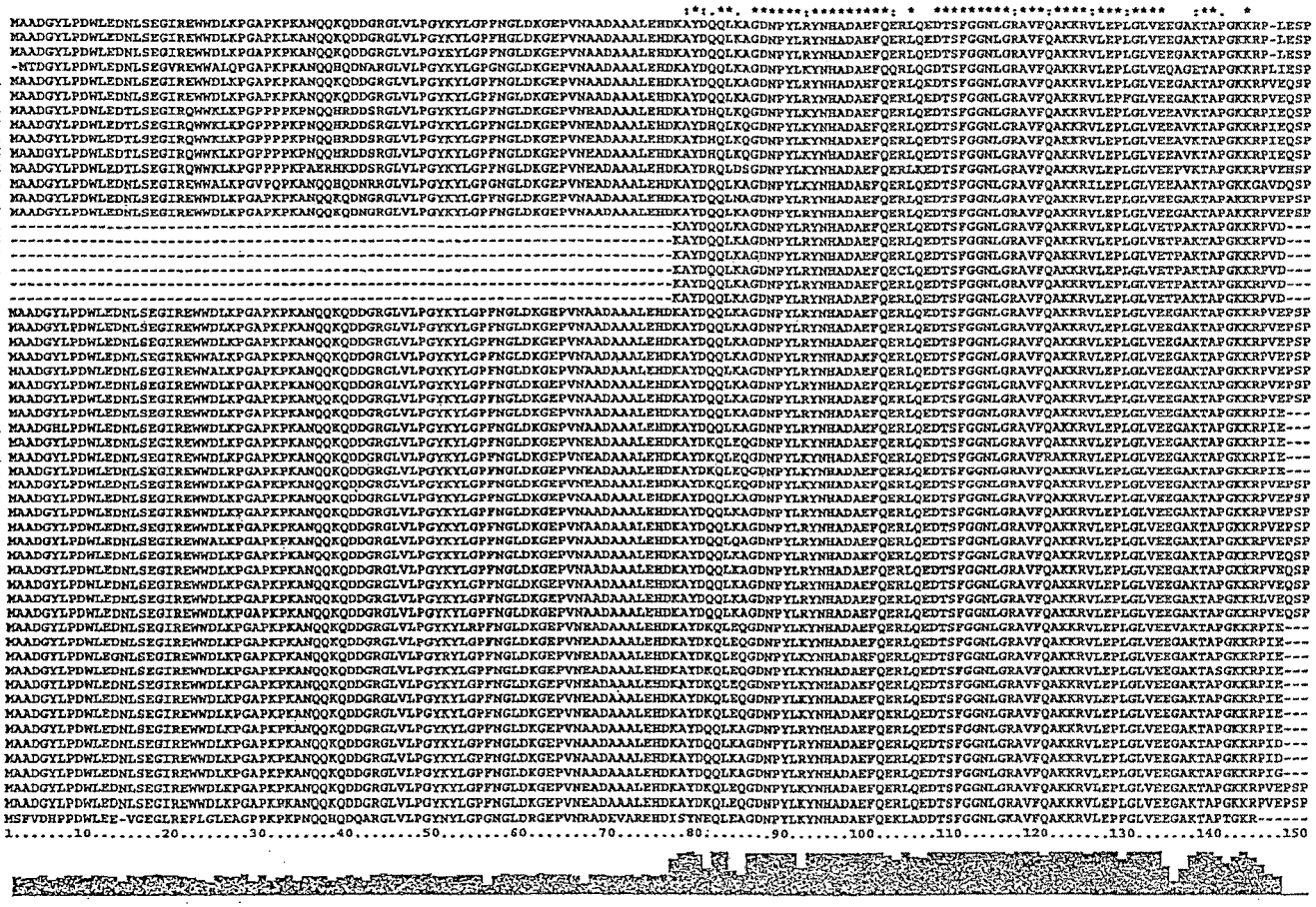

Fig. 2A

Fig. 2B

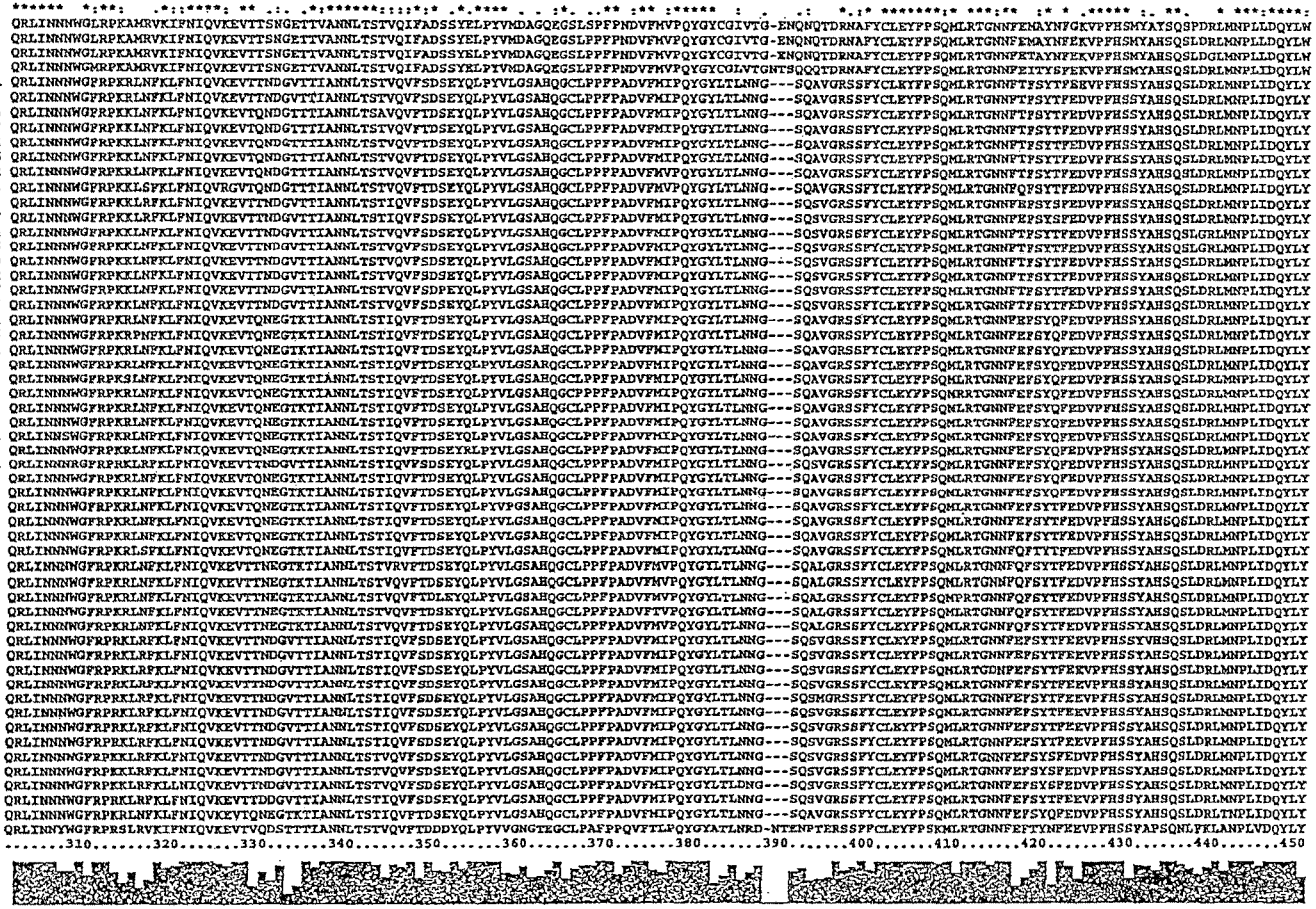
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Fig. 2C

Fig. 2D

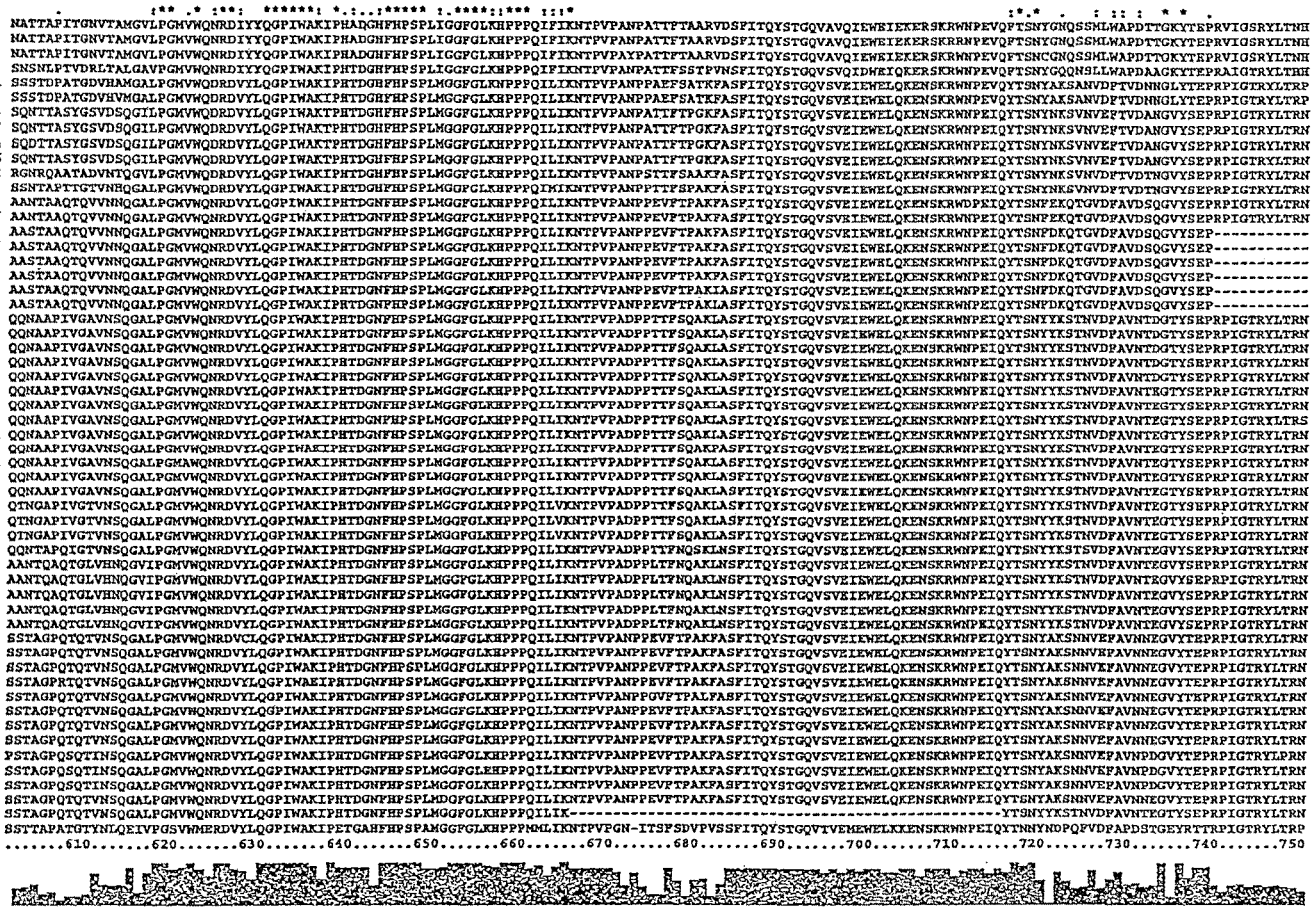
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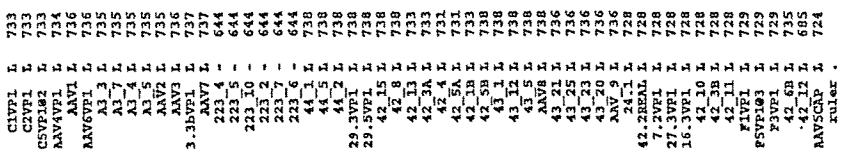
Fig. 2E

Fig. 2F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ruler .

Fig. 3A

```
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20                  25                  30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50                  55                  60

Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Val Leu Val Glu
                85                  90                  95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100                 105                 110

Arg Glu Lys Leu Val Gln Thr Ile Tyr Arg Gly Val Glu Pro Thr Leu
        115                 120                 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile
                165                 170                 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
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```

Fig. 3B

```
Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260                 265                 270

Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ser
        275                 280                 285

Leu Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
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Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
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Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445
```

Fig. 3C

```
Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
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Glu Val Lys Glu Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
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Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Ser Lys Arg Pro Ala
                485                 490                 495

Pro Asp Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
            500                 505                 510

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
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Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Ile Gln Met
    530                 535                 540

Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
545                 550                 555                 560

Cys Phe Thr His Gly Val Arg Asp Cys Leu Glu Cys Phe Pro Gly Val
                565                 570                 575

Ser Glu Ser Gln Pro Val Val Arg Lys Lys Thr Tyr Arg Lys Leu Cys
            580                 585                 590

Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
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Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
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SEQUENCE LISTING

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Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
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Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
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Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

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Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
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Leu Tyr Lys Gln Ile Ser Ser Glu Thr Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495
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Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
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Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
515 520 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
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Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
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Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
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Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
580 585 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
595 600 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
610 615 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
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Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
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Leu

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<212> PRT
<213> rep protein of adeno-associated virus serotype 7

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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50                  55                  60

Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Val Leu Val Glu
                85                  90                  95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100                 105                 110

Arg Glu Lys Leu Val Gln Thr Ile Tyr Arg Gly Val Glu Pro Thr Leu
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Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
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Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile
                165                 170                 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
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Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
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Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ser
        275                 280                 285

Leu Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
    290                 295                 300

Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
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Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Lys Glu Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
465                 470                 475                 480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Ser Lys Arg Pro Ala
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Pro Asp Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
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Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
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Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Ile Gln Met
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Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
545 550 555 560

Cys Phe Thr His Gly Val Arg Asp Cys Leu Glu Cys Phe Pro Gly Val
565 570 575

Ser Glu Ser Gln Pro Val Val Arg Lys Lys Thr Tyr Arg Lys Leu Cys
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Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
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Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
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tatctgaccc taaacaatgg cagtcaggct gtgggccgtt cctccttcta ctgcctggaa 2040

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<211> 3123
<212> DNA
<213> new AAV serotype, clone 43.12

<400> 41
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aaggccattc tcggcggcag caaggtgcgc gtggaccaaa agtgcaagtc gtccgcccag 180

atcgacccca cccccgtgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg 240

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<211> 3122
<212> DNA
<213> new AAV serotype, clone 43.20

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gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat gnaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg 1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat 1440

gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt 1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc 1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaagt ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gagtgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 49
<211> 1933
<212> DNA
<213> new AAV serotype, clone 223.2

<400> 49
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagt gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gttgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccctg 600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggtgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggact cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

ttctcagatg ctgagaacgg gcaacaactt caccttagc tacaccttcg aggacgtgcc 1020

tttccacagc agctacgcgc acagccagag tctggaccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttctccc cttcgagcgg 1380

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gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt 1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc 1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacgccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaagt ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gagtgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 50
<211> 1933
<212> DNA
<213> new AAV serotype, clone 223.4

<400> 50
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gccagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca cggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccctg 600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggcgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggact cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

ttctcagatg ctgagaacgg gcaacaactt caccttttagc tacaccttcg aggacgtgcc 1020

tttccacagc agctacgcgc acagccagag tctgggccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg 1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat 1440

gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt 1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc 1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaagt ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gaatgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 51
<211> 1933
<212> DNA
<213> new AAV serotype, clone 223.5

<400> 51
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gccagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca cggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccccctg 600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggcgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggact cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

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ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg 1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat 1440

gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt 1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc 1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaagt ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gaatgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 52
<211> 1933
<212> DNA
<213> new AAV serotype, clone 223.6

<400> 52
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aatagcgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccccctg 600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggtgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggact cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

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tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

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tttccacagc agctacgcgc acagccagag tctggaccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg 1380

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aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

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caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaagc ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gagtgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 53
<211> 1933
<212> DNA
<213> new AAV serotype, clone 223.7

<400> 53
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccctg 600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggcgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggacc cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

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tttccacagc agctacgcgc acagccagag tctggaccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg 1380

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gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga 1740

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cgttgagatc gagtgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 54
<211> 3123
<212> DNA
<213> new AAV serotype, clone A3.4

<400> 54
gaattcgccc tttctacggc tgcgtcaact ggaccaatga aaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggaaagat gaccgccaag gtcgtggaat 120

ctgccaaagc cattctgggt ggaagcaagg ttcgtgtgga ccagaaatgc aagtcttcgg 180

cccagatcga cccgactccg gtgattgtca cctctaacac caacatgtgc gccgtgattg 240

acggaaactc gaccaccttc gagcaccagc agccgttgca agaccggatg ttcaaatttg 300

aacttacccg ccgtttggat catgactttg ggaaggtcac caagcaggaa gtcaaagact 360

ttttccggtg ggctcaagat cacgtgactg aggtggagca tgagttctac gtcaaaaagg 420

gtggagccaa gaaaaggccc gcccccgatg atgtatatat aaatgagccc aagcgggcgc 480

gcgagtcagt tgcgcagcca tcgacgtcag acgcggaagc ttcgataaac tacgcgggca 540

ggtaccaaaa caaatgttct cgtcacgtgg gcatgaatct gatgctgttt ccctgtcgac 600

aatgcgaaag aatgaatcag aattcaaata tctgcttcac acacgggcaa aaagactgtt 660

tggaatgctt tcccgtgtca gaatctcaac ccgtttctgt cgtcagaaaa acgtatcaga 720

aactttgtta cattcatcat atcatgggaa aagaaccaga cgcctgcact gcctgcgacc 780

tggtaaatgt ggacttggat gactgtattt ctgagcaata aatgacttaa atcaggtatg 840

gctgctgacg gttatcttcc agattggctc gaggacactc tctctgaagg aatcagacag 900

tggtggaagc tcaaacctgg cccaccaccg ccgaaaccta accaacaaca ccgggacgac 960

agtaggggtc ttgtgcttcc tgggtacaag tacctcggac ccttcaacgg actcgacaaa 1020

ggagagccgg tcaacgaggc agacgccgcg gccctcgagc acgacaaagc ctacgaccac 1080

cagctcaagc aaggggacaa cccgtacctc aaatacaacc acgcggacgc tgaatttcag 1140

gagcgtcttc aagaagatac gtctttcggg ggcaacctcg ggcgagcagt cttccaggcc 1200

aaaaagaggg tactcgagcc tcttggtctg gttgaggaag ctgttaagac ggctcctgga 1260

aaaaagagac ctatagagca gtctcctgca gaaccggact cttcctcggg catcggcgaa 1320

tcaggccagc agcccgctaa gaaaagactc aattttggtc agactggcga cacagagtca 1380

gtcccagacc ctcaaccaat cggagaaccc cccgcagccc cctctggtgt gggatctaat 1440

acaatggctt caggcggtgg ggcaccaatg gcagacgata acgaaggcgc cgacggagtg 1500

ggtaattcct cgggaaattg gcattgcgat tccacatgga tgggcgacag agttatcacc 1560

accagcacaa gaacctgggc cctccccacc tacaataatc acctctacaa gcaaatctcc 1620

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tttgacttta acagattcca ctgtcacttc tcaccacgtg actggcagcg actcatcaac 1740

aacaactggg gatttagacc caagaaactc aatttcaagc tcttcaacat ccaagtcaag 1800

gaggtcacgc agaatgatgg aaccacgacc atcgccaata accttaccag cacggtgcag 1860

gtcttcacag actctgagta ccagctgccc tacgtcctcg gttcggctca ccagggctgc 1920

cttccgccgt tcccagcaga cgtcttcatg attcctcagt acggctactt gactctgaac 1980

aatggcagcc aagcggtagg acgttcttca ttctactgtc tagagtattt tccctctcag 2040

atgctgagga cgggaaacaa cttcaccttc agctacactt ttgaagacgt gcctttccac 2100

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ctgtattacc tgagcaaaac tcagggtaca agtggaacaa cgcagcaatc gagactgcag 2220

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agctaccgac agcagcgaat gtctaagacg gctaatgaca acaacaacag tgaatttgct 2340

tggactgcag ccaccaaata ttacctgaat ggaagaaatt ctctggtcaa tcccgggccc 2400

ccaatggcca gtcacaagga cgatgaggaa aagtatttcc ccatgcacgg aaatctcatc 2460

tttggaaaac aaggcacagg aactaccaat gtggacattg aatcagtgct tattacagac 2520

gaagaagaaa tcagaacaac taatcctgtg gctacagaac aatacggaca ggttgccacc 2580

aaccatcaga gtcaggacac cacagcttcc tatggaagtg tggacagcca gggaatctta 2640

cctggaatgg tgtggcagga ccgcgatgtc tatcttcaag gtcccatttg ggccaaaact 2700

cctcacacgg acggacactt tcatccttct ccgctcatgg gaggctttgg actgaaacac 2760

cctcctcccc agatcctgat caaaaacaca cctgtgccag cgaatcccgc gaccactttc 2820

actcctggaa agtttgcttc gttcattacc cagtattcca ccggacaggt cagcgtggaa 2880

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cta 3123

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<212> DNA
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tcgcgagtgg tgggacttga aacctggagc cccgaaaccc aaagccaacc agcaaaagca 960
ggacgacggc cggggtctgg tgcttcctgg ctacaagtac ctcggaccct tcaacggact 1020
cgacaagggg gagcccgtca acgcggcgga cgcagcggcc ctcgagcacg acaaggccta 1080
cgaccagcag ctcaaagcgg gtgacaatcc gtacctgcgg tataaccacg ccgacgccga 1140
gtttcaggag cgtctgcaag aagatacgtc ttttgggggc aacctcgggc gagcagtctt 1200
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cgacggagtg ggtagttcct caggaaattg gcattgcgat tccacatggc tgggcgacag 1560
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gcagcgactc atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt 1800
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taccagcacg attcaggtct ttacggactc ggaataccag ctcccgtacg tcctcggctc 1920
tgcgcaccag ggctgcctgc ctccgttccc ggcggacgtc ttcatgattc ctcagtacgg 1980

gtacctgact ctgaacaatg gcagtcaggc cgtgggccgt tcctccttct actgcctgga 2040

gtactttcct tctcaaatgc tgagaacggg caacaacttt gagttcagct accagtttga 2100

ggacgtgcct tttcacagca gctacgcgca cagccaaagc ctggaccggc tgatgaaccc 2160

cctcatcgac cagtacctgt actacctgtc tcggactcag tccacgggag gtaccgcagg 2220

aactcagcag ttgctatttt ctcaggccgg gcctaataac atgtcggctc aggccaaaaa 2280

ctggctaccc gggccctgct accggcagca acgcgtctcc acgacactgt cgcaaaataa 2340

caacagcaac tttgcctgga ccggtgccac caagtatcat ctgaatggca gagactctct 2400

ggtaaatccc ggtgtcgcta tggcaaccca caaggacgac gaagagcgat tttttccgtc 2460

cagcggagtc ttaatgtttg ggaaacaggg agctggaaaa gacaacgtgg actatagcag 2520

cgttatgcta accagtgagg aagaaattaa aaccaccaac ccagtggcca cagaacagta 2580

cggcgtggtg gccgataacc tgcaacagca aaacgccgct cctattgtag gggccgtcaa 2640

cagtcaagga gccttacctg gcatggtctg gcagaaccgg gacgtgtacc tgcagggtcc 2700

tatctgggcc aagattcctc acacggacgg aaactttcat ccctcgccgc tgatgggagg 2760

ctttggactg aaacacccgc ctcctcagat cctgattaag aatacacctg ttcccgcgga 2820

tcctccaact accttcagtc aagctaagct ggcgtcgttc atcacgcagt acagcaccgg 2880

acaggtcagc gtggaaattg aatgggagct gcagaaagaa aacagcaaac gctggaaccc 2940

agagattcaa tacacttcca actactacaa atctacaaat gtggactttg ctgttaacac 3000

agatggcact tattctgagc ctcgccccat cggcacccgt tacctcaccc gtaatctgta 3060

attgcttgtt aatcaataaa ccggttgatt cgtttcagtt gaactttggt ctctgcgaag 3120

ggcgaattc 3129

<210> 60
<211> 733
<212> PRT
<213> capsid protein of AAV serotype, clone C1VP1

<400> 60

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320
```

```
Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Ser Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Met Ala Tyr Asn Phe Gly Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala Tyr Ser Gln Ser Pro Asp Arg Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575
```

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
580 585 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
595 600 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
610 615 620

His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625 630 635 640

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
645 650 655

Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
675 680 685

Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
690 695 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705 710 715 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
725 730

<210> 61
<211> 733
<212> PRT
<213> capsid protein of AAV serotype, clone C2VP1

<400> 61
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Leu
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe His Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335
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Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
340 345 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
355 360 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
370 375 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385 390 395 400

Asn Phe Glu Met Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
405 410 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp
420 425 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
435 440 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
450 455 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465 470 475 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
485 490 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
500 505 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
515 520 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
530 535 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545 550 555 560

Gly Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
565 570 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
580 585 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
595 600 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
610 615 620

His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625 630 635 640

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
645 650 655

Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
675 680 685

Ser Lys Arg Arg Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
690 695 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705 710 715 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
725 730

<210> 62
<211> 733
<212> PRT
<213> capsid protein of AAV serotype, clone C5VP1@2

<400> 62
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Glu Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350
```

```
Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Thr Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala His Ser Gln Ser Leu Asp Gly Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605
```

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
610 615 620

His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625 630 635 640

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Tyr Pro Ala
645 650 655

Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
675 680 685

Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Cys Gly Asn
690 695 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705 710 715 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
725 730

<210> 63
<211> 734
<212> PRT
<213> capsid protein of AAV serotype, clone AAV4VP1

<400> 63
Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1 5 10 15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
50 55 60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65 70 75 80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
100 105 110

```
Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365
```

```
Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620
```

```
Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730
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<210> 64
<211> 736
<212> PRT
<213> capsid protein of AAV serotype, clone AAV1

<400> 64

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380
```

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
435 440 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 65
<211> 736
<212> PRT
<213> capsid protein of AAV serotype, clone AAV6VP1

<400> 65
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400
```

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
435 440 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 66
<211> 735
<212> PRT
<213> capsid protein of AAV serotype, clone A3.3

<400> 66

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Thr Glu Ser Val Pro Gly Pro Gln Pro Ile Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Ala Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
435 440 445

Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
450 455 460

Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465 470 475 480

Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
485 490 495

Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly
500 505 510

Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Val Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
530 535 540

Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Gln Val Ala Thr Asn His Gln Ser Gln Asn Thr Thr Ala Ser Tyr
580 585 590

Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Thr Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 67
<211> 735
<212> PRT
<213> capsid protein of AAV serotype, clone A3.7

<400> 67
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn Arg Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
435 440 445

Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
450 455 460

Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465 470 475 480

Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
485 490 495

Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly
500 505 510

Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
530 535 540

Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Gln Val Ala Thr Asn His Gln Ser Gln Asn Thr Thr Ala Ser Tyr
580 585 590

Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Thr Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 68
<211> 735
<212> PRT
<213> capsid protein of AAV serotype, clone A3.4

<400> 68
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Glu Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

```
Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asp Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430
```

```
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445

Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly
            500                 505                 510

Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Gln Val Ala Thr Asn His Gln Ser Gln Asp Thr Thr Ala Ser Tyr
            580                 585                 590

Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Thr Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685
```

```
Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 69
<211> 735
<212> PRT
<213> capsid protein of AAV serotype, clone A3.5

<400> 69

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190
```

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
435 440 445

```
Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Asn Gln
    450                 455                 460

Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Pro Asn Gly
            500                 505                 510

Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Gln Val Ala Thr Asn Arg Gln Ser Gln Asn Thr Thr Ala Ser Tyr
            580                 585                 590

Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Thr Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700
```

Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 70
<211> 735
<212> PRT
<213> capsid protein of AAV serotype, clone AAV2

<400> 70
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190

```
Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445
```

```
Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700
```

```
Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 71
<211> 736
<212> PRT
<213> capsid protein of AAV serotype, clone AAV3

<400> 71

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly
    130                 135                 140

Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
435 440 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
450 455 460

```
Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720
```

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 72
<211> 737
<212> PRT
<213> capsid protein of AAV serotype, clone 3.3bVP1

<400> 72

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Asn Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Ala Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
210 215 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Glu Gln Ile Ser Ser Glu Thr Ala Gly Ser Thr Asn Asp Asn
260 265 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
370 375 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser
405 410 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
435 440 445

Arg Thr Gln Ser Asp Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
450 455 460

```
Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asp Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720
```

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 73
<211> 644
<212> PRT
<213> capsid protein of AAV serotype, clone 223-4

<400> 73
Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1 5 10 15

Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
20 25 30

Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
35 40 45

Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
50 55 60

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65 70 75 80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
85 90 95

Gly Asp Ser Glu Pro Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
100 105 110

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
115 120 125

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
130 135 140

Ser Gly Asn Trp His Cys Asp Ser Thr Arg Leu Gly Asp Arg Val Ile
145 150 155 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
165 170 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
180 185 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
195 200 205

```
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380

Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385                 390                 395                 400

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430

Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460
```

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465 470 475 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
485 490 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
500 505 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
515 520 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
530 535 540

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545 550 555 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
565 570 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
580 585 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
595 600 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
610 615 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625 630 635 640

Tyr Ser Glu Pro

<210> 74
<211> 644
<212> PRT
<213> capsid protein of AAV serotype, clone 223.5

<400> 74
Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1 5 10 15

Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
20 25 30

Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
35 40 45

Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
50 55 60

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65 70 75 80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
85 90 95

Gly Asp Ser Glu Pro Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
100 105 110

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
115 120 125

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
130 135 140

Ser Gly Asn Trp His Cys Asp Ser Thr Arg Leu Gly Asp Arg Val Ile
145 150 155 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
165 170 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
180 185 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
195 200 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
210 215 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225 230 235 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
245 250 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
260 265 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
275 280 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
290 295 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305 310 315 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
325 330 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly
340 345 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
355 360 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
370 375 380

Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385 390 395 400

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
405 410 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
420 425 430

Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
435 440 445

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
450 455 460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465 470 475 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
485 490 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
500 505 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
515 520 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
530 535 540

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545 550 555 560

```
Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                565                 570                 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
            580                 585                 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        595                 600                 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    610                 615                 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625                 630                 635                 640

Tyr Ser Glu Pro
```

<210> 75
<211> 644
<212> PRT
<213> capsid protein of AAV serotype, clone 223.10

<220>
<221> MISC_FEATURE
<222> (434)..(434)
<223> can be any amino acid

<400> 75

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Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1               5                   10                  15

Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
            20                  25                  30

Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
        35                  40                  45

Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
    50                  55                  60

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65                  70                  75                  80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                85                  90                  95

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            100                 105                 110
```

```
Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
        115                 120                 125

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    130                 135                 140

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
145                 150                 155                 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165                 170                 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180                 185                 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195                 200                 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365
```

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
370 375 380

Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385 390 395 400

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
405 410 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
420 425 430

Asn Xaa Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
435 440 445

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
450 455 460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465 470 475 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
485 490 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
500 505 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
515 520 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
530 535 540

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545 550 555 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
565 570 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
580 585 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
595 600 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
610 615 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625 630 635 640

Tyr Ser Glu Pro

<210> 76
<211> 644
<212> PRT
<213> capsid protein of AAV serotype, clone 223.2

<400> 76
Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1 5 10 15

Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Cys Leu Gln Glu Asp Thr
20 25 30

Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
35 40 45

Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
50 55 60

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65 70 75 80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
85 90 95

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
100 105 110

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Val Ala Gly Gly Gly
115 120 125

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
130 135 140

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
145 150 155 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
165 170 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
180 185 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
195 200 205

```
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380

Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385                 390                 395                 400

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430

Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445

Lys Asp Asp Glu Glu Arg Phe Ser Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460
```

```
Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
                485                 490                 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
            500                 505                 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        515                 520                 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    530                 535                 540

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545                 550                 555                 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                565                 570                 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
            580                 585                 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        595                 600                 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    610                 615                 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625                 630                 635                 640

Tyr Ser Glu Pro
```

<210> 77
<211> 644
<212> PRT
<213> capsid protein of AAV serotype, clone 223.7

<400> 77

```
Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1               5                   10                  15

Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
            20                  25                  30
```

```
Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
        35                  40                  45

Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
    50                  55                  60

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65                  70                  75                  80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                85                  90                  95

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            100                 105                 110

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
        115                 120                 125

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    130                 135                 140

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
145                 150                 155                 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165                 170                 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180                 185                 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195                 200                 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Pro Glu Tyr Gln Leu Pro
            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285
```

```
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380

Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385                 390                 395                 400

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430

Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
                485                 490                 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
            500                 505                 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        515                 520                 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    530                 535                 540
```

```
Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545                 550                 555                 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                565                 570                 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Ile Ala Ser Phe Ile Thr
            580                 585                 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        595                 600                 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    610                 615                 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625                 630                 635                 640

Tyr Ser Glu Pro
```

<210> 78
<211> 644
<212> PRT
<213> capsid protein of AAV serotype, clone 223.6

<400> 78

```
Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1               5                   10                  15

Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
            20                  25                  30

Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
        35                  40                  45

Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
    50                  55                  60

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65                  70                  75                  80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                85                  90                  95

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            100                 105                 110

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
        115                 120                 125
```

```
Ala Pro Met Ala Asp Asn Ser Glu Gly Ala Asp Gly Val Gly Asn Ala
    130                 135                 140

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
145                 150                 155                 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165                 170                 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180                 185                 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195                 200                 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380
```

```
Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385                 390                 395                 400

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430

Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
                485                 490                 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
            500                 505                 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        515                 520                 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    530                 535                 540

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545                 550                 555                 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                565                 570                 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Leu Ala Ser Phe Ile Thr
            580                 585                 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        595                 600                 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    610                 615                 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625                 630                 635                 640
```

Tyr Ser Glu Pro

<210> 79
<211> 738
<212> PRT
<213> capsid protein of AAV serotype, clone 44.1

<400> 79

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
450 455 460

```
Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720
```

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 80
<211> 738
<212> PRT
<213> capsid protein of AAV serotype, clone 44.5

<400> 80

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

```
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Pro Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460
```

```
Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720
```

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 81
<211> 738
<212> PRT
<213> capsid protein of AAV serotype, clone 44.2

<400> 81
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
450 455 460

```
Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720
```

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 82
<211> 738
<212> PRT
<213> capsid protein of AAV serotype, clone 29.3VP1

<400> 82

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Thr Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala Arg Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
450 455 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
515 520 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
530 535 540

Phe Gly Lys Gln Gly Ala Gly Lys Gly Asn Val Asp Tyr Ser Ser Val
545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
580 585 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 83
<211> 738
<212> PRT
<213> capsid protein of AAV serotype, clone 29.5VP1

<400> 83

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Gly Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Ser Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

```
Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asp Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700
```

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 84
<211> 738
<212> PRT
<213> capsid protein of AAV serotype, clone 42.15

<400> 84

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Pro Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Arg Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

```
Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700
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Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 85
<211> 738
<212> PRT
<213> capsid protein of AAV serotype, clone 42.8

<400> 85

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
450 455 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
515 520 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
530 535 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
580 585 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 86
<211> 733
<212> PRT
<213> amino acid of AAV serotype, clone 42.13

<400> 86
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
180 185 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
195 200 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp
210 215 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225 230 235 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
245 250 255

Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly
260 265 270

Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His
275 280 285

Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe
290 295 300

Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu
305 310 315 320

Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser
325 330 335

Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu
340 345 350

Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe
355 360 365

Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala
370 375 380

Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met
385 390 395 400

Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val
405 410 415

Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met
420 425 430

Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser
435 440 445

Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly
450 455 460

Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys
465 470 475 480

Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser
485 490 495

Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp
500 505 510

Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His Lys Gly Asp Glu
515 520 525

Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly
530 535 540

Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu
545 550 555 560

Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val
565 570 575

Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala
580 585 590

Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp
595 600 605

Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
610 615 620

Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro
625 630 635 640

Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro
645 650 655

Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys
690 695 700

Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu
705 710 715 720

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Ser Leu
725 730

<210> 87
<211> 733
<212> PRT
<213> capsid protein of AAV serotype, clone 42.3A

<400> 87
Met Ala Ala Asp Gly His Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
180 185 190

```
Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly
            260                 265                 270

Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His
        275                 280                 285

Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Ser Trp Gly Phe
    290                 295                 300

Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu
305                 310                 315                 320

Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser
                325                 330                 335

Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu
            340                 345                 350

Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe
        355                 360                 365

Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala
    370                 375                 380

Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met
385                 390                 395                 400

Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val
                405                 410                 415

Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met
            420                 425                 430

Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser
        435                 440                 445
```

Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly
450 455 460

Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys
465 470 475 480

Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser Gln Asn Asn Asn Ser
485 490 495

Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp
500 505 510

Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu
515 520 525

Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly
530 535 540

Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu
545 550 555 560

Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val
565 570 575

Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala
580 585 590

Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp
595 600 605

Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
610 615 620

Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro
625 630 635 640

Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro
645 650 655

Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys
690 695 700

Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu
705 710 715 720

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 88
<211> 731
<212> PRT
<213> capsid protein of AAV serotype, clone 42.4

<400> 88
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
180 185 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
195 200 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
210 215 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225 230 235 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
245 250 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
260 265 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
275 280 285

Ser Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
290 295 300

Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305 310 315 320

Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
325 330 335

Gln Val Phe Thr Asp Ser Glu Tyr Arg Leu Pro Tyr Val Leu Gly Ser
340 345 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
355 360 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val Gly
370 375 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385 390 395 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val Pro Phe
405 410 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
420 425 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser Thr Gly
435 440 445

Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly Pro Asn
450 455 460

Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465 470 475 480

Gln Gln Arg Val Ser Thr Thr Leu Ser Gln Asn Asn Asn Ser Asn Phe
485 490 495

Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
500 505 510

Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
515 520 525

Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
530 535 540

Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu Glu Glu
545 550 555 560

Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
565 570 575

Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala Val Asn
580 585 590

Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr
595 600 605

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
610 615 620

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
625 630 635 640

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Thr
645 650 655

Phe Ser Gln Ala Lys Pro Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
660 665 670

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
675 680 685

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Thr
690 695 700

Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu Pro Arg
705 710 715 720

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 89
<211> 731
<212> PRT
<213> capsid protein of AAV serotype, clone 42.5A

<400> 89
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Arg Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
180 185 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
195 200 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
210 215 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225 230 235 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
245 250 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
260 265 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
275 280 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Arg Gly Phe Arg Pro
290 295 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305 310 315 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
325 330 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
340 345 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
355 360 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
370 375 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385 390 395 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val Pro Phe
405 410 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
420 425 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser Thr Gly
435 440 445

Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly Pro Asn
450 455 460

Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465 470 475 480

Gln Gln Arg Val Ser Thr Thr Leu Ser Gln Asn Asn Asn Ser Asn Phe
485 490 495

Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
500 505 510

Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
515 520 525

Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
530 535 540

Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu Glu Glu
545 550 555 560

Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
565 570 575

Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala Val Asn
580 585 590

Ser Gln Gly Ala Leu Pro Gly Met Ala Trp Gln Asn Arg Asp Val Tyr
595 600 605

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
610 615 620

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
625 630 635 640

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Thr
645 650 655

Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
660 665 670

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
675 680 685

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Thr
690 695 700

Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu Pro Arg
705 710 715 720

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 90
<211> 733
<212> PRT
<213> capsid protein of AAV serotype, clone 42.1B

<400> 90
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Arg Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
180 185 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
195 200 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp
210 215 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225 230 235 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
245 250 255

Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly
260 265 270

Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His
275 280 285

Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe
290 295 300

Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu
305 310 315 320

Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser
325 330 335

Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu
340 345 350

Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe
355 360 365

Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala
370 375 380

Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met
385 390 395 400

Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val
405 410 415

Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met
420 425 430

Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser
435 440 445

Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly
450 455 460

Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys
465 470 475 480

```
Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser
                485                 490                 495

Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp
            500                 505                 510

Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His Lys Gly Asp Glu
        515                 520                 525

Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly
    530                 535                 540

Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val
                565                 570                 575

Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala
            580                 585                 590

Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
    610                 615                 620

Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro
                645                 650                 655

Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670

Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
        675                 680                 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys
    690                 695                 700

Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu
705                 710                 715                 720

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730
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<210> 91
<211> 738
<212> PRT
<213> capsid protein of AAV serotype, clone 42.5B

<400> 91
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
450 455 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

```
Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
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<210> 92
<211> 738
<212> PRT
<213> capsid protein of AAV serotype, clone 43.1

<400> 92
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
450 455 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
515 520 525

```
His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
            580                 585                 590

Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Val Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
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<210> 93
<211> 738
<212> PRT
<213> capsid protein of AAV serotype, clone 43.12

<400> 93
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
450 455 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

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Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
      515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
            580                 585                 590

Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Val Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
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<210> 94
<211> 738
<212> PRT
<213> capsid protein of AAV serotype, clone 43.5

<400> 94
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

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Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510
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Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
            580                 585                 590

Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Val Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
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<210> 95
<211> 738
<212> PRT
<213> capsid protein of AAV serotype, clone AAV8

<400> 95

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
180 185 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
405 410 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
450 455 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
500 505 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
515 520 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
530 535 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
565 570 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
580 585 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 96
<211> 736
<212> PRT
<213> capsid protein of AAV serotype, clone 43.21

<400> 96

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
260 265 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Arg Val Phe Thr Asp Ser Glu Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
370 375 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
405 410 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
435 440 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
450 455 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Ser
485 490 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
500 505 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
515 520 525

Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
530 535 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
565 570 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
580 585 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
595 600 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 97
<211> 736
<212> PRT
<213> capsid protein of AAV serotype, clone 43.25

<400> 97
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225 230 235 240

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Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495
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Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
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<210> 98
<211> 736
<212> PRT
<213> capsid protein of AAV serotype, clone 43.23

<400> 98
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
260 265 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Leu Glu Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
370 375 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Pro Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
405 410 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
435 440 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
450 455 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
485 490 495

```
Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 99
<211> 736
<212> PRT
<213> capsid protein of AAV serotype, clone 43.20

<400> 99
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Leu Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225 230 235 240

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Thr Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
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<210> 100
<211> 736
<212> PRT
<213> capsid protein of AAV serotype, clone AAV9

400> 100

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Glu Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510
```

```
Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 101
<211> 728
<212> PRT
<213> capsid protein of AAV serotype, clone 24.1

<400> 101

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
```

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Arg Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Val Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
180 185 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
195 200 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
210 215 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225 230 235 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
245 250 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Ser Tyr Ser
260 265 270

```
Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Val His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525
```

```
Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Cys Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 102
<211> 728
<212> PRT
<213> capsid protein of AAV serotype, clone 42.2REAL

<400> 102

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
```

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
180 185 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
195 200 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
210 215 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225 230 235 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
245 250 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
260 265 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
275 280 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
290 295 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305 310 315 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
325 330 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
340 345 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
355 360 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
370 375 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385 390 395 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
405 410 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
420 425 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
435 440 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
450 455 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465 470 475 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
485 490 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
500 505 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
515 520 525

```
Pro Ile Asn Gly Val Leu Val Phe Gly Glu Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 103
<211> 728
<212> PRT
<213> capsid protein of AAV serotype, clone 7.2VP1

<400> 103

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Gly Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
145                 150                 155                 160

Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285
```

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
290 295 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305 310 315 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
325 330 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
340 345 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
355 360 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
370 375 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385 390 395 400

Thr Gly Asp Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
405 410 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
420 425 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
435 440 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
450 455 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465 470 475 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
485 490 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
500 505 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
515 520 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
530 535 540

```
Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 104
<211> 728
<212> PRT
<213> capsid protein of AAV serotype, clone 27.3VP1

<400> 104

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Ser Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285
```

```
Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Cys Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Val
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Leu
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540
```

```
Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Arg Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Glu Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 105
<211> 728
<212> PRT
<213> capsid protein of AAV serotype, clone 16.3VP1

<400> 105

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300
```

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305 310 315 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
325 330 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
340 345 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
355 360 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Met Gly
370 375 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385 390 395 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
405 410 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
420 425 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
435 440 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
450 455 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465 470 475 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
485 490 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
500 505 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Gly Gln Phe Phe
515 520 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
530 535 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545 550 555 560

```
Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Gly Val Phe Thr Pro
                645                 650                 655

Ala Leu Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 106
<211> 728
<212> PRT
<213> capsid protein of AAV serotype, clone 42.10

<400> 106

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Arg Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300
```

```
Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560
```

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
565 570 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
580 585 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
595 600 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
610 615 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625 630 635 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
645 650 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
660 665 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
675 680 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
690 695 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 107
<211> 728
<212> PRT
<213> capsid protein of AAV serotype, clone 42.3B

<400> 107
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320
```

```
Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Thr Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575
```

```
Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 108
<211> 728
<212> PRT
<213> capsid protein of AAV serotype, clone 42.11

<400> 108

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320
```

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
325 330 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
340 345 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
355 360 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
370 375 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385 390 395 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
405 410 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
420 425 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
435 440 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
450 455 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Arg Gln
465 470 475 480

Arg Leu Ser Lys Asp Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
485 490 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
500 505 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
515 520 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
530 535 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545 550 555 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
565 570 575

```
Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 109
<211> 729
<212> PRT
<213> capsid protein of AAV serotype, clone F1VP1

<400> 109

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335
```

```
Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
                405                 410                 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
        435                 440                 445

Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
    450                 455                 460

Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465                 470                 475                 480

Gln Gly Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
                485                 490                 495

Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
            500                 505                 510

Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
        515                 520                 525

Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
    530                 535                 540

Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
545                 550                 555                 560

Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
                565                 570                 575

Leu Gln Pro Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
            580                 585                 590
```

Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
595 600 605

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
610 615 620

Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
625 630 635 640

Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
645 650 655

Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
660 665 670

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
675 680 685

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
690 695 700

Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
705 710 715 720

Gly Thr Arg Tyr Leu Pro Arg Asn Leu
725

<210> 110
<211> 729
<212> PRT
<213> capsid protein of AAV serotype, clone F5VP1@3

<400> 110
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Thr Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350
```

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
355 360 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
370 375 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385 390 395 400

Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
405 410 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
420 425 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
435 440 445

Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
450 455 460

Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465 470 475 480

Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
485 490 495

Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
500 505 510

Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
515 520 525

Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
530 535 540

Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
545 550 555 560

Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
565 570 575

Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
580 585 590

Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
595 600 605

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
610 615 620

Ser Pro Leu Met Gly Gly Phe Gly Leu Glu His Pro Pro Pro Gln Ile
625 630 635 640

Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
645 650 655

Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
660 665 670

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
675 680 685

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
690 695 700

Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
705 710 715 720

Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 111
<211> 729
<212> PRT
<213> capsid protein of AAV serotype, clone F3VP1

<400> 111
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Gly Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Arg Phe Lys Leu Leu Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350
```

```
Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asp Asn Gly Ser Gln Ser Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
                405                 410                 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
        435                 440                 445

Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
    450                 455                 460

Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465                 470                 475                 480

Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
                485                 490                 495

Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
            500                 505                 510

Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
        515                 520                 525

Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
    530                 535                 540

Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
545                 550                 555                 560

Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
                565                 570                 575

Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
            580                 585                 590

Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
        595                 600                 605
```

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
610 615 620

Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
625 630 635 640

Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
645 650 655

Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
660 665 670

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
675 680 685

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
690 695 700

Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
705 710 715 720

Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 112
<211> 735
<212> PRT
<213> capsid protein of AAV serotype, clone 42.6B

<400> 112
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Arg Lys Leu Arg Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Thr Asp Asp Gly Val Thr Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365
```

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Thr Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ala Arg Thr Gln Ser Thr Thr Gly Ser Thr Arg Glu Leu Gln Phe His
450 455 460

Gln Ala Gly Pro Asn Thr Met Ala Glu Gln Ser Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Asn Ile Asp Ser Asn
485 490 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
500 505 510

Gly Arg Asn Ser Leu Thr Asn Pro Gly Val Ala Met Ala Thr Asn Lys
515 520 525

Asp Asp Glu Asp Gln Phe Phe Pro Ile Asn Gly Val Leu Val Phe Gly
530 535 540

Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met Thr
545 550 555 560

Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr
565 570 575

Gly Val Val Ser Ser Asn Leu Gln Ser Ser Thr Ala Gly Pro Gln Thr
580 585 590

Gln Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly Asn Phe His Pro Ser Pro Leu Met Asp Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Ala Lys Ser Asn Asn Val Glu Phe Ala Val Asn Asn Glu Gly Val Tyr
705 710 715 720

Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 113
<211> 685
<212> PRT
<213> capsid protein of AAV serotype, clone 42.12

<400> 113
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365
```

```
Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Thr Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ala Arg Thr Gln Ser Thr Thr Gly Ser Thr Arg Gly Leu Gln Phe His
    450                 455                 460

Gln Ala Gly Pro Asn Thr Met Ala Glu Gln Ser Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Asn Ile Asp Ser Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Thr Asn Pro Gly Val Ala Met Ala Thr Asn Lys
        515                 520                 525

Asp Asp Glu Asp Gln Phe Phe Pro Ile Asn Gly Val Leu Val Phe Gly
    530                 535                 540

Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met Thr
545                 550                 555                 560

Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr
                565                 570                 575

Gly Val Val Ser Ser Asn Leu Gln Ser Ser Thr Ala Gly Pro Gln Thr
            580                 585                 590

Gln Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Tyr Thr Ser Asn Tyr Tyr Lys
645 650 655

Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu
660 665 670

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
675 680 685

<210> 114
<211> 724
<212> PRT
<213> capsid protein of AAV serotype, clone AAV5CAP

<400> 114
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
165 170 175

```
Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430
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Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
435 440 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
450 455 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465 470 475 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
485 490 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
500 505 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
515 520 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
530 535 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545 550 555 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
565 570 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
580 585 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
595 600 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 115
<211> 9
<212> DNA
<213> DraIII restriction enzyme site

<400> 115

caccacgtc 9

<210> 116
<211> 28
<212> DNA
<213> AV2cas

<400> 116

cgcagagacc aaagttcaac tgaaacga 28

<210> 117
<211> 255
<212> DNA
<213> adeno-associated virus serotype 10

<400> 117
ggtaattcct ccggaaattg gcattgcgat tccacatggc tgggcgacag agtcatcacc 60

accagcaccc gaacctgggt cctgcccacc tacaacaacc acatctacaa gcaaatctcc 120

agcgagacag gagccaccaa cgacaaccac tacttcggct acagcacccc ctgggggtat 180

tttgacttta acagattcca ctgccacttt tcaccacgtg actggcagcg actcatcaac 240

aacaactggg gattc 255

<210> 118
<211> 258
<212> DNA
<213> adeno-associated virus serotype 11

<400> 118
ggtaattcct ccggaaattg gcattgcgat tccacatggc tgggcgacag agtcatcacc 60

accagcaccc gaacctgggc cctgccaacc tacaacaacc acctctacaa acaaatctcc 120

agcgcttcaa cgggggccag caacgacaac cactactttg gctacagcac cccctggggg 180

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatc 240

aacaacaact ggggattc 258

<210> 119
<211> 255
<212> DNA
<213> adeno-associated virus serotype 12

<400> 119
ggtaattcct ccggaaattg gcattgcgat tccacatggc tgggcgaccg agtcattacc 60

accagcaccc ggacttgggc cctgcccacc tacaacaacc acctctacaa gcaaatctcc 120

agccaatcgg gtgccaccaa cgacaaccac tacttcggct acagcacccc ttgggggtat 180

tttgatttca acagattcca ctgccatttc tcaccacgtg actggcagcg actcatcaac 240

aacaactggg gattc 255

<210> 120
<211> 2205
<212> DNA
<213> adeno-associated virus serotype, clone A3.1vp1

<400> 120
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaatcaga 60

cagtggtgga agctcaaacc tggcccacca ccgccgaaac ctaaccaaca acaccgggac 120

gacagtaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

caccagctca agcaagggga caacccgtac ctcaaataca accacgcgga cgctgaattt 300

caggagcgtc ttcaagaaga tacgtctttc gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga gggtactcga gcctcttggt ctggttgagg aagctgttaa gacggctcct 420

ggaaaaaaga gacctataga gcagtctcct gcagaaccgg actcttcctc gggcatcggc 480

aaatcaggcc agcagcccgc taagaaaaga ctcaattttg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa ccccccgcag ccccctctgg tgtgggatct 600

aatacaatgg cttcaggcgg tggggcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagttatc 720

accaccagca caagaacctg ggccctcccc acctacaata atcacctcta caagcaaatc 780

tccagcgaat cgggagccac caacgacaac cactacttcg gctacagcac cccctggggg 840

tattttgact ttaacagatt ccactgtcac ttctcaccac gtgactggca gcgactcatc 900

aacaacaact ggggatttag acccaagaaa ctcaatttca agctcttcaa catccaagtc 960

aaggaggtca cgcagaatga tggaaccacg accatcgcca ataaccttac cagcacggtg 1020

caggtcttca cagactctga gtaccagctg ccctacgtcc tcggttcggc tcaccagggc 1080

tgccttccgc cgttcccagc agacgtcttc atgattcctc agtacggcta cttgactctg 1140

aacaatggca gccaagcggt aggacgttct tcattctact gtctagagta ttttccctct 1200

cagatgctga ggacgggaaa caacttcacc ttcagctaca cttttgaaga cgtgcctttc 1260

cacagcagct acgcgcacag ccagagtctg gatcggctga tgaatcctct cattgaccag 1320

tacctgtatt acctgagcaa aactcagggt acaagtggaa caacgcagca atcgagactg 1380

cagttcagcc aagctgggcc tagctccatg gctcagcagg ccaaaaactg gctaccggga 1440

cccagctacc gacagcagcg aatgtctaag acggctaatg acaacaacaa cagtgaattt 1500

gcttggactg cagccaccaa atattacctg aatggaagaa attctctggt caatcccggg 1560

cccccaatgg ccagtcacaa ggacgatgag gaaaagtatt tccccatgca cggaaatctc 1620

atctttggaa aacaaggcac aggaactacc aatgtggaca ttgaatcagt gcttattaca 1680

gacgaagaag aaatcagaac aactaatcct gtggctacag aacaatacgg acaggttgcc 1740

accaaccatc agagtcagaa caccacagct tcctatggaa gtgtggacag ccagggaatc 1800

ttacctggaa tggtgtggca ggaccgcgat gtctatcttc aaggtcccat ttgggccaaa 1860

actcctcaca cggacggaca ctttcatcct tctccgctca tgggaggctt tggactgaaa 1920

caccctcctc cccagatcct gatcaaaaac acacctgtgc cagcgaatcc cgcgaccact 1980

ttcactcctg gaaagtttgc ttcgttcatt acccagtatt ccaccggaca ggtcagcgtg 2040

gaaatagagt gggagctgca gaaagaaaac agcaaacgct ggaacccaga aattcagtac 2100

acctccaact acaacaagtc ggtgaatgtg gagtttaccg tggacgcaaa cggtgtttat 2160

tctgaacccc gccctattgg cactcgttac cttacccgga acttg 2205