FIG. 1A

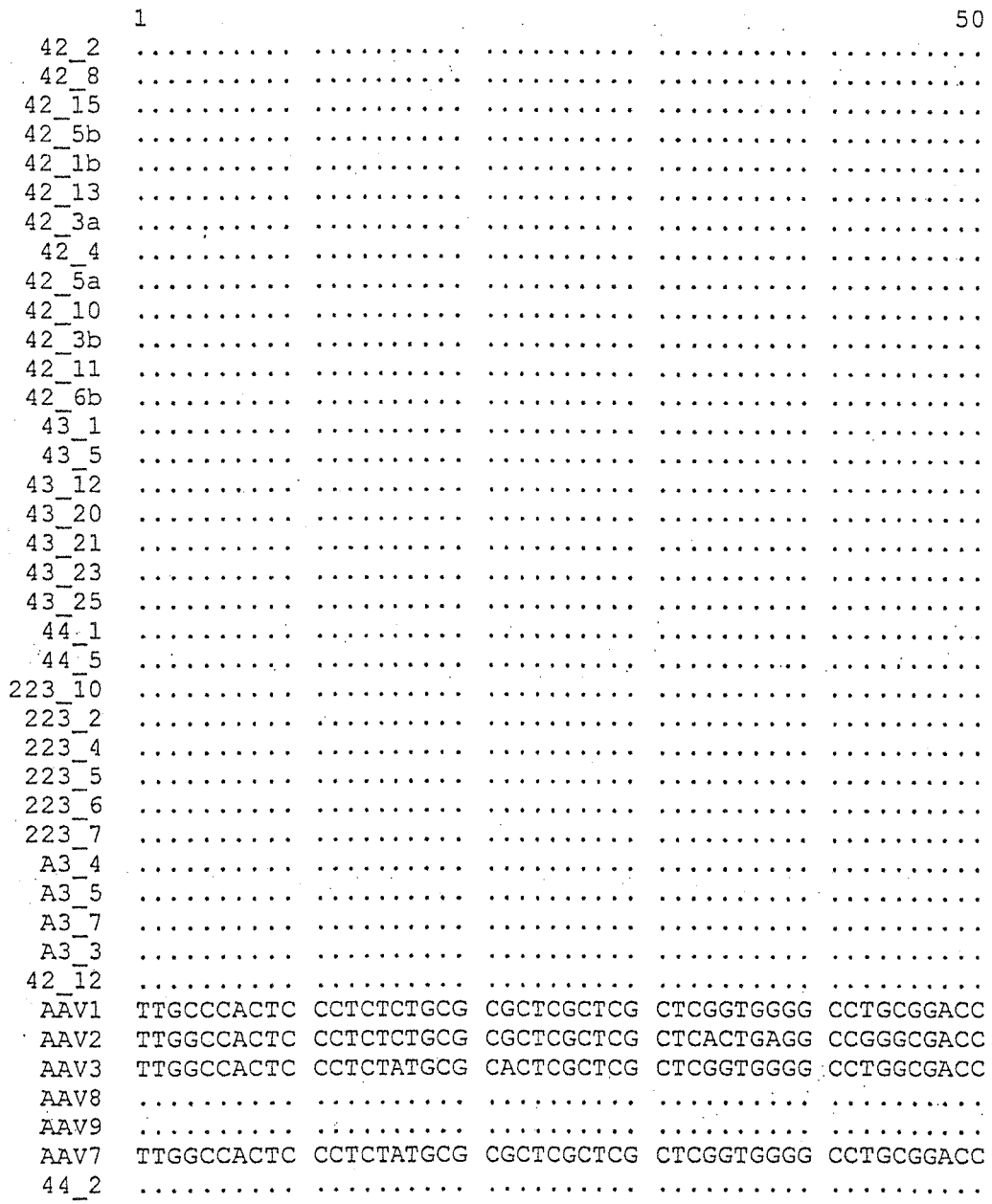

1
50
42_2 ....
42_8 ....
42_15 ....
42_5b ....
42_1b ....
42_13 ....
42_3a ....
42_4 ....
42_5a ....
42_10 ....
42_3b ....
42_11 ....
42_6b ....
43_1 ....
43_5 ....
43_12 ....
43_20 ....
43_21 ....
43_23 ....
43_25 ....
44_1 ....
44_5 ....
223_10 ....
223_2 ....
223_4 ....
223_5 ....
223_6 ....
223_7 ....
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

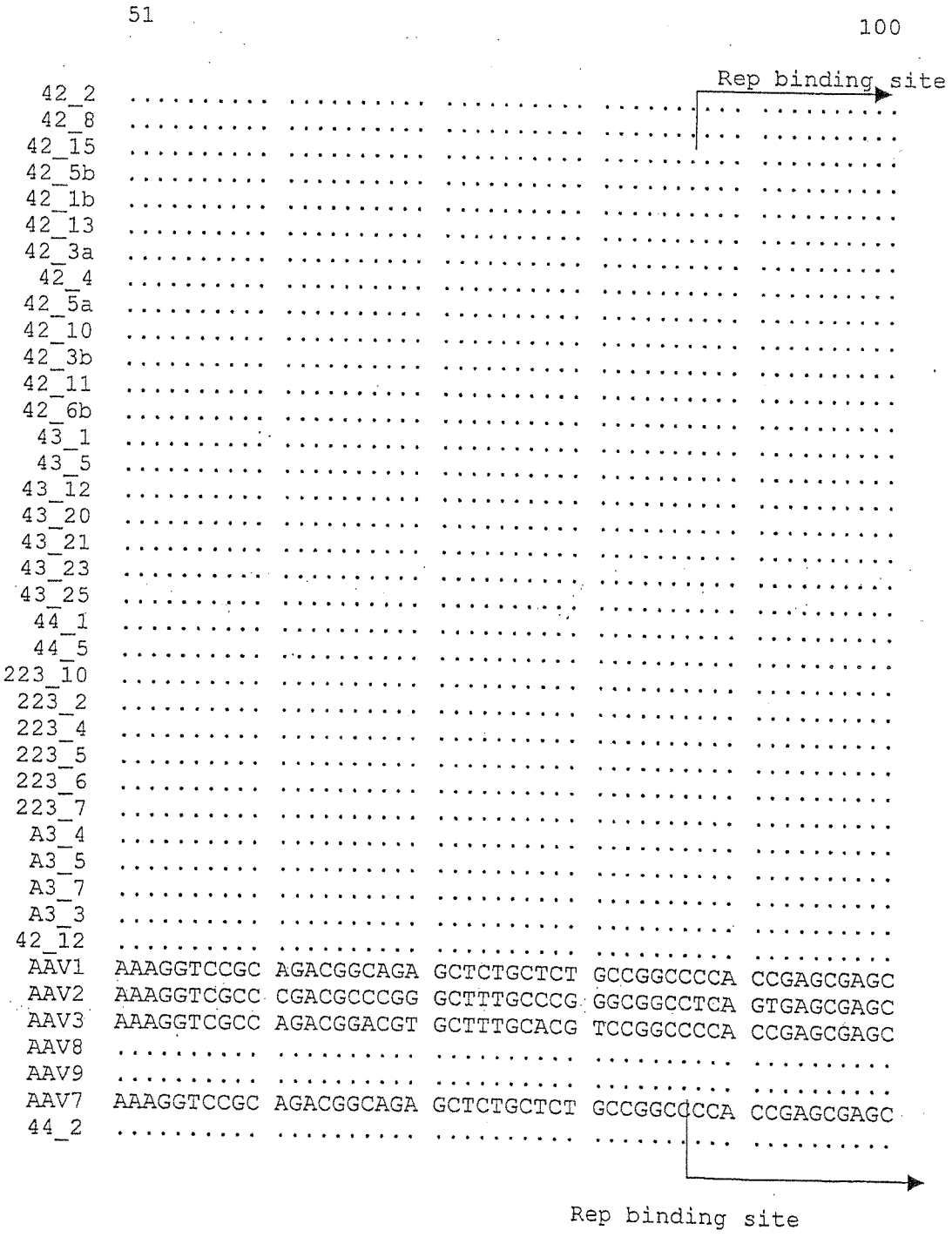

51
100
Rep binding site
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 AAAGGTCCGC AGACGGCAGA GCTCTGCTCT GCCGGCCCCA CCGAGCGAGC
AAV2 AAAGGTCGCC CGACGCCCGG GCTTTGCCCG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

Fig. 1C

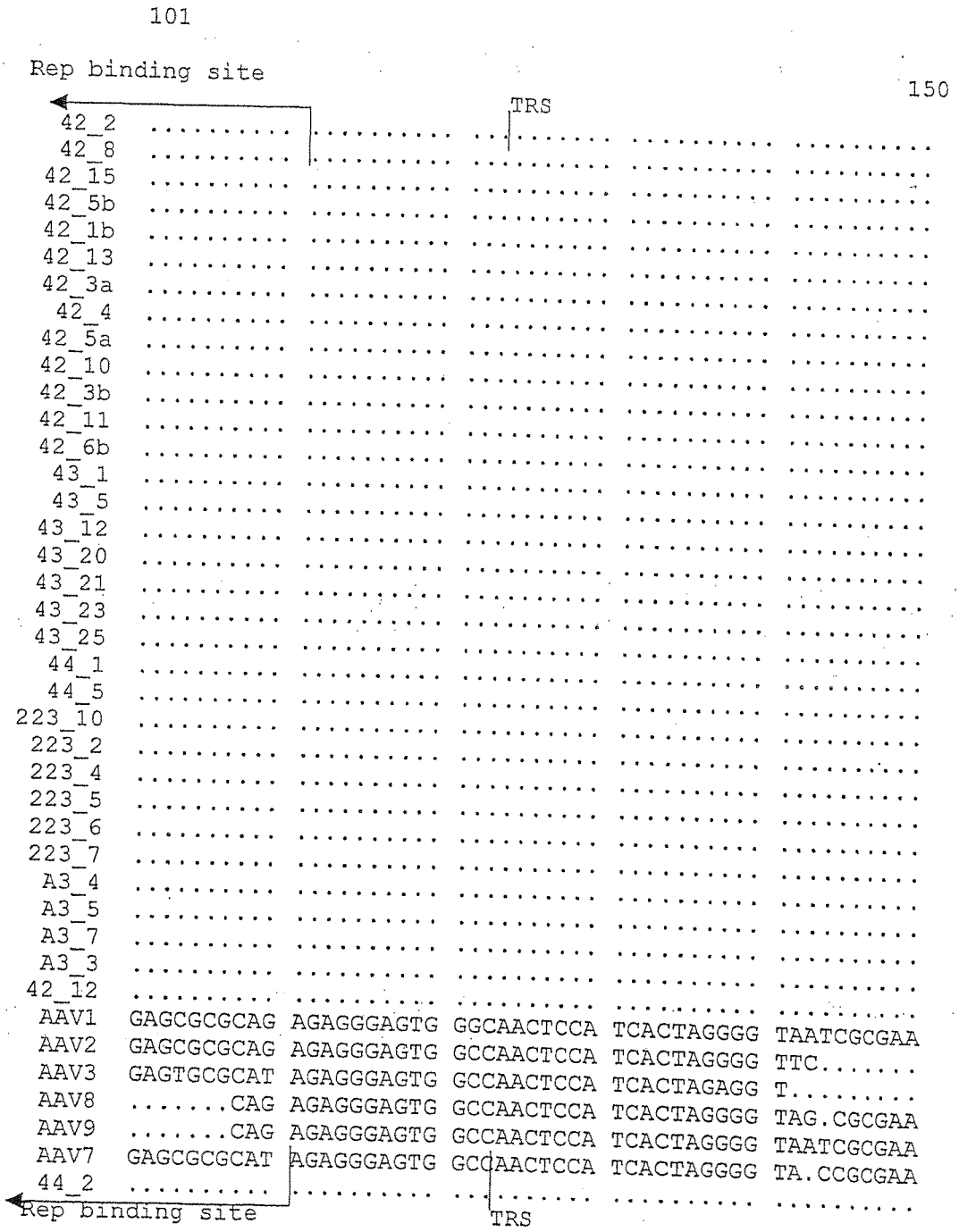

101
Rep binding site
150
TRS
42_2 ....
42_8 ....
42_15 ....
42_5b ....
42_1b ....
42_13 ....
42_3a ....
42_4 ....
42_5a ....
42_10 ....
42_3b ....
42_11 ....
42_6b ....
43_1 ....
43_5 ....
43_12 ....
43_20 ....
43_21 ....
43_23 ....
43_25 ....
44_1 ....
44_5 ....
223_10 ....
223_2 ....
223_4 ....
223_5 ....
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

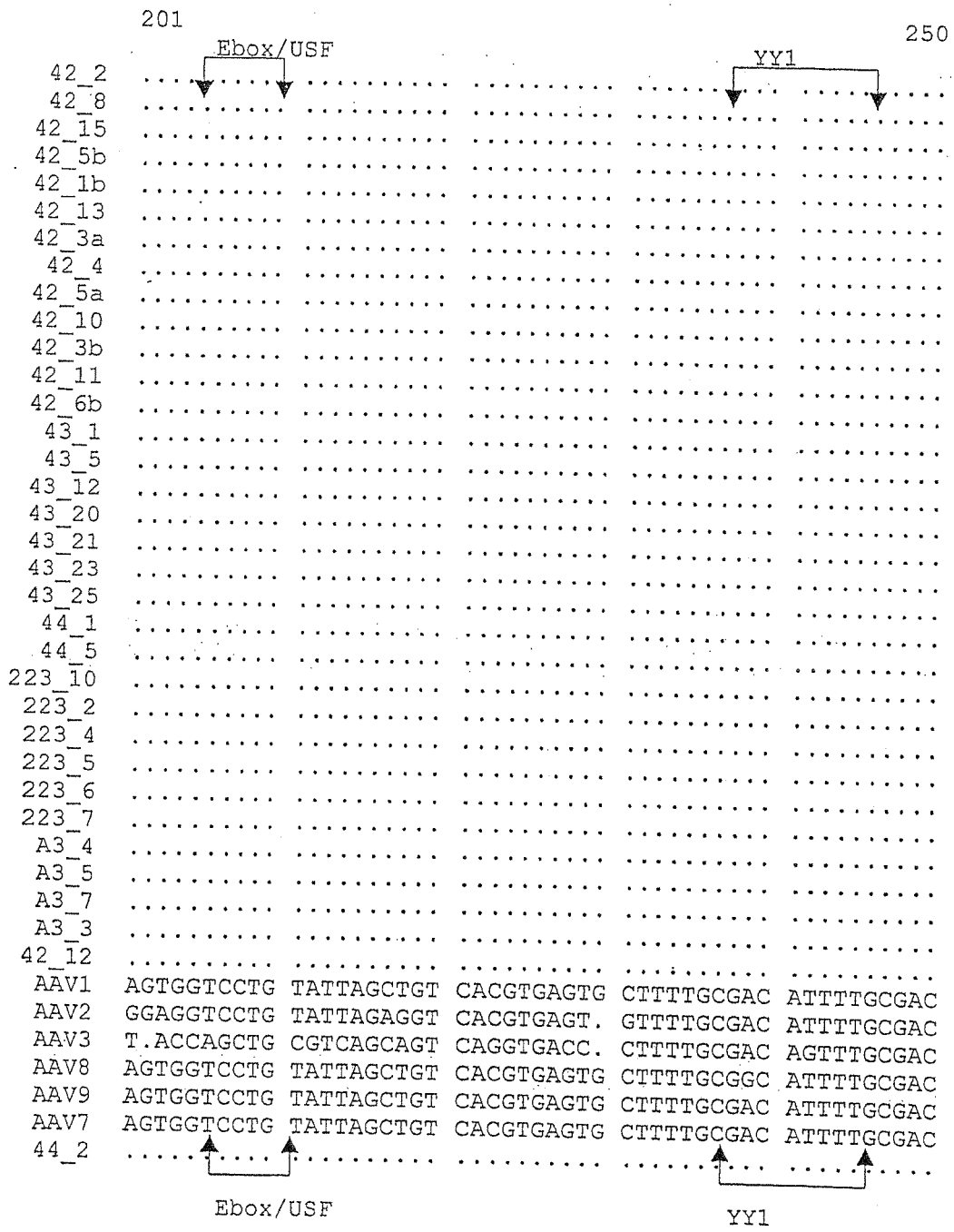

201
250
Ebox/USF
YY1
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 AGTGGTCCTG TATTAGCTGT CACGTGAGTG CTTTTGCGAC ATTTTGCGAC
AAV2 GGAGGTCCTG TATTAGAGGT CACGTGAGT.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

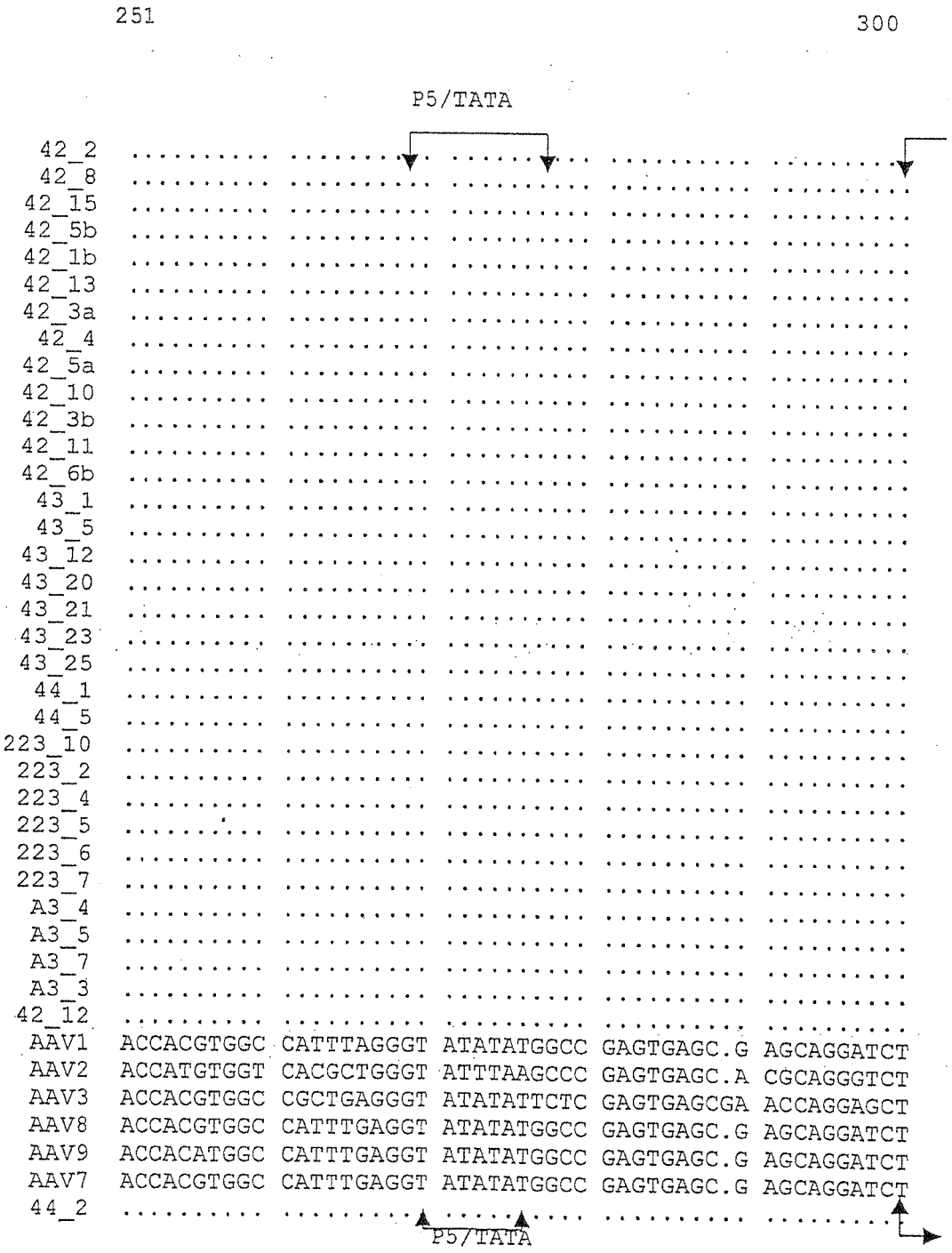

251
300
P5/TATA
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 ACCACGTGGC CATTTAGGGT ATATATGGCC GAGTGAGC.G AGCAGGATCT
AAV2 ACCATGTGGT CACGCTGGGT ATTTAAGCCC 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

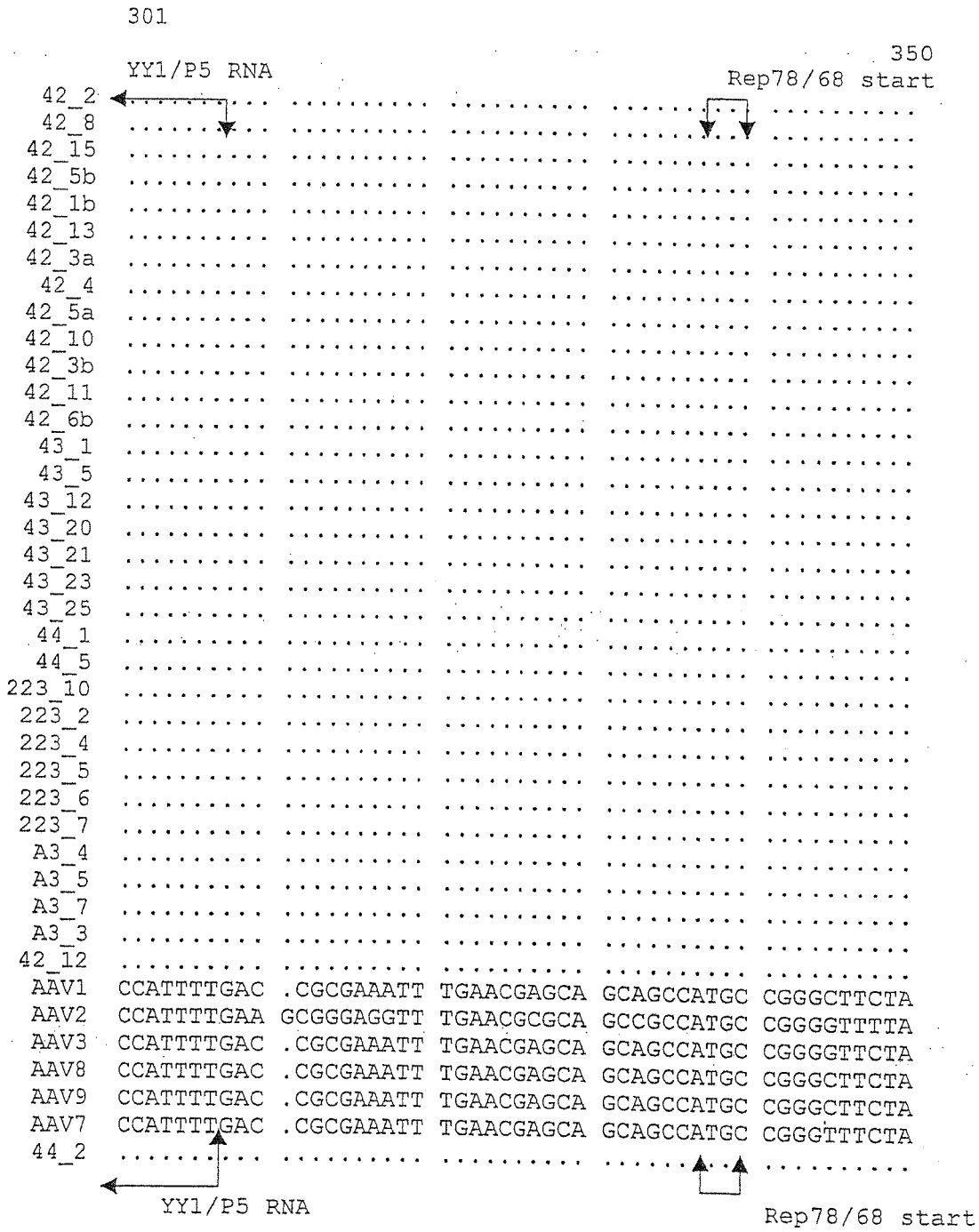

301
350
YY1/P5 RNA
Rep78/68 start
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 CCATTTTGAC .CGCGAAATT TGAACGAGCA GCAGCCATGC CGGGCTTCTA
AAV2 CCATTTTGAA GCGGGAGGTT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

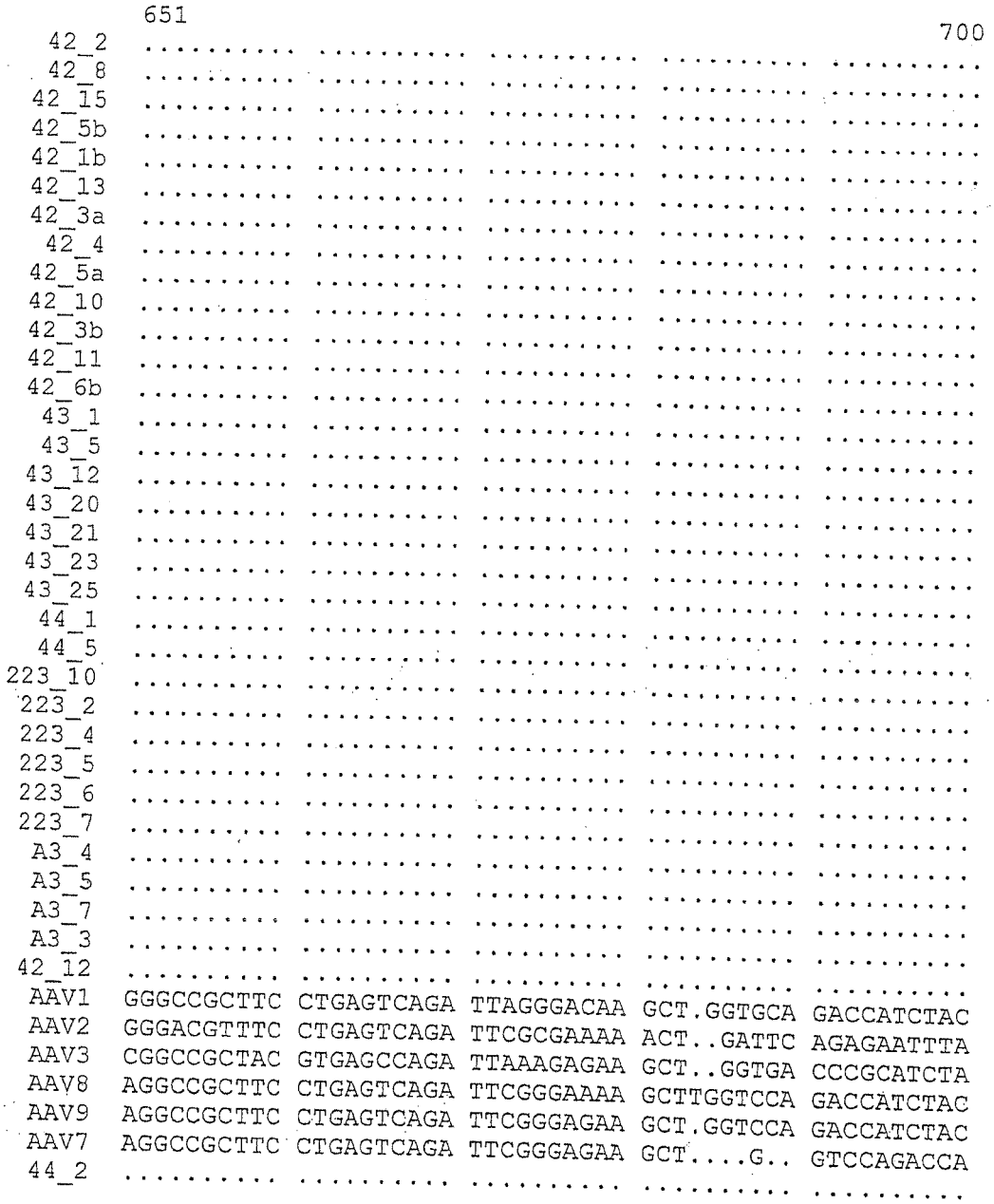

651
700
42_2 ....
42_8 ....
42_15 ....
42_5b ....
42_1b ....
42_13 ....
42_3a ....
42_4 ....
42_5a ....
42_10 ....
42_3b ....
42_11 ....
42_6b ....
43_1 ....
43_5 ....
43_12 ....
43_20 ....
43_21 ....
43_23 ....
43_25 ....
44_1 ....
44_5 ....
223_10 ....
223_2 ....
223_4 ....
223_5 ....
223_6 ....
223_7 ....
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 GACCAA.GAC
  AAV3    CCGCGGGGTC GAGCCG.CAG CTTCCGAACT GGTTCGCGGT CACAAA...G
  AAV8    CCGCGGGGTC GAGCCCCACC TTGCCCAACT GGTTCGCGGT GACCAA...A
  AAV9    C.GCGGGATC GAGCCG.ACC CTGCCCAACT GGTTCGCGGT GACCAAAGAC
  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

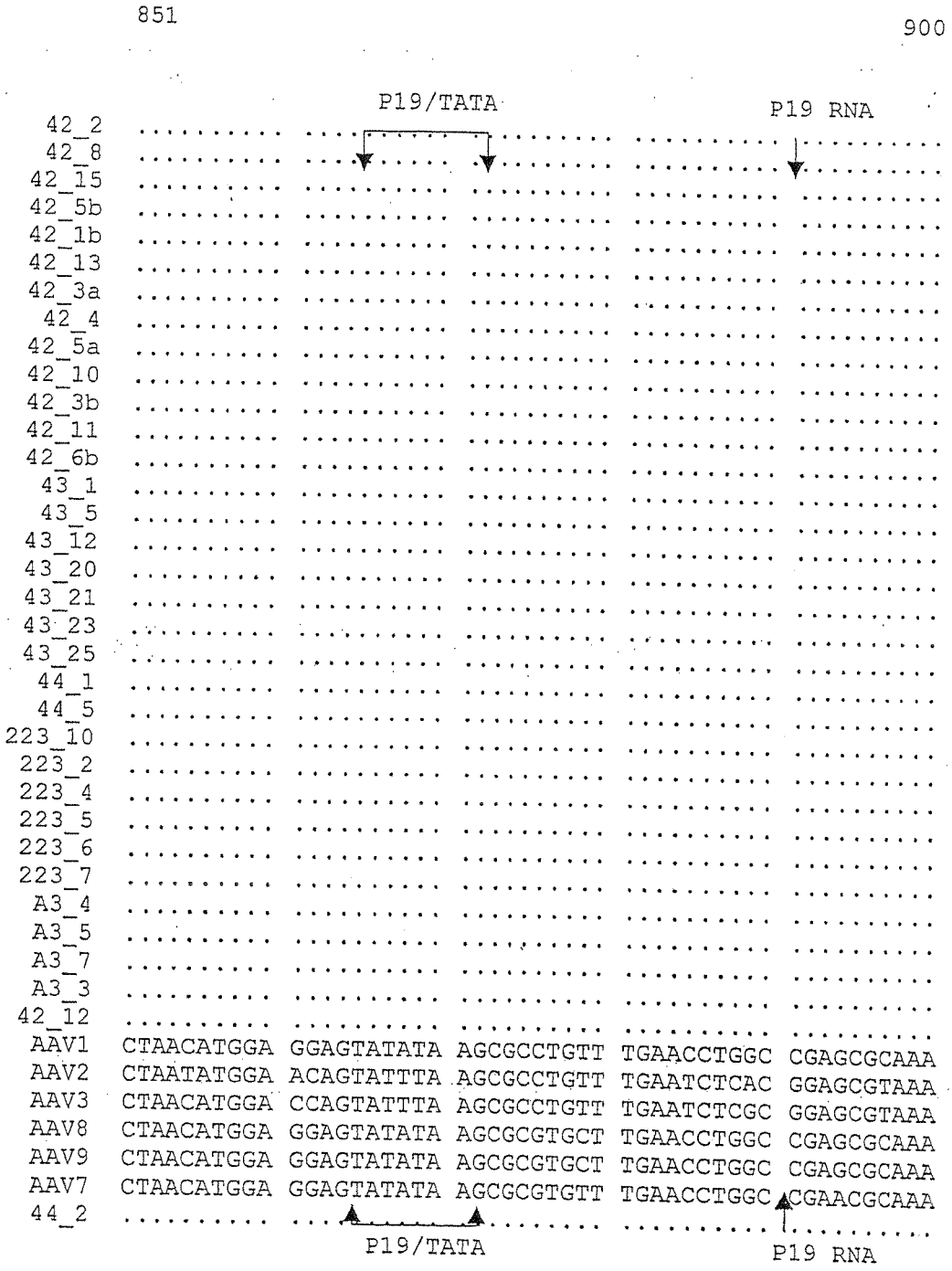

851
900
P19/TATA
P19 RNA
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 CTAACATGGA GGAGTATATA AGCGCCTGTT TGAACCTGGC CGAGCGCAAA
AAV2 CTAATATGGA ACAGTATTTA AGCGCCTGTT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

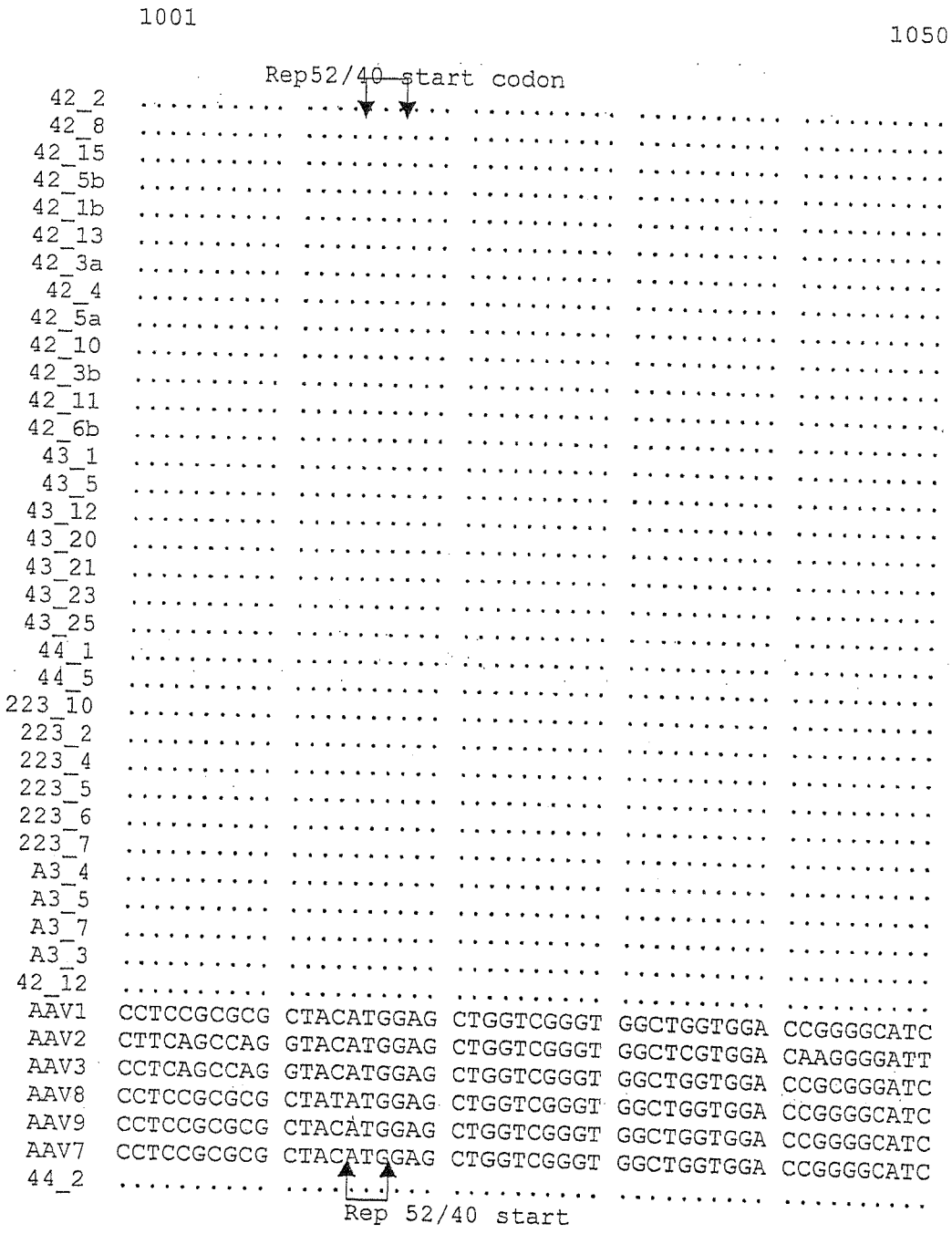

1001
1050
Rep52/40 start codon
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 CCTCCGCGCG CTACATGGAG CTGGTCGGGT GGCTGGTGGA CCGGGGCATC
AAV2 CTTCAGCCAG GTACATGGAG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

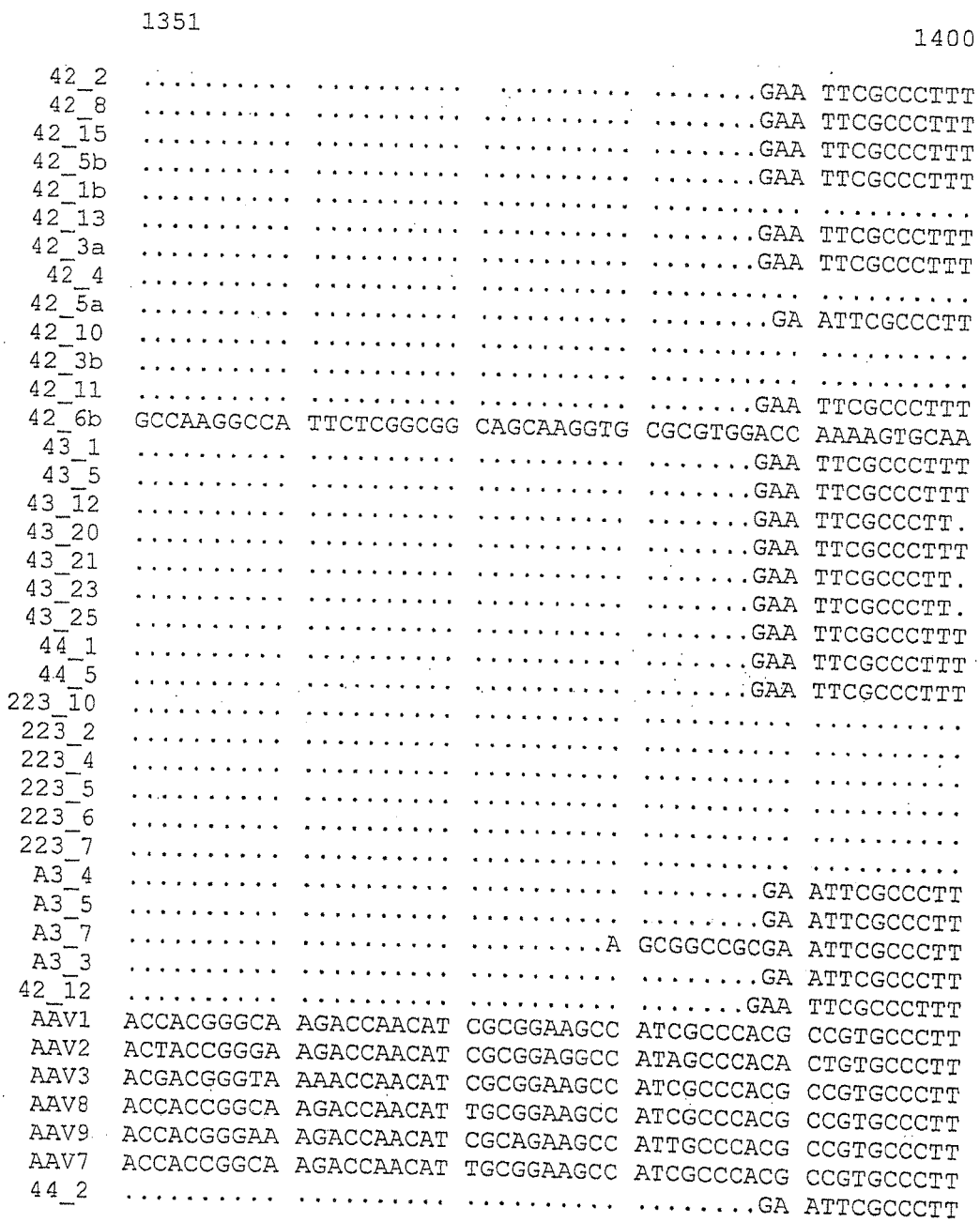

1351
1400
42_2 ....GAA TTCGCCCTTT
42_8 ....GAA TTCGCCCTTT
42_15 ....GAA TTCGCCCTTT
42_5b ....GAA TTCGCCCTTT
42_1b ....
42_13 ....GAA TTCGCCCTTT
42_3a ....GAA TTCGCCCTTT
42_4 ....
42_5a ....GA ATTCGCCCTT
42_10 ....
42_3b ....
42_11 ....GAA TTCGCCCTTT
42_6b GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC AAAAGTGCAA
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 CAACGATTGC
 AAV2    .CTACGGGTG CGTAAACTGG ACCAATGAGA ACTTTCCCTT CAATGATTGC
 AAV3    .CTACGGCTG CGTAAACTGG ACCAATGAGA ACTTTCCCTT CAACGACTGT
 AAV8    .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC
 AAV9    .CTACGGCTG CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAATGATTGC
 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 GGGAACAGCA CCACCTTCGA
 43_21    TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCG 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

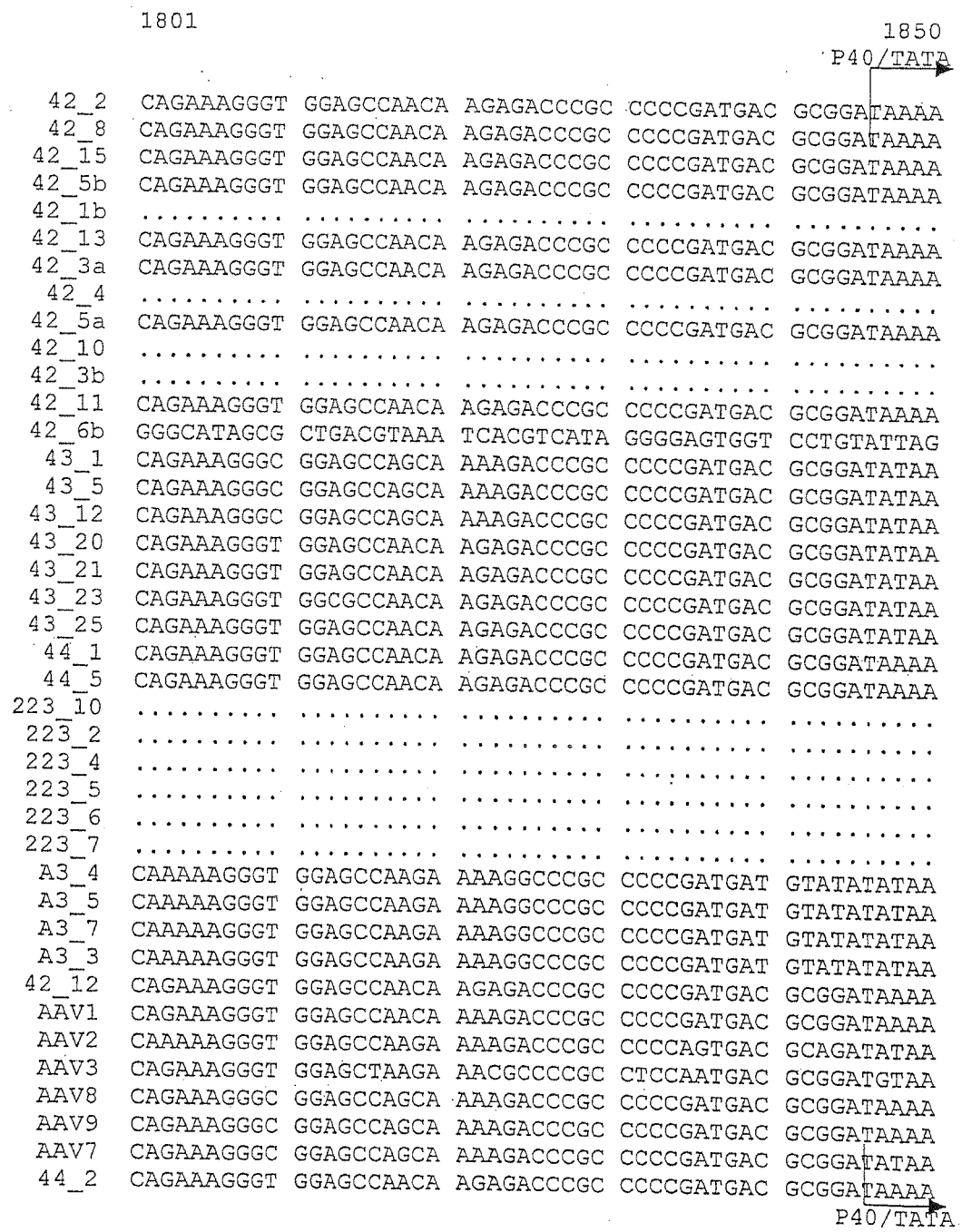

1801
1850
P40/TATA
42_2 CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATAAAA
42_8 CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATAAAA
42_15 CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATAAAA
42_5b CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATAAAA
42_1b ....
42_13 CAGAAAGGGT GGAGCCAACA AGAGACCCGC 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 GCGGATATAA
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 GACATGCGAG
 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 ACGCACGGGC AAAAAGACTG
 AAV1     AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCACGGGA CCAGAGACTG
 AAV2     AGAATGAATC AGAATTCAAA TATCTGCTTC ACGCACGGGA CGAGAGACTG
 AAV3     AGAATGAATC AAATTTCCAA TGTCTGTTTT ACTCACGGAC AGAAAGACTG
 AAV8     AGAATGAATC AGAATTTCAA CATTTGCTTC ACGCATGGTC AAAGAGACTG
 AAV9     AGAATGAATC AGAATTTCAA CATTTGCTTC ACACACGGGG TCAGAGACTG
 AAV7     AGAATGAATC AGAATTTCAA CATTTGCTTC ACACACGGGG TCAGAGACTG
 44_2     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

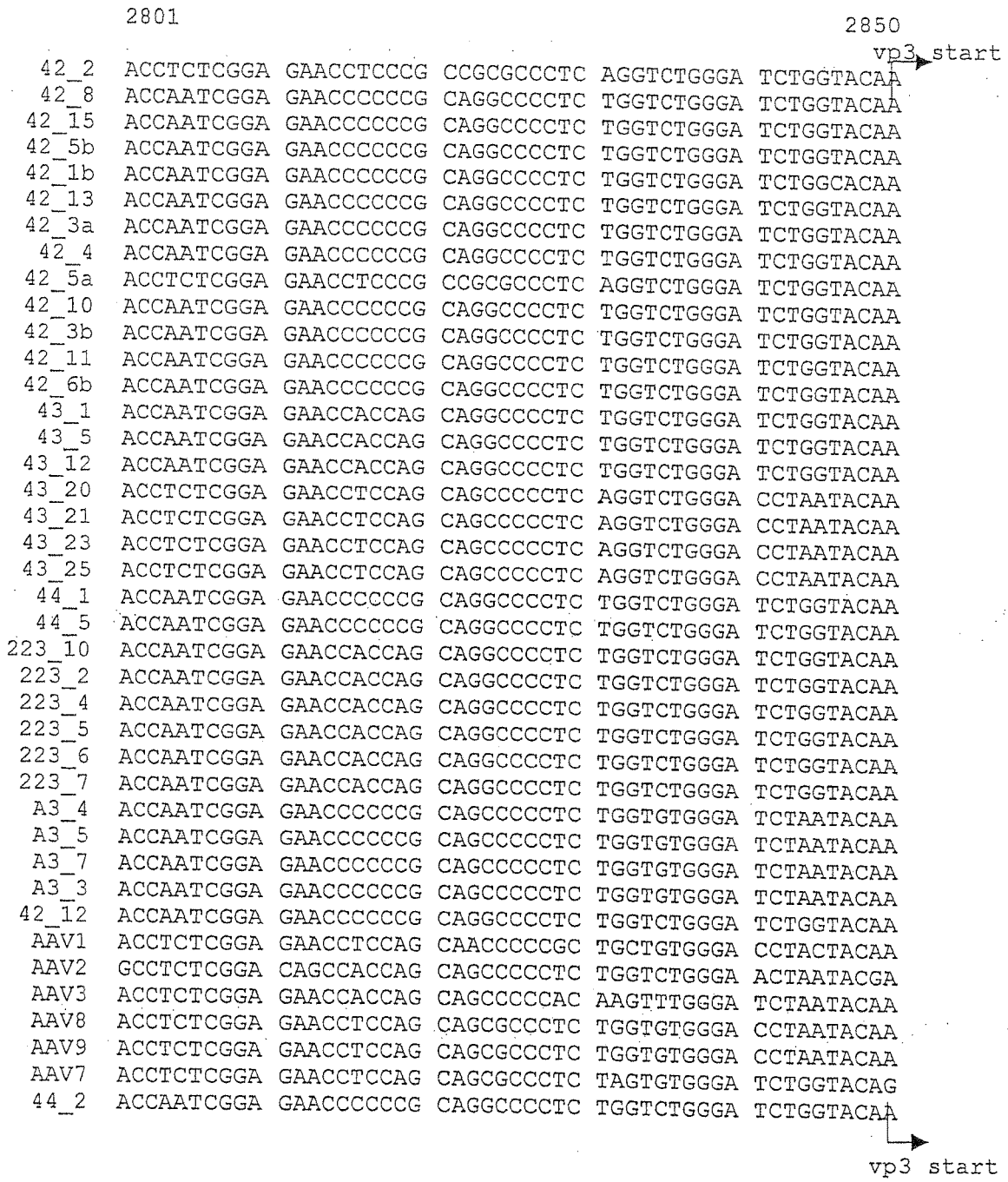

2801
2850
vp3 start
42_2 ACCTCTCGGA GAACCTCCCG CCGCGCCCTC AGGTCTGGGA TCTGGTACAA
42_8 ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
42_15 ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
42_5b ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
42_1b ACCAATCGGA GAACCCCCCG CAGGCCCCTC 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

```
          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 ACAATGGAAG
  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

```
          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

```
          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 TGAATGGCAG AGACTCTCTG
 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 TGAATGGTAG AAATTCATTA
  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 AAATTCATTG
 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 AAGAGCGATT
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 AGGACCAGTT
 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 AAGAGCGATT
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 AGGAACGCTT
 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 AAGAAAAGTT
 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    .......... .......... ....
```

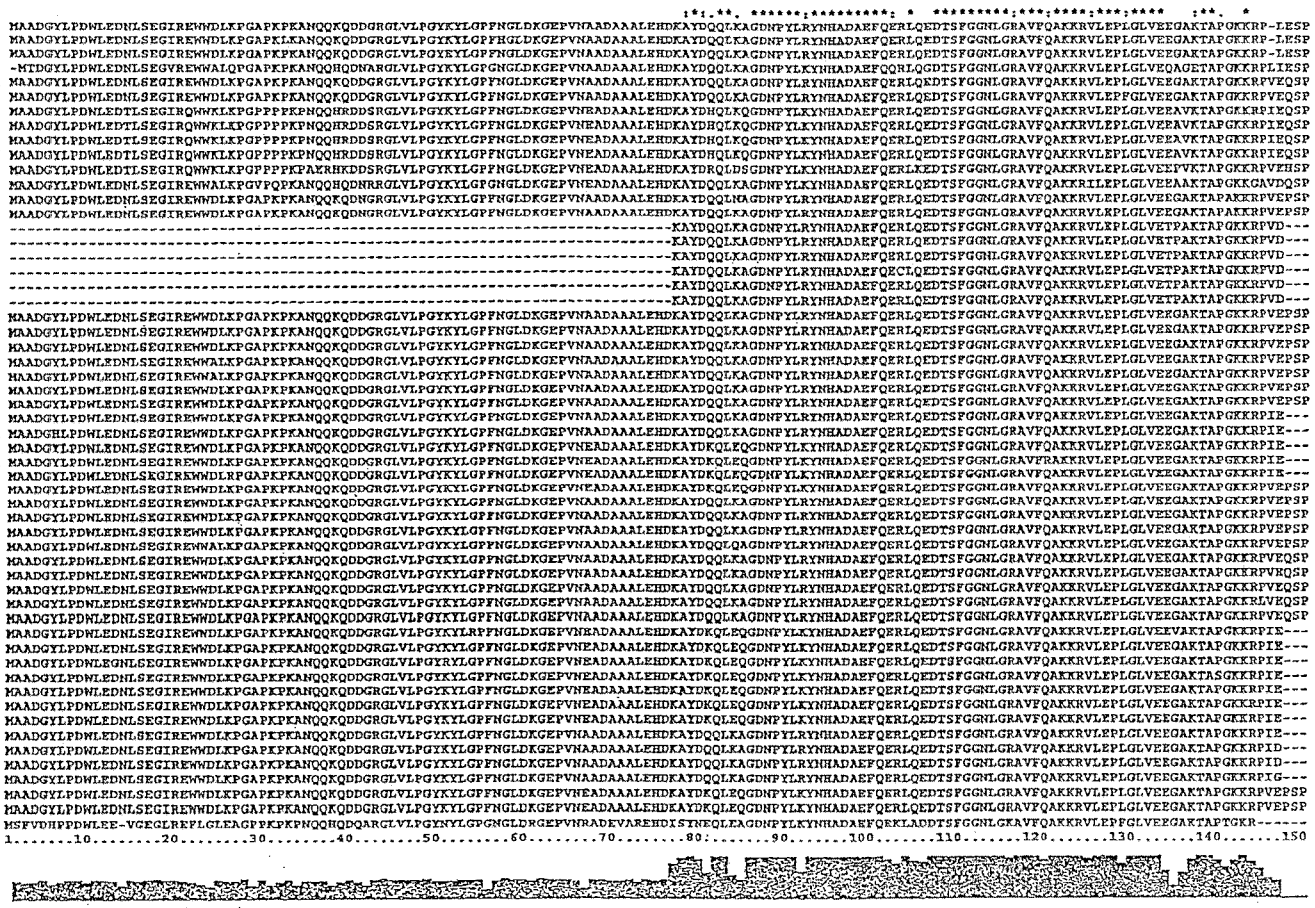
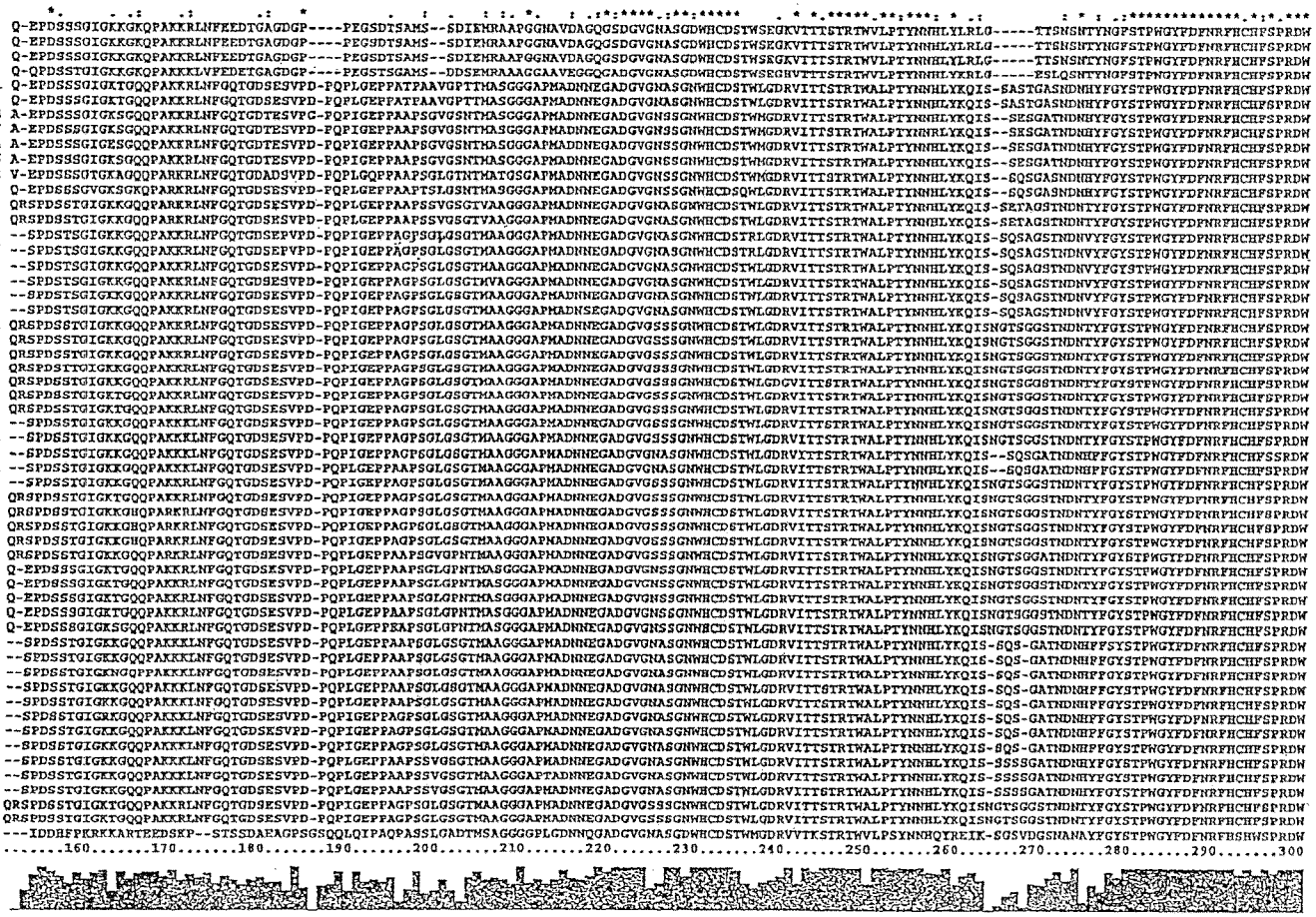


Fig. 2A



98/105

Fig. 2B

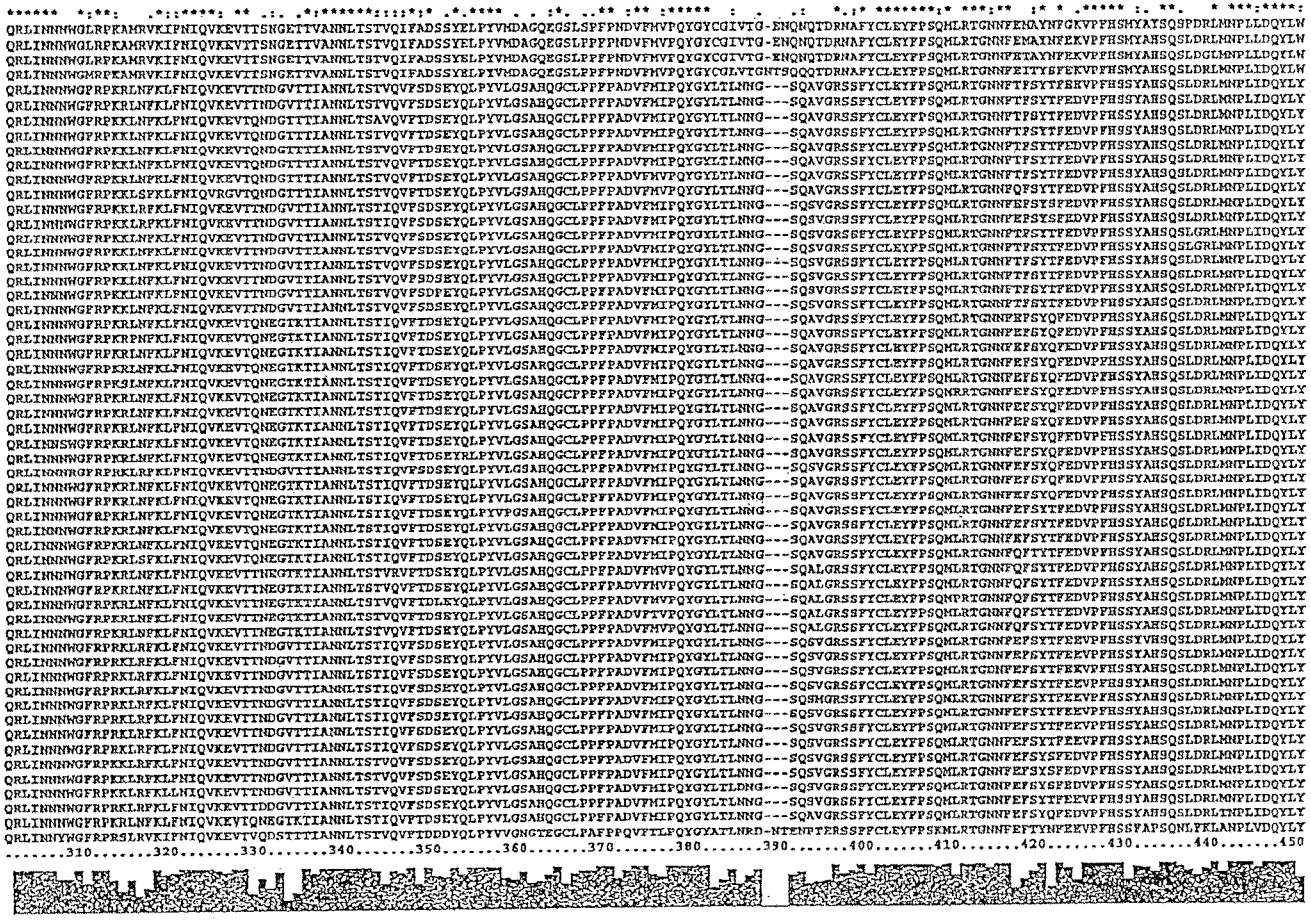


Fig. 2C

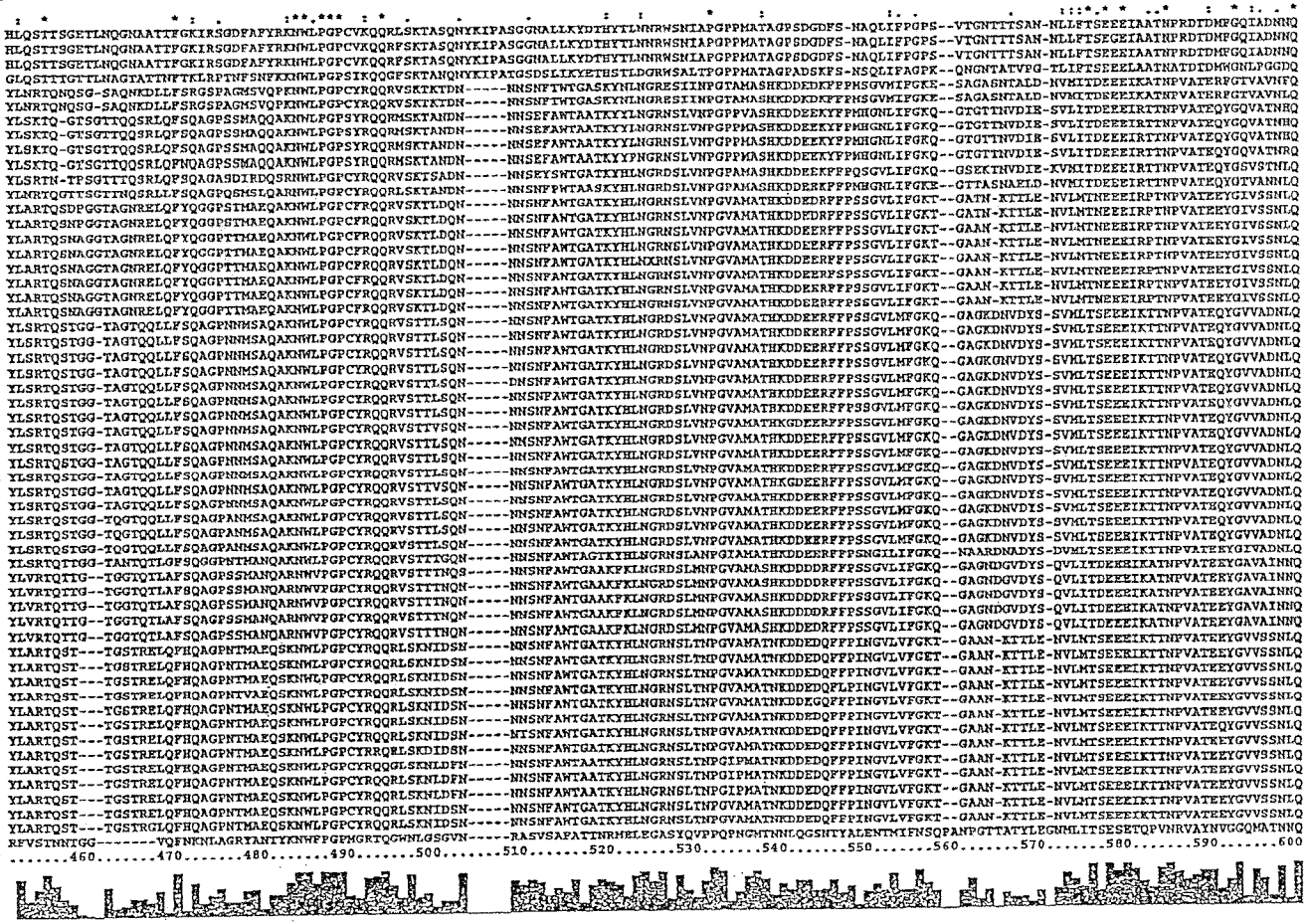


Fig. 2D

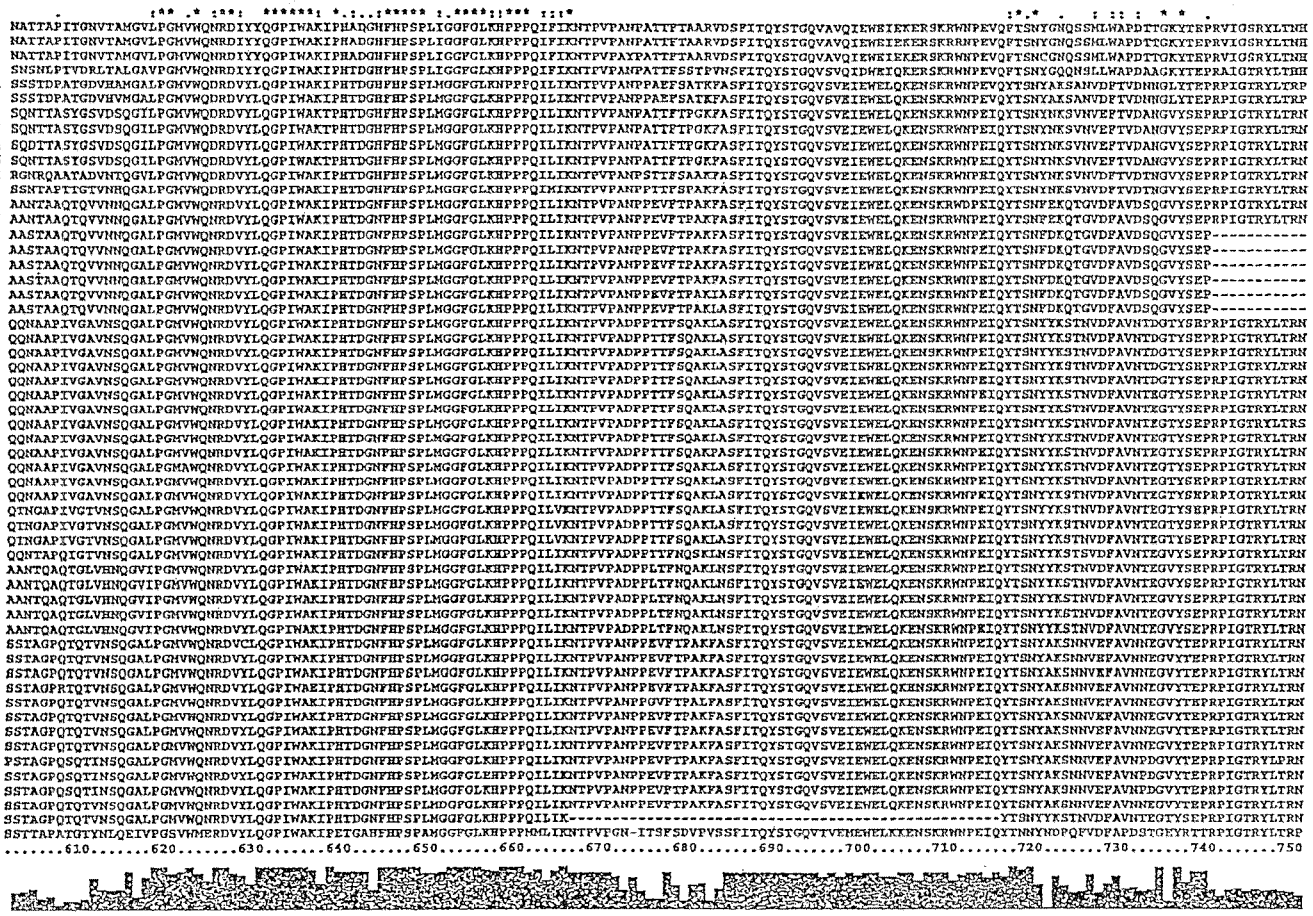

C1VP1
C2VP1
C5VP1@2
AAV4VP1
AAV1
AAV6VP1
A3_3
A3_7
A3_4
A3_5
AAV2
AAV3
3.3bVP1
AAV7
223_4
223_5
223_10
223_2
223_7
223_6
44_1
44_5
44_2
29.3VP1
29.5VP1
42_15
42_8
42_13
42_3A
41_4
42_5A
42_1B
42_5B
43_1
43_12
43_5
AAV8
43_21
43_25
43_23
43_20
AAV_9
24_1
42.2REAL
7.2VP1
27.3VP1
16.3VP1
42_10
42_3B
42_11
F1VP1
F5VP1@3
F3VP1
42_6B
42_12
AAV5CAP
ruler
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750

Fig. 2E

Fig. 2F

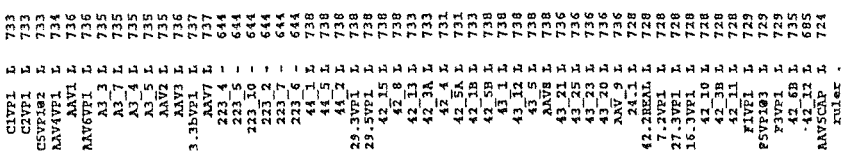

C1VP1 L 733
C2VP1 L 733
C5VP1#2 L 733
AAV4VP1 L 734
AAV1 L 736
AAV6VP1 L 736
A3_3 L 735
A3_7 L 735
A3_4 L 735
A3_5 L 735
AAV2 L 735
AAV3 L 736
3.3bVP1 L 737
AAV7 L 737
223_4 - 644
223_5 - 644
223_10 - 644
223_2 - 644
223_7 - 644
223_6 - 644
44_1 L 738
44_5 L 738
44_2 L 738
29.3VP1 L 738
29.5VP1 L 738
42_15 L 738
42_8 L 738
42_13 L 733
42_3A L 733
42_4 L 731
42_5A L 731
42_1B L 733
42_5B L 738
43_1 L 738
43_12 L 738
43_5 L 738
AAV8 L 738
43_21 L 736
43_25 L 736
43_23 L 736
43_20 L 736
AAV_9 L 736
24_1 L 728
42.2BRAL L 728
7.2VP1 L 728
27.3VP1 L 728
16.3VP1 L 728
42_10 L 728
42_3B L 728
42_11 L 728
KIVP1 L 729
PSVP1#3 L 729
P3VP1 L 729
42_6B L 735
42_12 L 695
AAV5CAP L 724
Point -

Fig. 3A

```
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1               5                  10                  15

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
    210                 215                 220
```

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
    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
                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
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
                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
        515                 520                 525

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
        595                 600                 605

Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
    610                 615                 620
```

SEQUENCE LISTING

<110> The Trustees of The University of Pennsylvania

<120> A Method of Detecting and/or Identifying Adeno-Associated Virus (AAV) Sequences and Isolating Novel Sequences Identified Thereby

<130> SP6203B

<150> US 60/350,607
<151> 2001-11-13

<150> US 60/341,117
<151> 2001-12-17

<150> US 60/377,066
<151> 2002-05-01

<150> US 60/386,675
<151> 2002-06-05

<160> 120

<170> PatentIn version 3.1

<210> 1
<211> 4721
<212> DNA
<213> adeno-associated virus serotype 7

<400> 1
ttggccactc cctctatgcg cgctcgctcg ctcggtgggg cctgcggacc aaaggtccgc 60

agacggcaga gctctgctct gccggcccca ccgagcgagc gagcgcgcat agagggagtg 120

gccaactcca tcactagggg taccgcgaag cgcctcccac gctgccgcgt cagcgctgac 180

gtaaatcacg tcatagggga gtggtcctgt attagctgtc acgtgagtgc ttttgcgaca 240

ttttgcgaca ccacgtggcc atttgaggta tatatggccg agtgagcgag caggatctcc 300

attttgaccg cgaaatttga acgagcagca gccatgccgg gtttctacga gatcgtgatc 360

aaggtgccga gcgacctgga cgagcacctg ccgggcattt ctgactcgtt tgtgaactgg 420

gtggccgaga aggaatggga gctgcccccg gattctgaca tggatctgaa tctgatcgag 480

caggcacccc tgaccgtggc cgagaagctg cagcgcgact tcctggtcca atggcgccgc 540

gtgagtaagg ccccggaggc cctgttcttt gttcagttcg agaagggcga gagctacttc 600

caccttcacg ttctggtgga gaccacgggg gtcaagtcca tggtgctagg ccgcttcctg 660

agtcagattc gggagaagct ggtccagacc atctaccgcg gggtcgagcc cacgctgccc 720

aactggttcg cggtgaccaa gacgcgtaat ggcgccggcg gggggaacaa ggtggtggac 780

gagtgctaca tccccaacta cctcctgccc aagacccagc ccgagctgca gtgggcgtgg 840

actaacatgg aggagtatat aagcgcgtgt ttgaacctgg ccgaacgcaa acggctcgtg 900

gcgcagcacc tgacccacgt cagccagacg caggagcaga acaaggagaa tctgaacccc 960
aattctgacg cgcccgtgat caggtcaaaa acctccgcgc gctacatgga gctggtcggg 1020
tggctggtgg accggggcat cacctccgag aagcagtgga tccaggagga ccaggcctcg 1080
tacatctcct tcaacgccgc ctccaactcg cggtcccaga tcaaggccgc gctggacaat 1140
gccggcaaga tcatggcgct gaccaaatcc gcgcccgact acctggtggg gccctcgctg 1200
cccgcggaca ttaaaaccaa ccgcatctac cgcatcctgg agctgaacgg gtacgatcct 1260
gcctacgccg gctccgtctt tctcggctgg gcccagaaaa agttcgggaa gcgcaacacc 1320
atctggctgt ttgggcccgc caccaccggc aagaccaaca ttgcggaagc catcgcccac 1380
gccgtgccct tctacggctg cgtcaactgg accaatgaga actttccctt caacgattgc 1440
gtcgacaaga tggtgatctg gtgggaggag ggcaagatga cggccaaggt cgtggagtcc 1500
gccaaggcca ttctcggcgg cagcaaggtg cgcgtggacc aaaagtgcaa gtcgtccgcc 1560
cagatcgacc ccaccccccgt gatcgtcacc tccaacacca acatgtgcgc cgtgattgac 1620
gggaacagca ccaccttcga gcaccagcag ccgttgcagg accggatgtt caaatttgaa 1680
ctcacccgcc gtctggagca cgactttggc aaggtgacga agcaggaagt caaagagttc 1740
ttccgctggg ccagtgatca cgtgaccgag gtggcgcatg agttctacgt cagaaagggc 1800
ggagccagca aaagacccgc ccccgatgac gcggatataa gcgagcccaa gcgggcctgc 1860
ccctcagtcg cggatccatc gacgtcagac gcggaaggag ctccggtgga ctttgccgac 1920
aggtaccaaa acaaatgttc tcgtcacgcg ggcatgattc agatgctgtt tccctgcaaa 1980
acgtgcgaga gaatgaatca gaatttcaac atttgcttca cacacggggt cagagactgt 2040
ttagagtgtt tccccggcgt gtcagaatct caaccggtcg tcagaaaaaa gacgtatcgg 2100
aaactctgcg cgattcatca tctgctgggg cgggcgcccg agattgcttg ctcggcctgc 2160
gacctggtca acgtggacct ggacgactgc gtttctgagc aataaatgac ttaaaccagg 2220
tatggctgcc gatggttatc ttccagattg gctcgaggac aacctctctg agggcattcg 2280
cgagtggtgg gacctgaaac ctggagcccc gaaacccaaa gccaaccagc aaaagcagga 2340
caacggccgg ggtctggtgc ttcctggcta caagtacctc ggacccttca acggactcga 2400
caaggggggag cccgtcaacg cggcggacgc agcggccctc gagcacgaca aggcctacga 2460
ccagcagctc aaagcgggtg acaatccgta cctgcggtat aaccacgccg acgccgagtt 2520
tcaggagcgt ctgcaagaag atacgtcatt tgggggcaac ctcgggcgag cagtcttcca 2580
ggccaagaag cgggttctcg aacctctcgg tctggttgag gaaggcgcta agacggctcc 2640
tgcaaagaag agaccggtag agccgtcacc tcagcgttcc cccgactcct ccacgggcat 2700
cggcaagaaa ggccagcagc ccgccagaaa gagactcaat ttcggtcaga ctggcgactc 2760
agagtcagtc cccgaccctc aacctctcgg agaacctcca gcagcgccct ctagtgtggg 2820

atctggtaca gtggctgcag gcggtggcgc accaatggca gacaataacg aaggtgccga 2880

cggagtgggt aatgcctcag gaaattggca ttgcgattcc acatggctgg gcgacagagt 2940

cattaccacc agcacccgaa cctgggccct gcccacctac aacaaccacc tctacaagca 3000

aatctccagt gaaactgcag gtagtaccaa cgacaacacc tacttcggct acagcacccc 3060

ctgggggtat tttgacttta acagattcca ctgccacttc tcaccacgtg actggcagcg 3120

actcatcaac aacaactggg gattccggcc caagaagctg cggttcaagc tcttcaacat 3180

ccaggtcaag gaggtcacga cgaatgacgg cgttacgacc atcgctaata accttaccag 3240

cacgattcag gtattctcgg actcggaata ccagctgccg tacgtcctcg gctctgcgca 3300

ccagggctgc ctgcctccgt tcccggcgga cgtcttcatg attcctcagt acggctacct 3360

gactctcaac aatggcagtc agtctgtggg acgttcctcc ttctactgcc tggagtactt 3420

cccctctcag atgctgagaa cgggcaacaa ctttgagttc agctacagct tcgaggacgt 3480

gcctttccac agcagctacg cacacagcca gagcctggac cggctgatga atcccctcat 3540

cgaccagtac ttgtactacc tggccagaac acagagtaac ccaggaggca cagctggcaa 3600

tcgggaactg cagttttacc agggcgggcc ttcaactatg gccgaacaag ccaagaattg 3660

gttacctgga ccttgcttcc ggcaacaaag agtctccaaa acgctggatc aaaacaacaa 3720

cagcaacttt gcttggactg gtgccaccaa atatcacctg aacggcagaa actcgttggt 3780

taatcccggc gtcgccatgg caactcacaa ggacgacgag gaccgctttt tcccatccag 3840

cggagtcctg atttttggaa aaactggagc aactaacaaa actacattgg aaaatgtgtt 3900

aatgacaaat gaagaagaaa ttcgtcctac taatcctgta gccacggaag aatacgggat 3960

agtcagcagc aacttacaag cggctaatac tgcagcccag acacaagttg tcaacaacca 4020

gggagccttа cctggcatgg tctggcagaa ccgggacgtg tacctgcagg gtcccatctg 4080

ggccaagatt cctcacacgg atggcaactt tcacccgtct cctttgatgg gcggctttgg 4140

acttaaacat ccgcctcctc agatcctgat caagaacact cccgttcccg ctaatcctcc 4200

ggaggtgttt actcctgcca agtttgcttc gttcatcaca cagtacagca ccggacaagt 4260

cagcgtggaa atcgagtggg agctgcagaa ggaaaacagc aagcgctgga acccggagat 4320

tcagtacacc tccaactttg aaaagcagac tggtgtggac tttgccgttg acagccaggg 4380

tgtttactct gagcctcgcc ctattggcac tcgttacctc acccgtaatc tgtaattgca 4440

tgttaatcaa taaaccggtt gattcgtttc agttgaactt tggtctcctg tgcttcttat 4500

cttatcggtt tccatagcaa ctggttacac attaactgct tgggtgcgct tcacgataag 4560

aacactgacg tcaccgcggt acccctagtg atggagttgg ccactccctc tatgcgcgct 4620

cgctcgctcg gtggggcctg cggaccaaag gtccgcagac ggcagagctc tgctctgccg 4680

gccccaccga gcgagcgagc gcgcatagag ggagtggcca a 4721

<210> 2
<211> 737
<212> PRT
<213> capsid protein of adeno-associated virus serotpye 7

<400> 2
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 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 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 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
```

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 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
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> 3
<211> 623
<212> PRT
<213> rep protein of adeno-associated virus serotype 7

<400> 3

```
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1               5                  10                  15

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
    210                 215                 220

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
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
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

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
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
515 520 525

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
595 600 605

Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
610 615 620

<210> 4
<211> 4393
<212> DNA
<213> adeno-associated virus serotype 8

<400> 4
cagagaggga gtggccaact ccatcactag gggtagcgcg aagcgcctcc cacgctgccg 60

cgtcagcgct gacgtaaatt acgtcatagg ggagtggtcc tgtattagct gtcacgtgag 120

tgcttttgcg gcattttgcg acaccacgtg gccatttgag gtatatatgg ccgagtgagc 180

gagcaggatc tccattttga ccgcgaaatt tgaacgagca gcagccatgc cgggcttcta 240

cgagatcgtg atcaaggtgc cgagcgacct ggacgagcac ctgccgggca tttctgactc 300

gtttgtgaac tgggtggccg agaaggaatg ggagctgccc ccggattctg acatggatcg 360

gaatctgatc gagcaggcac ccctgaccgt ggccgagaag ctgcagcgcg acttcctggt 420

ccaatggcgc cgcgtgagta aggccccgga ggccctcttc tttgttcagt tcgagaaggg 480

cgagagctac tttcacctgc acgttctggt cgagaccacg ggggtcaagt ccatggtgct 540

aggccgcttc ctgagtcaga ttcgggaaaa gcttggtcca gaccatctac ccgcgggggtc 600

gagccccacc ttgcccaact ggttcgcggt gaccaaagac gcggtaatgg cgccggcggg 660

ggggaacaag gtggtggacg agtgctacat ccccaactac ctcctgccca agactcagcc 720

cgagctgcag tgggcgtgga ctaacatgga ggagtatata agcgcgtgct tgaacctggc 780

cgagcgcaaa cggctcgtgg cgcagcacct gacccacgtc agccagacgc aggagcagaa 840

caaggagaat ctgaacccca attctgacgc gcccgtgatc aggtcaaaaa cctccgcgcg 900

ctatatggag ctggtcgggt ggctggtgga ccggggcatc acctccgaga agcagtggat 960

ccaggaggac caggcctcgt acatctcctt caacgccgcc tccaactcgc ggtcccagat 1020

caaggccgcg ctggacaatg ccggcaagat catggcgctg accaaatccg cgcccgacta 1080

cctggtgggg ccctcgctgc ccgcggacat tacccagaac cgcatctacc gcatcctcgc 1140

tctcaacggc tacgaccctg cctacgccgg ctccgtcttt ctcggctggg ctcagaaaaa 1200

gttcgggaaa cgcaacacca tctggctgtt tggacccgcc accaccggca agaccaacat 1260

tgcggaagcc atcgcccacg ccgtgccctt ctacggctgc gtcaactgga ccaatgagaa 1320

ctttcccttc aatgattgcg tcgacaagat ggtgatctgg tgggaggagg gcaagatgac 1380

ggccaaggtc gtggagtccg ccaaggccat tctcggcggc agcaaggtgc gcgtggacca 1440

aaagtgcaag tcgtccgccc agatcgaccc cacccccgtg atcgtcacct ccaacaccaa 1500

catgtgcgcc gtgattgacg ggaacagcac caccttcgag caccagcagc ctctccagga 1560

ccggatgttt aagttcgaac tcacccgccg tctggagcac gactttggca aggtgacaaa 1620

gcaggaagtc aaagagttct tccgctgggc cagtgatcac gtgaccgagg tggcgcatga 1680

gttttacgtc agaaagggcg gagccagcaa aagacccgcc cccgatgacg cggataaaag 1740

cgagcccaag cgggcctgcc cctcagtcgc ggatccatcg acgtcagacg cggaaggagc 1800

tccggtggac tttgccgaca ggtaccaaaa caaatgttct cgtcacgcgg gcatgcttca 1860

gatgctgttt ccctgcaaaa cgtgcgagag aatgaatcag aatttcaaca tttgcttcac 1920

acacggggtc agagactgct cagagtgttt ccccggcgtg tcagaatctc aaccggtcgt 1980

cagaaagagg acgtatcgga aactctgtgc gattcatcat ctgctggggc gggctcccga 2040

gattgcttgc tcggcctgcg atctggtcaa cgtggacctg gatgactgtg tttctgagca 2100

ataaatgact taaaccaggt atggctgccg atggttatct tccagattgg ctcgaggaca 2160

acctctctga gggcattcgc gagtggtggg cgctgaaacc tggagccccg aagcccaaag 2220

ccaaccagca aaagcaggac gacggccggg gtctggtgct tcctggctac aagtacctcg 2280

gacccttcaa cggactcgac aaggggagc ccgtcaacgc ggcggacgca gcggccctcg 2340

agcacgacaa ggcctacgac cagcagctgc aggcgggtga caatccgtac ctgcggtata 2400

accacgccga cgccgagttt caggagcgtc tgcaagaaga tacgtctttt gggggcaacc 2460

tcgggcgagc agtcttccag gccaagaagc gggttctcga acctctcggt ctggttgagg 2520

aaggcgctaa gacggctcct ggaaagaaga gaccggtaga gccatcaccc cagcgttctc 2580

cagactcctc tacgggcatc ggcaagaaag gccaacagcc cgccagaaaa agactcaatt 2640

ttggtcagac tggcgactca gagtcagttc cagaccctca acctctcgga gaacctccag 2700

cagcgccctc tggtgtggga cctaatacaa tggctgcagg cggtggcgca ccaatggcag 2760

acaataacga aggcgccgac ggagtgggta gttcctcggg aaattggcat tgcgattcca 2820

catggctggg cgacagagtc atcaccacca gcacccgaac ctgggccctg cccacctaca 2880

acaaccacct ctacaagcaa atctccaacg ggacatcggg aggagccacc aacgacaaca 2940

cctacttcgg ctacagcacc ccctgggggt attttgactt taacagattc cactgccact 3000

tttcaccacg tgactggcag cgactcatca acaacaactg gggattccgg cccaagagac 3060

tcagcttcaa gctcttcaac atccaggtca aggaggtcac gcagaatgaa ggcaccaaga 3120

ccatcgccaa taacctcacc agcaccatcc aggtgtttac ggactcggag taccagctgc 3180

cgtacgttct cggctctgcc caccagggct gcctgcctcc gttcccggcg gacgtgttca 3240

tgattcccca gtacggctac ctaacactca acaacggtag tcaggccgtg ggacgctcct 3300

ccttctactg cctggaatac tttccttcgc agatgctgag aaccggcaac aacttccagt 3360

ttacttacac cttcgaggac gtgcctttcc acagcagcta cgcccacagc cagagcttgg 3420

accggctgat gaatcctctg attgaccagt acctgtacta cttgtctcgg actcaaacaa 3480

caggaggcac ggcaaatacg cagactctgg gcttcagcca aggtgggcct aatacaatgg 3540

ccaatcaggc aaagaactgg ctgccaggac cctgttaccg ccaacaacgc gtctcaacga 3600

caaccgggca aaacaacaat agcaactttg cctggactgc tgggaccaaa taccatctga 3660

atggaagaaa ttcattggct aatcctggca tcgctatggc aacacacaaa gacgacgagg 3720

agcgtttttt tcccagtaac gggatcctga tttttggcaa acaaaatgct gccagagaca 3780

atgcggatta cagcgatgtc atgctcacca gcgaggaaga aatcaaaacc actaaccctg 3840

tggctacaga ggaatacggt atcgtggcag ataacttgca gcagcaaaac acggctcctc 3900

aaattggaac tgtcaacagc caggggggct tacccggtat ggtctggcag aaccgggacg 3960

tgtacctgca gggtcccatc tgggccaaga ttcctcacac ggacggcaac ttccacccgt 4020

ctccgctgat gggcggcttt ggcctgaaac atcctccgcc tcagatcctg atcaagaaca 4080

cgcctgtacc tgcggatcct ccgaccacct tcaaccagtc aaagctgaac tctttcatca 4140

cgcaatacag caccggacag gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca 4200

gcaagcgctg gaaccccgag atccagtaca cctccaacta ctacaaatct acaagtgtgg 4260

actttgctgt taatacagaa ggcgtgtact ctgaaccccg ccccattggc acccgttacc 4320

tcacccgtaa tctgtaattg cctgttaatc aataaaccgg ttgattcgtt tcagttgaac 4380

tttggtctct gcg 4393

<210> 5
<211> 4385
<212> DNA
<213> adeno-associated virus serotype 9

<400> 5

cagagaggga gtggccaact ccatcactag gggtaatcgc gaagcgcctc ccacgctgcc 60

gcgtcagcgc tgacgtagat tacgtcatag gggagtggtc ctgtattagc tgtcacgtga 120

gtgcttttgc gacattttgc gacaccacat ggccatttga ggtatatatg gccgagtgag 180

cgagcaggat ctccattttg accgcgaaat ttgaacgagc agcagccatg ccgggcttct 240

acgagattgt gatcaaggtg ccgagcgacc tggacgagca cctgccgggc atttctgact 300

cttttgtgaa ctgggtggcc gagaaggaat gggagctgcc cccggattct gacatggatc 360

ggaatctgat cgagcaggca cccctgaccg tggccgagaa gctgcagcgc gacttcctgg 420

tccaatggcg ccgcgtgagt aaggccccgg aggccctctt ctttgttcag ttcgagaagg 480

gcgagagcta ctttcacctg cacgttctgg tcgagaccac gggggtcaag tccatggtgc 540

taggccgctt cctgagtcag attcgggaga agctggtcca gaccatctac cgcgggatcg 600

agccgaccct gcccaactgg ttcgcggtga ccaagacgcg taatggcgcc ggcgggggga 660

acaaggtggt ggacgagtgc tacatcccca actacctcct gcccaagact cagcccgagc 720

tgcagtgggc gtggactaac atggaggagt atataagcgc gtgcttgaac ctggccgagc 780

gcaaacggct cgtggcgcag cacctgaccc acgtcagcca gacgcaggag cagaacaagg 840

agaatctgaa ccccaattct gacgcgcccg tgatcaggtc aaaaacctcc gcgcgctaca 900

tggagctggt cgggtggctg gtggaccggg gcatcacctc cgagaagcag tggatccagg 960

aggaccaggc ctcgtacatc tccttcaacg ccgcctccaa ctcgcggtcc cagatcaagg 1020

ccgcgctgga caatgccggc aagatcatgg cgctgaccaa atccgcgccc gactacctgg 1080

taggcccttc acttccggtg gacattacgc agaaccgcat ctaccgcatc ctgcagctca 1140

acggctacga ccctgcctac gccggctccg tctttctcgg ctgggcacaa aagaagttcg 1200

ggaaacgcaa caccatctgg ctgtttgggc cggccaccac gggaaagacc aacatcgcag 1260

aagccattgc ccacgccgtg cccttctacg gctgcgtcaa ctggaccaat gagaactttc 1320

ccttcaacga ttgcgtcgac aagatggtga tctggtggga ggagggcaag atgacggcca 1380

aggtcgtgga gtccgccaag gccattctcg gcggcagcaa ggtgcgcgtg gaccaaaagt 1440

gcaagtcgtc cgcccagatc gaccccactc ccgtgatcgt cacctccaac accaacatgt 1500

gcgccgtgat tgacgggaac agcaccacct tcgagcacca gcagcctctc caggaccgga 1560

tgtttaagtt cgaactcacc cgccgtctgg agcacgactt tggcaaggtg acaaagcagg 1620

aagtcaaaga gttcttccgc tgggccagtg atcacgtgac cgaggtggcg catgagtttt 1680

acgtcagaaa gggcggagcc agcaaaagac ccgcccccga tgacgcggat aaaagcgagc 1740

ccaagcgggc ctgcccctca gtcgcggatc catcgacgtc agacgcggaa ggagctccgg 1800

tggactttgc cgacaggtac caaaacaaat gttctcgtca cgcgggcatg cttcagatgc 1860

tgcttccctg caaaacgtgc gagagaatga atcagaattt caacatttgc ttcacacacg 1920

gggtcagaga ctgctcagag tgtttccccg gcgtgtcaga atctcaaccg gtcgtcagaa 1980

agaggacgta tcggaaactc tgtgcgattc atcatctgct ggggcgggct cccgagattg 2040

cttgctcggc ctgcgatctg gtcaacgtgg acctggatga ctgtgtttct gagcaataaa 2100

tgacttaaac caggtatggc tgccgatggt tatcttccag attggctcga ggacaacctc 2160

tctgagggca ttcgcgagtg gtgggcgctg aaacctggag ccccgaagcc caaagccaac 2220

cagcaaaagc aggacgacgg ccggggtctg gtgcttcctg gctacaagta cctcggaccc 2280

ttcaacggac tcgacaaggg ggagcccgtc aacgcggcgg acgcagcggc cctcgagcac 2340

ggcaaggcct acgaccagca gctgcaggcg ggtgacaatc cgtacctgcg gtataaccac 2400

gccgacgccg agtttcagga gcgtctgcaa gaagatacgt cttttgggggg caacctcggg 2460

cgagcagtct tccaggccaa gaagcgggtt ctcgaacctc tcggtctggt tgaggaaggc 2520

gctaagacgg ctcctggaaa gaagagaccg gtagagccat caccccagcg ttctccagac 2580

tcctctacgg gcatcggcaa gaaaggccaa cagcccgcca gaaaaagact caattttggt 2640

cagactggcg actcagagtc agttccagac cctcaacctc tcggagaacc tccagcagcg 2700

ccctctggtg tgggacctaa tacaatggct gcaggcggtg gcgcaccaat ggcagacaat 2760

aacgaaggcg ccgacggagt gggtaattcc tcgggaaatt ggcattgcga ttccacatgg 2820

ctgggggaca gagtcatcac caccagcacc cgaacctggg cattgcccac ctacaacaac 2880

cacctctaca agcaaatctc caatggaaca tcgggaggaa gcaccaacga caacacctac 2940

tttggctaca gcaccccctg ggggtatttt gacttcaaca gattccactg ccacttctca 3000

ccacgtgact ggcagcgact catcaacaac aactggggat tccggccaaa gagactcaac 3060

ttcaagctgt tcaacatcca ggtcaaggag gttacgacga acgaaggcac caagaccatc 3120

gccaataacc ttaccagcac cgtccaggtc tttacggact cggagtacca gctaccgtac 3180

gtcctaggct ctgcccacca aggatgcctg ccaccgtttc ctgcagacgt cttcatggtt 3240

cctcagtacg gctacctgac gctcaacaat ggaagtcaag cgttaggacg ttcttctttc 3300

tactgtctgg aatacttccc ttctcagatg ctgagaaccg gcaacaactt tcagttcagc 3360

tacactttcg aggacgtgcc tttccacagc agctacgcac acagccagag tctagatcga 3420

ctgatgaacc ccctcatcga ccagtaccta tactacctgg tcagaacaca gacaactgga 3480

actgggggaa ctcaaacttt ggcattcagc caagcaggcc ctagctcaat ggccaatcag 3540

gctagaaact gggtacccgg gccttgctac cgtcagcagc gcgtctccac aaccaccaac 3600

caaaataaca acagcaactt tgcgtggacg ggagctgcta aattcaagct gaacgggaga 3660

gactcgctaa tgaatcctgg cgtggctatg gcatcgcaca aagacgacga ggaccgcttc 3720

tttccatcaa gtggcgttct catatttggc aagcaaggag ccgggaacga tggagtcgac 3780

tacagccagg tgctgattac agatgaggaa gaaattaaag ccaccaaccc tgtagccaca 3840

gaggaatacg gagcagtggc catcaacaac caggccgcta acacgcaggc gcaaactgga 3900

cttgtgcata accagggagt tattcctggt atggtctggc agaaccggga cgtgtacctg 3960

cagggcccta tttgggctaa aatacctcac acagatggca actttcaccc gtctcctctg 4020

atgggtggat ttggactgaa acacccacct ccacagattc taattaaaaa tacaccagtg 4080

ccggcagatc ctcctcttac cttcaatcaa gccaagctga actctttcat cacgcagtac 4140

agcacgggac aagtcagcgt ggaaatcgag tgggagctgc agaaagaaaa cagcaagcgc 4200

tggaatccag agatccagta tacttcaaac tactacaaat ctacaaatgt ggactttgct 4260

gtcaatacca aaggtgttta ctctgagcct cgccccattg gtactcgtta cctcacccgt 4320

aatttgtaat tgcctgttaa tcaataaacc ggttaattcg tttcagttga actttggtct 4380

ctgcg 4385

<210> 6
<211> 4718
<212> DNA
<213> adeno-associated virus serotype 1

<400> 6
ttgcccactc cctctctgcg cgctcgctcg ctcggtgggg cctgcggacc aaaggtccgc 60

agacggcaga gctctgctct gccggcccca ccgagcgagc gagcgcgcag agagggagtg 120

ggcaactcca tcactagggg taatcgcgaa gcgcctccca cgctgccgcg tcagcgctga 180

cgtaaattac gtcatagggg agtggtcctg tattagctgt cacgtgagtg cttttgcgac 240

attttgcgac accacgtggc catttagggt atatatggcc gagtgagcga gcaggatctc 300

cattttgacc gcgaaatttg aacgagcagc agccatgccg ggcttctacg agatcgtgat 360

caaggtgccg agcgacctgg acgagcacct gccgggcatt tctgactcgt ttgtgagctg 420

ggtggccgag aaggaatggg agctgccccc ggattctgac atggatctga atctgattga 480

gcaggcaccc ctgaccgtgg ccgagaagct gcagcgcgac ttcctggtcc aatggcgccg 540

cgtgagtaag gccccggagg ccctcttctt tgttcagttc gagaagggcg agtcctactt 600

ccacctccat attctggtgg agaccacggg ggtcaaatcc atggtgctgg gccgcttcct 660

gagtcagatt agggacaagc tggtgcagac catctaccgc gggatcgagc cgaccctgcc 720

caactggttc gcggtgacca agacgcgtaa tggcgccgga ggggggaaca aggtggtgga 780

cgagtgctac atccccaact acctcctgcc caagactcag cccgagctgc agtgggcgtg 840

gactaacatg gaggagtata taagcgcctg tttgaacctg gccgagcgca aacggctcgt 900

ggcgcagcac ctgacccacg tcagccagac ccaggagcag aacaaggaga atctgaaccc 960

caattctgac gcgcctgtca tccggtcaaa aacctccgcg cgctacatgg agctggtcgg 1020

gtggctggtg gaccggggca tcacctccga gaagcagtgg atccaggagg accaggcctc 1080

gtacatctcc ttcaacgccg cttccaactc gcggtcccag atcaaggccg ctctggacaa 1140

tgccggcaag atcatggcgc tgaccaaatc cgcgcccgac tacctggtag gccccgctcc 1200

gcccgcggac attaaaacca accgcatcta ccgcatcctg gagctgaacg gctacgaacc 1260

tgcctacgcc ggctccgtct ttctcggctg ggcccagaaa aggttcggga agcgcaacac 1320

catctggctg tttgggccgg ccaccacggg caagaccaac atcgcggaag ccatcgccca 1380

cgccgtgccc ttctacggct gcgtcaactg gaccaatgag aactttccct tcaatgattg 1440

cgtcgacaag atggtgatct ggtgggagga gggcaagatg acggccaagg tcgtggagtc 1500

cgccaaggcc attctcggcg gcagcaaggt gcgcgtggac caaaagtgca agtcgtccgc 1560

ccagatcgac cccacccccg tgatcgtcac ctccaacacc aacatgtgcg ccgtgattga 1620

cgggaacagc accaccttcg agcaccagca gccgttgcag gaccggatgt tcaaatttga 1680

actcacccgc cgtctggagc atgactttgg caaggtgaca aagcaggaag tcaaagagtt 1740

cttccgctgg gcgcaggatc acgtgaccga ggtggcgcat gagttctacg tcagaaaggg 1800

tggagccaac aaaagacccg cccccgatga cgcggataaa agcgagccca agcgggcctg 1860

cccctcagtc gcggatccat cgacgtcaga cgcggaagga gctccggtgg actttgccga 1920

caggtaccaa aacaaatgtt ctcgtcacgc gggcatgctt cagatgctgt ttccctgcaa 1980

gacatgcgag agaatgaatc agaatttcaa catttgcttc acgcacggga cgagagactg 2040

ttcagagtgc ttccccggcg tgtcagaatc tcaaccggtc gtcagaaaga ggacgtatcg 2100

gaaactctgt gccattcatc atctgctggg gcgggctccc gagattgctt gctcggcctg 2160

cgatctggtc aacgtggacc tggatgactg tgtttctgag caataaatga cttaaaccag 2220

gtatggctgc cgatggttat cttccagatt ggctcgagga caacctctct gagggcattc 2280

gcgagtggtg ggacttgaaa cctggagccc cgaagcccaa agccaaccag caaaagcagg 2340

acgacggccg gggtctggtg cttcctggct acaagtacct cggacccttc aacggactcg 2400

acaaggggga gcccgtcaac gcggcggacg cagcggccct cgagcacgac aaggcctacg 2460

accagcagct caaagcgggt gacaatccgt acctgcggta taaccacgcc gacgccgagt 2520

ttcaggagcg tctgcaagaa gatacgtctt ttgggggcaa cctcgggcga gcagtcttcc 2580

aggccaagaa gcgggttctc gaacctctcg gtctggttga ggaaggcgct aagacggctc 2640

ctggaaagaa acgtccggta gagcagtcgc cacaagagcc agactcctcc tcgggcatcg 2700

gcaagacagg ccagcagccc gctaaaaaga gactcaattt tggtcagact ggcgactcag 2760

agtcagtccc cgatccacaa cctctcggag aacctccagc aacccccgct gctgtgggac 2820

ctactacaat ggcttcaggc ggtggcgcac caatggcaga caataacgaa ggcgccgacg 2880

gagtgggtaa tgcctcagga aattggcatt gcgattccac atggctgggc gacagagtca 2940

tcaccaccag cacccgcacc tgggccttgc ccacctacaa taaccacctc tacaagcaaa 3000

tctccagtgc ttcaacgggg gccagcaacg acaaccacta cttcggctac agcacccct 3060

gggggtattt tgatttcaac agattccact gccacttttc accacgtgac tggcagcgac 3120

tcatcaacaa caattgggga ttccggccca agagactcaa cttcaaactc ttcaacatcc 3180

aagtcaagga ggtcacgacg aatgatggcg tcacaaccat cgctaataac cttaccagca 3240

cggttcaagt cttctcggac tcggagtacc agcttccgta cgtcctcggc tctgcgcacc 3300

agggctgcct ccctccgttc ccggcggacg tgttcatgat tccgcaatac ggctacctga 3360

cgctcaacaa tggcagccaa gccgtgggac gttcatcctt ttactgcctg gaatatttcc 3420

cttctcagat gctgagaacg ggcaacaact ttaccttcag ctacaccttt gaggaagtgc 3480

ctttccacag cagctacgcg cacagccaga gcctggaccg gctgatgaat cctctcatcg 3540

accaatacct gtattacctg aacagaactc aaaatcagtc cggaagtgcc caaaacaagg 3600

acttgctgtt tagccgtggg tctccagctg gcatgtctgt tcagcccaaa aactggctac 3660

ctggaccctg ttatcggcag cagcgcgttt ctaaaacaaa aacagacaac aacaacagca 3720

attttacctg gactggtgct tcaaaatata acctcaatgg gcgtgaatcc atcatcaacc 3780

ctggcactgc tatggcctca cacaaagacg acgaagacaa gttctttccc atgagcggtg 3840

tcatgatttt tggaaaagag agcgccggag cttcaaacac tgcattggac aatgtcatga 3900

ttacagacga agaggaaatt aaagccacta accctgtggc caccgaaaga tttgggaccg 3960

tggcagtcaa tttccagagc agcagcacag accctgcgac cggagatgtg catgctatgg 4020

gagcattacc tggcatggtg tggcaagata gagacgtgta cctgcagggt cccatttggg 4080

ccaaaattcc tcacacagat ggacactttc acccgtctcc tcttatgggc ggctttggac 4140

tcaagaaccc gcctcctcag atcctcatca aaaacacgcc tgttcctgcg aatcctccgg 4200

cggagttttc agctacaaag tttgcttcat tcatcaccca atactccaca ggacaagtga 4260

gtgtggaaat tgaatgggag ctgcagaaag aaaacagcaa gcgctggaat cccgaagtgc 4320

agtacacatc caattatgca aaatctgcca acgttgattt tactgtggac aacaatggac 4380

tttatactga gcctcgcccc attggcaccc gttaccttac ccgtcccctg taattacgtg 4440

ttaatcaata aaccggttga ttcgtttcag ttgaactttg gtctcctgtc cttcttatct 4500

tatcggttac catggttata gcttacacat taactgcttg gttgcgcttc gcgataaaag 4560

acttacgtca tcgggttacc cctagtgatg gagttgccca ctccctctct gcgcgctcgc 4620

tcgctcggtg gggcctgcgg accaaaggtc cgcagacggc agagctctgc tctgccggcc 4680

ccaccgagcg agcgagcgcg cagagaggga gtgggcaa 4718

<210> 7
<211> 4675
<212> DNA
<213> adeno-associated virus serotype 2

<400> 7
ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc 60
cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg 120
gccaactcca tcactagggg ttcctggagg ggtggagtcg tgacgtgaat tacgtcatag 180
ggttagggag gtcctgtatt agaggtcacg tgagtgtttt gcgacatttt gcgacaccat 240
gtggtcacgc tgggtattta agcccgagtg agcacgcagg gtctccattt tgaagcggga 300
ggtttgaacg cgcagccgcc atgccggggt tttacgagat tgtgattaag gtccccagcg 360
accttgacgg gcatctgccc ggcatttctg acagctttgt gaactgggtg gccgagaagg 420
aatgggagtt gccgccagat tctgacatgg atctgaatct gattgagcag gcacccctga 480
ccgtggccga gaagctgcag cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc 540
cggaggccct tttctttgtg caatttgaga agggagagag ctacttccac atgcacgtgc 600
tcgtggaaac caccggggtg aaatccatgg ttttgggacg tttcctgagt cagattcgcg 660
aaaaactgat tcagagaatt taccgcggga tcgagccgac tttgccaaac tggttcgcgg 720
tcacaaagac cagaaatggc gccggaggcg ggaacaaggt ggtggatgag tgctacatcc 780
ccaattactt gctccccaaa acccagcctg agctccagtg ggcgtggact aatatggaac 840
agtatttaag cgcctgtttg aatctcacgg agcgtaaacg gttggtggcg cagcatctga 900
cgcacgtgtc gcagacgcag gagcagaaca aagagaatca gaatcccaat tctgatgcgc 960
cggtgatcag atcaaaaact tcagccaggt acatggagct ggtcgggtgg ctcgtggaca 1020
aggggattac ctcggagaag cagtggatcc aggaggacca ggcctcatac atctccttca 1080
atgcggcctc caactcgcgg tcccaaatca aggctgcctt ggacaatgcg ggaaagatta 1140
tgagcctgac taaaaccgcc cccgactacc tggtgggcca gcagcccgtg gaggacattt 1200
ccagcaatcg gatttataaa attttggaac taaacgggta cgatccccaa tatgcggctt 1260
ccgtctttct gggatgggcc acgaaaaagt tcggcaagag gaacaccatc tggctgtttg 1320
ggcctgcaac taccgggaag accaacatcg cggaggccat agcccacact gtgcccttct 1380
acgggtgcgt aaactggacc aatgagaact ttcccttcaa cgactgtgtc gacaagatgg 1440
tgatctggtg ggaggagggg aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc 1500
tcggaggaag caaggtgcgc gtggaccaga aatgcaagtc ctcggcccag atagacccga 1560
ctcccgtgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg aactcaacga 1620
ccttcgaaca ccagcagccg ttgcaagacc ggatgttcaa atttgaactc acccgccgtc 1680
tggatcatga ctttgggaag gtcaccaagc aggaagtcaa agacttttttc cggtgggcaa 1740
aggatcacgt ggttgaggtg gagcatgaat tctacgtcaa aaagggtgga gccaagaaaa 1800
gacccgcccc cagtgacgca gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc 1860
agccatcgac gtcagacgcg gaagcttcga tcaactacgc agacaggtac caaaacaaat 1920

gttctcgtca cgtgggcatg aatctgatgc tgtttccctg cagacaatgc gagagaatga 1980

atcagaattc aaatatctgc ttcactcacg gacagaaaga ctgtttagag tgctttcccg 2040

tgtcagaatc tcaacccgtt tctgtcgtca aaaaggcgta tcagaaactg tgctacattc 2100

atcatatcat gggaaaggtg ccagacgctt gcactgcctg cgatctggtc aatgtggatt 2160

tggatgactg catctttgaa caataaatga tttaaatcag gtatggctgc cgatggttat 2220

cttccagatt ggctcgagga cactctctct gaaggaataa gacagtggtg gaagctcaaa 2280

cctggcccac caccaccaaa gcccgcagag cggcataagg acgacagcag gggtcttgtg 2340

cttcctgggt acaagtacct cggacccttc aacggactcg acaagggaga gccggtcaac 2400

gaggcagacg ccgcggccct cgagcacgta caaagcctac gaccggcagc tcgacagcgg 2460

agacaacccg tacctcaagt acaaccacgc cgacgcggag tttcaggagc gccttaaaga 2520

agatacgtct tttgggggca acctcggacg agcagtcttc caggcgaaaa agagggttct 2580

tgaacctctg ggcctggttg aggaacctgt taagacggct ccgggaaaaa agaggccggt 2640

agagcactct cctgtggagc cagactcctc ctcgggaacc ggaaaggcgg gccagcagcc 2700

tgcaagaaaa agattgaatt ttggtcagac tggagacgca gactcagtac ctgaccccca 2760

gcctctcgga cagccaccag cagccccctc tggtctggga actaatacga tggctacagg 2820

cagtggcgca ccaatggcag acaataacga gggcgccgac ggagtgggta attcctccgg 2880

aaattggcat tgcgattcca catggatggg cgacagagtc atcaccacca gcacccgaac 2940

ctgggccctg cccacctaca acaaccacct ctacaaacaa atttccagcc aatcaggagc 3000

ctcgaacgac aatcactact ttggctacag caccccttgg gggtattttg acttcaacag 3060

attccactgc cacttttcac cacgtgactg gcaaagactc atcaacaaca actggggatt 3120

ccgacccaag agactcaact tcaagctctt taacattcaa gtcaaagagg tcacgcagaa 3180

tgacggtacg acgacgattg ccaataacct taccagcacg gttcaggtgt ttactgactc 3240

ggagtaccag ctcccgtacg tcctcggctc ggcgcatcaa ggatgcctcc cgccgttccc 3300

agcagacgtc ttcatggtgc cacagtatgg atacctcacc ctgaacaacg ggagtcaggc 3360

agtaggacgc tcttcatttt actgcctgga gtactttcct tctcagatgc tgcgtaccgg 3420

aaacaacttt accttcagct acacttttga ggacgttcct ttccacagca gctacgctca 3480

cagccagagt ctggaccgtc tcatgaatcc tctcatcgac cagtacctgt attacttgag 3540

cagaacaaac actccaagtg gaaccaccac gcagtcaagg cttcagtttt ctcaggccgg 3600

agcgagtgac attcgggacc agtctaggaa ctggcttcct ggaccctgtt accgccagca 3660

gcgagtatca aagacatctg cggataacaa caacagtgaa tactcgtgga ctggagctac 3720

caagtaccac ctcaatggca gagactctct ggtgaatccg gccatggcaa gccacaagga 3780

cgatgaagaa aagtttttc ctcagagcgg ggttctcatc tttgggaagc aaggctcaga 3840

gaaaacaaat gtgaacattg aaaaggtcat gattacagac gaagaggaaa tcggaacaac 3900

caatcccgtg gctacggagc agtatggttc tgtatctacc aacctccaga gaggcaacag 3960

acaagcagct accgcagatg tcaacacaca aggcgttctt ccaggcatgg tctggcagga 4020

cagagatgtg taccttcagg ggcccatctg ggcaaagatt ccacacacgg acggacattt 4080

tcacccctct cccctcatgg gtggattcgg acttaaacac cctcctccac agattctcat 4140

caagaacacc ccggtacctg cgaatccttc gaccaccttc agtgcggcaa agtttgcttc 4200

cttcatcaca cagtactcca cgggacacgg tcagcgtgga gatcgagtgg gagctgcaga 4260

aggaaaacag caaacgctgg aatcccgaaa ttcagtacac ttccaactac aacaagtctg 4320

ttaatcgtgg acttaccgtg gatactaatg gcgtgtattc agagcctcgc cccattggca 4380

ccagatacct gactcgtaat ctgtaattgc ttgttaatca ataaaccgtt taattcgttt 4440

cagttgaact ttggtctctg cgtatttctt tcttatctag tttccatggc tacgtagata 4500

agtagcatgg cgggttaatc attaactaca aggaacccct agtgatggag ttggccactc 4560

cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc cgacgcccgg 4620

gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg gccaa 4675

<210> 8
<211> 4726
<212> DNA
<213> adeno-associated virus serotype 3

<400> 8
ttggccactc cctctatgcg cactcgctcg ctcggtgggg cctggcgacc aaaggtcgcc 60

agacggacgt gctttgcacg tccggcccca ccgagcgagc gagtgcgcat agagggagtg 120

gccaactcca tcactagagg tatggcagtg acgtaacgcg aagcgcgcga agcgagacca 180

cgcctaccag ctgcgtcagc agtcaggtga ccctttttgcg acagtttgcg acaccacgtg 240

gccgctgagg gtatatattc tcgagtgagc gaaccaggag ctccattttg accgcgaaat 300

ttgaacgagc agcagccatg ccggggttct acgagattgt cctgaaggtc ccgagtgacc 360

tggacgagcg cctgccgggc atttctaact cgtttgttaa ctgggtggcc gagaaggaat 420

gggacgtgcc gccggattct gacatggatc cgaatctgat tgagcaggca cccctgaccg 480

tggccgaaaa gcttcagcgc gagttcctgg tggagtggcg ccgcgtgagt aaggccccgg 540

aggccctctt ttttgtccag ttcgaaaagg gggagaccta cttccacctg cacgtgctga 600

ttgagaccat cggggtcaaa tccatggtgg tcggccgcta cgtgagccag attaaagaga 660

agctggtgac ccgcatctac cgcggggtcg agccgcagct tccgaactgg ttcgcggtga 720

ccaaaacgcg aaatggcgcc gggggcggga acaaggtggt ggacgactgc tacatcccca 780

actacctgct ccccaagacc cagcccgagc tccagtgggc gtggactaac atggaccagt 840

atttaagcgc ctgtttgaat ctcgcggagc gtaaacggct ggtggcgcag catctgacgc 900

acgtgtcgca gacgcaggag cagaacaaag agaatcagaa ccccaattct gacgcgccgg 960

tcatcaggtc aaaaacctca gccaggtaca tggagctggt cgggtggctg gtggaccgcg 1020

ggatcacgtc agaaaagcaa tggattcagg aggaccaggc ctcgtacatc tccttcaacg 1080

ccgcctccaa ctcgcggtcc cagatcaagg ccgcgctgga caatgcctcc aagatcatga 1140

gcctgacaaa gacggctccg gactacctgg tgggcagcaa cccgccggag gacattacca 1200

aaaatcggat ctaccaaatc ctggagctga acgggtacga tccgcagtac gcggcctccg 1260

tcttcctggg ctgggcgcaa aagaagttcg ggaagaggaa caccatctgg ctctttgggc 1320

cggccacgac gggtaaaacc aacatcgcgg aagccatcgc ccacgccgtg cccttctacg 1380

gctgcgtaaa ctggaccaat gagaactttc ccttcaacga ttgcgtcgac aagatggtga 1440

tctggtggga ggagggcaag atgacggcca aggtcgtgga gagcgccaag gccattctgg 1500

gcggaagcaa ggtgcgcgtg gaccaaaagt gcaagtcatc ggcccagatc gaacccactc 1560

ccgtgatcgt cacctccaac accaacatgt gcgccgtgat tgacgggaac agcaccacct 1620

tcgagcatca gcagccgctg caggaccgga tgtttgaatt tgaacttacc cgccgtttgg 1680

accatgactt tgggaaggtc accaaacagg aagtaaagga ctttttccgg tgggcttccg 1740

atcacgtgac tgacgtggct catgagttct acgtcagaaa gggtggagct aagaaacgcc 1800

ccgcctccaa tgacgcggat gtaagcgagc caaaacggga gtgcacgtca cttgcgcagc 1860

cgacaacgtc agacgcggaa gcaccggcgg actacgcgga caggtaccaa aacaaatgtt 1920

ctcgtcacgt gggcatgaat ctgatgcttt ttccctgtaa aacatgcgag agaatgaatc 1980

aaatttccaa tgtctgtttt acgcatggtc aaagagactg tggggaatgc ttccctggaa 2040

tgtcagaatc tcaacccgtt tctgtcgtca aaaagaagac ttatcagaaa ctgtgtccaa 2100

ttcatcatat cctgggaagg gcacccgaga ttgcctgttc ggcctgcgat ttggccaatg 2160

tggacttgga tgactgtgtt tctgagcaat aaatgactta aaccaggtat ggctgctgac 2220

ggttatcttc cagattggct cgaggacaac ctttctgaag gcattcgtga gtggtgggct 2280

ctgaaacctg gagtccctca acccaaagcg aaccaacaac accaggacaa ccgtcggggt 2340

cttgtgcttc cgggttacaa atacctcgga cccggtaacg gactcgacaa aggagagccg 2400

gtcaacgagg cggacgcggc agccctcgaa cacgacaaag cttacgacca gcagctcaag 2460

gccggtgaca acccgtacct caagtacaac cacgccgacg ccgagtttca ggagcgtctt 2520

caagaagata cgtcttttgg gggcaacctt ggcagagcag tcttccaggc caaaaagagg 2580

atccttgagc ctcttggtct ggttgaggaa gcagctaaaa cggctcctgg aaagaagggg 2640

gctgtagatc agtctcctca ggaaccggac tcatcatctg gtgttggcaa atcgggcaaa 2700

cagcctgcca gaaaaagact aaatttcggt cagactggag actcagagtc agtcccagac 2760

cctcaacctc tcggagaacc accagcagcc cccacaagtt tgggatctaa tacaatggct 2820

tcaggcggtg gcgcaccaat ggcagacaat aacgagggtg ccgatggagt gggtaattcc 2880

tcaggaaatt ggcattgcga ttcccaatgg ctgggcgaca gagtcatcac caccagcacc 2940

agaacctggg ccctgcccac ttacaacaac catctctaca agcaaatctc cagccaatca 3000

ggagcttcaa acgacaacca ctactttggc tacagcaccc cttgggggta ttttgacttt 3060

aacagattcc actgccactt ctcaccacgt gactggcagc gactcattaa caacaactgg 3120

ggattccggc ccaagaaact cagcttcaag ctcttcaaca tccaagttag aggggtcacg 3180

cagaacgatg gcacgacgac tattgccaat aaccttacca gcacggttca agtgtttacg 3240

gactcggagt atcagctccc gtacgtgctc gggtcggcgc accaaggctg tctcccgccg 3300

tttccagcgg acgtcttcat ggtccctcag tatggatacc tcaccctgaa caacggaagt 3360

caagcggtgg gacgctcatc cttttactgc ctggagtact tcccttcgca gatgctaagg 3420

actggaaata acttccaatt cagctatacc ttcgaggatg taccttttca cagcagctac 3480

gctcacagcc agagtttgga tcgcttgatg aatcctctta ttgatcagta tctgtactac 3540

ctgaacagaa cgcaaggaac aacctctgga acaaccaacc aatcacggct gctttttagc 3600

caggctgggc ctcagtctat gtctttgcag gccagaaatt ggctacctgg gccctgctac 3660

cggcaacaga gactttcaaa gactgctaac gacaacaaca acagtaactt tccttggaca 3720

gcggccagca aatatcatct caatggccgc gactcgctgg tgaatccagg accagctatg 3780

gccagtcaca aggacgatga agaaaaattt ttccctatgc acggcaatct aatatttggc 3840

aaagaaggga caacggcaag taacgcagaa ttagataatg taatgattac ggatgaagaa 3900

gagattcgta ccaccaatcc tgtggcaaca gagcagtatg gaactgtggc aaataacttg 3960

cagagctcaa atacagctcc cacgactgga actgtcaatc atcagggggc cttacctggc 4020

atggtgtggc aagatcgtga cgtgtacctt caaggaccta tctgggcaaa gattcctcac 4080

acggatggac actttcatcc ttctcctctg atgggaggct ttggactgaa acatccgcct 4140

cctcaaatca tgatcaaaaa tactccggta ccggcaaatc ctccgacgac tttcagcccg 4200

gccaagtttg cttcatttat cactcagtac tccactggac aggtcagcgt ggaaattgag 4260

tgggagctac agaaagaaaa cagcaaacgt tggaatccag agattcagta cacttccaac 4320

tacaacaagt ctgttaatgt ggactttact gtagacacta atggtgttta tagtgaacct 4380

cgccctattg gaacccggta tctcacacga aacttgtgaa tcctggttaa tcaataaacc 4440

gtttaattcg tttcagttga actttggctc ttgtgcactt ctttatcttt atcttgtttc 4500

catggctact gcgtagataa gcagcggcct gcggcgcttg cgcttcgcgg tttacaactg 4560

ctggttaata tttaactctc gccatacctc tagtgatgga gttggccact ccctctatgc 4620

gcactcgctc gctcggtggg gcctggcgac caaaggtcgc cagacggacg tgctttgcac 4680

gtccggcccc accgagcgag cgagtgcgca tagagggagt ggccaa 4726

<210> 9
<211> 3098
<212> DNA
<213> new AAV serotype, clone 42.2

<400> 9
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcttccg 180

cccagatcga tcccacccca gtgatcgtca cttccaacac caacatgtgc gctgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgacc gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaagggag agccggtcaa cgaggcagac gccgcggccc tcgagcacga caaggcctac 1080

gacaagcagc tcgagcaggg ggacaacccg tacctcaagt acaaccacgc cgacgccgag 1140

tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagacccat agaatccccc gactcctcca cgggcatcgg caagaaaggc 1320

cagcagcccg ctaaaaagaa gctcaacttt gggcagactg gcgactcaga gtcagtgccc 1380

gacccccaac ctctcggaga acctcccgcc gcgccctcag gtctgggatc tggtacaatg 1440

gctgcaggcg gtggcgcacc aatggcagac aataacgaag gcgccgacgg agtgggtaat 1500

gcctccggaa attggcattg cgattccaca tggctgggcg acagagtcat caccaccagc 1560

acccgcacct gggccctgcc cacctacaac aaccacctct acaagcagat atcaagtcag 1620

agcggggcta ccaacgacaa ccacttcttc ggctacagca ccccctgggg ctattttgac 1680

ttcaacagat tccactgcca cttctcacca cgtgactggc agcgactcat caacaacaac 1740

tggggattcc ggcccagaaa gctgcggttc aagttgttca acatccaggt caaggaggtc 1800

acgacgaacg acggcgttac gaccatcgct aataacctta ccagcacgat tcaggtcttc 1860

tcggactcgg agtaccaact gccgtacgtc ctcggctctg cgcaccaggg ctgcctccct 1920

ccgttccctg cggacgtgtt catgattcct cagtacggat atctgactct aaacaacggc 1980

agtcagtctg tgggacgttc ctccttctac tgcctggagt actttccttc tcagatgctg 2040

agaacgggca ataactttga attcagctac acctttgagg aagtgccttt ccacagcagc 2100

tatgcgcaca gccagagcct ggaccggctg atgaatcccc tcatcgacca gtacctgtac 2160

tacctggccc ggacccagag cactacgggg tccacaaggg agctgcagtt ccatcaggct 2220

gggcccaaca ccatggccga gcaatcaaag aactggctgc ccggaccctg ttatcggcag 2280

cagagactgt caaaaaacat agacagcaac aacaacagta actttgcctg gaccggggcc 2340

actaaatacc atctgaatgg tagaaattca ttaaccaacc cgggcgtagc catggccacc 2400

aacaaggacg acgaggacca gttctttccc atcaacggag tgctggtttt tggcgaaacg 2460

ggggctgcca acaagacaac gctggaaaac gtgctaatga ccagcgagga ggagatcaaa 2520

accaccaatc ccgtggctac agaagaatac ggtgtggtct ccagcaacct gcaatcgtct 2580

acggccggac cccagacaca gactgtcaac agccaggggg ctctgcccgg catggtctgg 2640

cagaaccggg acgtgtacct gcagggtccc atctgggcca aaattcctca cacggacggc 2700

aactttcacc cgtctccccc gatgggcgga tttggactca aacacccgcc tcctcaaatt 2760

ctcatcaaaa acaccccggt acctgctaat cctccagagg tgtttactcc tgccaagttt 2820

gcctcattta tcacgcagta cagcaccggc caggtcagcg tggagatcga gtgggaactg 2880

cagaaagaaa acagcaaacg ctggaatcca gagattcagt acacctcaaa ttatgccaag 2940

tctaataatg tggaatttgc tgtcaacaac gaaggggttt atactgagcc tcgccccatt 3000

ggcacccgtt acctcacccg taacctgtaa ttgcctgtta atcaataaac cggttaattc 3060

gtttcagttg aactttggtc tctgcgaagg gcgaattc 3098

<210> 10
<211> 3098
<212> DNA
<213> new AAV serotype, clone 16.3

<400> 10
gaattcgccc ttcgcagaga ccaaagttca actgaaacga atcaaccggt ttattgatta 60

acaagtaatt acaggttacg ggtgaggtaa cgggtgccaa tggggcgagg ctcagtataa 120

acccccttcgt tgttgacagc aaattccaca ttattagact tggcataatt tgaggtgtac 180

tgaatctctg gattccagcg tttgctgttt tctttctgca gttcccactc gatctccacg 240

ctgacctggc cggtgctgta ctgcgtgata aatgaggcaa actaggcagg agtaaacacc 300
cctggaggat tagcaggtac cggggtgttt ttgatgagaa tttgaggagg cgggtgtttg 360
agtccaaatc cgcccatcag gggagacggg tgaaagttgc cgtccgtgtg aggaattttg 420
gcccagatgg gaccctgcag gtacacgtcc cggttctgcc agaccatgcc gggcagagcc 480
ccctggctgt tgacagtctg tgtctggggt ccggccgtag acgattgcag gttgctggag 540
accacaccgt attcttctgt agccacggga ttggtggttt tgatctcctc ctcgctggtc 600
attagcacgt tttccagcgt tgtcttgttg gcagcccccg ttttgccaaa aaccagcact 660
ccgttgatgg gaaagaactg gccctcgtcg tccttgttgg tggccatggc tacgcccggg 720
ttggttaatg aatttctacc attcagatgg tatttagtgg ccccggtcca ggcaaagtta 780
ctgttgttgt tgctgtctat gttttttgac agtctctgct gccgataaca gggtccgggc 840
agccagttct ttgattgctc ggccatggtg ttgggcccag cctgatggaa ctgcagctcc 900
cttgtggacc ccgtagtgct ctgggtccgg gccaggtagt acaggtactg gtcgatgagg 960
ggattcatca gccggtccag gctctggctg tgcgcatagc tgctgtggaa aggcacttcc 1020
tcaaaggtgt agctgaattc aaagttattg cccgttctca gcatctgaga aggaaagtac 1080
tccaggcagt agaaggagga acgtcccata gactgactgc cgttgtttag agtcagatat 1140
ccgtactgag gaatcatgaa cacgtccgca gggaacggag ggaggcagcc ctggtgcgca 1200
gagccgagga cgtacggcag ttggtactcc gagtccgaga agacctgaat cgtgctggta 1260
aggttattag cgatggtcgt aacgccgtcg ttcgtcgtga cctccttgac ctggatgttg 1320
aacaacttga accgcagctt tctgggccgg aatccccagt tgttgttgat gagtcgctgc 1380
cagtcacgtg gtgagaagtg gcagtggaat ctgttgaagt caaaatagcc ccaggggtg 1440
ctgtagccga agaagtggtt gtcgttggta gccccgctct gacttgatat ctgcttgtag 1500
aggtggttgt tgtaggtggg cagggcccag gtgcgggtgc tggtggtgat gactctgtcg 1560
cccagccatg tggaatcgca atgccaattt ccggaggcat tacccactcc gtcggcgcct 1620
tcgttattgt ctgccattgg tgcgccaccg cctgcagcca ttgtaccaga tcccagacct 1680
gagggcgcgg cgggaggttc tccgagaggt tgggggtcgg gcactgactc tgagtcgcca 1740
gtctgcccaa agttgagctt ctttttagcg ggctgctggc ctttcttgcc gatgcccgtg 1800
gaggagtcgg gggattctat gggtctcttc tttccaggag ccgtcttagc gccttcctca 1860
accagaccga gaggttcgag aacccgcttc ttggcctgga agactgctcg cccgaggttg 1920
cccccaaaag acgtatcttc ttgaagacgc tcctgaaact cagcgtcggc gtggttgtac 1980
ttgaggtacg ggttgtcccc ctgctcgagc tgcttgtcgt aggccttgtc gtgctcgagg 2040
gccgcggcgt ctgcctcgtt gaccggctct cccttgtcga gtccgttgaa gggtccgagg 2100
tacttgtagc caggaagcac cagaccccgg ccgtcgtcct gcttttgctg gttggctttg 2160

ggtttcgggg ctccaggttt caagtcccac cactcgcgaa tgccctcaga gaggttgtcc 2220

tcgagccaat ctggaagata accatcggca gccatacctg gtttaagtca tttattgctc 2280

agaaacacag tcatccaggt ccacgttgac cagatcgcag gccgagcaag caatctcggg 2340

agcccgcccc agcagatgat gaatggcaca gagtttccga tacgtcctct ttctgacgac 2400

cggttgagat tctgacacgc cggggaaaca ttctgaacag tctctggtcc cgtgcgtgaa 2460

gcaaatgttg aaattctgat tcattctctc gcatgtcttg cagggaaaca gcatctgaag 2520

catgcccgcg tgacgagaac atttgttttg gtacctgtcg gcaaagtcca ccggagctcc 2580

ttccgcgtct gacgtcgatg gatccgcgac tgaggggcag gcccgcttgg gctcgctttt 2640

atccgcgtca tcgggggcgg gcctcttgtt ggctccaccc tttctgacgt agaactcatg 2700

cgccacctcg gtcacgtgat cctgcgccca gcggaagaac tctttgactt cctgctttgt 2760

caccttgcca aagtcctgct ccagacggcg ggtgagttca aatttgaaca tccggtcttg 2820

taacggctgc tggtgctcga aggtggtgct gttcccgtca atcacggcgc acatgttggt 2880

gttggaagtg acgatcacgg gggtgggatc gatctgggcg gacgacttgc acttttggtc 2940

cacgcgcacc ttgctgccgc cgagaatggc cttggcggac tccacgacct tggccgtcat 3000

cttgccctcc tcccaccaga tcaccatctt gtcgacgcaa tcgttgaagg gaaagttctc 3060

attggtccag ttgacgcagc cgtagaaagg gcgaattc 3098

<210> 11
<211> 3121
<212> DNA
<213> new AAV serotype, clone 29.3

<400> 11
gaattcgccc ttcgcagaga ccaaagttca actgaaacga atcaaccggt ttattgatta 60

acaagcaatt acagattacg ggtgaggtaa cgggtgccga tggggcgagg ctcagaataa 120

gtgccatctg tgttaacagc aaagtccaca tttgtagatt tgtagtagtt ggaagtgtat 180

tgaatctctg ggttccagcg tttgctgttt tctttctgca gctcccattc aatttccacg 240

ctgacctgtc cggtgctgta ctgcgtgatg aacgacgcca gcttagcttg actgaaggta 300

gttggaggat ccgcgggaac aggtgtattc ttaatcagga tctgaggagg cgggtgtttc 360

agtccaaagc cccccatcag cggcgaggga tgaaagtttc cgtccgtgtg aggaatcttg 420

gcccagatag gaccctgcag gtacacgtcc cggttctgcc agaccatgcc aggtaaggct 480

ccttgactgt tgacggcccc tacaatagga gcggcgtttt gctgttgcag gttatcggcc 540

accacgccgt actgttctgt ggccactggg ttggtggttt taatttcttc ctcactggtt 600

agcataacgc tgctatagtc cacgttgcct tttccagctc cctgtttccc aaacattaag 660

actccgctgg acggaaaaaa tcgctcttcg tcgtccttgt gggttgccat agcgacaccg 720

ggatttacca gagagtctct gccattcaga tgatacttgg tggcaccggt ccaggcaaag 780

ttgctgttgt tattttgcga cagtgtcgtg gagacgcgtt gctgccggta gcagggcccg 840
ggtagccagt ttttggcctg agccgacatg ttattaggcc cggcctgaga aaatagcaac 900
tgctgagttc ctgcggtacc tcccgtggac tgagtccgag acaggtagta caggtactgg 960
tcgatgaggg ggttcatcag ccggtccagg ctttggctgt gcgcgtagct gctgtgaaaa 1020
ggcacgtcct caaactggta gctgaactca aagttgttgc ccgttctcag catttgagaa 1080
ggaaagtact ccaggcagta gaaggaggaa cggcccacgg cctgactgcc attgttcaga 1140
gtcaggtacc cgtactgagg aatcatgaag acgtccgccg ggaacggagg caggcagccc 1200
tggcgcgcag agccgaggac gtacgggagc tggtattccg agtccgtaaa gacctgaatc 1260
gtgctggtaa ggttattggc gatggtcttg gtgccttcat tctgcgtgac ctccttgacc 1320
tggatgttga agagcttgaa gttgagtctc ttgggccgga atccccagtt gttgttgatg 1380
agtcgctgcc agtcacgtgg tgagaagtgg cagtggaatc tgttaaagtc aaaatacccc 1440
caggggtgtc tgtagccgaa gtaggtgttg tcgttggtgc ttcctcccga agtcccgttg 1500
gagatttgct tgtagaggtg gttgttgtag gtggggaggg cccaggttcg ggtgctggtg 1560
gtgatgactc tgtcgcccag ccatgtggaa tcgcaatgcc aatttcctga ggaactaccc 1620
actccgtcgg cgccttcgtt attgtctgcc attggagcgc caccgcctgc agccattgta 1680
ccagatccca gaccagaggg gcctgcgggg ggttctccga ttggttgagg gtcgggcact 1740
gactctgagt cgccagtctg cccaaagttg agtctctttt tcgcgggctg ctggcctttc 1800
ttgccgatgc ccgtagtgga gtctggagaa cgctggggtg atggctctac cggtctcttc 1860
tttccaggag ccgtcttagc gccttcctca accagaccga gaggttcgag aacccgcttc 1920
ttggcctgga agactgctcg tccgaggttg cccccaaaag acgtatcttc ttgcagacgc 1980
tcctgaaact cggcgtcggc gtggttatac cgcaggtacg gattgtcacc cgctttgagc 2040
tgctggtcgt aggccttgtc gtgctcgagg gccgctgcgt ccgccgcgtt gacgggctcc 2100
cccttgtcga gtccgttgaa gggtccgagg tacttgtagc caggaagcac cagaccccgg 2160
ccgtcgtcct gcttttgctg gttggctttg ggcttcgggg ctccaggttt cagcgcccac 2220
cactcgcgaa tgccctcaga gaggttgtcc tcgagccaat ctggaagata accatcggca 2280
gccatacctg atctaaatca tttattgttc aaagatgcag tcatccaaat ccacattgac 2340
cagatcgcag gcagtgcaag cgtctggcac ctttcccatg atatgatgaa tgtagcacag 2400
tttctgatac gccttttga cgacagaaac gggttgagat tctgacacgg gaaagcactc 2460
taaacagtct ttctgtccgt gagtgaagca gatatttgaa ttctgattca ttctctcgca 2520
ttgtctgcag ggaaacagca tcagattcat gcccacgtga cgagaacatt tgttttggta 2580
cctgtccgcg tagttgatcg aagcttccgc gtctgacgtc gatggctgcg caactgactc 2640
gcgcacccgt ttgggctcac ttatatctgc gtcactgggg gcgggtcttt tcttggctcc 2700

acccttttttg acgtagaatt catgctccac ctcaaccacg tgatcctttg cccaccggaa 2760

aaagtctttg acttcctgct tggtgacctt cccaaagtca tgatccagac ggcgggtgag 2820

ttcaaatttg aacatccggt cttgcaacgg ctgctggtgt tcgaaggtcg ttgagttccc 2880

gtcaatcacg gcgcacatgt tggtgttgga ggtgacgatc acgggagtcg ggtctatctg 2940

ggccgaggac ttgcatttct ggtccacgcg caccttgctt cctccgagaa tggctttggc 3000

cgactccacg accttggcgg tcatcttccc ctcctcccac cagatcacca tcttgtcgac 3060

acagtcgttg aagggaaagt tctcattggt ccagttgacg cagccgtaga agggcgaatt 3120

c 3121

<210> 12
<211> 3121
<212> DNA
<213> new AAV serotype, clone 29.4

<400> 12
gaattcgccc ttctacggct gcgtcaactg gaccaatgag aactttccct tcaacgactg 60

tgtcgacaag atggtgatct ggtgggagga ggggaagatg accgccaagg tcgtggagtc 120

ggccaaagcc attctcggag gaagcaaggt gcgcgtggac cagaaatgca agtcctcggc 180

ccagatagac ccgactcccg tgatcgtcac ctccaacacc aacatgtgcg ccgtgattga 240

cgggaactca acgaccttcg aacaccagca gccgttgcaa gaccggatgt tcaaatttga 300

actcacccgc cgtctggatc atgactttgg gaaggtcacc aagcaggaag tcaaagactt 360

tttccggtgg gcaaaggatc acgtggttga ggtggagcac gaattctacg tcaaaaaggg 420

tggagccaag aaaagacccg cccccagtga cgcagatata agtgagccca aacgggtgcg 480

cgagtcagtt gcgcagccat cgacgtcaga cgcggaagct tcgatcaact acgcagacag 540

gtaccaaaac aaatgttctc gtcacgcggg catgaatctg atgctgtttc cctgcagaca 600

atgcgagaga atgaatcaga attcaaatat ctgcttcact cacggacaga aagactgttt 660

agagtgcttt cccgtgtcag aatctcaacc cgtttctgtc gtcaaaaagg cgtatcagaa 720

actgtgctac attcatcata tcatgggaaa ggtgccagac gcttgcactg cctgcgatct 780

ggtcgatgtg gatttggatg actgcatctt tgaacaataa atgatttaaa tcaggtatgg 840

ctgccgatgg ttatcttcca gattggctcg aggacaacct ctctgagggc attcgcgagt 900

ggtgggcgct gaaacctgga gccccgaagc ccaaagccaa ccagcaaaag caggacggcg 960

gccggggtct ggtgcttcct ggctacaagt acctcggacc cttcaacgga ctcgacaagg 1020

gggagcccgt caacgcggcg gacgcagcgg ccctcgagca cgacaaggcc tacgaccagc 1080

agctcaaagc gggtgacaat ccgtacctgc ggtataacca cgccgacgcc gagtttcagg 1140

agcgtctgca agaagatacg tcttttgggg gcaacctcgg gcgagcagtc ttccaggcca 1200

agaagcgggt tctcgaacct ctcggtctgg ttgaggaagg cgctaagacg gctcctggaa 1260

agaagagacc ggtagagcca tcaccccagc gttctccaga ctcctctacg ggcatcggca 1320

agaaaggcca gcagcccgcg aaaaagagac tcaactttgg gcagactggc gactcagagt 1380

cagtgcccga ccctcaacca atcggagaac cccccgcagg cccctctggt ctgggatctg 1440

gtacaatggc tgcaggcggt ggcgctccaa tggcagacaa taacgaaggc gccgacggag 1500

tgggtagttc ctcaggaaat tggcattgcg attccacatg gctgggcgac tgagtcatca 1560

ccaccagcac ccgaacctgg gccctcccca cctacaacaa ccacctctac aagcaaatct 1620

ccaacgggac ttcgggagga agcaccaacg acaacaccta cttcggctac agcacccccc 1680

gggggtattt tgactttaac agattccact gccacttctc accacgtgac tggcagcgac 1740

tcatcaacaa caactgggga ttccggccca agagactcaa cttcaagctc ttcaacatcc 1800

aggtcaagga ggtcacgcag aatgaaggca ccaagaccat cgccaataac cttaccagca 1860

cgattcaggt ctttacggac tcggaatacc agctcccgta cgtcctcggc tctgcgcacc 1920

agggctgcct gcctccgttc ccggcggacg tcttcatgat tcctcagtac gggtacctga 1980

ctctgaacaa tggcagtcag gccgtgggcc gttcctcctt ctactgcctg gagtactttc 2040

cttctcaaat gctgagaacg ggcaacaact ttgagttcag ctaccagttt gaggacgtgc 2100

cttttcacag cagctacgcg cacagccaaa gcctggaccg gctgatgaac cccctcatcg 2160

accagtacct gtactacctg tctcggactc agtccacggg aggtaccgca ggaactcagc 2220

agttgctatt ttctcaggcc gggcctaata acatgtcggc tcaggccaaa aactggctac 2280

ccgggccctg ctaccggcag taacgcgtct ccacgacact gtcgcaaaat aacaacagca 2340

actttgtctg gaccggtgcc accaagtatc atctgaatgg cagagactct ctggtagatc 2400

ccggtgtcgc tatggcaacc cacaaggacg acgaagagcg atttttttccg tccagcggag 2460

tcataatgtt tgggaaacag ggagctggaa aagacaacgt ggactatagc agcgtcatgc 2520

taaccagtga ggaagaaatt aaaaccacca acccagtggc cacagaacag tacggcgtgg 2580

tggccgataa cctgcaacag caaaacgccg ctcctattgt aggggccgtc aacagtcaag 2640

gagccttacc tggcatggtc tggcagaacc gggacgtgta cctgcagggt cctacctggg 2700

ccaagattcc tcacacggac ggaaactttc atccctcgcc gctgatggga ggctttggac 2760

tgaaacaccc gcctcctcag atcctgatta agaatacacc tgttcccgcg gatcctccaa 2820

ctaccttcag tcaagctaag ctggcgtcgt tcatcacgca gtacagcacc ggacaggtca 2880

gcgtggaaat tgaatgggag ctgcaggaag aaaacagcaa acgctggaac ccagagattc 2940

aatacacttc caactactac aaatctacaa atgtggactt tgctgttaac acagatggca 3000

cttattctga gcctcgcccc atcggcaccc gttacctcac ccgtaatctg taattgcttg 3060

ttaatcaata aaccggttga ttcgtttcag ttgaactttg gtctctgcga agggcgaatt 3120

<210> 13
<211> 3121
<212> DNA
<213> new AAV serotype, clone 29.5

<400> 13
gaattcgccc ttcgcgagac caaagttcaa ctgaaacgaa tcaaccggtt tattgattaa 60
caagcaatta cagattacgg gtgaggtaac gggtgccgat ggggcgaggc tcagaataag 120
tgccatctgt gttaacagca aagtccacat ttgtagattt gtagtagttg gaagtgtatt 180
gaatctctgg gttccagcgt ttgctgtttt ctttctgcag ctcccattca atttccacgc 240
tgacctgtcc ggtgctgtac tgcgtgatga acgacgccag cttagcttga ctgaaggtag 300
ttggaggatc cgcgggaaca ggtgtattct taatcaggat ctgaggaggc gggtgtttca 360
gtccaaagcc tcccatcagc ggcgagggat gaaagtttcc gtccgtgtga ggaatcttgg 420
cccagatagg accctgcagg tacacgtccc ggttctgcca gaccatgcca ggtaaggctc 480
cttgactgtt gacggccccc acaataggag cggcgttttg ctgttgcagg ttatcggcca 540
ccacgccgta ctgttctgtg gccactgggt tggtggtttt aatttcttcc tcactggtta 600
gcataacgct gctatagtcc acgttgtctt ttccagctcc ctgtttccca aacattaaga 660
ctccgctgga cggaaaaaat cgctcttcgt cgtccttgtg ggttgccata gcgacaccgg 720
gatttaccag agagtctctg ccattcagat gatacttggt ggcaccggtc caggcaaagt 780
tgctgttgtc attttgcgac agtgtcgtgg agacgcgttg ctgccggtag cagggcccgg 840
gtagccagtt tttggcctga gccgacatgt tattaggccc ggcctgagaa aatagcaact 900
gctgagttcc tgcggtacct cccgtggact gagtccgaga caggtagtac aggtactggt 960
cgatgagggg gttcatcagc cggtccaggc tttggctgtg cgcgtagctg ctgtgaaaag 1020
gcacgtcctc aaactggtag ctgaactcaa agttgttgcc cgttctcagc atttgagaag 1080
gaaagtactc caggcagtag aaggaggaac ggcccacggc ctgactgcca ttgttcagag 1140
tcaggtaccc gtactgagga atcatgaaga cgtccgccgg gaacggaggc aggcagccct 1200
ggtgcgcaga gccgaggacg tacgggagct ggtattccga gtccgtaaag acctgaatcg 1260
tgctggtaag gttattggcg atggtcttgg tgccttcatt ctgcgtgacc tccttgacct 1320
ggatgttgaa gagcttgaag ttgaggctct tgggccggaa tccccagttg ttgttgatga 1380
gtcgctgcca gtcacgtggt gagaagtggc agtggaatct gttaaagtca aaataccccc 1440
agggggtgct gtagccgaag taggtgttgt cgttggtgct tcctcccgaa gtcccgttgg 1500
agatttgctt gtagaggtgg ttgttgtagg tggggagggc ccaggttcgg gtgctggtgg 1560
tgatgactcc gtcgcccagc catgtggaat cgcaatgcca atttcctgag gaactaccca 1620
ctccgtcggc gccttcgtta ttgtctgcca ttggagcgcc accgcctgca gccattgtac 1680

cagatcccag accagagggg cctgcggggg gttctccgat tggttgaggg tcgggcactg 1740

actctgagtc gccagtctgc ccaaagttga gtctcttttt cgcgggctgc tggcctttct 1800

tgccgatgcc cgtagaggag tctggagaac gctggggtga tggctctacc ggtctcttct 1860

ttccaggagc cgtcttagcg ccttcctcaa ccagaccgag aggttcgaga acccgcttct 1920

tggcctggaa gactgctcgc ccgaggttgc ccccaaaaga cgtatcttct tgcagacgct 1980

cctgaaactc ggcgtcggcg tggttatacc gcaggtacgg attgtcaccc gctttgagct 2040

gctggtcgta ggccttgtcg tgctcgaggg ccgctgcgtc cgccgcgttg acgggctccc 2100

ccttgtcgag tccgttgaag ggtccgaggt acttgtagcc aggaagcacc agaccccggc 2160

cgtcgtcctg cttttgctgg ttggctttgg gcttcggggc tccaggtttc agcgcccacc 2220

actcgcgaat gccctcagag aggttgtcct cgagccaatc tggaagataa ccatcggcag 2280

ccatacctga tttaaatcat ttattgttca aagatgcagt catccaaatc cacattgacc 2340

agatcgcagg cagtgcaagc gtctggcacc tttcccatga tatgatgaat gtagcacagt 2400

ttctgatacg ccttttttgac gacagaaacg ggttgagatt ctgacacggg aaagcactct 2460

aaacagtctt tctgtccgtg agtgaagcag atatttgaat tctgattcat tctctcgcat 2520

tgtctgcagg gaaacagcat cagattcatg cccacgtgac gagaacattt gttttggtac 2580

ctgtctgcgt agttgatcga agcttccgcg tctgacgtcg atggctgcgc aactgactcg 2640

cgcacccgtt tgggctcact tatatctgcg tcactggggg cgggtctttt cttggctcca 2700

ccctttttga cgtagaattc atgctccacc tcaaccacgt gatcctttgc ccaccggaaa 2760

aagtctttga cttcctgctt ggtgaccttc ccaaagtcat gatccagacg gcgggtgagt 2820

tcaaatttga acatccggtc ttgcaacggc tgctggtgtt cgaaggtcgt tgagttcccg 2880

tcaatcacgg cgcacatgtt ggtgttggag gtgacgatca cgggagtcgg gtctatctgg 2940

gccgaggact tgcatttctg gtccacgcgc accttgcttc ctccgagaat ggctttggcc 3000

gactccacga ccttggcggt catcttcccc tcctcccacc agatcaccat cttgtcgaca 3060

cagtcgttga agggaaagtt ctcattggtc cagttgacgc agccgtagaa agggcgaatt 3120

c 3121

<210> 14
<211> 3131
<212> DNA
<213> new AAV serotype, clone 1-3

<400> 14
gcggccgcga attcgccctt ggctgcgtca actggaccaa tgagaacttt cccttcaatg 60

attgcgtcga caagatggtg atctggtggg aggagggcaa gatgacggcc aaggtcgtgg 120

agtccgccaa ggccattctc ggcggcagca aggtgcgcgt ggaccaaaag tgcaagtcgt 180

ccgcccagat cgaccccacc cccgtgatcg tcacctccaa caccaacatg tgcgccgtga 240

ttgacgggaa cagcaccacc ttcgagcacc agcagcctct ccaggaccgg atgtttaagt 300

tcgaactcac ccgccgtctg gagcacgact ttggcaaggt gacaaagcag gaagtcaaag 360

agttcttccg ctgggccagt gatcacgtga ccgaggtggc gcatgagttt tacgtcagaa 420

agggcggagc cagcaaaaga cccgcccccg atgacgcgga taaaagcgag cccaagcggg 480

cctgcccctc agtcgcggat ccatcgacgt cagacgcgga aggagctccg gtggactttg 540

ccgacaggta ccaaaacaaa tgttctcgtc acgcgggcat gcttcagatg ctgtttccct 600

gcaaaacgtg cgagagaatg aatcggaatt tcaacatttg cttcacacac ggggtcagag 660

actgctcaga gtgtttcccc ggcgtgtcag aatctcaacc ggtcgtcaga aagaggacgt 720

atcggaaact ccgtgcgatt catcatctgc tggggcgggc tcccgagatt gcttgctcgg 780

cctgcgatct ggtcaacgtg gacctggatg actgtgtttc tgagcaataa atgacttaaa 840

ccaggtatgg ctgccgatgg ttatcttcca gattggctcg aggacaacct ctctgagggc 900

attcgcgagt ggtgggcgct gaaacctgga gccccgaagc ccaaagccaa ccagcaaaag 960

caggacgacg gccggggtct ggtgcttcct ggctacaagt acctcggacc cttcaacgga 1020

ctcgacaagg gggagcccgt caacgcggcg gacgcagcgg ccctcgagca cgacaaggct 1080

tacgaccagc agctgcaggc gggtgacaat ccgtacctgc ggtataacca cgccgacgcc 1140

gagtttcagg agcgtctgca agaagatacg tcttttgggg gcaacctcgg gcgagcagtc 1200

ttccaggcca agaagcgggt tctcgaacct ctcggtctgg ttgaggaagg cgctaagacg 1260

gctcctggaa agaagagacc ggtagagcca tcaccccagc gttctccaga ctcctctacg 1320

ggcatcggca agaaaggcca acagcccgcc agaaaaagac tcaattttgg tcagactggc 1380

gactcagagt cagttccaga ccctcaacct ctcggagaac ctccagcagc gccctctggt 1440

gtgggaccta atacaatggc tgcaggcggt ggcgcaccaa tggcagacaa taacgaaggc 1500

gccgacggag tgggtagttc ctcgggaaat tggcattgcg attccacatg gctgggcgac 1560

agagtcatca ccaccagcac ccgaacctgg gccctgccca cctacaacaa ccacctctac 1620

aagcaaatct ccaacgggac atcgggagga gccaccaacg acaacaccta cttcggctac 1680

agcacccccc tggggtattt tgactttaac agattccact gccacctttc accacgtgac 1740

tggcagcgac tcatcaacaa caactgggga ttccgaccca agagactcag cttcaagctc 1800

ttcaacatcc aggtcaagga ggtcacgcag aatgaaggca ccaagaccat cgccaataac 1860

ctcaccagca ccatccaggt gtttacggac tcggagtacc agctgccgta cgttctcggc 1920

tctgtccacc agggctgcct gcctccgttc ccggcggacg tgttcatgat tccccagtac 1980

ggctacctaa cactcaacaa cggtagtcag gccgtgggac gctcctcctt ctactgcctg 2040

gaatactttc cttcgcagat gctgagaacc ggcaacaact tccagtttac ttacaccttc 2100

gaggacgtgc ctttccacag cagctacgcc cacagctaga gcttggaccg gctgatgaat 2160

cctctgattg accagtacct gtactacttg tctcggactc aaacaacagg aggcacggca 2220

aatacgcaga ctctgggctt cagccaaggt gggcctaata caatggccaa tcaggcaaag 2280

aactggctgc caggaccctg ttaccgccaa caacgcgtct caacgacaac cgggcaaaac 2340

aacaatagca actttgcctg gactgctggg accaaatacc atctgaatgg aagaaattca 2400

ttggctaatc ctggcatcgc tatggcaaca cacaaagacg acgaggagcg ttttttttccc 2460

agtaacggga tcctgatttt tggcaaacaa aatgctgcca gagacaatgc ggattacagc 2520

gatgtcatgc tcaccagcga ggaagaaatc aaaaccacta accctgtggc tacagaggaa 2580

tacggtatcg tggcagataa cttgcagcag caaaacacgg ctcctcaaat tggaactgtc 2640

aacagccagg gggccttacc cggtatggtc tggcagaacc gggacgtgta cctgcagggt 2700

cccatctggg ccaagattcc tcacacggac ggcaacttcc acccgtctcc gctgatgggc 2760

ggctttggcc tgaaacatcc tccgcctcag atcctgatca agaacacgcc tgtacctgcg 2820

gatcctccga ccaccttcaa ccagtcaaag ctgaactctt tcatcacgca atacagcacc 2880

ggacaggtca gcgtggaaat tgaatgggag ctgcagaagg aaaacagcaa gcgctggaac 2940

cccgagatcc agtacacctc caactactac aaatctataa gtgtggactt tgctgttaat 3000

acagaaggcg tgtactctga accccgcccc attggcaccc gttacctcac ccgtaatctg 3060

taattgcctg ttaatcaata aaccggttga ttcgtttcag ttgaactttg gtctctgcga 3120

agggcgaatt c 3131

<210> 15
<211> 3127
<212> DNA
<213> new AAV serotype, clone 13-3b

<400> 15
gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat caaccggttt 60

attgattaac atgcaattac agattacggg tgaggtaacg agtgccaata gggcgaggct 120

cagagtaaac accctggctg tcaacggcaa agtccacacc agtctgcttt tcaaagttgg 180

aggtgtactg aatctccggg tcccagcgct tgctgttttc cttctgcagc tcccactcga 240

tttccacgct gacttgtccg gtgctgtact gtgtgatgaa cgaagcaaac ttggcaggag 300

taaacacctc cggaggatta gcgggaacgg gagtgttctt gatcaggatc tgaggaggcg 360

gatgtttaag tccaaagccg cccatcaaag gagacgggtg aaagttgcca tccgtgtgag 420

gaatcttggc ccagatggga ccctgcaggt acacgtcccg gttctgccag accatgccag 480

gtaaggctcc ctggttgttg acaacttgtg tctgggctgc agtattagcc gcttgtaagt 540

tgctgctgac tatcccgtat tcttccgtgg ctacaggatt agtaggacga atttcttctt 600

catttgtcat taacacattt tccaatgtag ttttgttagt tgctccagtt tttccaaaaa 660

tcaggactcc gctggatggg aaaaagcggt cctcgtcgtc cttgtgagtt gccatggcga 720

cgccgggatt aaccaacgag tttctgccgt tcaggtgata tttggtggca ccagtccaag 780

caaagttgct gttgttgttt tgatccagcg ttttggagac cctttgttgc cggaagcagg 840

gtccaggtaa ccaattcttg gcttgttcgg ccatagttga aggcccgccc tggtaaaact 900

gcagttcccg attgccagct gtgcctcctg ggtcactctg tgttctggcc aggtagtaca 960

agtactggtc gatgagggga ttcatcagcc ggtccaggct ctggctgtgt gcgtagctgc 1020

tgtggaaagg cacgtcctcg aagctgtagc tgaactcaaa gttgttgccc gttctcagca 1080

tctgagaggg gaagtactcc aggcagtaga aggaggaacg tcccacagac tgactgccat 1140

tgttgagagt caggtagccg tactgaggaa tcatgaagac gtccgccggg aacggaggca 1200

ggcagccctg gtgcgcagag ccgaggacgt acggcagctg gtattccgag tccgagaata 1260

cctgaatcgt gctggtaagg ttattagcga tggtcgtaac gccgtcattc gtcgtgacct 1320

ccttgacctg gatgttgaag agcttgaacc gcagcttctt gggccggaat ccccagttgt 1380

tgttgatgag tcgctgccag tcacgtggtg agaagtggca gtggaatctg ttaaagtcaa 1440

aatacccccа gggggtgctg tagccgaagt aggtgttgtc gttggtacta cctgcagttt 1500

cactggagat ttgctcgtag aggtggttgt tgtaggtggg cagggcccag gttcgggtgc 1560

tggtggtaat gactctgtcg cccagccatg tggaatcgca atgccaattt cctgaggcat 1620

tacccactcc gtcggcacct tcgttattgt ctgccattgg tgcgccaccg cctgcagcca 1680

ctgtaccaga tcccacacta gagggcgctg ctggaggttc tccgagaggt tgagggtcgg 1740

ggactgactc tgagtcgcca gtctgaccga aattgagtct ctttctggcg ggctgctggc 1800

ccttcttgcc gatgcccgtg gaggagtcgg gggaacgctg aggtgacggc tctaccggtc 1860

tcttctttgc aggagccgtc ttagcgcctt cctcaaccag accgagaggt tcgagaaccc 1920

gcttcttggc ctggaagact gctcgcccga ggttgccccc aaatgacgta tcttcttgca 1980

gacgctcctg aaactcggcg tcggcgtggt tataccgcag gtacgggttg tcacccgcat 2040

tgagctgctg gtcgtaggcc ttgtcgtgct cgagggccgc tgcgtccgcc gcgttgacgg 2100

gctcccccct gtcgagtccg ttgaagggtc cgaggtactt gtagccagga agcaccagac 2160

cccggccgtt gtcctgcttt tgctggttgg ctttgggttt cggggctcca ggtttcaggt 2220

cccaccactc gcgaatgccc tcagagaggt tgtcctcgag ccaatctgga agataaccat 2280

cggcagccat acctgattta aatcatttat tgttcaaaga tgcagtcatc caaatccaca 2340

ttgaccagat cgcaggcagt gcaagcgtct ggcacctttc ccatgatatg atgaatgtag 2400

cacagtttct gatacgcctt tttgacgaca gaaacgggtt tagattctga cacgggaaag 2460

cactctaaac agtctttctg tccgtgagtg aagcagatat ttgaattctg attcattctc 2520

tcgcattgtc tgcagggaaa cagcatcaga ttcatgccca cgtgacgaga acatttgttt 2580

tggtacctgt ctgcgtagtt gatcgaagct tccgcgtctg acgtcgatgg ctgcgcaact 2640

gactcgcgca cccgtttggg ctcacttata tctgcgtcac tgggggcggg tcttttcttg 2700

gctccaccct ttttgacgta gaattcatgc tccacctcaa ccacgtaatc ctttgcccac 2760

cggaaaaagt ctttgacttc ctgcttggtg accttcccaa agtcatgatc cagacggcgg 2820

gtgagttcaa atttgaacat ccggtcttgc aacggctgct ggtgttcgaa ggtcgttgag 2880

ttcccgtcga tcacggcgca catgttggtg ttggagatga cgatcgcggg agtcgggtct 2940

atctgggccg aggacttgca tttctggtcc acgcgcacct tgcttcctcc gagaatggct 3000

ttggccgact ccacgacctt ggcggtcatc ttcccctcct cccaccagat caccatcttg 3060

tcgacacagt cgttgaaggg aaagttctca ttggtccagt tgacgcagcc gtagaaaggg 3120

cgaattc 3127

<210> 16
<211> 3106
<212> DNA
<213> new AAV serotype, clone 24-1

<400> 16
gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat caaccggttt 60

attgattaac aagtaattac aggttacggg tgaggtaacg ggtgccaatg gggcgaggct 120

cagtataaac cccttcgttg ttgacagcaa attccacatt attagacttg gcataatttg 180

aggtgtactg aatctctgga ttccagcgtt tgctgttttc tttctgcagt tcccactcga 240

tctccacgct gacctggccg gtgctgtact gcgtgataaa tgaggcaaac ttggcaggag 300

taaacacctc tggaggatta gcaggtaccg gggtgttttt gatgagaatt tgaggaggcg 360

ggtgtttgag tccaaatccg cccatcaggg gagacgggtg aaagttgccg tccgtgtgag 420

gaattttggc ccagatggga ccctgcaggc acacgtcccg gttctgccag accatgccgg 480

gcagagcccc ctggctgttg acagtctgtg tctggggtcc ggccgtagac gattgcaggt 540

tgctggagac cacaccgtat tcttctgtag ccacgggatt ggtggttttg atctcctcct 600

cgctggtcat tagcacgttt tccagcgttg tcttgttggc agcccccgtt ttgccaaaaa 660

ccagcactcc gttgatggga aagaactggt cctcgtcgtc cttgttggtg gccatggcta 720

cgcccgggtt ggttaatgaa tttctaccat tcagatggta tttagtggcc ccggtccagg 780

caaagttact gttgttgttg ctgtctatgt tttttgacag tctctgctgc cgataacagg 840

gtccgggcag ccagttcttt gattgctcgg ccatggtgtt gggcccagcc tgatggaact 900

gcagctccct tgtggacccc gtagtgctct gggtccgggc caggtagtac aggtactggt 960

cgatgagggg attcatcagc cggtctaggc tctggctgtg cacatagctg ctgtggaaag 1020

gcacttcctc aaaggtgtag ctgaattcaa agttattgcc cgttctcagc atctgagaag 1080

gaaagtactc caggcagtag aaggaggaac gtcccacaga ctgactgccg ttgtttagag 1140

tcagatatcc gtactgagga atcatgaaca cgtccgcagg gaacggaggg aggcagccct 1200

ggtgcgcaga gccgaggacg tacggcagtt ggtactccga gtccgagaag acctgaatcg 1260

tgctggtaag gttattagcg atggtcgtaa cgccgtcgtt cgtcgtgacc tccttgacct 1320

ggatgttgaa caacttgaac cgcagctttc tgggccggaa tccccagttg ttgttgatga 1380

gtcgctgcca gtcacgtggt gagaagtggc agtggaatct gttgaagtca aaatagcccc 1440

agggggtgct gtagctgaag aagtggttgt cgttggtagc cccgctctga cttgatatct 1500

gcttgtagag gtggttgttg taggtgggca gggcccaggt gcgggtgctg gtggtgatga 1560

ctctgtcgcc cagccatgtg gaatcgcaat gccaatttcc ggaggcatta cccactccgt 1620

cggcgccttc gttattgtct gccattggtg cgccaccgcc tgcagccatt gtaccagatc 1680

ccagacctga gggcgcggcg ggaggttctc cgagaggttg ggggtcgggc actgactctg 1740

agtcgccagt ctgcccaaag ttgagcttct ttttagcggg ctgctggcct ttcttgccga 1800

tgcccgtgga ggagtcgggg gattctatgg gtctcttctt tccaggagcc gtcttagcga 1860

cttcctcaac cagaccgaga ggttcgagaa cccgcttctt ggcctggaag actgctcgcc 1920

cgaggttgcc cccaaaagac gtatcttctt gaagacgctc ctgaaactcg gcgtcggcgt 1980

ggttgtactt gaggtacggg ttgtcccccc gctcgagctg cttgtcgtag gccttgtcgt 2040

gctcgagggc cgcggcgtct gcctcgttga ccggctctcc cttgtcgagt ccgttgaagg 2100

gtctgaggta cttgtagcca ggaagcacca gaccccggcc gtcgtcctgc ttttgctggt 2160

tggctttggg tttcggggct ccaggtttca agtcccacca ctcgcgaatg ccctcagaga 2220

ggttgtcctc gagccaatct ggaagataac catcggcagc catacctggt ttaagtcatt 2280

tattgctcag aaacacagtc atccaggtcc acgttgacca gatcgcaggc cgagcaagca 2340

atctcgggag cccgccccag cagatgatga atggcacaga gtttccgata cgtcctcttt 2400

ctgacgaccg gttgagattc tgacacgccg gggaaacatt ctgaacagtc tctggtcccg 2460

tgcgtgaagc aaatgttgaa attctgattc actctctcgc atgtcttgca gggaaacagc 2520

atctgaagca tgcccgcgtg acgagaacat ttgttttggt acctgtcggc aaagtccacc 2580

ggagctcctt ccgcgtctga cgtcgatgga ttcgcgactg aggggcaggc ccgcttgggc 2640

tcgcttttat ccgcgtcatc gggggcgggt ctcttgttgg ccccaccctt tctgacgtag 2700

aacccatgcg ccacctcggt cacgtgatcc tgcgcccagc ggaagaacct tttgacttcc 2760

tgctttgtca ccttgccaaa gttatgctcc agacggcggg tgggttcaaa tttgaacatc 2820

cggtcctgca acggctgctg gtgctcgaag gtggcgctgt tcccgtcaat cacggcgcac 2880

atgttggtgt tggaggtgac ggtcacgggg gtggggtcga tctgggcgga cgacttgcac 2940

ttttggtcca cgcgcacctt gctgccgccg agaatggcct tggcggactc cacgaccttg 3000

gccgtcatct tgccctcctc ccaccagatc accatcttgt cggcgcaatc gttgaaggga 3060

aagttctcat tggtccagtt gacgcagccg tagaaagggc gaattc 3106

<210> 17
<211> 3102
<212> DNA
<213> new AAV serotype, clone 27-3

<400> 17
gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat caaccggttt 60

attgattaac aagtaattac aggttacggg tgaggtaacg ggtgccaatg gggcgaggct 120

cagtataaac cccttcgttg ttgacagcaa attccacatt attagacttg gcataatttg 180

aggtgtactg aatctctgga ttccagcgtt tgctgttttc tttctgcagt tcccactcga 240

tctccacgct gacctggccg gtgctgtact gcgtgataaa tgaggcaaac ttggcaggag 300

taaacacctc tggaggatta gcaggtaccg gggtgttttt gatgagaatt tgaggaggcg 360

ggtgtttgag tccaaatccg cccatcaggg gagacgggtg aaagttgccg tccgtgtgag 420

gaatttcggc ccagatggga ccctgcaggt acacgtcccg gttctgccag accatgccgg 480

gcagagcccc ctggctgttg acagtctgtg tccggggtcc ggccgtagac gattgcaggt 540

tgctggagac cacaccgtat tcttctgtag ccacgggatt ggtggttttg atctcctcct 600

cgctggtcat tagcacgttt tccagcgttg tcttgttggc agcccccgtt ttgccaaaaa 660

ccagcactcc gttgatggga aggaactggt cctcgtcgtc cttgttggtg gccatggcta 720

cgcccgggtt ggttaatgaa tttctaccat tcagatggta tttagtggcc ccggtccagg 780

caaagttact gttgttgttg ctgtctatgt tttttgacag tctctgctgc cgataacagg 840

gtccgggcag ccagttcttt gattgctcgg ccacggtgtt gggcccagcc tgatggaact 900

gcagctccct tgtggacccc gtagtgctct gggtccgggc caggtagtac aggtactggt 960

cgatgagggg attcatcagc cggtccaggc tctggctgtg cgcatagctg ctgtggaaag 1020

gcacttcctc aaaggtgtag ctgaattcaa agttattgcc cgttctcagc atctgagaag 1080

gaaagtactc caggcagcag aaggaggaac gtcccacaga ctgactgccg ttgtttagag 1140

tcagatatcc gtactgagga atcatgaaca cgtccgcagg gaacggaggg aggcagccct 1200

ggtgcgcaga gccgaggacg tacggcagtt ggtactccga gtccgagaag acctgaatcg 1260

tgctggtaag gttattagcg atggtcgtaa cgccgtcgtt cgtcgtgacc tccttgacct 1320

ggatgttgaa caacttgaac cgcagctttc tgggccggaa tccccagttg ttgttgatga 1380

gtcgctgcca gtcacgtggt gagaagtggc agtggaatct gttgaagtca aaatagcccc 1440

agggggtgct gtagccgaag aagtggttgt cgttggtagc cccgctctga cttgatatct 1500

gcttgtagag gtggttgttg taggtgggca gggcccaggt gcgggtgctg gtggtgatga 1560

ctctgtcgcc cagccatgtg gaatcgcaat gccaatttcc ggaggcatta cccactccgt 1620

cggcgccttc gttattgtct gccattggtg cgccaccgcc tgcagccatt gtaccagatc 1680

ccagacctga gggcgcggcg ggaggttctc cgagaggttg ggggtcgggc actgactctg 1740

agtcgccagt ctgcccaaag ttgagcttct ttttagcggg ctgctggcct ttcttgccga 1800

tgcccgtgga ggagtcgggg gattctatgg gtctcttctt tccggaagcc gtcttagcgc 1860

cttcctcaac cagaccgaga ggttcgagaa cccgcttctt ggcctggaag actgctcgcc 1920

cgaggttgcc cccaaaagac gtatcttctt gaagacgctc ctgaaactcg gcgtcggcgt 1980

ggttgtactt gaggtacggg ttgtcccccc gctcgagctg cttgtcgtag gccttgtcgt 2040

gctcgagggc cgcggcgtct gcctcgttga ccggctctcc cttgtcgagt ccgttgaagg 2100

gtccgaggta cttgtagcca ggaagcacca gaccccggcc gtcgtcctgc ttttgctggt 2160

tggctttggg tttcgggggct ccaggtttca agtcccacca ctcgcgaatg ccctcagaga 2220

ggttgtcctc gagccaatct ggaagataac catcggcagc catacctggt ttaagtcatt 2280

tattgctcag aaacacagtc atccaggtcc acgttgacca gatcgcaggc cgagcaagca 2340

atctcgggag cccgccccag cagatgatga atggcacaga gtttccgata cgtcctcttt 2400

ctgacgaccg gttgagattc tgacacgccg gggaaacatt ctgaacagtc tctggtcccg 2460

tgcgtgaagc aaatgttgaa attctgattc attctctcgc atgtcttgca gggaaacagc 2520

atctgaagca tgcccgcgtg acgagaacat ttgttttggt acctgtcggc aaagtccacc 2580

ggagctcctt ccgcgtctga cgtcgatgga tccgcgactg aggggcaagc ccgcttgggc 2640

tcgcttttat ccgcgtcatc gggggcgggt ctcttgttgg ctccaccctt tctgacgtag 2700

aactcatgcg ccacctcggt cacgtgatcc tgcgcccagc ggaagaactc tttgacttcc 2760

tgctttgtca ccttgccaaa gtcatgctcc agacggcggg tgagttcaaa tttgaacatc 2820

cggtcttgta acggctgctg gtgctcgaag gtggtgctgt tcccgtcaat cacggcgcac 2880

atgttggtgt tggaagtgac gatcacgggg gtgggatcga tctgggcgga cgacttgcac 2940

ttttggtcca cgcgcacctt gctgccgccg agaatggcct tggcggactc cacgaccttg 3000

gccgtcatct tgccctcctc ccaccagatc accatcttgt cgacgcaatc gttgaaggga 3060

aagttctcat tggtccagtt gacgcagccg aagggcgaat tc 3102

<210> 18
<211> 3106
<212> DNA
<213> new AAV serotype, clone 7-2

<400> 18
gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat cagccggttt 60

attgattaac aagtaattac aggttacggg tgaggtaacg ggtgccaatg gggcgaggct 120

cagtataaac cccttcgttg ttgacagcaa attccacatt attagacttg gcataatttg 180

aggtgtactg aatctctgga ttccagcgtt tgctgttttc tttctgcagt tcccactcga 240

tctccacgct gacctggccg gtgctgtact gcgtgataaa tgaggcaaac ttggcaggag 300

taaacacctc tggaggatta gcaggtaccg gggtgttttt gatgagaatt tgaggaggcg 360

ggtgtttgag tccaaatccg cccatcaggg gagacgggtg aaagttgccg tccgtgtgag 420

gaattttggc ccagatggga ccctgcaggt acacgtcccg gttctgccag accatgccgg 480

gcagagcccc ctggctgttg acagtctgtg tctggggtcc ggccgtagac gattgcaggt 540

tgctggagac cacaccgtat tctttctgtag ccacgggatt ggtggttttg atctcctcct 600

cgctggtcat tagcacgttt tccagcgttg tcttgttggc agcccccgtt ttgccaaaaa 660

ccagcactcc gttgatggga aagaactggt cctcgtcgtc cttgttggtg gccatggcta 720

cgcccgggtt ggttaatgaa tttctaccat tcagatggta tttagtggcc ccggtccagg 780

caaagttact gttgttgttg ctgtctatgt tttttgacag tctctgctgc cgataacagg 840

gtccgggcag ccagttcttt gattgctcgg ccatggtgtt gggcccagcc tgatggaact 900

gcagctccct tgtggacccc gtagtgctct gggtccgggc caggtagtac aggtactggt 960

cgatgagggg attcatcagc cggtccaggc tctggctgtg cgcatagctg ctgtggaaag 1020

gcacttcctc aaaggtgtag ctgaattcaa agttatcgcc cgttctcagc atctgagaag 1080

gaaagtactc caggcagtag aaggaggaac gtcccacaga ctgactgccg ttgtttagag 1140

tcagatatcc gtactgagga atcatgaaca cgtccgcagg gaacggaggg aggcagccct 1200

ggtgcgcaga gccgaggacg tacggcagtt ggtactccga gtccgagaag acctgaatcg 1260

tgctggtaag gttattagcg atggtcgtaa cgccgtcgtt cgtcgtgacc tccttgacct 1320

ggatgttgaa caacttgaac cgcagctttc tgggccggaa tccccagttg ttgttgatga 1380

gtcgctgcca gtcacgtggt gagaagtggc agtggaatct gttgaagtca aaatagcccc 1440

agggggtgct gtagccgaag aagtggttgt cgttggtagc cccgctctga cttgatatct 1500

gcttgtagag gtggttgttg taggtgggca gggcccaggt gcgggtgctg gtggtgatga 1560

ctctgtcgcc cagccatgtg gaatcgcaat gccaatttcc ggaggcatta cccactccgt 1620

cggcgccttc gttattgtct gccattggtg cgccaccgcc tgcagccatt gtaccagatc 1680

ccagacctga gggcgcggcg ggaggttctc cgagaggttg ggggtcgggc actgactctg 1740

agtcgccagt ctgcccaaag ttgagcttct ttttagcggg cggctggccg ttcttgccga 1800

tgcccgtgga ggagtcgggg gattctatgg gtctcttctt tccaggagcc gtcttagcgc 1860

cttcctcaac cagaccgaga ggttcgagaa cccgcttctt ggcctggaag actgctcgcc 1920

cgaggtttgcc cccaaaagac gtatcttctt gaagacgctc ctgaaactcg gcgtcggcgt 1980

ggttgtactt gaggtacggg ttgtcccccc gctcgagctg cttgtcgtag gccttgtcgt 2040

gctcgagggc cgcggcgtct gcctcgttga ccggctctcc cttgtcgagt ccgttgaagg 2100

gtccgaggta cctgtagcca ggaagcacca gaccccggcc gtcgtcctgc ttttgctggt 2160

tggctttggg tttcggggct ccaggtttca agtcccacca ctcgcgaatg ccctcagaga 2220

ggttgccctc gagccaatct ggaagataac catcggcagc catacctggt ttaagtcatt 2280

tattgctcag aaacacagtc atccaggtcc acgttggcca gatcgcaggc cgagcaagca 2340

atctcgggag cccgccccag cagatgatga atggcacaga gtttccgata cgtcctcttt 2400

ctgacgaccg gttgagattc tgacacgccg gggaaacatt ctgaacagtc tctggtcccg 2460

tgcgtgaagc aaatgttgaa attctgattc attctctcgc atgtcttgca ggggaacagc 2520

atctgaagca tgcccgcgtg acgagaacat ttgttttggt acctgtcggc aaagtccacc 2580

ggagctcctt ccgcgtctga cgtcgatgga tccgcgactg aggggcaggc ccgcttgggc 2640

tcgcttttat ccgcgtcatc gggggcgggt ctcttgttgg ctccaccctt tctgacgtag 2700

aactcatacg ccacctcggt cacgtgatcc tgcgcccagc ggaagaactc tttgacttcc 2760

tgctttgtca ccttgccaaa gtcatgctcc agacggcggg tgagttcaaa tttgaacatc 2820

cggtcttgta acggctgctg gtgctcgaag gtggtgctgt tcccgtcaat cacggcgcac 2880

atgttggtgt tggaagtgac gatcacgggg gtgggatcga tctgggcgga cgacttgcac 2940

ttttggtcca cgcgcacctt gctgccgccg agaatggcct tggcggactc cacgaccttg 3000

gccgtcatcc tgccctcctc ccaccagatc accatcttgt cgacgcaatc gttgaaggga 3060

aagttctcat tggtccagtt gacgcagccg tagaaagggc gaattc 3106

<210> 19
<211> 3105
<212> DNA
<213> new AAV serotype, clone C1

<400> 19
gaattcgccc ttgctgcgtc aactggacca atgagaactt tcccttcaac gattgcgtcg 60

acaagatggt gatctggtgg gaggagggca agatgaccgc caaggtcgtg gagtccgcca 120

aggccattct gggcggaagc aaggtgcgcg tggaccaaaa gtgcaagtca tcggcccaga 180

tcgaccccac gcccgtgatc gtcacctcca acaccaacat gtgcgccgtg atcgacggga 240

acagcaccac cttcgagcac cagcagccgc tgcaggaccg catgttcaag ttcgagctca 300

cccgccgtct ggagcacgac tttggcaagg tgaccaagca ggaagtcaaa gagttcttcc 360

gctgggctca ggatcacgtg actgaggtgg cgcatgagtt ctacgtcaga aagggcggag 420

ccaccaaaag acccgccccc agtgacgcgg atataagcga gcccaagcgg gcctgccgct 480

cagttgcgga gccatcgacg tcagacgcgg aagcaccggt ggactttgcg gacaggtacc 540

aaaacaaatg ttctcgtcac gcgggcatgc ttcagatgct gtttccctgc aagacatgcg 600

agagaatgaa tcagaatttc aacgtctgct tcacgcacgg ggtcagagac tgctcagagt 660

gcttccccgg cgcgtcagaa tctcaacccg tcgtcagaaa aaagacgtat cagaaactgt 720

gcgcgattca tcatctgctg gggcgggcac ccgagattgc gtgttcggcc cgcgatctcg 780

tcaacgtgga cttggatgac tgtgtttctg agcaataaat gacttaaacc aggtatggct 840

gctgacggtt atcttccaga ttggctcgag gacaacctct ctgagggcat tcgcgagtgg 900

tgggacctga aacctggagc ccccaagccc aaggccaacc agcagaagca ggacgacggc 960

cggggtctgg tgcttcctgg ctacaagtac ctcggaccct tcaacggact cgacaagggg 1020

gagcccgtca acgcggcgga cgcagcggcc ctcgagcacg acaaggccta cgaccagcag 1080

ctcaaagcgg gtgacaatcc gtacctgcgg tataaccacg ccgacgccga gtttcaggag 1140

cgtctgcaag aagatacgtc ttttgggggc aacctcgggc gagcagtctt ccaggccaag 1200

aagagggtac tcgaacctct gggcctggtt gaagaaggtg ctaagacggc tcctggaaag 1260

aagagaccgt tagagtcacc acaagagccc gactcctcct caggaatcgg caaaaaaggc 1320

aaacaaccag ccaaaaagag actcaacttt gaagaggaca ctggagccgg agacggaccc 1380

cctgaaggat cagataccag cgccatgtct tcagacattg aaatgcgtgc agcaccgggc 1440

ggaaatgctg tcgatgcggg acaaggttcc gatggagtgg gtaatgcctc gggtgattgg 1500

cattgcgatt ccacctggtc tgagggcaag gtcacaacaa cctcgaccag aacctgggtc 1560

ttgcccacct acaacaacca cttgtacctg cggctcggaa caacatcaaa cagcaacacc 1620

tacaacggat tctccacccc ctggggatac tttgacttta acagattcca ctgtcacttc 1680

tcaccacgtg actggcaaag actcatcaac aacaactggg gactacgacc aaaagccatg 1740

cgcgttaaaa tcttcaatat ccaagttaag gaggtcacaa cgtcgaacgg cgagactacg 1800

gtcgctaata accttaccag cacggttcag atatttgcgg actcgtcgta tgagctcccg 1860

tacgtgatgg acgctggaca agagggaagt ctgtctcctt tccccaatga cgtcttcatg 1920

gtgcctcaat atggctactg tggcattgtg actggcgaaa atcagaacca gacggacaga 1980

aatgctttct actgcctgga gtattttcct tcacaaatgc tgagaactgg caataacttt 2040

gaaatggctt acaactttgg gaaggtgccg ttccactcaa tgtatgctta cagccagagc 2100

ccggacagac tgatgaatcc cctcctggac cagtacctgt ggcacttaca gtcgaccacc 2160

tctggagaga ctctgaatca aggcaatgca gcaaccacat ttggaaaaat caggagtgga 2220

gactttgcct tttacagaaa gaactggctg cctgggcctt gtgttaaaca gcagagactc 2280

tcaaaaactg ccagtcaaaa ttacaagatt cctgccagcg ggggcaacgc tctgttaaag 2340

tatgacaccc actatacctt aaacaaccgc tggagcaaca tagcgcctgg acctccaatg 2400

gcaacagctg gaccttcaga tggggacttc agcaacgccc agctcatctt ccctggacca 2460

tcagtcaccg gaaacacaac aacctcagca aacaatctgt tgtttacatc agaagaagaa 2520

attgctgcca ccaacccaag agacacggac atgtttggtc agattgctga caataatcag 2580

aatgctacaa ctgctcccat aaccggcaac gtgactgcta tgggagtgct tcctggcatg 2640

gtgtggcaaa acagagacat ttactaccaa gggccaattt gggccaagat cccacacgcg 2700

gacggacatt ttcatccttc accgctaatt ggcggttttg gactgaaaca tccgcctccc 2760

cagatatttta tcaaaaacac ccccgtacct gccaatcctg cgacaacctt cactgcagcc 2820

agagtggact ctttcatcac acaatacagc accggccagg tcgctgttca gattgaatgg 2880

gaaatcgaaa aggaacgctc caaacgctgg aatcctgaag tgcagtttac ttcaaactat 2940

gggaaccagt cttctatgtt gtgggctccc gatacaactg ggaagtatac agagccgcgg 3000

gttattggct ctcgttattt gactaatcat ttgtaactgc ctagttaatc aataaaccgt 3060

gtgattcgtt tcagttgaac tttggtctct gcgaagggcg aattc 3105

<210> 20
<211> 3105
<212> DNA
<213> new AAV serotype, clone C3

<400> 20
gaattcgccc ttgctgcgtc aactggacca atgagaactt tcccttcaac gattgcgtcg 60

acaagatggt gatctggtgg gaggagggca agatgaccgc caaggtcgtg gagtccgcca 120

aggccattct gggcggaagc aaggtgcgcg tggaccaaaa gtgcaagtca tcggcccaga 180

tcgaccccac gcccgtgatc gtcacctcca acaccaacat gtgcgccgtg atcgacggga 240

acagcaccac cttcgagcac cagcagccgc tgcaggaccg catgttcaag ttcgagctca 300

cccgccgtct ggagcacgac tttggcaagg tgaccaagca ggaagtcaaa gagttcttcc 360

gctgggctca ggatcacgtg actgaggtgg cgcatgagtt ctacgtcaga aagggcggag 420

ccaccaaaag acccgccccc agtgacgcgg atataagcga gcccaagcgg gcctgccact 480

cagttgcgga gccatcgacg tcagacgcgg aagcaccggt ggactttgcg gacaggtacc 540

aaaacaaatg ttctcgtcac gcgggcatgc ttcagatgct gtttccctgc aagacatgcg 600

agagaatgaa tcagaatttc aacgtctgct tcacgcacgg ggtcagagac tgctcagagt 660

gcttccccgg cgcgtcagaa tctcaacccg tcgtcagaaa aaagacgtat cagaaactgt 720

gcgcgattca tcatctgctg gggcgggcac ccgagattgc gtgttcggcc tgcgatctcg 780

tcaacgtgga cttggatgac tgtgtttctg agcaataaat gacttaaacc aggtatggct 840

gctgacggtt atcttccaga ttggctcgag gacaacctct ctgagggcat tcgcgagtgg 900

tgggacctga aacctggagc ccccaagctc aaggccaacc agcagaagca ggacgacggc 960

cggggtctgg tgcttcctgg ctacaagtac ctcggaccct tccacggact cgacaagggg 1020

gagcccgtca acgcggcgga cgcagcggcc ctcgagcacg acaaggccta cgaccagcag 1080

ctcaaagcgg gtgacaatcc gtacctgcgg tataaccacg ccgacgccga gtttcaggag 1140

cgtctgcaag aagatacgtc ttttgggggc aacctcgggc gagcagtctt ccaggccaag 1200

aagagggtac tcgaaccact gggcctggtt gaagaaggtg ctaagacggc tcctggaaag 1260

aagagaccgt tagagtcacc acaagagccc gactcctcct caggaatcgg caaaaaaggc 1320

aaacaaccag ccaaaaagag actcaacttt gaagaggaca ctggagccgg agacggaccc 1380

cctgaaggat cagataccag cgccatgtct tcagacattg aaatgcgtgc agcaccgggc 1440

ggaaatgctg tcgatgcggg acaaggttcc gatggagtgg gtaatgcctc gggtgattgg 1500

cattgcgatt ccacctggtc tgagggcaag gtcacaacaa cctcgaccag aacctgggtc 1560

ttgcccacct acaacaacca cttgtacctg cggctcggaa caacatcaaa cagcaacacc 1620

tacaacggat tctccacccc ctggggatac tttgacttta acagattcca ctgtcacttc 1680

tcaccacgtg actggcaaag actcatcaac aacaactggg gactacgacc aaaagccatg 1740

cgcgttaaaa tcttcaatat ccaagttaag gaggtcacaa cgtcgaacgg cgagactacg 1800

gtcgctaata accttaccag cacggttcag atatttgcgg actcgtcgta tgagctcccg 1860

tacgtgatgg acgctggaca agagggaagt ctgcctcctt tccccaatga cgtcttcatg 1920

gtgcctcaat atggctactg tggcattgtg actggcgaaa atcagaacca gacggacaga 1980

aatgctttct actgcctgga gtattttcct tcacaaatgc tgagaactgg caataacttt 2040

gaaatggctt acaactttga gaaggtgccg ttccactcaa tgtatgctca cagccagagc 2100

ctggacagac tgatgaatcc cctcctggac cagtacctgt ggcacttaca gtcgaccacc 2160

tctggagaga ctctgaatca aggcaatgca gcaaccacat ttggaaaaat caggagtgga 2220

gactttgcct tttacagaaa gaactggctg cctgggcctt gtgttaaaca gcagagattc 2280

tcaaaaactg ccagtcaaaa ttacaagatt cctgccagcg ggggcaacgc tctgttaaag 2340

tatgacaccc actatacctt aaacaaccgc tggagcaaca tagcgcctgg acctccaatg 2400

gcaacagctg gaccttcaga tggggacttc agcaacgccc agctcatctt ccctggacca 2460

tcagtcaccg gaaacacaac aacctcagca aacaatctgt tgtttacatc agaaggagaa 2520

attgctgcca ccaacccaag agacacggac atgtttggtc agattgctga caataatcag 2580

aatgctacaa ctgctcccat aaccggcaac gtgactgcta tgggagtgct tcctggcatg 2640

gtgtggcaaa acagagacat ttactaccaa gggccaattt gggccaagat cccacacgcg 2700

gacggacatt ttcatccttc accgctaatt ggcggttttg gactgaaaca tccgcctccc 2760

cagatatttc tcaaaaacac ccccgtacct gccaatcctg cgacaacctt cactgcagcc 2820

agagtggact ctttcatcac acaatacagc accggccagg tcgctgttca gattgaatgg 2880

gaaatcgaaa aggaacgctc caaacgccgg aatcctgaag tgcagtttac ttcaaactat 2940

gggaaccagt cttctatgtt gtgggctccc gatacaactg ggaagtatac agagccgcgg 3000

gttattggct ctcgttattt gactaatcat ttgtaactgc ctagttaatc aataaaccgt 3060

gtgattcgtt tcagttgaac tttggtctct gcgaagggcg aattc 3105

<210> 21
<211> 3105
<212> DNA
<213> new AAV serotype, clone C5

<400> 21
gaattcgccc ttcgcagaga ccaaagttca actgaaacga atcacacggt ttattgatta 60

actaggcagt tacaaatgat tagtcaaata acgagagcca ataacccgcg gctctgtata 120

cttcccagtt gtatcgggag cccacaacat agaagactgg ttcccacagt ttgaagtaaa 180

ctgcacttca ggattccagc gtttggagcg ttccttttcg atttcccatt caatctgaac 240

agcgacctgg ccggtgctgt attgtgtgat gaaagagtcc actctggctg cagtgaaggt 300

tgtcgcagga taggcaggta cgggggtgtt tttgataaat atctggggag gcggatgttt 360

cagtccaaaa ccgccaatta gcggtgaagg atgaaaatgt ccgtccgcgt gtgggatctt 420

ggcccaaatt ggcccttggt agtaaatgtc tctgttttgc cacaccatgc caggaagcac 480

tcccatagca gtcacgttgc cggttatggg agcagttgta gcattctgat tattgtcagc 540

aatctgacca aacatgtccg tgtctcttgg gttggtggca gcaatttctt cttctgatgt 600

aaacaacaga ttgtttgctg aggttgttgt gtttccggtg actgatggtc cagggaagat 660

gagctgggcg ttgctgaagt ccccatctga aggtccagct gttgccattg gaggtccagg 720

cgctatgttg ctccagcggt tgtttaaggt atagtgggtg tcatacttta acagagcgtt 780

gcccccgctg gcaggaatct tgtaattttg actggcagtt tttgagaatc tctgctgttt 840

aacacaaggc ccaggcagcc agttctttct gtaaaaggca aagtctccac tcctgatttt 900

tccaaatgtg gttgctgcat tgccttgatt cagagtctct ccagaggtgg tcgactgtaa 960

gtgccacagg tactggtcca ggaggggatt catcagtccg tccaggctct ggctgtgagc 1020

atacattgag tggaacggca ccttctcaaa gttgtaagcc gtttcaaagt tattgccagt 1080

tctcagcatt tgtgaaggaa aatactccag gcagtagaaa gcatttctgt ccgtctggtt 1140

ctgattttcg ccagtcacaa tgccacagta gccatattga ggcaccatga agacgtcatt 1200

ggggaaagga ggcagacttc cctcttgtcc agcgtccatc acgtacggga gctcatacga 1260

cgagtccgca aatatctgaa ccgtgctggt aaggttatta gcgaccgtag tctcgccgtt 1320

cgacgttgtg acctccttaa cttggatatt gaagatttta acgcgcatgg cttttggtcg 1380

tagtccccag ttgttgttga tgagtctttg ccagtcacgt ggtgagaagt gacagtggaa 1440

tctgttaaag tcaaagtatc cccagggggt ggagaatccg ttgtaggtgt tgctgtttga 1500

tgttgttccg agccgcaggt acaagtggtt gttgtaggtg ggcaagaccc aggttctggt 1560

cgaggttgtt gtgaccttgc cctcagacca ggtggaatcg caatgccaat cacccgaggc 1620

attacccact ccatcggaac cttgtcccgc atcgacagca tttccgcccg gtgctgcacg 1680

catttcaatg tctgaagaca tggcgctggt atctgatcct tcaggggtc cgtctccggc 1740

tccagtgtcc tcttcaaagt tgagtctctt tttggctggt tgtttgcctt ttttgccgat 1800

tcctgaggag gagtcgggct cttgtggtga ctctaacggt ctcttctttc caggagccgt 1860

cttagcacct tcttcaacca ggcccagagg ttcgagtacc ctcttcttgg cctggaagac 1920

tgctcgcccg aggttgcccc caaaagacgt atcttcttgc agacgctcct gaaactcggc 1980

gtcggcgtgg ttataccgca ggtacggatt gtcacccgct ttgagctgct ggtcgtaggc 2040

cttgtcgtgc tcgagggccg ctgcgtccgc cgcgttgacg ggctcccctt tgtcgagtcc 2100

gttgaagggt ccgaggtact cgtagccagg aagcaccaga ccccggccgt cgtcctgctt 2160

ctgctggttg gccttgggct tgggggctcc aggtttcagg tcccaccact cgcgaatgcc 2220

ctcagagagg ttgtcctcga gccaatctgg aagataaccg tcagcagcca tacctggttt 2280

aagtcattta ttgctcagaa acacagtcat ccaagtccac gttgacgaga tcgcaggccg 2340

aacacgcaat ctcgggtgcc cgccccagca gatgatgaat cgcgcacagt ttctgatacg 2400

tctttttttct gacgacgggt tgagattctg acgcgccggg gaagcactct gagcagtctc 2460

tgaccccgtg cgtgaagcag acgttgaaat tctgattcat tctctcgcat gtcttgcagg 2520

gaaacagcat ctgaagcatg cccgcgtgac gagaacattt gttttggtac ctgtccgcaa 2580

ggtccaccgg tgcttccgcg tctgacgtcg atggctccgc aactgagggg caggcccgct 2640

tgggctcgct tatatccgcg tcactggggg cgggtctttt ggtggctccg cctttctga 2700

cgtagaactc atgcgccacc tcagtcacgt gatcctgagc ccagcggaag aactctttga 2760

cttcctgctt ggtcaccttg ccaaagtcgt gctccagacg gcgggtgagc tcgaacttga 2820

acatgcggtc ctgcagcggc tgctggtgct cgaaggtggt gctgttcccg tcgatcacgg 2880

cgcacatgtt ggtgttggag gtgacgatca cgggcgtggg gtcgatctgg gccgatgact 2940

tgcacttttg gtccacgcgc accttgcttc cgcccagaat ggccttggcg gactccacga 3000

ccttggcggt catcttgccc tcctcccacc agatcaccat cttgtcgacg caatcgttga 3060

agggaaagtt ctcattggtc cagttgacgc agcaagggcg aattc 3105

<210> 22
<211> 3094
<212> DNA
<213> new AAV serotype, clone F1

<400> 22
gaattcgccc ttgctgcgtc aactggacca agagaacttt cccttcaacg attgcgtcga 60

caagatggtg atctggtggg aggagggcaa gatgacggcc aaggtcgtgg agtccgccaa 120

agccattctg ggcggaagca aggtgcgcgt cgaccaaaag tgcaagtcct cggcccagat 180

cgatcccacc cccgtgatcg tcacctccaa caccaacatg tgcgccgtga tcgacgggaa 240

cagcaccacc ttcgagcacc agcagccgtt gcaggaccgg atgttcaaat ttgaactcac 300

ccgccgtctg gaacacgact ttggcaaggt gaccaagcag gaagtcaaag agttcttccg 360

ctgggctagt gatcacgtga ctgaggtgac gcatgagttc tacgtcagaa agggcggagc 420

cagcaaaaga cccgcccccg atgacgcgga tataagcgag cccaagcggg cctgtccctc 480

agtcacggac ccatcgacgt cagacgcgga aggagctccg gtggactttg ccgacaggta 540

ccaaaacaaa tgttctcgtc acgcgggcat gcttcagatg ctgtttccct gcaaaacgtg 600

cgagagaatg aatcagaatt tcaacatttg cttcacgcac ggggtcagag actgtttaga 660

atgtttcccc ggcgtgtcag aatctcaacc ggtcgtcaga aaaaagacgt atcggaagct 720

gtgtgcgatt catcatctgc tggggcgggc acccgagatt gcttgctcgg cctgcgacct 780

ggtcaacgtg gacctggacg actgtgtttc tgagcaataa atgacttaaa ccgggtatgg 840

ctgccgatgg ttatcttcca gattggctcg aggacaacct ctctgagggc attcgcgagt 900

ggtgggacct gaaacctgga gccccgaaac ccaaagccaa ccagcaaaag caggacgacg 960

gccggggtct ggtgcttcct ggctacaagt acctcggacc cttcaacgga ctcgacaagg 1020

gggagcccgt caacgcggcg gacgcagcgg ccctcgagca cgacaaggcc tacgaccagc 1080

agctcaaagc gggtgacaat ccgtacctgc ggtataacca cgccgacgcc gagtttcagg 1140

agcgtctgca agaagatacg tcatttgggg gcaacctcgg gcgagcagtc ttccaggcca 1200

agaagcgggt tctcgaacct ctcggtctgg ttgaggaagg cgctaagacg gctcctggaa 1260

agaagagacc catagactct ccagactcct ccacgggcat cggcaaaaaa ggccagcagc 1320

ccgctaaaaa gaagctcaat tttggtcaga ctggcgactc agagtcagtc cccgaccctc 1380

aacctcttgg agaacctcca gcagcgccct ctagtgtggg atctggtaca atggctgcag 1440

gcggtggcgc accaatggca gacaataacg aaggtgccga cggagtgggt aatgcctcag 1500

gaaattggca ttgcgattcc acatggctgg gcgacagagt catcaccacc agcaccagaa 1560

cctgggccct ccccacctac aacaaccacc tctacaagca aatctccagc agcagctcag 1620

gagccaccaa tgacaaccac tacttcggct acagcacccc ctgggggtat tttgacttta 1680

acagattcca ctgccacttc tcaccacgtg actggcagcg actcatcaac aacaactggg 1740

gattccggcc caagaagctg cggttcaagc tcttcaacat ccaggtcaag gaggtcacaa 1800

cgaatgacgg cgtcacgacc atcgctaata accttaccag cacggttcag gtcttctcgg 1860

actcggaata ccagctgccg tacgtcctcg gctctgcgca ccagggctgc ctgcctccgt 1920

tcccggcgga cgtcttcatg attcctcagt acggctacct gactctgaac aacggcagcc 1980

aatcggtggg ccgttcctcc ttctactgcc tggaatattt cccctctcaa atgctgagaa 2040

cgggcaacaa ctttgagttc agttacagct tcgaggacgt gcctttccac agcagctacg 2100

cgcacagcca gagcctagac cggctgatga accctctcat cgaccagtac ctgtactacc 2160

tggcccggac ccagagcacc acgggttcca ccagggaact gcaatttcat caagctgggc 2220

ccaatactat ggccgagcag tcaaagaact ggctgcctgg accctgctat aggcaacagg 2280

gactgtcaaa gaacttggac tttaacaaca acagcaattt tgcctggact gctgccacta 2340

aatatcatct gaatggcaga aactctttga ccaatcctgg cattcccatg gcaaccaaca 2400

aggatgatga ggaccagttc tttcccatca acggggtact ggtttttggc aagacgggag 2460

ctgccaacaa aactacgctg gaaaacgttc tgatgaccag cgaggaggag atcaagacca 2520

ctaaccctgt ggctacagaa gaatacggtg tggtctccag caacctgcag ccgtctacag 2580

ccgggcctca atcacagact atcaacagcc agggagcact gcctggcatg gtctggcaga 2640

accgggacgt gtatctgcag ggtcccatct gggccaaaat tcctcacacg gatggcaact 2700

ttcacccgtc tcctctgatg ggcggttttg gactcaaaca cccgcctcca cagatcctga 2760

tcaaaaacac acctgtacct gctaatcctc cggaggtgtt tactcctgcc aagtttgcct 2820

ccttcatcac gcagtacagc accggacaag tcagcgtgga aatcgagtgg gagctgcaga 2880

aagaaaacag caagcgctgg aacccagaaa ttcagtatac ttccaattat gccaagtcta 2940

ataatgttga atttgctgtg aaccctgatg gtgtttatac tgagcctcgc cccattggca 3000

ctcgttacct cccccgtaat ctgtaattgc ttgttaatca ataaaccggt tgattcgttt 3060

cagttgaact ttggtctctg cgaagggcga attc 3094

<210> 23
<211> 3095
<212> DNA
<213> new AAV serotype, clone F3

<400> 23
gaattcgccc ttcgcagaga ccaaagttca actgaaacga atcaaccggt ttattgatta 60

acaagcaatt acagattacg ggtgaggtaa cgagtgccaa tggggcgagg ctcagtataa 120

acaccatcag ggttcacagc aaattcaaca ttattagact tggcataatt ggaagtatac 180

tgaatttctg ggttccagcg cttgctgttt tctttctgca gctcccactc gatttccacg 240

ctgacttgtc cggtgctgta ctgcgtgatg aaggaggcaa acttggcagg agtaaacacc 300

tccggaggat tagcaggtac aggtgtgttt ttgatcagga tctgtggagg cgggtgtttg 360

agtccaaaac cgcccatcag aggagacggg tgaaagttgc catccgtgtg aggaattttg 420

gcccagatgg gaccctgcag atacacgtcc cggttctgcc agaccatgcc aggcagtgct 480

ccctggctgt tgatagtctg tgattgaggc ccggctgtag acgactgcag gttgctggag 540

accacaccgt attcttctgt agccacaggg ttagtggtct tgatctcctc ctcgctggtc 600

atcagaacgt tttccagcgt agttttgttg gcagctcccg tcttgccaaa aaccagtacc 660

ccgttgatgg gaaagaactg gtcctcatca tccttgttgg ttgccatggg aatgccagga 720

ttggtcaaag agtttctgcc attcagatga tatttagtgg cagcagtcca ggcaaaattg 780

ctgttgttgt taaagtccaa gttcttttgac agtctctgtt gcctatagca gggtccaggc 840

agccagttct ttgactgctc ggccatagta ttgggcccag cttgatgaaa ttgcagttcc 900

ctggtggaac ccgtggtgct ctgggtccgg gccaggtagt acaggtactg gtcgatgaga 960

gggttcatca gccggtctag gctctggctg tgcgcgtagc tgctgtggaa aggcacgtcc 1020

tcgaagctgt aactgaactc aaagttgttg cccgttctca gcatttgaga ggggaaatat 1080

tccaggcagt agaaggagga acggcccacc gattggctgc cgttgtccag agtcaggtag 1140

ccgtactgag gaatcatgaa gacgtccgcc gggaacggag gcaggcagcc ctggtgcgca 1200

gagccgagga cgtacggcag ctggtattcc gagtccgaga agacctgaac cgtgctggta 1260

aggttattag cgatggtcgt gacgccgtca ttcgttgtga cctccttgac ctggatgttg 1320

aggagcttga accgcagctt cttgggccgg aatccccagt tgttgttgat gagtcgctgc 1380

cagtcacgtg gtgagaagtg gcagtggaat ctgttaaagt caaaataccc ccaggggtg 1440

ctgtagccga agtagtggtt gtcattggtg gctcctgagc tgctgctgga gatttgcttg 1500

tagaggtggt tgttgtaggt ggggagggcc caggttctgg tgctggtggt gatgactctg 1560

tcgcccagcc atgtggaatc gcaatgccaa tttcctgagg cattacccac tccgtcggca 1620

ccttcgttat tgtctgccat tggtgcgcca ccgcctgcag ccattgtacc agatcccaca 1680

ctagagggcg ctgctggagg ttctccaaga ggttgagggt cggggactga ctctgagtcg 1740

ccagtctgac caaaattgag cttcttttta gcgggctgct ggccttttt gccgatgccc 1800

gtggaggagt ctggagagcc tatgggtctc ttctttccag gagccgtctt agcgccttcc 1860

tcaaccagac cgagaggttc gagaacccgc ttcttggcct ggaagactgc tcgcccgagg 1920

ttgcccccaa atgacgtatc ttcttgcaga cgctcctgaa actcggcgtc ggcgtggtta 1980

taccgcaggt acggattgtc acccgctttg agctgctggt cgtaggcctt gtcgtgctcg 2040

agggccgctg cgtccgccgc gttgacgggc tccccttgt cgagtccgtt gaagggtccg 2100

aggtacttgt agccaggaag caccagaccc cggccgtcgt cctgcttttg ctggttggct 2160

ttgggtttcg gggctccagg tttcaggtcc caccactcgc gaatgccctc agagaggttg 2220

tcctcgagcc aatctggaag ataaccatcg gcagccatac ctggtttaag tcatttattg 2280

ctcagaaaca cagtcgtcca ggtccacgtt gaccaggtcg caggccgagc aagcaatctc 2340

gggtgcccgc cccagcagat gatgaatcgc acacagcttc cgatacgtct tttttctgac 2400

gaccggttga gattctgaca cgccggggaa acattctaaa cagtctctga ccccgtgcgt 2460

gaagcaaatg ttgaaattct gattcattct ctcgcacgtt ttgcagggaa acagcacctg 2520

aagcatgccc gcgtgacgag aacatttgtt ttggtacctg tcggcaaagt ccaccggagc 2580

tccttccgcg tctgacgtcg atgggtccgt gactgaggga cgggcccgct tgggctcgct 2640

tatatccgcg tcatcggggg cgggtctttt gctggctccg ccctttctga cgtagaactc 2700

atgcgtcacc tcagtcacgt gatcactagc ccagcggaag aactctttga cttcctgctt 2760

tgtcaccttg ccaaagtcgt gttccagacg gcgggtgagt tcaaatttga acatccggtc 2820

ctgcaacggt tgctggtgct cgaaggtggt gctgttcccg tcgatcacgg cgcacatgtt 2880

ggtgttggag gtgacgatca cgggggtggg atcgatctgg gcggacgact tgcacttttg 2940

gtccacgcgc accttgctgc cgccgagaat ggccttggcg gactccacga ccttggccgt 3000

catcttgccc tcctcccacc agatcaccat cttgtcgacg caatcgttga agggaaagtt 3060

ctcattggtc cagttgacgc agcaagggcg aattc 3095

<210> 24
<211> 3095
<212> DNA
<213> new AAV serotype, clone F5

<400> 24
gaattcgccc ttcgcagaga ccaaagttca actgaaacga atcaaccggt ttattgatta 60

acaagcaatt acagattacg ggtgaggtaa cgagtgccaa tggggcgagg ctcagtataa 120

acaccatcag ggttcacagc aaattcaaca ttattagact tggcataatt ggaagtatac 180

tgaatttctg ggttccagcg cttgctgttt tctttctgca gctcccactc gatttccacg 240

ctgacttgtc cggtgctgta ctgcgtgatg aaggaggcaa acttggcagg agtaaacacc 300

tccggaggat tagcaggtac aggtgtgttt ttgatcagga tctgtggagg cgggtgttcg 360

agtccaaaac cgcccatcag aggagacggg tgaaagttgc catccgtgtg aggaattttg 420

gcccagatgg gaccctgcag atacacgtcc cggttctgcc agaccatgcc aggcagtgct 480

ccctggctgt tgatagtctg tgattgaggc ccggctgtag acgactgcag gttgctggag 540

accacaccgt attcttctgt agccacaggg ttagtggtct tgatctcctc ctcgctggtc 600

atcagaacgt tttccagcgt agttttgttg gcagctcccg tcttgccaaa aaccagtacc 660

ccgttgatgg gaaagaactg gtcctcatca tccttgttgg ttgccatggg aatgccagga 720

ttggtcaaag agtttctgcc attcagatga tatttagtgg cagcagtcca ggcaaaattg 780

ctgttgttgt taaagtccaa gtttctttgac agtctctgtt gcctatagca gggtccaggc 840

agccagttct ttgactgctc ggccatagta ttgggcccag cttgatgaaa ttgcagttcc 900

ctggtggaac ccgtggtgct ctgggtccgg gccaggtagt acaggtactg gtcgatgaga 960

gggttcatca gccggtctag gctctggctg tgcgcgtagc tgctgtggaa aggcacgtcc 1020

tcgaagctgt aactgaactc aaagttgttg cccgttctca gcatttgaga ggggaaatat 1080

tccaggcagt agaaggagga acggcccacc gattggctgc cgttgttcag agtcaggtag 1140

ccgtactgag gaatcatgaa gacgtccgcc gggaacggag gcaggcagcc ctggtgcgca 1200

gagccgagga cgtacggcag ctggtattcc gagtccgaga agacctgaac cgtgctggta 1260

aggttattag cgatggtcgt gacgccgtca ttcgttgtga cctccttgac ctggatgttg 1320

aagagcttga accgcagctt cttgggccgg aatccccagt tgttgttgat gagtcgctgc 1380

cagtcacgtg gtgagaagtg gcagtggaat ctgttaaagt caaaatacce ccaggggtg 1440

ctgtagccga agtagtggtt gtcattggtg gctcctgagc tgctgctgga gatttgcttg 1500

tagaggtggt tgttgtaggt ggggagggcc caggttctgg tgctggtggt gatgactctg 1560

tcgcccagcc atgtggaatc gcaatgccaa tttcctgagg cattacccac tccgtcggca 1620

ccttcgttat tgtctgccgt tggtgcgcca ccgcctgcag ccattgtacc agatcccaca 1680

ctagagggcg ctgctggagg ttctccaaga ggttgagggt cggggactga ctctgagtcg 1740

ccagtctgac caaaattgag cttcttttta gcgggctgct ggccttttt gccgatgccc 1800

gtggaggagt ctggagagtc tatgggtctc ttctttccag gagccgtctt agcgccttcc 1860

tcaaccagac cgagaggttc gagaacccgc ttcttggcct ggaagactgc tcgcccgagg 1920

ttgcccccaa atgacgtatc ttcttgcagg cgctcctgaa actcggcgtc ggcgtggtta 1980

taccgcaggt acggattgtc acccgctttg agctgctggt cgtaggcctt gtcgtgctcg 2040

agggccgctg cgtccgccgc gttgacgggc tccccttgt cgagtccgtt gaagggtccg 2100

aggtacttgt agccaggaag caccagaccc cggccgtcgt cctgcttttg ctggttggct 2160

ttgggtttcg gggctccagg tttcaggtcc caccactcgc gaatgccctc agagaggttg 2220

tcctcgagcc aatctggaag ataaccatcg gcagccatac ctggtttaag ccatttattg 2280

ctcagaaaca cagtcgtcca ggtccacgtt gaccaggtcg caggccgagc aggcaatctc 2340

gggtgcccgc cccagcagat gatgaatcgc acacagcttc cgatacgtct tttttctgac 2400

gaccggttga gattctgaca cgccggggaa acattctaaa cagtctctga ccccgtgcgt 2460

gaagcaaatg ttgaaattct gattcattct ctcgcacgtt ttgcagggaa acagcatctg 2520

aagcatgccc gcgtggcgag aacatttgtt ttggtacctg tcggcaaagt ccaccggagc 2580

tccttccgcg tctgacgtcg atgggtccgt gactgaggga caggcccgct tgggctcgct 2640

tatatccgcg tcatcggggg cgggtctttt gctggctccg ccctttctga cgtagaactc 2700

atgcgtcacc tcagtcacgt gatcactagc ccagcggaag aactctttga cttcctgctt 2760

tgtcaccttg ccaaagtcgt gttccagacg gcgggtgagt tcaaatttga acatccggtc 2820

ctgcaacggc tgctggtgct cgaaggtggt gctgttcccg tcgatcacgg cgcgcatgtt 2880

ggtgttggag gtgacgatca cgggggtggg atcgatctgg gcggacgact tgcacttttg 2940

gtccacgcgc accttgctgc cgccgagaat ggccttggcg gactccacga ccttggccgt 3000

catcttgccc tcctcccacc agatcaccat cttgtcgacg caatcgttga agggaaagtt 3060

ctcattggtc cagttgacgc agcaagggcg aattc 3095

<210> 25
<211> 3142
<212> DNA
<213> new AAV serotype, clone H6

<400> 25
aaaacgacgg gccagtgatt gtaatacgac tcactatagg gcgaaattga aattagcggc 60

cgcgaattcg cctttcgcag agaccaaagt tcaactgaaa cgaattaaac ggtttattga 120

ttaacaagca attacagatt acgagtcagg tatctggtgc caatggggcg aggctctgaa 180

tacacaccat tagtgtccac agtaaagtcc acattaacag acttgttgta gttggaagtg 240

tactgaattt cgggattcca gcgtttgctg ttctccttct gcagctccca ctcgatctcc 300

acgctgacct gtcccgtgga atactgtgtg atgaaagaag caaacttggc agaactgaag 360

tttgtgggag gattggctgg aacgggagtg tttttgatca tgatctgagg aggcgggtgt 420

ttgagtccaa aacctcccat cagtggagaa ggatgaaagt gtccatcggt gtgaggaatc 480

ttggcccaaa tgggtccctg caggtacacg tctcgatcct gccacaccat accaggtaac 540

gctccttggt gattgacagt tccagtagtt ggaccagtgt ttgagttttg caaattattt 600

gacacagtcc cgtactgctc cgtagccacg ggattggtgg ccctgatttc ttcttcatct 660

gtaatcatga cattttccaa atccgcgtcg ttggcatttg ttccttgttt accaaatatc 720

agggttccat gcatggggaa aaacttttct tcgtcatcct tgtgactggc catagctggt 780

cctggattaa ccaacgagtc ccggccattt agatgatact ttgtagctgc agtccaggga 840

aagttgctgt tgttgttgtc gtttgcctgt tttgacagac gctgctgtct gtagcaaggt 900

ccaggcagcc agtttttagc ttgaagagac atgttggttg gtccagcttg gctaaacagt 960

agccgagact gctgaagagt tccactattt gtttgtgtct tgttcagata atacaggtac 1020

tggtcgatca gaggattcat cagccgatcc agactctggc tgtgagcgta gctgctgtgg 1080

aaaggcacgt cttcaaaagt gtagctgaac tgaaagttgt ttccagtacg cagcatctga 1140

gaaggaaagt actccaggca gtaaaaggaa gagcgtccta ccgcctgact cccgttgttc 1200

agggtgaggt atccatactg tgggaccatg aagacgtccg ctggaaacgg cgggaggcat 1260

ccttgatgcg ccgagcccag gacgtacggg agctggtact ccgagtcagt aaacacctga 1320

accgtgctgg taaggttatt ggcaatcgtc gtcgtaccgt cattctgcgt gacctctttg 1380

acttgaatat taaagagctt gaagttgagt cttttgggcc ggaatccccg gttgttgttg 1440

acgagtcttt gccagtcacg tggtgaaaag tggcagtgga atctgttgaa gtcaaaatac 1500

ccccaggggg tgctgtagcc aaagtagtgg ttgtcgttgc tggctcctga ttggctggag 1560

atttgcttgt agaggtggtt gttgtatgtg ggcagggccc aggttcgggt gctggtggtg 1620

atgactctgt cgcccagcca ttgggaatcg caatgccaat ttcctgagga attacccact 1680

ccatcggcac cctcgttatt gtctgccatt ggtgcgccac tgcctgtagc cattgtagta 1740

gatcccagac cagaggggge tgctggtggc tgtccgagag gctgggggtc aggtacggag 1800

tctgcgtctc cagtctgacc aaaatttaat ctttttcttg caggctgctg gcccgctttt 1860

ccggttcccg aggaggagtc tggctccaca ggagagtgct ctaccggcct ctttttttccc 1920

ggagccgtct taacaggctc ctcaaccagg cccagaggtt caagaaccct ctttttcgcc 1980

tggaagactg ctcgtccgag gttgccccca aaagacgtat cttctttaag gcgctcctga 2040

aactctgcgt cggcgtggtt gtacttgagg tacgggttgt ctccgctgtc gagctgccgg 2100

tcgtaggcct tgtcgtgctc gagggccgcg gcgtctgcct cgttgaccgg ctcccccttg 2160

tcgagtccgt tgaagggtcc gaggtacttg tacccaggaa gcacaagacc cctgctgtcg 2220

tccttatgcc gctctgcggg ctttggtggt ggtgggccag gtttgagctt ccaccactgt 2280

cttattcctt cagagagagt gtcctcgagc caatctggaa gataaccatc ggcagccata 2340

cctgatttaa atcatttatt gttcagagat gcagtcatcc aaatccacat tgaccagatc 2400

gcaggcagtg caagcgtctg gcacctttcc catgatatga tgaatgtagc acagtttctg 2460

atacgccttt ttgacgacag aaacgggttg agattctgac acgggaaagc actctaaaca 2520

gtctttctgt ccgtgagtga agcagatatt tgaattctga ttcattctct cgcattgtct 2580

gcagggaaac agcatcagat tcatgcccac gtgacgagaa catttgtttt ggtacctgtc 2640

cgcgtagttg atcgaagctt ccgcgtctga cgtcgatggc tgcgcaactg actcgcgcgc 2700

ccgtttgggc tcacttatat ctgcgtcact gggggcgggt cttttcttag ctccaccctt 2760

tttgacgtag aattcatgct ccacctcaac cacgtgatcc tttgcccacc ggaaaaagtc 2820

tttcacttcc tgcttggtga cctttccaaa gtcatgatcc agacggcggg taagttcaaa 2880

tttgaacatc cggtcttgca acggctgctg gtgctcgaag gtcgttgagt tcccgtcaat 2940

cacggcgcac atgttggtgt tggaggtgac gatcacggga gtcgggtcta tctgggccga 3000

ggacttgcat ttctggtcca cacgcacctt gcttcctcca agaatggctt tggccgactc 3060

cacgaccttg gcggtcatct tcccctcctc ccaccagatc accatcttgt cgacgcaatg 3120

gtaaaaggaa agttctcatt gg 3142

<210> 26
<211> 3075
<212> DNA
<213> new AAV serotype, clone H2

<400> 26
tgagaacttt cctttcaacg attgcgtcgg acaagatggt gatctggtgg gaggagggga 60

agatgaccgc caaggtcgtg gagtcggcca aagccattct tggaggaagc aaggtgcgtg 120

tggaccagaa atgcaagtcc tcggcccaga tagacccgac tcccgtgatc gtcacctcca 180

acaccaacat gtgcgccgtg attgacggga actcaacgac cttcgagcac cagcagccgt 240

tgcaagaccg gatgttcaaa tttgaactta cccgccgtct ggatcatgac tttggaaagg 300

tcaccaagca ggaagtgaaa gacttttttcc ggtgggcaaa ggatcacgtg gttgaggtgg 360

agcatgaatt ctacgtcaaa aagggtggag ctaagaaaag acccgccccc agtgacgcag 420

atataagtga gcccaaacgg gcgcgcgagt cagttgcgca gccatcaacg tcagacgcgg 480

aagcttcgat caactacgcg gacaggtacc aaaaacaaat gttctcgtca cgtgggcatg 540

aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 600

ttcactcacg gacagaaaga ctgtttagag tgctttcccg tgtcagaatc tcaacccgtt 660

tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaaggtg 720

ccagacgctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catctctgaa 780

caataaatga tttaaatcag gtatggctgc cgatggttat cctccagatt ggctcgagga 840

cactctctct gaagggataa gacagtggtg gaagctcaaa cctggcccac caccaccaaa 900

gcccgcagag cggcataagg acgacagcag gggtcttgtg cttcctgggt acaagtacct 960

cggacccttc aacggactcg acaaggggga gccggtcaac gaggcagacg ccgcggccct 1020

cgagcacgac aaggcctacg accggcagct cgacagcgga gacaacccgt acctcaagta 1080

caaccacgcc gacgcagagt ttcaggagcg ccttaaagaa gatacgtctt ttgggggcaa 1140

cctcggacga gcagtcttcc aggcgaaaaa gagggttctt gaacctctgg gcctggttga 1200

ggaacctgtt aagacggctc cgggaaaaaa gaggccggta gagcactctc ctgtggagcc 1260

agactcctcc tcgggaaccg gaaaagcggg ccagcggcct gcaagaaaaa gattaaattt 1320

tggtcagact ggagacgcag actccgtacc tgacccccag cctctcggac agccaccagc 1380

agcccccctct ggtctgggat ctactacaat ggctacaggc agtggcgcac caatggcaga 1440

caataacgag ggtgccgatg gagtgggtaa ttcctcagga aattggcatt gcgattccca 1500

atggctgggc gacagagtca tcaccaccag cacccgaacc tgggccctgc ccacatacaa 1560

caaccacctc tacaagcaaa tctccagcca atcaggagcc agcaacgaca accactactt 1620

tggctacagc acccccctggg ggtatttttga cttcaacaga ttccactgcc acttttcacc 1680

acgtgactgg caaagactca tcaacaacaa ctggggattc cggcccaaaa gactcaactt 1740

caagctcttt aatattcaag tcaaagaggt cacgcagaat gacggtacga cgacgattgc 1800

caataacctt accagcacgg ttcaggtgtt tactgactcg gagtaccagc tcccgtacgt 1860

cctgggctcg gcgcatcaag gatgcctccc gccgtttcca gcggacgtct tcatggtccc 1920

acagtatgga tacctcaccc tgaacaacgg gagtcaggcg gtaggacgct cttcctttta 1980

ctgcctggag tactttcctt ctcagatgct gcgtactgga aacaactttc agttcagcta 2040

cacttttgaa gacgtgcctt tccacagcag ctacgctcac agccagagtc tggatcggct 2100

gatgaatcct ctgatcgacc agtacctgta ttatctgaac aagacacaaa caaatagtgg 2160

aactcttcag cagtctcggc tactgtttag ccaagctgga ccaaccaaca tgtctcttca 2220

agctaaaaac tggctgcctg gaccttgcta cagacagcag cgtctgtcaa aacaggcaaa 2280

cgacaacaac aacagcaact ttccctggac tgcagctaca aagtatcatc taaatggccg 2340

ggactcgttg gttaatccag gaccagctat ggccagtcac aaggatgacg aagaaaagtt 2400

tttccccatg catggaaccc tgatatttgg taaacaagga acaaatgcca acgacgcgga 2460

tttggaaaat gtcatgatta cagatgaaga agaaatcagg gccaccaatc ccgtggctac 2520

ggagcagtac gggactgtgt caaataattt gcaaaactca aacactggtc caactactgg 2580

aactgtcaat cgccaaggag cgttacctgg tatggtgtgg caggatcgag acgtgtacct 2640

gcagggaccc atttgggcca agattcctca caccgatgga cactttcatc cttctccact 2700

gatgggaggt tttggactca aacacccgcc tcctcagatc atgatcaaaa acactcccgt 2760

tccagccaat cctcccacaa acttcagttc tgccaagttt gcttctttca tcacacagta 2820

ttccacggga caggtcagcg tggagatcga gtgggagctg cagaaggaga acagcaaacg 2880

ctggaatccc gaaattcagt acacttccaa ctacaacaag tctgttaatg tggactttac 2940

tgtggacact aatggtgtgt attcagagcc tcgccccatt ggcaccagat acctgactcg 3000

taatctgtaa ttgcttgtta atcaataaac cgtttaattc gtttcagttg aactttggtc 3060

tctgcgaagg gcgaa 3075

<210> 27
<211> 3128
<212> DNA
<213> new AAV serotype, clone 42.8

<400> 27
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcttccg 180

cccagatcga tcccacccca gtgatcgtca cttccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctag ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

atcggcaaga caggccagca gcccgcgaaa aagagactca actttgggca gactggcgac 1380

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacatc gggaggaagc accaacgaca acacctactt cggctacagc 1680

acccccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920

gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tacctgactc tgaacaacgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag 2100

gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc 2160

ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220

actcagcagt tgctattttc tcaggccggg cctaataaca tgtcggctca ggccaaaaac 2280

tggctacccg ggccctgcta ccggcagcaa cgcgtctcca cgacactgtc gcaaaataac 2340

aacagcaact ttgcttggac cggtgccacc aagtatcatc tgaatggcag agactctctg 2400

gtaaatcccg gtgtcgctat ggcaacgcac aaggacgacg aagagcgatt ttttccatcc 2460

agcggagtct tgatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc 2520

gttatgctaa ccagtgagga agaaatcaaa accaccaacc cagtggccac agaacagtac 2580

ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac 2640

agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct 2700

atctgggcca agattcctca cacggacggc aactttcatc cttcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat 2820

cctccaacta ccttcagtca agccaagctg gcgtcgttca tcacgcagta cagcaccgga 2880

caggtcagcg tggaaattga atgggagctg cagaaagaga acagcaagcg ctggaaccca 2940

gagattcagt atacttccaa ctactacaaa tctacaaatg tggactttgc tgtcaatact 3000

gagggtactt attcagagcc tcgccccatt ggcacccgtt acctcacccg taacctgtaa 3060

ttgcctgtta atcaataaac cggctaattc gtttcagttg aactttggtc tctgcgaagg 3120

gcgaattc 3128

<210> 28
<211> 3128
<212> DNA
<213> new AAV serotype, clone 42.15

<400> 28
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaaatttg 300

aactcacccg ccgtctggag catgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcgcggg accagagact 660

gttcagaatg tttcccgggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

atcggcaaga caggccagca gcccgcgaaa aagagactca actttgggca gactggcgac 1380

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacatc gggaggaagc accaacgaca acacctactt cggctacagc 1680

acccccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920

gcgcaccagg gctgcccgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tacctgactc tgaacaacgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgcg gagaacgggc aacaactttg agttcagcta ccagtttgag 2100

gacgtgcctt ttcacagcag ctacgcgcat agccaaagcc tggaccggct gatgaacccc 2160

ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220

actcagcagt tgctattttc tcaggccggg cctaataaca tgtcggctca ggccaaaaac 2280

tggctacccg ggccctgcta ccggcagcaa cgcgtctcca cgacactgtc gcaaaataac 2340

aacagcaact ttgcttggac cggtgccacc aagtatcatc tgaatggcag agactctctg 2400

gtaaatcccg gtgtcgctat ggcaacgcac aaggacgacg aagagcgatt ttttccatcc 2460

agcggagtct tgatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc 2520

gttatgctaa ccagtgagga agaaatcaaa accaccaacc cagtggccac agaacagtac 2580

ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac 2640

agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct 2700

atctgggcca agattcctca cacggacggc aactttcatc cttcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat 2820

cctccaacta ccttcagtca agccaagctg gcgtcgttca tcacgcagta cagcaccgga 2880

caggtcagcg tggaaattga atgggagctg cagaaagaga acagcaagcg ctggaaccca 2940

gagattcagt atacttccaa ctactacaaa tctacaaatg tggactttgc tgtcaatact 3000

gagggtactt attcagagcc tcgccccatt ggcacccgtt acctcacccg taacctgtaa 3060

ttgcctgtta atcaataaac cggttaattc gtttcagttg aactttggtc tctgcgaagg 3120

gcgaattc 3128

<210> 29
<211> 3197
<212> DNA
<213> new AAV serotype. clone 42.5b

<400> 29
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaagggag agccggtcaa cgaggcagac gccgcggccc tcgagcacga caaggcctac 1080

gacaagcagc tcgagcaggg ggacaacccg tacctcaagt acaaccacgc cgacgccgag 1140

tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

atcggcaaga caggccagca gcccgcgaaa aagagactca actttgggca gactggcgac 1380

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacatc gggaggaagc accaacgaca acacctactt cggctacagc 1680

acccccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920

gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tacctgactc tgaacaacgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag 2100

gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc 2160

ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220

actcagcagt tgctattttc tcaggccggg cctaataaca tgtcggctca ggccaaaaac 2280

tggctacccg ggccctgcta ccggcagcaa cgcgtctcca cgacactgtc gcaaaataac 2340

aacagcaact ttgcttggac cggtgccacc aagtatcatc tgaatggcag agactctctg 2400

gtaaatcccg gtgtcgctat ggcaacgcac aaggacgacg aagagcgatt ttttccatcc 2460

agcggagtct tgatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc 2520

gttatgctaa ccagtgagga agaaatcaaa accaccaacc cagtggccac agaacagtac 2580

ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac 2640

agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct 2700

atctgggcca agattcctca cacggacggc aactttcatc cttcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat 2820

cctccaacta ccttcagtca agccaagctg gcgtcgttca tcacgcagta cagcaccgga 2880

caggtcagcg tggaaattga atgggagctg cagaaagaga acagcaagcg ctggaaccca 2940

gagattcagt atacttccaa ctactacaaa tctacaaatg tggactttgc tgtcaatact 3000

gagggtactt attcagagcc tcgccccatt ggcacccgtt acctcacccg taacctgtaa 3060

ttgcctgtta atcaataaac cggttaattc gtttcagttg aactttggtc tctgcgaagg 3120

gcgaattcgt ttaaacctgc aggactagtc cctttagtga gggttaattc tgagcttggc 3180

gtaatcatgg gtcatag 3197

<210> 30
<211> 2501
<212> DNA
<213> new AAV serotype, clone 42.1b

<400> 30
gaattcgccc ttggctgcgt caactggacc aatgagaact ttcccttcaa cgattgcgtc 60

gacaagatgg tgatctggtg ggaggagggc aagatgacgg ccaaggtcgt ggagtccgcc 120

aaggccattc atcatctgct ggggcgggct cccgagattg cttgctcggc ctgcgatctg 180

gtcaacgtgg acctggatga ctgtgtttct gagcaataaa tgacttaaac caggtatggc 240

tgccgatggt tatcttccag attggctcga ggacaacctc tctgagggca ttcgcgagtg 300

gtgggacttg agacctggag ccccgaaacc caaagccaac cagcaaaagc aggacgacgg 360

ccggggtctg gtgcttcctg gctacaagta cctcggaccc ttcaacggac tcgacaaggg 420

agagccggtc aacgaggcag acgccgcggc cctcgagcac gacaaggcct acgacaagca 480

gctcgagcag ggggacaacc cgtacctcaa gtacaaccac gccgacgccg agtttcagga 540

gcgtcttcaa gaagatacgt cttttgggggg caacctcggg cgagcagtct tccaggccaa 600

gaagcgggtt ctcgaacctc tcggtctggt tgaggaaggc gctaagacgg ctcctggaaa 660

gaagagaccc atagaatccc ccgactcctc cacgggcatc ggcaagaaag gccagcagcc 720

cgctaaaaag agactcaact ttgggcagac tggcgactca gagtcagtgc ccgaccctca 780

accaatcgga gaacccccg caggcccctc tggtctggga tctggcacaa tggctgcagg 840

cggtggcgct ccaatggcag acaataacga aggcgccgac ggagtgggta gttcctcagg 900

aaattggcat tgcgattcca catggctggg cgacagagtc atcaccacca gcacccgaac 960

ctgggccctc cccacctaca acaaccacct ctacaagcaa atctccaacg ggacatcggg 1020

aggaagcacc aacgacaaca cctacttcgg ctacagcacc ccctgggggt attttgactt 1080

taacagattc cactgccact tctcaccacg tgactggcag cgactcatca acaacaactg 1140

gggattccgg cccaagagac tcaacttcaa gctcttcaac atccaggtca aggaggtcac 1200

gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc agcacgattc aggtctttac 1260

ggactcggaa taccagctcc cgtacgtcct cggctctgcg caccagggct gcctgcctcc 1320

gttcccggcg gacgtcttca tgattcctca gtacgggtac ctgactctga acaacggcag 1380

tcaggccgtg ggccgttcct ccttctactg cctggagtac tttccttctc aaatgctgag 1440

aacgggcaac aactttgagt tcagctacca gtttgaggac gtgccttttc acagcagcta 1500

tgcgcacagc caaagcctgg accggctgat gaaccccctc atcgaccagt acctgtacta 1560

cctgtctcgg actcagtcca cgggaggtac cgcaggaact cagcagttgc tattttctca 1620

ggccgggcct aataacatgt cggctcaggc caaaaactgg ctacccgggc cctgctaccg 1680

gcagcaacgc gtctccacga cagtgtcgca aaataacaac agcaactttg cttggaccgg 1740

tgccaccaag tatcatctga atggcagaga ctctctggta aatcccggtg tcgctatggc 1800

aacgcacaag ggcgacgaag agcgatttttt tccatccagc ggagtcttga tgtttgggaa 1860

acagggagct ggaaaagaca acgtagacta tagcagcgtt atgctaacca gtgaggaaga 1920

aatcaaaacc accaacccag tggccacaga acagtacggc gtggtggccg ataacctgca 1980

acagcaaaac gccgctccta ttgtaggggc cgtcaacagt caaggagcct tacctggcat 2040

ggtctggcag aaccgggacg tgtacctgca gggtcctatc tgggccaaga ttcctcacac 2100

ggacggcaac tttcatcctt cgccgctgat gggaggcttt ggactgaaac acccgcctcc 2160

tcagatcctg attaagaata cacctgttcc cgcggatcct ccaactacct tcagtcaagc 2220

caagctggcg tcgttcatca cgcagtacag caccggacag gtcagcgtgg aaattgaatg 2280

ggagctgcag aaagagaaca gcaagcgctg gaacccagag attcagtata cttccaacta 2340

ctacaaatct acaaatgtgg actttgctgt caatactgag ggtacttatt cagagcctcg 2400

ccccattggc acccgttacc tcacccgtaa cctgtaattg cctgttaatc aataaaccgg 2460

ttgattcgtt tcagttgaac tttggtctca agggcgaatt c 2501

<210> 31
<211> 3113
<212> DNA
<213> new AAV serotype, clone 42.13

<400> 31
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga tcccaccccc gtgatcgtca cttccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag catgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagacccat agaatccccc gactcctcca cgggcatcgg caagaaaggc 1320

cagcagcccg ctaaaaagaa gctcaacttt gggcagactg gcgactcaga gtcagtgccc 1380

gaccctcaac caatcggaga acccccccgca ggcccctctg gtctgggatc tggtacaatg 1440

gctgcaggcg gtggcgctcc aatggcagac aataacgaag gcgccgacgg agtgggtagt 1500

tcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat caccaccagc 1560

acccgaacct gggccctccc cacctacaac aaccacctct acaagcaaat ctccaacggg 1620

acatcgggag gaagcaccaa cgacaacacc tacttcggct acagcacccc ctgggggtat 1680

tttgactttа acagattcca ctgccacttc tcaccacgtg actggcagcg actcatcaac 1740

aacaactggg gattccggcc caagagactc aacttcaagc tcttcaacat ccaggtcaag 1800

gaggtcacgc agaatgaagg caccaagacc atcgccaata accttaccag cacgattcag 1860

gtctttacgg actcggaata ccagctcccg tacgtcctcg gctctgcgca ccagggctgc 1920

ctgcctccgt tcccggcgga cgtcttcatg attcctcagt acgggtacct gactctgaac 1980

aacggcagtc aggccgtggg ccgttcctcc ttctactgcc tggagtactt tccttctcaa 2040

atgctgagaa cgggcaacaa ctttgagttc agctaccagt ttgaggacgt gcctttтcac 2100

agcagctatg cgcacagcca aagcctggac cggctgatga acccccтcat cgaccagtac 2160

ctgtactacc tgtctcggac tcagtccacg ggaggtaccg caggaactca gcagttgcta 2220

ttttctcagg ccgggcctaa taacatgtcg gctcaggcca aaaactggct acccgggccc 2280

tgctaccggc agcaacgcgt ctccacgaca gtgtcgcaaa ataacaacag caactttgct 2340

tggaccggtg ccaccaagta tcatctgaat ggcagagact ctctggtaaa tcccggtgtc 2400

gctatggcaa cgcacaaggg cgacgaagag cgatttтttc catccagcgg agtcttgatg 2460

tttgggaaac agggagctgg aaaagacaac gtggactata gcagcgttat gctaaccagt 2520

gaggaagaaa tcaaaaccac caacccagtg gccacagaac agtacggcgt ggtggccgat 2580

aacctgcaac agcaaaacgc cgctcctatt gtaggggccg tcaacagtca aggagcctta 2640

cctggcatgg tctggcagaa ccgggacgtg tacctgcagg gtcctatctg ggccaagatt 2700

cctcacacgg acggcaactt tcatccttcg ccgctgatgg gaggctttgg actgaaacac 2760

ccgcctcctc agatcctgat taagaataca cctgttcccg cggatcctcc aactaccttc 2820

agtcaagcca agctggcgtc gttcatcacg cagtacagca ccggacaggt cagcgtggaa 2880

attgaatggg agctgcagaa agagaacagc aagcgctgga acccagagat tcagtatact 2940

tccaactact acaaatctac aaatgtggac tttgctgtca atactgaggg tacttattca 3000

gagcctcgcc ccattggcac ccgttacctc acccgtagcc tgtaattgcc tgttaatcaa 3060

taaaccggtt gattcgtttc agttgaactt tggtctctgc gaagggcgaa ttc 3113

<210> 32
<211> 3113
<212> DNA
<213> new AAV serotype, clone 42.3a

<400> 32
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60
gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120
ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180
cccagatcga tcccaccccc gtgatcgtca cttccaacac caacatgtgc gccgtgattg 240
acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300
aactcacccg ccgtctggag catgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360
tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420
gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480
gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540
acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg cttccctgca 600
agacatgcga gagaatgaat cagaatttca gcatttgctt cacgcacggg accagagact 660
gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720
ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780
gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840
ggtatggctg ccgatggtca tcttccagat tggctcgagg acaacctctc tgagggcatt 900
cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960
gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020
gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080
gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140
tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200
caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260
cctggaaaga agagacccat agaatccccc gactcctcca cgggcatcgg caagaaaggc 1320
cagcagcccg ctaaaaagaa gctcaacttt gggcagactg gcgactcaga gtcagtgccc 1380
gaccctcaac caatcggaga acccccccgca ggcccctctg gtctgggatc tggtacaatg 1440
gctgcaggcg gtggcgctcc aatggcagac aataacgaag gcgccgacgg agtgggtagt 1500
tcctcaggaa attggcattg cgattccaca tagctgggcg acagagtcat caccaccagc 1560
acccgaacct gggccctccc cacctacaac aaccacctct acaagcaaat ctccaacggg 1620
acatcgggag gaagcaccaa cgacaacacc tacttcggct acagcacccc ctgggggtat 1680
tttgacttta acagattcca ctgccacttc tcaccacgtg actggcagcg actcatcaac 1740
aacagctggg gattccggcc caagagactc aacttcaagc tcttcaacat ccaggtcaag 1800
gaggtcacgc agaatgaagg caccaagacc atcgccaata accttaccag cacgattcag 1860
gtctttacgg actcggaata ccagctcccg tacgtcctcg gctctgcgca ccagggctgc 1920

ctgcctccgt tcccggcgga cgtcttcatg attcctcagt acgggtacct gactctgaac 1980

aacggcagtc aggccgtggg ccgttcctcc ttctactgcc tggagtactt tccttctcaa 2040

atgctgagaa cgggcaacaa ctttgagttc agctaccagt ttgaggacgt gcctttttcac 2100

agcagctacg cgcacagcca aagcctggac cggctgatga acccccctcat cgaccagtac 2160

ctgtactacc tgtctcggac tcagtccacg ggaggtaccg caggaactca gcagttgcta 2220

ttttctcagg ccgggcctaa taacatgtcg gctcaggcca aaaactggct acccgggccc 2280

tgctaccggc agcaacgcgt ctccacgaca ctgtcgcaaa ataacaacag caactttgct 2340

tggaccggtg ccaccaagta tcatctgaat ggcagagact ctctggtaaa tcccggtgtc 2400

gctatggcaa cgcacaagga cgacgaagag cgatttttc catccagcgg agtcttgatg 2460

tttgggaaac agggagctgg aaaagacaac gtggactata gcagcgttat gctaaccagt 2520

gaggaagaaa tcaaaaccac caacccagtg gccacagaac agtacggcgt ggtggccgat 2580

aacctgcaac agcaaaacgc cgctcctatt gtaggggccg tcaacagtca aggagcctta 2640

cctggcatgg tctggcagaa ccgggacgtg tacctgcagg gtcctatctg ggccaagatt 2700

cctcacacgg acggcaactt tcatccttcg ccgctgatgg gaggctttgg actgaaacac 2760

ccgcctcctc agatcctgat taagaataca cctgttcccg cggatcctcc aactaccttc 2820

agtcaagcca agctggcgtc gttcatcacg cagtacagca ccggacaggt cagcgtggaa 2880

attgaatggg agctgcagaa agagaacagc aagcgctgga acccagagat tcagtatact 2940

tccaactact acaaatctac aaatgtggac tttgctgtca atactgaggg tacttattca 3000

gagcctcgcc ccattggcac ccgttacctc acccgtaacc tgtaattgcc tgttaatcaa 3060

taaaccggtt aattcgtttc agttgaactt tggtctctgc gaagggcgaa ttc 3113

<210> 33
<211> 2504
<212> DNA
<213> new AAV serotype, clone 42.4

<400> 33
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattcatcat ctgctggggc gggctcccga gattgcttgc tcggcctgcg 180

atctggtcaa cgtggacctg gatgactgtg tttctgagca ataaatgact taaaccaggt 240

atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 300

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 360

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 420

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 480

aagcagctcg agcaggggga caacccgtac ctcaagtaca accacgccga cgccgagttt 540

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 600

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 660

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcaa gaaaggccag 720

cagcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac 780

cctcaaccaa tcggagaacc ccccgcaggc ccctctggtc tgggatctgg tacaatggct 840

gcaggcggtg gcgctccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc 900

tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc 960

cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatatc aagtcagagc 1020

ggggctacca acgacaacca cttcttcggc tacagcaccc cctggggcta ttttgacttc 1080

aacagattcc actgccactt ctcatcacgt gactggcagc gactcatcaa caacaactgg 1140

ggattccggc ccaagagact caacttcaag ctcttcaaca tccaggtcaa ggaggtcacg 1200

cagaatgaag gcaccaagac catcgccaat aaccttacca gcacgattca ggtctttacg 1260

gactcggaat accggctccc gtacgtcctc ggctctgcgc accagggctg cctgcctccg 1320

ttcccggcgg acgtcttcat gattcctcag tacgggtacc tgactctgaa caacggcagt 1380

caggccgtgg gccgttcctc cttctactgc ctggagtact ttccttctca aatgctgaga 1440

acgggcaaca actttgagtt cagctaccag tttgaggacg tgccttttca cagcagctac 1500

gcgcacagcc aaagcctgga ccggctgatg aacccccctca tcgaccagta cctgtactac 1560

ctgtctcgga ctcagtccac gggaggtacc gcaggaactc agcagttgct attttctcag 1620

gccgggccta ataacatgtc ggctcaggcc aaaaactggc tacccgggcc ctgctaccgg 1680

cagcaacgcg tctccacgac actgtcgcaa aataacaaca gcaactttgc ttggaccggt 1740

gccaccaagt atcatctgaa tggcagagac tctctggtaa atcccggtgt cgctatggca 1800

acgcacaagg acgacgaaga gcgatttttt ccatccagcg gagtcttgat gtttgggaaa 1860

cagggagctg gaaaagacaa cgtggactat agcagcgtta tgctaaccag tgaggaagaa 1920

atcaaaacca ccaacccagt ggccacagaa cagtacggcg tggtggccga taacctgcaa 1980

cagcaaaacg ccgctcctat tgtaggggcc gtcaacagtc aaggagcctt acctggcatg 2040

gtctggcaga accgggacgt gtacctgcag ggtcctatct gggccaagat tcctcacacg 2100

gacggcaact ttcatccttc gccgctgatg ggaggctttg gactgaaaca cccgcctcct 2160

cagatcctga ttaagaatac acctgttccc gcggatcctc caactacctt cagtcaagcc 2220

aagccggcgt cgttcatcac gcagtacagc accggacagg tcagcgtgga aattgaatgg 2280

gagctgcaga aagagaacag caagcgctgg aacccagaga ttcagtatac ttccaactac 2340

tacaaatcta caaatgtgga ctttgctgtc aatactgagg gtacttattc agagcctcgc 2400

cccattggca cccgttacct cacccgtaac ctgtaattgc ctgttaatca ataaaccggt 2460

taattcgttt cagttgaact ttggtctctg cgaagggcga attc 2504

<210> 34
<211> 3106
<212> DNA
<213> new AAV serotype, clone 42.5a

<400> 34
gaattcgccc ttctacggct gcgtcaactg gaccaatgag aactttccct tcaacgattg 60

cgtcgacaag atggtgatct ggtgggagga gggcaagatg acggccaagg tcgtggagtc 120

cgccaaggcc attctcggcg gcagcaaggt gcgcgtggac caaaagtgca agtcgtccgc 180

ccagatcgac cccacccccg tgatcgtcac ctccaacacc aacatgtgcg ccgtgattga 240

cgggaacagc accaccttcg agcaccagca gccgttgcag gaccggatgt tcaaatttga 300

actcacccgc cgtctggagc atgactttgg caaggcgaca aagcaggaag tcaaagagtt 360

cttccgctgg gcgcaggatc acgtgaccga ggtggcgcat gagttctacg tcagaaaggg 420

tggagccaac aagagacccg cccccgatga cgcggataaa agcgagccca agcgggcccg 480

cccctcagtc gcggatccat cgacgtcaga cgcggaagga gctccggtgg actttgccga 540

caggtaccaa aacaaatgtt ctcgtcacgc gggcatgctt cagatgctgt ttccctgcaa 600

aacatgcgag agaatgaatc agaatttcaa catttgcttc acgcacggga ccagagactg 660

ttcagaatgt ttccccggcg tgtcagaatc tcaaccggtc gtcagaaaga ggacgtatcg 720

gaaactctgt gccattcatc atctgctggg gcgggctccc gagattgctt gctcggcctg 780

cgatctggtc aacgtggacc tggatgactg tgtttctgag caataaatga cttaaaccag 840

gtatggctgc cgatggttat cttccagatt ggctcgagga caacctctct gagggcattc 900

gcgagtggtg ggacttgaaa cctggagccc cgaaacccaa agccaaccag caaaagcagg 960

acgacggccg gggtctggtg cttcctggct acaagtacct cggacccttc aacggactcg 1020

acaagggaga gccggtcaac gaggcagacg ccgcggccct cgagcacgac aaggcctacg 1080

acaagcagct cgagcagggg gacaacccgt acctcaagta caaccacgcc gacgccgagt 1140

ttcaggagcg tcttcaagaa gatacgtctt ttgggggcaa cctcgggcga gcagtcttcc 1200

gggccaagaa gcgggttctc gaacctctcg gtctggttga ggaaggcgct aagacggctc 1260

ctggaaagaa gagacccata gaatcccccg actcctccac gggcatcggc aagaaaggcc 1320

agcagcccgc taaaaagaag ctcaactttg ggcagactgg cgactcagag tcagtgcccg 1380

acccccaacc tctcggagaa cctcccgccg cgccctcagg tctgggatct ggtacaatgg 1440

ctgcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga gtgggtaatg 1500

cctccggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc accaccagca 1560

cccgcacctg ggccctgccc acctacaaca accacctcta caagcagata tcaagtcaga 1620

gcggggctac caacgacaac cacttcttcg gctacagcac cccctggggc tattttgact 1680

tcaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatc aacaacaacc 1740

ggggattccg gcccagaaag ctgcggttca agttgttcaa catccaggtc aaggaggtca 1800

cgacgaacga cggcgttacg accatcgcta ataaccttac cagcacgatt caggtcttct 1860

cggactcgga gtaccaactg ccgtacgtcc tcggctctgc gcaccagggc tgcctccctc 1920

cgttccctgc ggacgtgttc atgattcctc agtacggata tctgactcta aacaacggca 1980

gtcagtctgt gggacgttcc tccttctact gcctggagta ctttccttct cagatgctga 2040

gaacgggcaa taactttgaa ttcagctacc agtttgagga cgtgcccttt cacagcagct 2100

acgcgcacag ccaaagcctg gaccggctga tgaacccccc catcgaccag tacctgtact 2160

acctgtctcg gactcagtcc acgggaggta ccgcaggaac tcagcagttg ctatttttctc 2220

aggccgggcc taataacatg tcggctcagg ccaaaaactg gctacccggg ccctgctacc 2280

ggcagcaacg cgtctccacg acactgtcgc aaaataacaa cagcaacttt gcttggaccg 2340

gtgccaccaa gtatcatctg aatggcagag actctctggt aaatcccggt gtcgctatgg 2400

caacgcacaa ggacgacgaa gagcgatttt ttccatccag cggagtcttg atgtttggga 2460

aacagggagc tggaaaagac aacgtggact atagcagcgt tatgctaacc agtgaggaag 2520

aaatcaaaac caccaaccca gtggccacag aacagtacgg cgtggtggcc gataacctgc 2580

aacagcaaaa cgccgctcct attgtagggg ccgtcaacag tcaaggagcc ttacctggca 2640

tggcctggca gaaccgggac gtgtacctgc agggtcctat ctgggccaag attcctcaca 2700

cggacggcaa ctttcatcct tcgccgctga tgggaggctt tggactgaaa cacccgcctc 2760

ctcagatcct gattaagaat acacctgttc ccgcggatcc tccaactacc ttcagtcaag 2820

ccaagctggc gtcgttcatc acgcagtaca gcaccggaca ggtcagcgtg gaaattgaat 2880

gggagctgca gaaagagaac agcaagcgct ggaacccaga gattcagtat acttccaact 2940

actacaaatc tacaaatgtg gactttgctg tcaatactga gggtacttat tcagagcctc 3000

gccccattgg cacccgttac ctcacccgta acctgtaatt gcctgttaat caataaaccg 3060

gttaattcgt ttcagttgaa ctttggtctc tgcgaagggc gaattc 3106

<210> 35
<211> 2489
<212> DNA
<213> new AAV serotype, clone 42.10

<400> 35
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtgaagt 120

ccgccaaggc cattcatcat ctgctggggc gggctcccga gattgcttgc tcggcctgcg 180

atctggtcaa cgtggacctg gatgactgtg tttctgagca ataaatgact taaaccaggt 240

atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 300

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 360

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 420

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 480

aagcagctcg agcaggggga caacccgtac ctcaagtaca accacgccga cgccgagttt 540

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 600

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 660

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcag gaaaggccag 720

cagcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac 780

cctcaaccaa tcggagaacc ccccgcaggc ccctctggtc tgggatctgg tacaatggct 840

gcaggcggtg gcgctccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc 900

tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc 960

cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatatc aagtcagagc 1020

ggggctacca acgacaacca cttcttcggc tacagcaccc cctggggcta ttttgacttc 1080

aacagattcc actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg 1140

ggattccggc ccagaaagct gcggttcaag ttgttcaaca tccaggtcaa ggaggtcacg 1200

acgaacgacg gcgttacgac catcgccaat aaccttacca gcacgattca ggtcttctcg 1260

gactcggagt accaactgcc gtacgtcctc ggctctgcgc accagggctg cctccctccg 1320

ttccctgcgg acgtgttcat gattcctcag tacggatatc tgactctaaa caacggcagt 1380

cagtctgtgg gacgttcctc cttctactgc ctggagtact ttccttctca gatgctgaga 1440

acgggcaata actttgaatt cagctacacc tttgaggaag tgcctttcca cagcagctat 1500

gcgcacagcc agagcctgga ccggctgatg aatccctca tcgaccagta cctgtactac 1560

ctggcccgga cccagagcac tacggggtcc acaagggagc tgcagttcca tcaggctggg 1620

cccaacacca tggccgagca atcaaagaac tggctgcccg gaccctgtta tcggcagcag 1680

agactgtcaa aaaacataga cagcaacaac aacagtaact ttgcctggac cggggccact 1740

aaataccatc tgaatggtag aaattcatta accaacccgg gcgtagccat ggccaccaac 1800

aaggacgacg aggaccagtt ctttcccatc aacggagtgc tggtttttgg caaaacgggg 1860

gctgccaaca agacaacgct ggaaaacgtg ctaatgacca gcgaggagga gatcaaaacc 1920

accaatcccg tggctacaga agaatacggt gtggtctcca gcaacctgca atcgtctacg 1980

gccggacccc agacacagac tgtcaacagc caggggctc tgcccggcat ggtctggcag 2040

aaccgggacg tgtacctgca gggtcccatc tgggccaaaa ttcctcacac ggacggcaac 2100

tttcacccgt ctcccctgat gggcggattt ggactcaaac acccgcctcc tcaaattctc 2160

atcaaaaaca ccccggtacc tgctaatcct ccagaggtgt ttactcctgc caagtttgcc 2220

tcatttatca cgcagtacag caccggccag gtcagcgtgg agatcgagtg ggaactgcag 2280

aaagaaaaca gcaaacgctg gaatccagag attcagtaca cctcaaatta tgccaagtct 2340

aataatgtgg aatttgctgt caacaacgaa ggggtttata ctgagcctcg ccccattggc 2400

acccgttacc tcacccgtaa cctgtaattg cctgttaatc aataaaccgg ttaattcgtt 2460

tcagttgaac tttggtcaag ggcgaattc 2489

<210> 36
<211> 2495
<212> DNA
<213> new AAV serotype, clone 42.3b

<400> 36
gaattcgccc tttctacggc tgcgtcaact agaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattcatcat ctgctggggc gggctcccga gattgcttgc tcggcctgcg 180

atctggtcaa cgtggacctg gatgactgtg tttctgagca ataaatgact taaaccaggt 240

atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 300

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 360

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 420

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 480

aagcagctcg agcaggggga caacccgtac ctcaagtaca accacgccga cgccgagttt 540

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 600

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 660

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcaa gaaaggccag 720

cagcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac 780

cctcaaccaa tcggagaacc ccccgcaggc ccctctggtc tgggatctgg tacaatggct 840

gcaggcggtg gcgctccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc 900

tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc 960

cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatatc aagtcagagc 1020

ggggctacca acgacaacca cttcttcggc tacagcaccc cctggggcta ttttgacttc 1080

aacagattcc actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg 1140

ggattccggc ccagaaagct gcggttcaag ttgttcaaca tccaggtcaa ggaggtcacg 1200

acgaacgacg gcgttacgac catcgctaat aaccttacca gcacgattca ggtcttctcg 1260

gactcggagt accaactgcc gtacgtcctc ggctctgcgc accagggctg cctccctccg 1320

ttccctgcgg acgtgttcat gattcctcag tacggatatc tgactctaaa caacggcagt 1380

cagtctgtgg gacgttcctc cttctactgc ctggagtact ttccttctca gatgctgaga 1440

acgggcaata actttgaatt cagctacacc tttgaggaag tgcctttcca cagcagctat 1500

gcgcacagcc agagcctgga ccggctgatg aatcccctca tcgaccagta cctgtactac 1560

ctggcccgga cccagagcac tacggggtcc acaagggagc tgcagttcca tcaggctggg 1620

cccaacacca tggccgagca atcaaagaac tggctgcccg gaccctgtta tcggcagcag 1680

agactgtcaa aaaacataga cagcaacaac accagtaact ttgcctggac cggggccact 1740

aaataccatc tgaatggtag aaattcatta accaacccgg gcgtagccat ggccaccaac 1800

aaggacgacg aggaccagtt ctttcccatc aacggagtgc tggtttttgg caaaacgggg 1860

gctgccaaca agacaacgct ggaaaacgtg ctaatgacca gcgaggagga gatcaaaacc 1920

accaatcccg tggctacaga acagtacggt gtggtctcca gcaacctgca atcgtctacg 1980

gccggacccc agacacagac tgtcaacagc caggggggctc tgcccggcat ggtctggcag 2040

aaccgggacg tgtacctgca gggtcccatc tgggccaaaa ttcctcacac ggacggcaac 2100

tttcacccgt ctcccctgat gggcggattt ggactcaaac acccgcctcc tcaaattctc 2160

atcaaaaaca ccccggtacc tgctaatcct ccagaggtgt ttactcctgc caagtttgcc 2220

tcatttatca cgcagtacag caccggccag gtcagcgtgg agatcgagtg ggaactgcag 2280

aaagaaaaca gcaaacgctg gaatccagag attcagtaca cctcaaatta tgccaagtct 2340

aataatgtgg aatttgctgt caacaacgaa ggggtttata ctgagcctcg ccccattggc 2400

acccgttacc tcacccgtaa cctgtaattg cctgttaatc aataaaccgg ttaattcgtt 2460

tcagttgaac tttggtctct gcgaagggcg aattc 2495

<210> 37
<211> 3098
<212> DNA
<213> new AAV serotype, clone 42.11

<400> 37
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcttccg 180

cccagatcga tcccaccccc gtgatcgtca cttccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accggagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaagggag agccggtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagacccat agaatccccc gactcctcca cgggcatcgg caagaaaggc 1320

cagcagcccg ctaaaaagaa gctcaacttt gggcagactg gcgactcaga gtcagtgccc 1380

gaccctcaac caatcggaga acccccccgca ggcccctctg gtctgggatc tggtacaatg 1440

gctgcaggcg gtggcgctcc aatggcagac aataacgaag gcgccgacgg agtgggtaat 1500

gcctccggaa attggcattg cgattccaca tggctgggcg acagagtcat caccaccagc 1560

acccgcacct gggccctgcc cacctacaac aaccacctct acaagcagat atcaagtcag 1620

agcggggcta ccaacgacaa ccacttcttc ggctacagca ccccctgggg ctattttgac 1680

ttcaacagat tccactgcca cttctcacca cgtgactggc agcgactcat caacaacaac 1740

tggggattcc ggcccagaaa gctgcggttc aagttgttca acatccaggt caaggaggtc 1800

acgacgaacg acggcgttac gaccatcgct aataacctta ccagcacgat tcaggtcttc 1860

tcggactcgg agtaccaact gccgtacgtc ctcggctctg cgcaccaggg ctgcctccct 1920

ccgttccctg cggacgtgtt catgattcct cagtacggat atctgactct aaacaacggc 1980

agtcagtctg tgggacgttc ctccttctac tgcctggagt actttccttc tcagatgctg 2040

agaacgggca ataactttga attcagctac acctttgagg aagtgccttt ccacagcagc 2100

tatgcgcaca gccagagcct ggaccggctg atgaatcccc tcatcgacca gtacctgtac 2160

tacctggccc ggacccagag cactacgggg tccacaaggg agctgcagtt ccatcaggct 2220

gggcccaaca ccatggccga gcaatcaaag aactggctgc ccggaccctg ttatcggcgg 2280

cagagactgt caaaagacat agacagcaac aacaacagta actttgcctg gaccggggcc 2340

actaaatacc atctgaatgg tagaaattca ttaaccaacc cgggcgtagc catggccacc 2400

aacaaggacg acgaggacca gttctttccc atcaacggag tgctggtttt tggcaaaacg 2460

ggggctgcca acaagacaac gctggaaaac gtgctaatga ccagcgagga ggagatcaaa 2520

accaccaatc ccgtggctac agaagaatac ggtgtggtct ccagcaacct gcaatcgtct 2580

acggccggac cccagacaca gactgtcaac agccaggggg ctctgcccgg catggtctgg 2640

cagaaccggg acgtgtacct gcagggtccc atctgggcca aaattcctca cacggacggc 2700

aactttcacc cgtctccccct gatgggcgga tttggactca aacacccgcc tcctcaaatt 2760

ctcatcaaaa acaccccggt acctgctaat cctccagagg tgtttactcc tgccaagttt 2820

gcctcattta tcacgcagta cagcaccggc caggtcagcg tggagatcga gtgggaactg 2880

cagaaagaga acagcaaacg ctggaatcca gagattcagt acacctcaaa ttatgccaag 2940

tctaataatg tggaatttgc tgtcaacaac gaaggggttt atactgagcc tcgccccatt 3000

ggcacccgtt acctcacccg taacctgtaa ttacttgtta atcaataaac cggttgattc 3060

gtttcagttg aactttggtc tctgcgaagg gcgaattc 3098

<210> 38
<211> 3276
<212> DNA
<213> new AAV serotype, clone 42.6a

<400> 38
gaattcgccc ttcgcagaga ccaaagttca actgaaacga attaaccggt ttattgatta 60

acaggcaatt acaggttacg ggtgaggtaa cgggtgccaa tggggcgagg ctcagtataa 120

acccccttcgt tgttgacagc aaattccaca ttattagact tggcataatt tgaggtgtac 180

tgaatctctg gattccagcg tttgctgttt tctttctgca gttcccactc gatctccacg 240

ctgacctggc cggtgctgta ctgcgtgata aatgaggcaa acttggcagg agtaaacacc 300

tctggaggat tagcaggtac cggggtgttt ttgatgagaa tttgaggagg cgggtgtttg 360

agtccaaatc cgtccatcag gggagacggg tgaaagttgc cgtccgtgtg aggaattttg 420

gcccagatgg gaccctgcag gtacacgtcc cggttctgcc agaccatgcc gggcagagcc 480

ccctggctgt tgacagtctg tgtctggggt ccggccgtag acgattgcag gttgctggag 540

accacaccgt attcttctgt agccacggga ttggtggttt tgatctcctc ctcgctggtc 600

attagcacgt tttccagcgt tgtcttgttg gcagcccccg ttttgccaaa aaccagcact 660

ccgttgatgg gaaagaactg gtcctcgtcg tccttgttgg tggccatggc tacgcccggg 720

ttggttaatg aatttctacc attcagatgg tatttagtgg ccccggtcca ggcaaagtta 780

ctgttgttgt tgctgtctat gttttttgac agtctctgct gccgataaca gggtccgggc 840

agccagttct ttgattgctc ggccatggtg ttgggcccag cctgatggaa ctgcagctcc 900

cttgtggacc ccgtagtgct ctgggtccgg gccaggtagt acaggtactg gtcgatgagg 960

ggattcatca gccggtccag gctctggcta tgcgcatagc tgctgtggaa aggcacttcc 1020

tcaaaggtgt agctgaattc aaagttattg cccgttctca gcatctgaga aggaaagtac 1080

tccaggcagt agaaggagga acgtcccaca gactgactgc cgttgtttag agtcagatat 1140

ccgtactgag gaatcatgaa cacgtccgca gggaacggag ggaggcagcc ctggtgcgca 1200

gagccgagga cgtacggcag ttggtactcc gagtccgaga agacctgaat cgtgctggta 1260

aggttattag cgatggtcgt aacgccgtcg tccgtcgtga cctccttgac ctggatgttg 1320

aacaacttga accgcagctt tctgggccgg aatccccagt tgttgttgat gagtcgctgc 1380

cagtcacgtg gtgagaagtg gcagtggaat ctgttaaagt caaaataccc ccagggggtg 1440

ctgtagccga agtaggtgtt gtcgttggtg cttcctcccg atgtcccgtt ggagatttgc 1500

ttgtagaggt ggttgttgta ggtggggagg gcccaggttc gggtgctggt ggtgatgact 1560

ctgtcgccca gccatgtgga atcgcaatgc caatttcctg aggaactacc cactccgtcg 1620

gcgccttcgt tattgtctgc cattggagcg ccaccgcctg cagccattgt accagatccc 1680

agaccagagg ggcctgcggg gggttctccg attggttgag ggtcgggcac tgactctgag 1740

tcgccagtct gcccaaagtt gagtctcttt ttcgcgggct gctggcctgt cttgccgatg 1800

cccgtagagg agtctggaga acgctggggt gatggctcta ccggtctctt ctttccagga 1860

gccgtcttag cgccttcctc aaccagaccg agaggttcga gaacccgctt cttggcctgg 1920

aagactgctc gcccgaggtt gcccccaaaa gacgtatctt cttgaagacg ctcctgaaac 1980

tcggcgtcgg cgtggttgta cttgaggtac gggttgtccc cctgctcgag ctgcttgtcg 2040

taggccttgt cgtgctcgag ggccgcggcg tctgcctcgt tgaccggctc tcccttgtcg 2100

agtccgttga agggtccgag gtacttgtag ccaggaagca ccagaccccg gccgtcgtcc 2160

tgcttttgct ggttggcttt gggtttcggg gctccaggtt tcaagtccca ccactcgcga 2220

atgccctcag agaggttgtc ctcgagccaa tctggaagat aaccatcggc agccatacct 2280

ggtttaagtc atttattgct cagaaacaca gtcatccagg tccacgttga ccagatcgca 2340

ggccgagcaa gcaatctcgg gagcccgccc cagcagatga tgaatggcac agagtttccg 2400

atacgtcctc tttctgacga ccggttgaga ttctgacacg ccggggaaac attctgaaca 2460

gtctctggtc ccgtgcgtga agcaaatgtt gaaattctga ttcattctct cgcatgtctt 2520

gcagggaaac agcatctgaa gcatgcccgc gtgacgagaa cacttgtttt ggtacctgtc 2580

ggcaaagtcc accggagctc cttccgcgtc tgacgtcgat ggatgcaaaa tgtcgcaaaa 2640

gcactcacgt gacagctaat acaggaccac tcccctatga cgtgatttac gtcagcgcta 2700

tgcccgcgtg acgagaacat ttgttttggt acctgtcggc aaagtccacc ggagctcctt 2760

ccgcgtctga cgtcgatgga tccgcgactg aggggcaggc ccgcttgggc tcgcttttat 2820

ccgcgtcatc gggggcgggt ctcttgttgg ctccaccctt tctgacgtag aactcatgcg 2880

ccacctcggt cacgtgatcc tgcgcccagc ggaagaactc tttgacttcc tgctttgtca 2940

ccttgccaaa gtcatgctcc agacggcggg tgagttcaaa tttgaacatc cggtcctgca 3000

acggctgctg gtgctcgaag gtggtgctgt tcccgtcaat cacggcgcac atgttggtgt 3060

tggaagtgac gatcacgggg gtgggatcga tctgggcgga agacttgcac ttttggtcca 3120

cgcgcacctt gctgccgccg agaatggcct tggcggactc cacgaccttg gccgtcatct 3180

tgccctcctc ccaccagatc accatcttgt cgacgcaatc gttgaaggga aagttctcat 3240

tggtccagtt gacgcagccg tagaaagggc gaattc 3276

<210> 39
<211> 3084
<212> DNA
<213> new AAV serotype, clone 43.1

<400> 39
gaattcgccc tttctacggc tgcatcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccacccca gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaagttcg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac caagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gcggagccag caaaagaccc gcccccgatg acgcggatat aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

aaacgtgcga gaaaatgaat cagaatttca acatttgctt cacgcacggg gtcagagact 660

gctcagaatg tttccccggt gcatcagaat ctcaaccggt cgtcagaaaa aaaacgtatc 720

agaaactgtg tgccattcat catctgctgg ggcgggcacc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggacgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggcttgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacctgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca cctcagcgtt cccccgactc ctccacgggc 1320

atcggcaaga aaggccacca gcccgcgaga aagagactga actttgggca gactggcgac 1380

tcggagtcag tccccgaccc tcaaccaatc ggagaaccac cagcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctgcccacct acaacaacca tctctacaag 1620

caaatctcca acgggacatc gggaggaagc actaacgaca acacctactt tggctacagc 1680

acccccctggg ggtattttga cttcaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaataa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtgtt tacggactcg gaataccagc tcccgtacgt ccccggctct 1920

gcgcaccagg gctgcctccc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tatctgaccc taaacaatgg cagtcaggct gtgggccgtt cctccttcta ctgcctggaa 2040

tacttccctt ctcaaatgct gaggacgggc aacaactttg aattcagcta caccttcgag 2100

gacgtgcctt tccacagcag ctacgcgcac agccagagcc tggaccggct gatgaaccct 2160

ctcatcgacc agtacctgta ttacttatcc agaactcagt ccacaggagg aactcaaggt 2220

actcagcaat tgttattttc tcaagccggg cccgcaaaca tgtcggctca ggccaagaac 2280

tggctacctg gaccgtgtta ccgtcagcaa cgagtttcca cgacactgtc gcaaaacaac 2340

aacagcaatt ttgcttggac cggtgccacc aagtatcacc tgaatggcag agactccctg 2400

gttaatcccg gcgttgccat ggctacccac aaggacgacg aggagcgctt cttcccgtca 2460

agcggagttc taatgtttgg caagcagggg gctggaaaag acaatgtgga ctacagcagc 2520

gtgatgctca ccagcgaaga agaaattaaa actactaacc cagtggctac agagcagtat 2580

ggtgtggtgg cagacaacct gcagcagacc aacggagctc ccattgtggg aactgtcaac 2640

agccaggggg ccttacctgg tatggtctgg caaaaccggg acgtgtacct gcagggcccc 2700

atctgggcca aaattcctca cacggacggc aactttcatc cttcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctggtgaaaa acactcctgt tcctgcggat 2820

cctccgacca ccttcagcca ggccaagctg gcttctttta tcacgcagta cagcaccgga 2880

caggtcagcg tggaaatcga atgggagctg cagaaagaaa acagcaagcg ctggaaccca 2940

gagattcagt atacttccaa ctactacaaa tctacaaatg tggactttgc tgtcaatact 3000

gagggtactt attcagagcc tcgccccatt ggcactcgtt atctcacccg taatctgtaa 3060

ttgcttgtta atcaataaac cggt 3084

<210> 40
<211> 2370
<212> DNA
<213> new AAV serotype, clone 43.5

<400> 40
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240
acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaagttcg 300
aactcacccg ccgtctggag cacgactttg gcaaggtgac caagcaggaa gtcaaagagt 360
tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420
gcggagccag caaaagaccc gcccccgatg acgcggatat aagcgagccc aagcgggcct 480
gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540
acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagacgctg tttccctgca 600
aaacgtgcga gagaatgaat cagaatttca acatttgctt cacgcacggg gtcagagact 660
gctcagaatg tttccccggt gcatcagaat ctcaaccggt cgtcagaaaa aaaacgtatc 720
agaaactgtg tgccattcat catctgctgg ggcgggcacc cgagattgct tgctcggcct 780
gcgatctggt caacgtggac ctggacgact gtgtttctga gcaataaatg acttaaacca 840
ggtatggctg ccgatggtta tcttccagat tggcttgagg acaacctctc tgagggcatt 900
cgcgagtggt gggacctgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960
gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020
gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080
gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140
tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200
caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260
cctggaaaga agagaccggt agagccatca cctcagcgtt cccccgactc ctccacgggc 1320
atcggcaaga aaggccacca gcccgcgaga aagagactga actttgggca gactggcgac 1380
tcggagtcag tccccgaccc tcaaccaatc ggagaaccac cagcaggccc ctctggtctg 1440
ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500
gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560
gtcatcacca ccagcacccg aacctgggcc ctgcccacct acaacaacca tctctacaag 1620
caaatctcca acgggacatc gggaggaagc actaacgaca acacctactt tggctacagc 1680
acccccctggg ggtattttga cttcaacaga ttccactgcc acttctcacc acgtgactgg 1740
cagcgactca tcaacaataa ctggggattc cggcccaaga gactcaactt caagctcttc 1800
aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860
accagcacga ttcaggtgtt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920
gcgcaccagg gctgcctccc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980
tatctgaccc taaacaatgg cagtcaggct gtgggccgtt cctccttcta ctgcctggaa 2040
tacttccctt ctcaaatgct gaggacgggc aacaactttg aattcagcta caccttcgag 2100

gacgtgcctt tccacagcag ctacgcgcac agccagagcc tggaccggct gatgaaccct 2160

ctcatcgacc agtacctgta ttacttatcc agaactcagt ccacaggagg aactcaaggt 2220

actcagcaat tgttattttc tcaagccggg cccgcaaaca tgtyggctca ggccaagaac 2280

tggctacctg gaccgtgtta ccgtcagcaa cgagtttcca cgacactgtc gcaaaacaac 2340

aacagcaatt ttgctggacc ggtgccacca 2370

<210> 41
<211> 3123
<212> DNA
<213> new AAV serotype, clone 43.12

<400> 41
gaattcgccc ttggctgcgt caactggacc aatgagaact ttcccttcaa cgattgcgtc 60

gacaagatgg tgatctggtg ggaggagggc aagatgacgg ccaaggtcgt ggagtccgcc 120

aaggccattc tcggcggcag caaggtgcgc gtggaccaaa agtgcaagtc gtccgcccag 180

atcgacccca cccccgtgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg 240

aacagcacca ccttcgagca ccagcagccg ttgcaggacc ggatgttcaa gttcgaactc 300

acccgccgtc tggagcacga ctttggcaag gtgaccaagc aggaagtcaa agagttcttc 360

cgctgggcgc aggatcacgt gaccgaggtg gcgcatgagt tctacgtcag aaagggcgga 420

gccagcaaaa gacccgcccc cgatgacgcg gatataagcg agcccaagcg ggcctgcccc 480

tcagtcgcgg atccatcgac gtcagacgcg gaaggagctc cggtggactt tgccgacagg 540

taccaaaaca aatgttctcg tcacgcgggc atgctccaga tgctgtttcc ctgcaaaacg 600

tgcgagagaa tgaatcagaa tttcaacatt tgcttcacgc acggggtcag agactgctca 660

gaatgtttcc ccggtgcatc agaatctcaa ccggtcgtca gaaaaaaaac gtatcagaaa 720

ctgtgtgcca ttcatcatct gctggggcgg gcacccgaga ttgcttgctc ggcctgcgat 780

ctggtcaacg tggacctgga cgactgtgtt tctgagcaat aaatgactta aaccaggtat 840

ggctgccgat ggttatcttc cagattggct tgaggacaac ctctctgagg gcattcgcga 900

gtggtgggac ctgaaacctg gagccccgaa acccaaagcc aaccagcaaa agcaggacga 960

cggccggggt ctggtgcttc ctggctacaa gtacctcgga cccttcaacg gactcgacaa 1020

gggggagccc gtcaacgcgg cggacgcagc ggccctcgag cacgacaagg cctacgacca 1080

gcagctcaaa gcgggtgaca atccgtacct gcggtataac cacgccgacg ccgagtttca 1140

ggagcgtctg caagaagata cgtcttttgg gggcaacctc gggcgagcag tcttccaggc 1200

caagaagcgg gttctcgaac ctctcggtct ggttgaggaa ggcgctaaga cggctcctgg 1260

aaagaagaga ccggtagagc catcacctca gcgttccccc gactcctcca cgggcatcgg 1320

caagaaaggc caccagcccg cgagaaagag actgaacttt gggcagactg gcgactcgga 1380

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 1440

tggtacaatg gctgcaggcg gtggcgctcc aatggcagac aataacgaag gcgccgacgg 1500

agtgggtagt tcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat 1560

caccaccagc acccgaacct gggccctgcc cacctacaac aaccatctct acaagcaaat 1620

ctccaacggg acatcgggag gaagcactaa cgacaacacc tactttggct acagcacccc 1680

ctgggggtat tttgacttca acagattcca ctgccacttc tcaccacgtg actggcagcg 1740

actcatcaac aataactggg gattccggcc caagagactc aacttcaagc tcttcaacat 1800

ccaggtcaag gaggtcacgc agaatgaagg caccaagacc atcgccaata accttaccag 1860

cacgattcag gtgtttacgg actcggaata ccagctcccg tacgtcctcg gctctgcgca 1920

ccagggctgc ctccctccgt tcccggcgga cgtcttcatg attcctcagt acgggtatct 1980

gaccctaaac aatggcagtc aggctgtggg ccgttcctcc ttctactgcc tggaatactt 2040

cccttctcaa atgctgagga cgggcaacaa ctttgaattc agctacacct tcgaggacgt 2100

gcctttccac agcagctacg cgcacagcca gagcctggac cggctgatga accctctcat 2160

cgaccagtac ctgtattact tatccagaac tcagtccaca ggaggaactc aaggtactca 2220

gcaattgtta ttttctcaag ccgggcccgc aaacatgtcg gctcaggcca agaactggct 2280

acctggaccg tgttaccgtc agcaacgagt ttccacgaca ctgtcgcaaa acaacaacag 2340

caattttgct tggaccggtg ccaccaagta tcacctgaat ggcagagact ccctggttaa 2400

tcccggcgtt gccatggcta cccacaagga cgacgaggag cgcttcttcc cgtcaagcgg 2460

agttctaatg tttggcaagc agggggctgg aaaagacaat gtggactaca gcagcgtgat 2520

gctcaccagc gaagaagaaa ttaaaactac taacccagtg gctacagagc agtatggtgt 2580

ggtggcagac aacctgcagc agaccaacgg agctcccatt gtgggaactg tcaacagcca 2640

gggggccttа cctggtatgg tctggcaaaa ccgggacgtg tacctgcagg gccccatctg 2700

ggccaaaatt cctcacacgg acggcaactt tcatccttcg ccgctgatgg gaggctttgg 2760

actgaaacac ccgcctcctc agatcctggt gaaaaacact cctgttcctg cggatcctcc 2820

gaccaccttc agccaggcca agctggcttc ttttatcacg cagtacagca ccggacaggt 2880

cagcgtggaa atcgaatggg agctgcagaa agaaaacagc aagcgctgga acccagagat 2940

tcagtatact tccaactact acaaatctac aaatgtggac tttgctgtca atactgaggg 3000

tacttattca gagcctcgcc ccattggcac tcgttatctc acccgtaatc tgtaattgct 3060

tgttaatcaa taaaccggtt aattcgtttc agttgaactt tggtctctgc gaagggcgaa 3120

ttc 3123

<210> 42
<211> 3122
<212> DNA
<213> new AAV serotype, clone 43.20

<400> 42
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60
gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120
ccgccaaggc cattctcggc ggcagcaagg tgcgtgtgga ccaaaagtgc aagtcttccg 180
cccagatcga tcccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240
acgggaacag cgccaccttc gagcaccagc agccgttgca ggaccggatg ttcaaatttg 300
aactcacccg ccgtctggag catgactttg gcaaggtgac gaagcaggaa gtcaaagagt 360
tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttccac gtcagaaagg 420
gtggagccaa caagagaccc gcccccgatg acgcggatat aagcgagccc aagcgggcct 480
gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540
acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600
agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660
gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720
ggaaactctg tgcgattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780
gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840
ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900
cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960
gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020
gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaagcctac 1080
gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataatcacgc cgacgccgag 1140
tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200
caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260
cctggaaaga agagactggt agagcagtcg ccacaagagc cagactcctc ctcgggcatc 1320
ggcaagacag gccagcagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca 1380
gagtcagtcc ccgacccaca acctctcgga gaacctccag cagccccctc aggtctggga 1440
cctaatacaa tggcttcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 1500
ggagtgggta attcctcggg aaattggcat tgcgattcca catggctggg ggacagagtc 1560
atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 1620
atctccaacg gcacctcggg aggaagcacc aacgacaaca cctattttgg ctacagcacc 1680
ccctgggggt attttgactt caacagattc cactgtcact tttcaccacg tgactggcaa 1740
cgactcatca acaacaattg gggattccgg cccaaaagac tcaacttcaa gctgttcaac 1800
atccaggtca aggaagtcac gacgaacgaa ggcaccaaga ccatcgccaa taatctcacc 1860
agcaccgtgc aggtctttac ggactcggag taccagttac cgtacgtgct aggatccgct 1920

caccagggat gtctgcctcc gttcccggcg gacgtcttca cggttcctca gtacggctat 1980

ttaactttaa acaatggaag ccaagccctg ggacgttcct ccttctactg tctggagtat 2040

ttcccatcgc agatgctgag aaccggcaac aactttcagt tcagctacac cttcgaggac 2100

gtgcctttcc acagcagcta cgcgcacagc cagagcctgg acaggctgat gaatcccctc 2160

atcgaccagt acctgtacta cctggtcaga acgcaaacga ctggaactgg agggacgcag 2220

actctggcat tcagccaagc gggtcctagc tcaatggcca accaggctag aaattgggtg 2280

cccggacctt gctaccggca gcagcgcgtc tccacgacaa ccaaccagaa caacaacagc 2340

aactttgcct ggacgggagc tgccaagttt aagctgaacg gccgagactc tctaatgaat 2400

ccgggcgtgg caatggcttc ccacaaggat gacgacgacc gcttcttccc ttcgagcggg 2460

gtcctgattt ttggcaagca aggagccggg aacgatggag tggattacag ccaagtgctg 2520

attacagatg aggaagaaat caaggctacc aaccccgtgg ccacagaaga atatggagca 2580

gtggccatca acaaccaggc cgccaatacg caggcgcaga ccggactcgt gcacaaccag 2640

ggggtgattc ccggcatggt gtggcagaat agagacgtgt acctgcaggg tcccatctgg 2700

gccaaaattc ctcacacgga cggcaacttt cacccgtctc ccctgatggg cggctttgga 2760

ctgaagcacc cgcctcctca aattctcatc aagaacacac cggttccagc ggacccgccg 2820

cttaccttca accaggccaa gctgaactct ttcatcacgc agtacagcac cggacaggtc 2880

agcgtggaaa tcgagtggga gctgcagaaa gaaaacagca aacgctggaa tccagagatt 2940

caatacactt ccaactacta caaatctaca aatgtggact ttgctgtcaa cacggaagga 3000

gtttatagcg agcctcgccc cattggcacc cgttacctca cccgcaacct gtaattacat 3060

gttaatcaat aaaccggtta attcgtttca gttgaacttt ggtctctgcg aagggcgaat 3120

tc 3122

<210> 43
<211> 3117
<212> DNA
<213> new AAV serotype, clone 43.21

<400> 43
gaattcgccc ttggctgcgt caactggacc aatgagaact ttcccttcaa cgattgcgtc 60

gacaagatgg tgatctggtg ggaggagggc aagatgacgg ccaaggtcgt ggagtccgcc 120

aaggccattc tcggcggcag caaggtgcgt gtggaccaaa agtgcaagtc ttccgcccag 180

atcgatccca ccccgtgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg 240

aacagcacca ccttcgagca ccagcagccg ttgcaggacc ggatgttcaa atttgaactc 300

acccgccgtc tggagcatga ctttggcaag gtgacgaagc aggaagtcaa agagttcttc 360

cgctgggcgc aggatcacgt gaccgaggtg gcgcatgagt tccacgtcag aaagggtgga 420

gccaacaaga gacccgcccc cgatgacgcg gatataagcg agcccaagcg ggcctgcccc 480
tcagtcgcgg atccatcgac gtcagacgcg gaaggagctc cggtggactt tgccgacagg 540
taccaaaaca aatgttctcg tcacgcgggc atgcttcaga tgctgtttcc ctgcaagaca 600
tgcgagagaa tgaatcagaa tttcaacatt tgcttcacgc acgggaccag agactgttca 660
gaatgtttcc ccggcgtgtc agaatctcaa ccggtcgtca gaaagaggac gtatcggaaa 720
ctctgtgcga ttcatcatct gctggggcgg gctcccgaga ttgcttgctc ggcctgcgat 780
ctggtcaacg tggacctgga tgactgtgtt tctgagcaat aaatgactta aaccaggtat 840
ggctgccgat ggttatcttc cagattggct cgaggacaac ctctctgagg gcattcgcga 900
gtggtgggac ttgaaacctg gagccccgaa acccaaagcc aaccagcaaa agcaggacga 960
cggccggggt ctggtgcttc ctggctacaa gtacctcgga cccttcaacg gactcgacaa 1020
gggggagccc gtcaacgcgg cggacgcagc ggccctcgag cacgacaaag cctacgacca 1080
gcagctcaaa gcgggtgaca atccgtacct gcggtataat cacgccgacg ccgagtttca 1140
ggagcgtctg caagaagata cgtcttttgg gggcaacctc gggcgagcag tcttccaggc 1200
caagaagcgg gttctcgaac ctctcggtct ggttgaggaa ggcgctaaga cggctcctgg 1260
aaagaagaga ccggtagagc agtcgccaca agagccagac tcctcctcgg gcatcggcaa 1320
gacaggccag cagcccgcta aaaagagact caattttggt cagactggcg actcagagtc 1380
agtccccgac ccacaacctc tcggagaacc tccagcagcc ccctcaggtc tgggacctaa 1440
tacaatggct tcaggcggtg gcgctccaat ggcagacaat aacgaaggcg ccgacggagt 1500
gggtaattcc tcgggaaatt ggcattgcga ttccacatgg ctgggggaca gagtcatcac 1560
caccagcacc cgaacctggg ccctgcccac ctacaacaac cacctctaca agcaaatctc 1620
caacggcacc tcgggaggaa gcaccaacga caacacctat tttggctaca gcaccccctg 1680
ggggtatttt gacttcaaca gattccactg tcacttttca ccacgtgact ggcaacgact 1740
catcaacaac aattggggat tccggcccaa aagactcaac ttcaagctgt tcaacatcca 1800
ggtcaaggaa gtcacgacga acgaaggcac caagaccatc gccaataatc tcaccagcac 1860
cgtgcgggtc tttacggact cggagtacca gttaccgtac gtgctaggat ccgctcacca 1920
gggatgtctg cctccgttcc cggcggacgt cttcatggtt cctcagtacg gctatttaac 1980
tttaaacaat ggaagccaag ccctgggacg ttcctccttc tactgtctgg agtatttccc 2040
atcgcagatg ctgagaaccg gcaacaactt tcagttcagc tacaccttcg aggacgtgcc 2100
tttccacagc agctacgcgc acagccagag cctggacagg ctgatgaatc ccctcatcga 2160
ccagtacctg tactacctgg tcagaacgca aacgactgga actggaggga cgcagactct 2220
ggcattcagc caagcgggtc ctagctcaat ggccaaccag gctagaaatt gggtgcccgg 2280
accttgctac cggcagcagc gcgtctccac gacaaccaac cagagcaaca acagcaactt 2340

tgcctggacg ggagctgcca agtttaagct gaacggccga gactctctaa tgaatccggg 2400

cgtggcaatg gcttcccaca aggatgacga cgaccgcttc ttcccttcga gcggggtcct 2460

gatttttggc aagcaaggag ccgggaacga tggagtggat tacagccaag tgctgattac 2520

agatgaggaa gaaatcaagg ctaccaaccc cgtggccaca gaagaatatg gagcagtggc 2580

catcaacaac caggccgcca atacgcaggc gcagaccgga ctcgtgcaca accaggggat 2640

gattcccggc atggtgtggc agaatagaga cgtgtacctg cagggtccca tctgggccaa 2700

aattcctcac acggacggca actttcaccc gtctcccctg atgggcggct ttggactgaa 2760

gcacccgcct cctcaaattc tcatcaagaa cacaccggtt ccagcggacc cgccgcttac 2820

cttcaaccag gccaagctga actctttcat cacgcagtac agcaccggac aggtcagcgt 2880

ggaaatcgag tgggagctgc agaaagaaaa cagcaaacgc tggaatccag agattcaata 2940

cacttccaac tactacaaat ctacaaatgt ggactttgct gtcaacacgg aaggagttta 3000

tagcgagcct cgccccattg gcacccgtta cctcacccgc aacctgtaat tacatgttaa 3060

tcaataaacc ggttaattcg tttcagttga actttggtct ctgcgaaggg cgaattc 3117

<210> 44
<211> 3121
<212> DNA
<213> new AAV serotype, clone 43.23

<400> 44
gaattcgccc ttctacggct gcgtcaactg gaccaatgag aactttccct tcaacgattg 60

cgtcgacaag atggtgatct ggtgggagga gggcaagatg acggccaagg tcgtggagtc 120

cgccaaggcc attctcggcg gcagcaaggt gcgtgtggac caaaagtgca agtcttccgc 180

ccagatcgat cccaccccca tgatcgtcac ctccaacacc aacatgtgcg ccgtgattga 240

cgggaacagc accaccttcg agcaccagca gccgttgcag gaccggatgt tcaaatttga 300

actcacccgc cgtctggagc atgactttgg caaggtgacg aagcaggaag tcaaagagtt 360

cttccgctgg gcgcaggatc acgtgaccga ggtggcgcat gagttccacg tcagaaaggg 420

tggcgccaac aagagacccg cccccgatga cgcggatata agcgagccca agcgggcctg 480

cccctcagtc gcggatccat cgacgtcaga cgcggaagga gctccggtgg actttgccga 540

caggtaccaa aacaaatgtt ctcgtcacgc gggcatgctt cagatgctgt ttccctgcaa 600

gacatgcgag agaatgaatc agaatttcaa catttgcttc acgcacggga ccagagactg 660

ttcagaatgt ttccccggcg tgtcagaatc tcaaccggtc gtcagaaaga ggacgtatcg 720

gaaactctgt gcgattcatc atctgctggg gcgggctccc gagattgctt gctcggcctg 780

cgatctggtc aacgtggacc tggatgactg tgtttctgag caataaatga cttaaaccag 840

gtatggctgc cgatggttat cttccagatt ggctcgagga caacctctct gagggcattc 900

gcgagtggtg ggacttgaaa cctggagccc cgaaacccaa agccaaccag caaaagcagg 960

acgacggccg gggtctggtg cttcctggct acaagtacct cggacccttc aacggactcg 1020

acaaggggga gcccgtcaac gcggcggacg cagcggccct cgagcacgac aaagcctacg 1080

accagcagct caaagcgggt gacaatccgt acctgcggta taatcacgcc gacgccgagt 1140

ttcaggagcg tctgcaagaa gatacgtcct ttgggggcaa cctcgggcga gcagtcttcc 1200

aggccaagaa gcgggttctc gaacctctcg gtctggttga ggaaggcgct aagacggctc 1260

ctggaaagaa gagaccggta gagcagtcgc cacaagagcc agactcctcc tcgggcatcg 1320

gcaagacagg ccagcagccc gctaaaaaga gactcaattt tggtcagact ggcgactcag 1380

agtcagtccc cgacccacaa cctctcggag aacctccagc agccccctca ggtctgggac 1440

ctaatacaat ggcttcaggc ggtggcgctc caatggcaga caataacgaa ggcgccgacg 1500

gagtgggtaa ttcctcggga aattggcatt gcgattccac atggctgggg gacagagtca 1560

tcaccaccag cacccgaacc tgggccctgc ccacctacaa caaccacctc tacaagcaaa 1620

tctccaacgg cacctcggga ggaagcacca acgacaacac ctattttggc tacagcaccc 1680

cctgggggta ttttgacttc aacagattcc actgtcactt ttcaccacgt gactggcaac 1740

gactcatcaa caacaattgg ggattccggc ccaaaagact caacttcaag ctgttcaaca 1800

tccaggtcaa ggaagtcacg acgaacgaag gcaccaagac catcgccaat aatctcacca 1860

gcaccgtgca ggtctttacg gacttggagt accagttacc gtacgtgcta ggatccgctc 1920

accagggatg tctgcctccg ttcccggcgg acgtcttcat ggttcctcag tacggctatt 1980

taactttaaa caatggaagc caagccctgg gacgttcctc cttctactgt ctggagtatt 2040

tcccatcgca gatgccgaga accggcaaca actttcagtt cagctacacc ttcgaggacg 2100

tgcctttcca cagcagctac gcgcacagcc agagcctgga caggctgatg aatcccctca 2160

tcgaccagta cctgtactac ctggtcagaa cgcaaacgac tggaactgga gggacgcaga 2220

ctctggcatt cagccaagcg ggtcctagct caatggccaa ccaggctaga aattgggtgc 2280

ccggaccttg ctaccggcag cagcgcgtct ccacgacaac caaccagaac aacaacagca 2340

actttgcctg gacgggagct gccaagttta agctgaacgg ccgagactct ctaatgaatc 2400

cgggcgtggc aatggcttcc cacaaggatg acgacgaccg cttcttccct tcgagcgggg 2460

tcctgatttt tggcaagcaa ggagccggga acgatggagt ggattacagc caagtgctga 2520

ttacagatga ggaagaaatc aaggctacca accccgtggc cacagaagaa tatggagcag 2580

tggccatcaa caaccaggcc gccaatacgc aggcgcagac cggactcgtg cacaaccagg 2640

gggtgattcc cggcatggtg tggcagaata gagacgtgta cctgcagggt cccatctggg 2700

ccaaaattcc tcacacggac ggcaactttc acccgtctcc cctgatgggc ggctttggac 2760

tgaagcaccc gcctcctcaa attctcatca agaacacacc ggttccagcg gacccgccgc 2820

ttaccttcaa ccaggccaag ctgaactctt tcatcacgca gtacagcacc ggacaggtca 2880

gcgtggaaat cgagtgggag ctgcagaaag aaaacagcaa acgctggaat ccagagattc 2940

aatacacttc caactactac aaatctacaa atgtggactt tgctgtcaac acggaaggag 3000

tttatagcga gcctcgcccc attggcaccc gttacctcac ccgcaacctg taattacatg 3060

ttaatcaata aaccggttaa ttcgtttcag ttgaactttg gtctctgcga agggcgaatt 3120

c 3121

<210> 45
<211> 3122
<212> DNA
<213> new AAV serotype, clone 43.25

<400> 45
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgtgtgga ccaaaagtgc aagtcttccg 180

cccagatcga tcccacccca gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaaatttg 300

aactcacccg ccgtctggag catgactttg gcaaggtgac gaagcaggaa gtcaaagggt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttccac gtgcgagccc 420

aagcgggcct gccctcagt cgcggatcca tcgacgtcag accagaaagg gtggagccaa 480

caagagaccc gcccccgatg acgcggatat aagcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgcgattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaagcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataatcacgc cgacgccgag 1140

tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagcagtcg ccacaagagc cagactcctc ctcgggcatc 1320

ggcaagacag gccagcagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca 1380

gagtcagtcc ccgacccaca acctctcgga gaacctccag cagccccctc aggtctggga 1440

cctaatacaa tggcttcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 1500

ggagtgggta attcctcggg aaattggcat tgcgattcca catggctggg ggacagagtc 1560

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 1620

atctccaacg gcacctcggg aggaagcacc aacgacaaca cctattttgg ctacagcacc 1680

ccctgggggt attttgactt caacagattc cactgtcact tttcaccacg tgactggcaa 1740

cgactcatca acaacaattg gggattccgg cccaaaagac tcaacttcaa gctgttcaac 1800

atccaggtca aggaagtcac gacgaacgaa ggcaccaaga ccatcgccaa taatctcacc 1860

agcaccgtgc aggtctttac ggactcggag taccagttac cgtacgtgct aggatccgct 1920

caccagggat gtctgcctcc gttcccggcg gacgtcttca tggttcctca gtacggctat 1980

ttaactttaa acaatggaag ccaagccctg ggacgttcct ccttctactg tctggagtat 2040

ttcccatcgc agatgctgag aaccggcaac aactttcagt tcagctacac cttcgaggac 2100

gtgcctttcc acagcagcta cgcgcacagc cagagcctgg acaggctgat gaatcccctc 2160

atcgaccagt acctgtacta cctggtcaga acgcaaacga ctggaactgg agggacgcag 2220

actctggcat tcagccaagc gggtcctagc tcaatggcca accaggctag aaattgggtg 2280

cccggacctt gctaccggca gcagcgcgtc tccacgacaa ccaaccagaa caacaacagc 2340

aactttgcct ggacgggagc tgccaagttt aagctgaacg gccgagactc tctaatgaat 2400

ccgggcgtgg caatggcttc ccacaaggat gacgacgacc gcttcttccc ttcgagcggg 2460

gtcctgattt ttggcaagca aggagccggg aacgatggag tggattacag ccaagtgctg 2520

attacagatg aggaagaaat caaggctacc aaccccgtgg ccacagaaga atatggagca 2580

gtggccatca acaaccaggc cgccaatacg caggcgcaga ccggactcgt gcacaaccag 2640

ggggtgattc ccggcatggt gtggcagaat agagacgtgt acctgcaggg tcccatctgg 2700

gccaaaattc ctcacacgga cggcaacttt cacccgtctc ccctgatggg cggctttgga 2760

ctgaagcacc cgcctcctca aattctcatc aagaacacac cggttccagc ggacccgccg 2820

cttaccttca accaggccaa gctgaactct ttcatcacgc agtacagcac cggacaggtc 2880

agcgtggaaa tcgagtggga gctgcagaaa gaaaacagca aacgctggaa tccagagatt 2940

caatacactt ccaactacta caaatctaca aatgtggact ttgctgtcaa cacggagggg 3000

gtttatagcg agcctcgccc cattggcacc cgttacctca cccgcaacct gtaattacat 3060

gttaatcaat aaaccggtta attcgtttca gttgaacttt ggtctctgcg aagggcgaat 3120

tc 3122

<210> 46
<211> 3128
<212> DNA
<213> new AAV serotype, clone 44.1

<400> 46

gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatgttgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaaag tgcgcgtgga ccaaaagtgc aagccgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgcg ggaccggatg ttcaagtttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcagagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca cgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

aaacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaaa aagacgtatc 720

ggaaactctg tgcgattcat catctgctgg ggcgggcacc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctagatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

atcggcaaga aaggccagca gcccgcgaaa aagagactca actttgggca gactggcgac 1380

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacttc gggaggaagc accaacgaca acacctactt cggctacagc 1680

acccccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920

gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tacctgactc tgaacaatgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag 2100

gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc 2160

ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220

actcagcagt tgctattttc tcaggccggg cctaataaca tgtcggctca ggccaaaaac 2280

tggctacccg ggccctgcta ccggcagcaa cgcgtctcca cgacactgtc gcaaaataac 2340

aacagcaact gtaaatcccg gtgtcgctat ggcaacccac aaggacgacg aagagcgatt 2400

ttgcctggac cggtgccacc aagtatcatc tgaatggcag agactctctg ttttccgtcc 2460

agcggagtct taatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc 2520

gttatgctaa ccagtgagga agaaattaaa accaccaacc cagtggccac ggaacagtac 2580

ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac 2640

agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct 2700

atctgggcca agattcctca cacggacgga aactttcatc cctcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat 2820

cctccaacta ccttcagtca agctaagctg gcgtcgttca tcacgcagta cagcaccgga 2880

caggtcagcg tggaaattga atgggagctg cagaaagaaa acagcaaacg ctggaaccca 2940

gagattcaat acacttccaa ctactacaaa tctacaaatg tggacttcgc tgttaacaca 3000

gatggcactt attctgagcc tcgccccatt ggcacccgtt acctcacccg taatctgtaa 3060

ttgctcgtta atcaataaac cggttgattc gtttcagttg aactttggtc tctgcgaagg 3120

gcgaattc 3128

<210> 47
<211> 3128
<212> DNA
<213> new AAV serotype, clone 44.5

<400> 47
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaaag tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccacccca gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaagtttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcagagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca cgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540
acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600
aaacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660
gttcagaatg tttccccggc gtgtcagaat ctcaaccggt tgtcagaaaa aagacgtatc 720
ggaaactctg tgcgattcat catctgctgg ggcgggcacc cgagattgct tgctcggcct 780
gcgatctggt caacgtggac ctagatgact gtgtttctga gcaataaatg acttaaacca 840
ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900
cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960
gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020
gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080
gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140
tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200
caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260
cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320
atcggcaaga aaggccagca gcccgcgaaa aagagactca actttgggca gactggcgac 1380
tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440
ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500
gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560
gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620
caaatctcca acgggacttc gggaggaagc accaacgaca acacctactt cggctacagc 1680
acccccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740
cagcgactca tcaacaacaa ctggggattc cggcccaaga gacccaactt caagctcttc 1800
aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860
accagcacga ttcaggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920
gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980
tacctgactc tgaacaatgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040
tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag 2100
gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc 2160
ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220
actcagcagt tgctattttc tcaggccggg cctaataaca tgtcggctca ggccaaaaac 2280
tggctacccg ggccctgcta ccggcagcaa cgcgtctcca cgacactgtc gcaaaataac 2340
aacagcaact ttgcctggac cggtgccacc aagtatcatc tgaatggcag agactctctg 2400

gtaaatcccg gtgtcgctat ggcaacccac aaggacgacg aagagcgatt ttttccgtcc 2460

agcggagtct taatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc 2520

gttatgctaa ccagtgagga agaaattaaa accaccaacc cagtggccac agaacagtac 2580

ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac 2640

agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct 2700

atctgggcca agattcctca cacggacgga aactttcatc cctcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat 2820

cctccaacta ccttcagtca agctaagctg gcgtcgttca tcacgcagta cagcaccgga 2880

caggtcagcg tggaaattga atgggagctg cagaaagaaa acagcaaacg ctggaaccca 2940

gagattcaat acacttccaa ctactacaaa tctacaaatg tggactttgc tgttaacaca 3000

gatggcactt attctgagcc tcgccccatt ggcacccgtt acctcacccg taatctgtaa 3060

ttgcttgtta atcaataaac cggttgattc gtttcagttg aactttggtc tctgcgaagg 3120

gcgaattc 3128

<210> 48
<211> 1933
<212> DNA
<213> new AAV serotype, clone 223.10

<220>
<221> misc_feature
<222> (1302)..(1302)
<223> can be a, c, g or t

<400> 48
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 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 caccttttagc 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 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 ggccccctctg 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 caccttttagc 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

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 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 ggccccctctg 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 gcaccccctg 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> 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 ggccccctctg 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
gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900
tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960
ttctcagatg ctgagaacgg gcaacaactt caccttttagc 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 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 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 gcaccccctg 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

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

ttctcagatg ctgagaacgg gcaacaactt caccttttagc 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 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 cctgccaaga ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

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
agcgaatcgg gagccaccaa cgacaaccac tacttcggct acagcacccc ctgggggtat 1680
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
agcagctacg cgcacagcca gagtctggat cggctgatga atcctctcat tgaccagtac 2160
ctgtattacc tgagcaaaac tcagggtaca agtggaacaa cgcagcaatc gagactgcag 2220
ttcagccaag ctgggcctag ctccatggct cagcaggcca aaaactggct accgggaccc 2280
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
atagagtggg agctgcagaa agaaaacagc aaacgctgga acccagaaat tcagtacacc 2940
tccaactaca acaagtcggt gaatgtggag tttaccgtgg acgcaaacgg tgtttattct 3000
gaacccgcgc ctattggcac tcgttacctt acccggaact tgtaatttcc tgttaatgaa 3060
taaaccgatt tatgcgtttc agttgaactt tggtctctgc gaagggcgaa ttcgcggccg 3120
cta 3123

<210> 55
<211> 3113
<212> DNA
<213> new AAV serotype, clone A3.5

<400> 55
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 tacgcggaca 540

ggtaccaaaa caaatgttct cgtcacgtgg gcatgaatct gatgctgttt ccctgtcgac 600

aatgcgaaag aatgaatcag aattcaaata tctgcttcac acacgggcaa aaagactgtt 660

tggaatgctt tcccgtgtca gaatctcaac ccgttcctgt cgtcagaaaa acgtatcaga 720

aactttgtta cattcatcat atcatgggaa aagtaccaga 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 catcggcaaa 1320

tcaggccagc agcccgctaa gaaaagactc aattttggtc agactggcga cacagagtca 1380

gtcccagacc ctcaaccaat cggagaaccc ccgcagccc cctctggtgt gggatctaat 1440

acaatggctt caggcggtgg ggcaccaatg gcagacaata acgaaggcgc cgacggagtg 1500

ggtaattcct cgggaaattg gcattgcgat tccacatgga tgggcgacag agttatcacc 1560

accagcacaa gaacctgggc cctccccacc tacaataatc acctctacaa gcaaatctcc 1620

agcgaatcgg gagccaccaa cgacaaccac tacttcggct acagcacccc ctgggggtat 1680

tttgacttta acagattcca ctgtcacttc tcaccacgtg actggcagcg actcatcaat 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

agcagctacg cgcacagcca gagtctggat cggctgatga atcctctcat tgaccagtac 2160

ctgtattacc tgagcaaaac tcagggtaca agtggaacaa cgcagcaatc gagactgcag 2220

ttcaaccaag ctgggcctag ctccatggct cagcaggcca aaaactggct accgggaccc 2280

agctaccgac agcagcgaat gtctaagacg gctaatgaca acaacaacag tgaatttgct 2340

tggactgcag ccaccaaata ttacccgaat ggaagaaatt ctctggtcaa tcccgggccc 2400

ccaatggcca gtcacaagga cgatgaggaa aagtatttcc ccatgcacgg aaatctcatc 2460

tttggaaaac aaggcacagg aactaccaat gtggacattg aatcagtgct tattacagac 2520

gaagaagaaa tcagaacgac taatcctgtg gctacagaac aatacggaca ggttgccacc 2580

aaccgtcaga gtcagaacac 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

atagagtggg agctgcagaa agaaaacagc aaacgctgga acccggaaat tcagtacacc 2940

tccaactaca acaagtcggt gaatgtggag tttaccgtgg acgcaaacgg tgtttattct 3000

gaaccccgcc ctattggcac tcgttacctt acccggaact tgtaatttcc tgttaatgaa 3060

taaaccgatt tatgcgtttc agttgaactt tggtctctgc gaagggcgaa ttc 3113

<210> 56
<211> 3122
<212> DNA
<213> new AAV serotype, clone A3.7

<400> 56
agcggccgcg aattcgccct ttctacggct gcgtcaactg gaccaatgaa aactttccct 60

tcaacgattg cgtcgacaag atggtgatct ggtgggagga gggaaagatg accgccaagg 120

tcgtggaatc tgccaaagcc attctgggtg gaagcaaggt tcgtgtggac cagaaatgca 180

ggtcttcggc ccagatcgac ccgactccgg tgattgtcac ctctaacacc aacatgtgcg 240

ccgtgattga cggaaactcg accaccttcg agcaccagca gccgttgcaa gaccggatgt 300

tcaaatttga acttacccgc cgtttggatc atgactttgg gaaggtcacc aagcaggaag 360

tcaaagactt tttccggtgg gctcaagatc acgtgactga ggtggagcat gagttctacg 420

tcaaaaaggg tggagccaag aaaaggcccg cccccgatga tgtatatata aatgagccca 480

agcgggcgcg cgagtcagtt gcgcagccat cgacgtcaga cgcggaagct tcgataaact 540

acgcggacag gtaccaaaac aaatgttctc gtcacgtggg catgaatctg atgctgtttc 600

cctgtcgaca atgcgaaaga atgaatcaga attcaaatat ctgcttcaca cacgggcaaa 660

aagactgttt ggaatgcttt cccgtgtcag aatctcaacc cgtttctgtc gtcagaaaaa 720

cgtatcagaa actttgttac attcatcata tcatgggaaa agtaccagac gcctgcactg 780

cctgcgacct ggtaaatgtg gacttggatg actgtatttc tgagcaataa atgacttaaa 840

tcaggtatgg ctgctgacgg ttatcttcca gattggctcg aggacactct ctctgaagga 900

atcagacagt ggtggaagct caaacctggc ccaccaccgc cgaaacctaa ccaacaacac 960

cgggacgaca gtaggggtct tgtgcttcct gggtacaagt acctcggacc cttcaacgga 1020

ctcgacaaag gagagccggt caacgaggca gacgccgcgg ccctcgagca cgacaaagcc 1080

tacgaccacc agctcaagca aggggacaac ccgtacctca aatacaacca cgcggacgct 1140

gaatttcagg agcgtcttca agaagatacg tctttcgggg gcaacctcgg gcgagcagtc 1200

ttccaggcca aaaagagggt actcgagcct cttggtctgg ttgaggaagc tgttaagacg 1260

gctcctggaa aaaagagacc tatagagcag tctcctgcag aaccggactc ttcctcgggc 1320

atcggcaaat caggccagca gcccgctaag aaaagactca attttggtca gactggcgac 1380

acagagtcag tcccagaccc tcaaccaatc ggagaacccc ccgcagcccc ctctggtgtg 1440

ggatctaata caatggcttc aggcggtggg gcaccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtaattcctc gggaaattgg cattgcgatt ccacatggat gggcgacaga 1560

gttatcacca ccagcacaag aacctgggcc ctccccacct acaataatcg cctctacaag 1620

caaatctcca gcgaatcggg agccaccaac gacaaccact acttcggcta cagcaccccc 1680

tgggggtatt ttgactttaa cagattccac tgtcacttct caccacgtga ctggcagcga 1740

ctcatcaaca acaactgggg atttagaccc aagaaactca atttcaagct cttcaacatc 1800

caagtcaagg aggtcacgca gaatgatgga accacgacca tcgccaataa ccttaccagc 1860

acggtgcagg tcttcacaga ctctgagtac cagctgccct acgtcctcgg ttcggctcac 1920

cagggctgcc ttccgccgtt cccagcagac gtcttcatga ttcctcagta cggctacttg 1980

actctgaaca atggcagcca agcggtagga cgttcttcat tctactgtct agagtatttt 2040

ccctctcaga tgctgaggac gggaaacaac ttcaccttca gctacacttt tgaagacgtg 2100

cctttccaca gcagctacgc gcacagccag agtctggatc ggctgatgaa tcctctcatt 2160

gaccagtacc tgtattacct gagcaaaact cagggtacaa gtggaacaac gcagcaatcg 2220

agactgcagt tcagccaagc tgggcctagc tccatggctc agcaggccaa aaactggcta 2280

ccgggaccca gctaccgaca gcagcgaatg tctaagacgg ctaatgacaa caacaacagt 2340

gaatttgctt ggactgcagc caccaaatat tacctgaatg gaagaaattc tctggtcaat 2400

cccgggcccc caatggccag tcacaaggac gatgaggaaa agtatttccc catgcacgga 2460

aatctcatct ttggaaaaca aggcacagga actaccaatg tggacattga atcagtgctt 2520

attacagacg aagaagaaat cagaacaact aatcctgtgg ctacagaaca atacggacag 2580

gttgccacca accatcagag tcagaacacc acagcttcct atggaagtgt ggacagccag 2640

ggaatcttac ctggaatggt gtggcaggac cgcgatgtct atcttcaagg tcccatttgg 2700

gccaaaactc ctcacacgga cggacacttt catccttctc cgctcatggg aggctttgga 2760

ctgaaacacc ctcctcccca gatcctgatc aaaaacacac ctgtgccagc gaatcccgcg 2820

accactttca ctcctggaaa gtttgcttcg ttcattaccc agtattccac cggacaggtc 2880

agcgtggaaa tagagtggga gctgcagaaa gaaaacagca aacgctggaa cccagaaatt 2940

cagtacacct ccaactacaa caagtcggtg aatgtggagt ttaccgtgga cgcaaacggt 3000

gtttattctg aaccccgccc tattggcact cgttacctta cccggaactt gtaatttcct 3060

gttaatgaat aaaccgattt atgcgtttca gttgaacttt ggtctctgcg aagggcgaat 3120

tc 3122

<210> 57
<211> 3123
<212> DNA
<213> new AAV serotype, clone A3.3

<400> 57
gaattcgccc tttctacggc tgcgtcaact ggaccaatga aaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggaaagat gaccgccaag gtcgtggaat 120

ctgccaaagc cattctgggt ggaggcaagg 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 tacgcggaca 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 aagtaccaga 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 catcggcaaa 1320

tcaggccagc agcccgctaa gaaaagactc aattttggtc agactggcga cacagagtca 1380

gtcccaggcc ctcaaccaat cggagaaccc cccgcagccc cctctggtgt gggatctaat 1440

acaatggctt caggcggtgg ggcaccaatg gcagacaata acgaaggcgc cgacggagtg 1500

ggtaattcct cgggaaattg gcattgcgat tccacatgga tgggcgacag agttatcacc 1560

accagcacaa gaacctgggc cctccccacc tacaataatc acctctacaa gcaaatctcc 1620

agcgaatcgg gagccaccaa cgacaaccac tacttcggct acagcacccc ctgggggtat 1680

tttgacttta acagattcca ctgtcacttc tcaccacgtg actggcagcg actcatcaac 1740

aacaactggg gatttagacc caagaaactc aatttcaagc tcttcaacat ccaagtcaag 1800

gaggtcacgc agaatgatgg aaccacgacc atcgccaata accttaccag cgcggtgcag 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

agcagctacg cgcacagcca gagtctggat cggctgatga atcctctcat tgaccagtac 2160

ctgtattacc tgagcaaaac tcagggtaca agtggaacaa cgcagcaatc gagactgcag 2220

ttcagccaag ctgggcctag ctccatggct cagcaggcca aaaactggct accgggaccc 2280

agctaccgac agcagcgaat gtctaagacg gctaatgaca acaacaacag tgaatttgct 2340

tggactgcag ccaccaaata ttacctgaat ggaagaaatt ctctggtcaa tcccgggccc 2400

ccagtggcca gtcacaagga cgatgaggaa aagtatttcc ccatgcacgg aaatctcatc 2460

tttggaaaac aaggcacagg aactaccaat gtggacattg aatcagtgct tattacagac 2520

gaagaagaaa tcagaacaac taatcctgtg gctacagaac aatacggaca ggttgccacc 2580

aaccatcaga gtcagaacac 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 cctgacaggt cagcgtggaa 2880

atagagtggg agctgcagaa agaaaacagc aaacgctgga acccagaaat tcagtacacc 2940

tccaactaca acaagtcggt gaatgtggag tttaccgtgg acgcaaacgg tgtttattct 3000

gaaccccgcc ctattggcac tcgttacctt acccggaact tgtaatttcc tgttaatgaa 3060

taagccgatt tatgcgtttc agttgaactt tggtctctgc gaagggcgaa ttcgtttaaa 3120

cct 3123

<210> 58
<211> 2969
<212> DNA
<213> new AAV serotype, clone 42.12

<400> 58
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatc 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaagggag agccggtcaa cgaggcagac gccgcggccc tcgagcacga caaggcctac 1080

gacaagcagc tcgagcaggg ggacaacccg tacctcaagt acaaccacgc cgacgccgag 1140

tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

atcggcaaga caggccagca gcccgcgaaa aagagactca actttgggca gactggcgac 1380

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacatc gggaggaagc accaacgaca acacctactt cggctacagc 1680

acccccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920

gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tacctgactc tgaacaacgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag 2100

gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gacgaacccc 2160

ctcatcgacc agtacctgta ctacctggcc cggacccaga gcactacggg gtccacaagg 2220

gggctgcagt tccatcaggc tgggcccaac accatggccg agcaatcaaa gaactggctg 2280

cccggaccct gttatcggca gcagagactg tcaaaaaaca tagacagcaa caacaacagt 2340

aactttgcct ggaccggggc cactaaatac catctgaatg gtagaaattc attaaccaac 2400

ccgggcgtag ccatggccac caacaaggac gacgaggacc agttctttcc catcaacgga 2460

gtgctggttt ttggcaaaac gggggctgcc aacaagacaa cgctggaaaa cgtgctaatg 2520

accagcgagg aggagatcaa aaccaccaat cccgtggcta cagaagaata cggtgtggtc 2580

tccagcaacc tgcaatcgtc tacggccgga ccccagacac agactgtcaa cagccagggg 2640

gctctgcccg gcatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 2700

aaaattcctc acacggacgg caactttcac ccgtctcccc tgatgggcgg atttggactc 2760

aaacacccgc ctcctcaaat tctcatcaag tatacttcca actactacaa atctacaaat 2820

gtggactttg ctgtcaatac tgagggtact tattcagagc ctcgccccat tggcacccgt 2880

tacctcaccc gtaacctgta attgcctgtt aatcaataaa ccggttaatt cgtttcagtt 2940

gaactttggt ctctgcgaag ggcgaattc 2969

<210> 59
<211> 3129
<212> DNA
<213> new AAV serotype, clone 44.2

<400> 59
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120
ccgccaaggc cattctcggc ggcagcaaag tgcgcgtgga ccaaaagtgc aagtcgtccg 180
cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240
acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaagtttg 300
aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcagagagt 360
tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca cgagttctac gtcagaaagg 420
gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480
gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540
acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600
aaacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660
gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaaa aagacgtatc 720
ggaaactctg tgcgattcat catctgctgg gggcgggcac ccgagattgc ttgctcggcc 780
tgcgatctgg tcaacgtgga cctagatgac tgtgtttctg agcaataaat gacttaaacc 840
aggtatggct gccgatggtt atcttccaga ttggctcgag gacaacctct ctgagggcat 900
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
ccaggccaag aagcgggttc tcgaacctct cggtctggtt gaggaaggcg ctaagacggc 1260
tcctggaaag aagagaccgg tagagccatc accccagcgt tctccagact cctctacggg 1320
catcggcaag aaaggccagc agcccgcgaa aaagagactc aactttgggc agactggcga 1380
ctcagagtca gtgcccgacc ctcaaccaat cggagaaccc cccgcaggcc cctctggtct 1440
gggatctggt acaatggctg caggcggtgg cgctccaatg gcagacaata acgaaggcgc 1500
cgacggagtg ggtagttcct caggaaattg gcattgcgat tccacatggc tgggcgacag 1560
agtcatcacc accagcaccc gaacctgggc cctccccacc tacaacaacc acctctacaa 1620
gcaaatctcc aacgggactt cgggaggaag caccaacgac aacacctact tcggctacag 1680
caccccctgg gggtattttg actttaacag attccactgc cacttctcac cacgtgactg 1740
gcagcgactc atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt 1800
caacatccag gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct 1860
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
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 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

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

<210> 64
<211> 736
<212> PRT
<213> capsid protein of AAV serotype, clone AAV1

<400> 64
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
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

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
```

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

<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

<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
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 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
```

<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

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

<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

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

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

<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

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 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> 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

<210> 100
<211> 736
<212> PRT
<213> capsid protein of AAV serotype, clone AAV9

400> 100

```
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

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

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

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