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Gao et al.

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(54) **METHOD OF DETECTING AND/OR IDENTIFYING ADENO-ASSOCIATED VIRUS (AAV) SEQUENCES AND ISOLATING NOVEL SEQUENCES IDENTIFIED THEREBY**

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(58) **Field of Classification Search**
None
See application file for complete search history.

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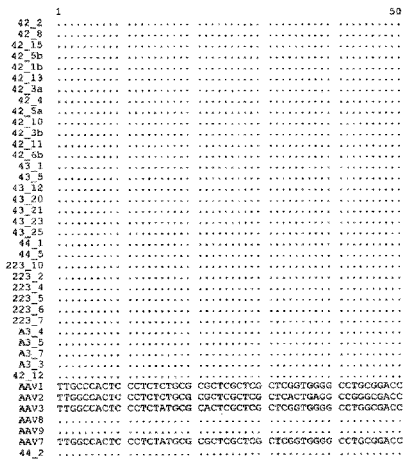
(57) **ABSTRACT**

Adeno-associated virus rh.10 sequences, vectors containing same, and methods of use are provided.

25 Claims, 112 Drawing Sheets

Specification includes a Sequence Listing.



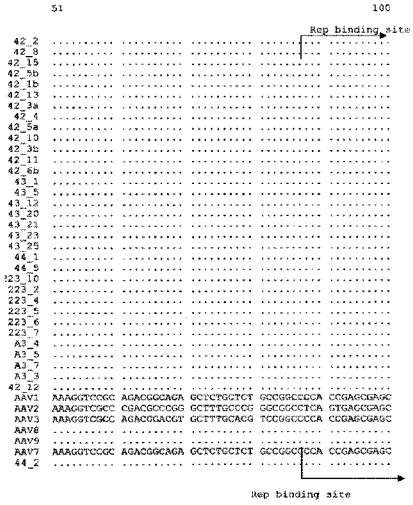


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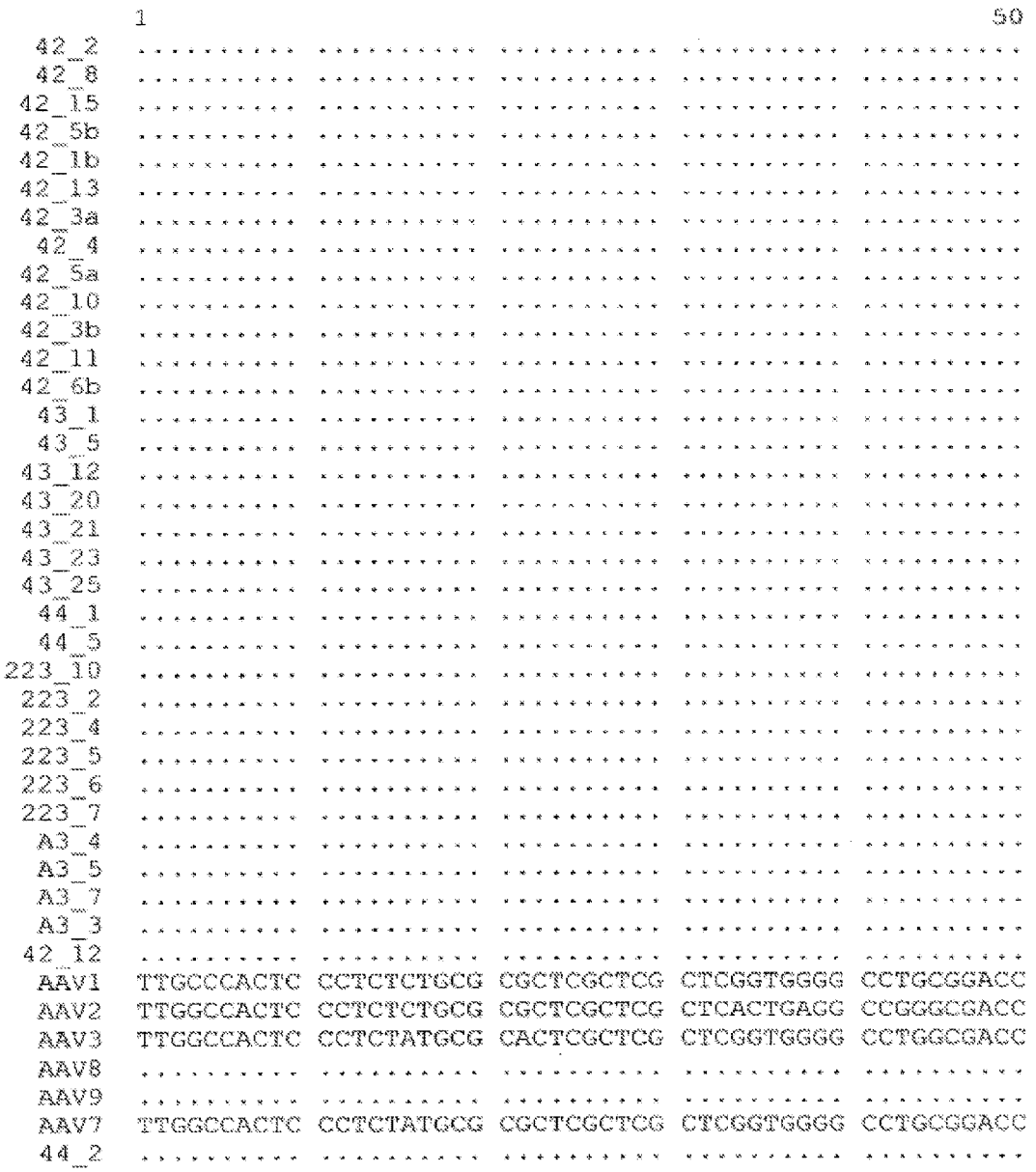
FIG. 1A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AAV9
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44_2

FIG. 1B

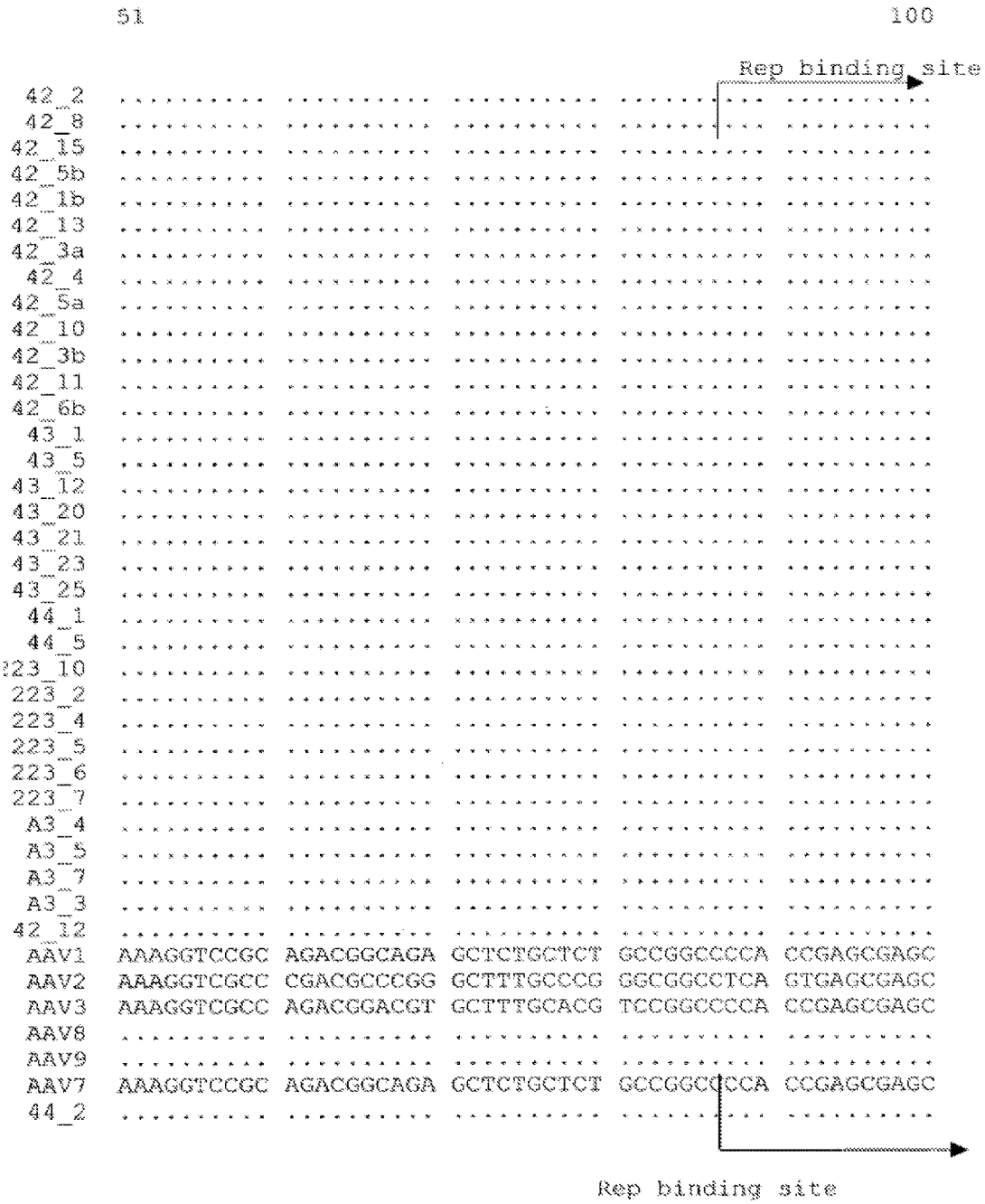
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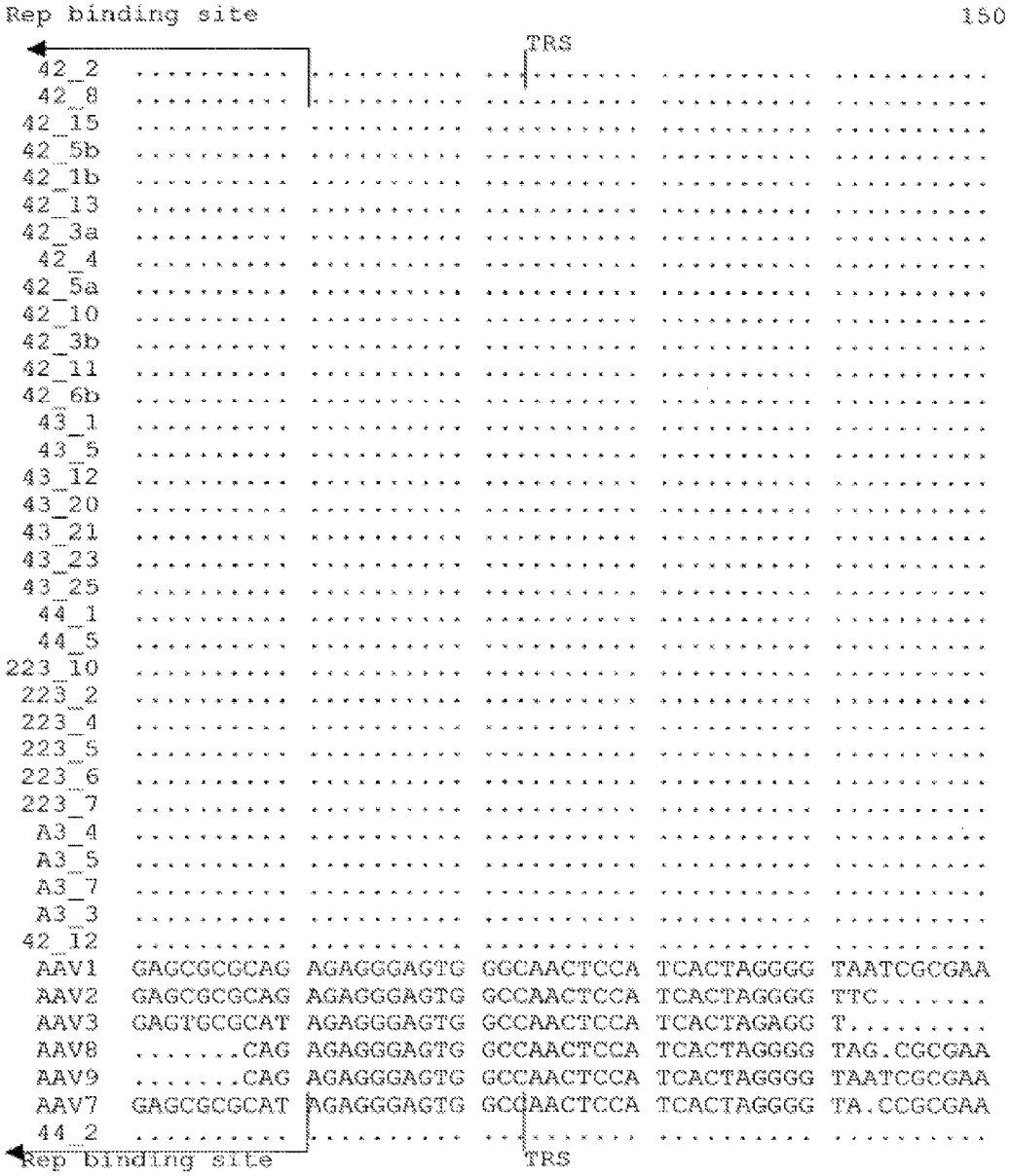
FIG. 1C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AAV2 GAGCGCGCAG AGAGGGAGTG GCCAACTCCA TCACTAGGGG TTC.....
AAV3 GAGTGCGCAT AGAGGGAGTG GCCAACTCCA TCACTAGAGG T.....
AAV8 .....CAG AGAGGGAGTG GCCAACTCCA TCACTAGGGG TAG.CGCGAA
AAV9 .....CAG AGAGGGAGTG GCCAACTCCA TCACTAGGGG TAATCGCGAA
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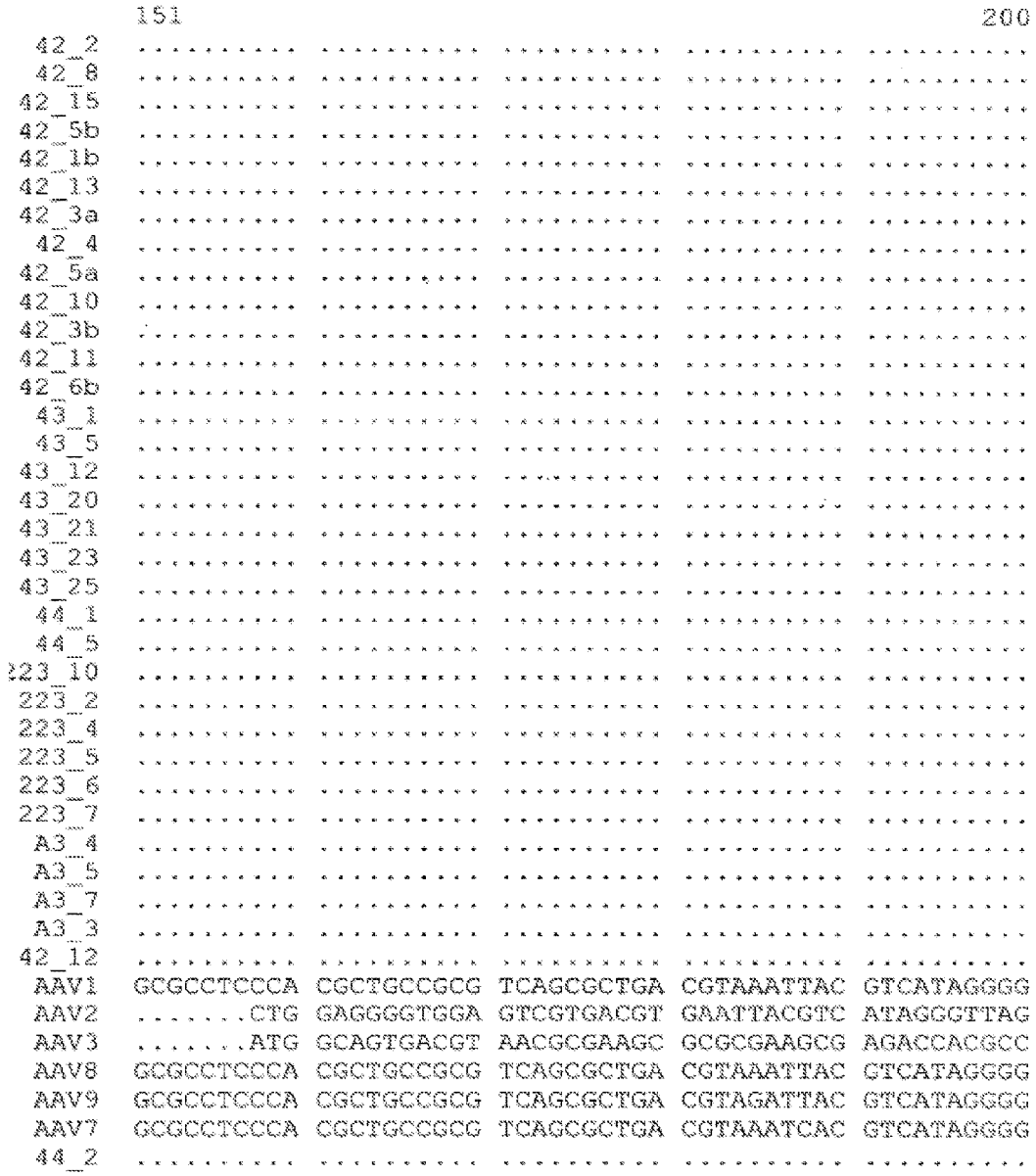
FIG. 1D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A3_3
42_12
AAV1 GCGCCTCCCA CGCTGCCGCG TCAGCGCTGA CGTAAATTAC GTCATAGGGG
AAV2 .....CTG GAGGGGTGGA GTCGTGACGT GAATTACGTC ATAGGGTTAG
AAV3 .....ATG GCAGTGACGT AACGCGAAGC GCGCGAAGCG AGACCACGCC
AAV8 GCGCCTCCCA CGCTGCCGCG TCAGCGCTGA CGTAAATTAC GTCATAGGGG
AAV9 GCGCCTCCCA CGCTGCCGCG TCAGCGCTGA CGTAGATTAC GTCATAGGGG
AAV7 GCGCCTCCCA CGCTGCCGCG TCAGCGCTGA CGTAAATCAC GTCATAGGGG
44_2

FIG. 1E

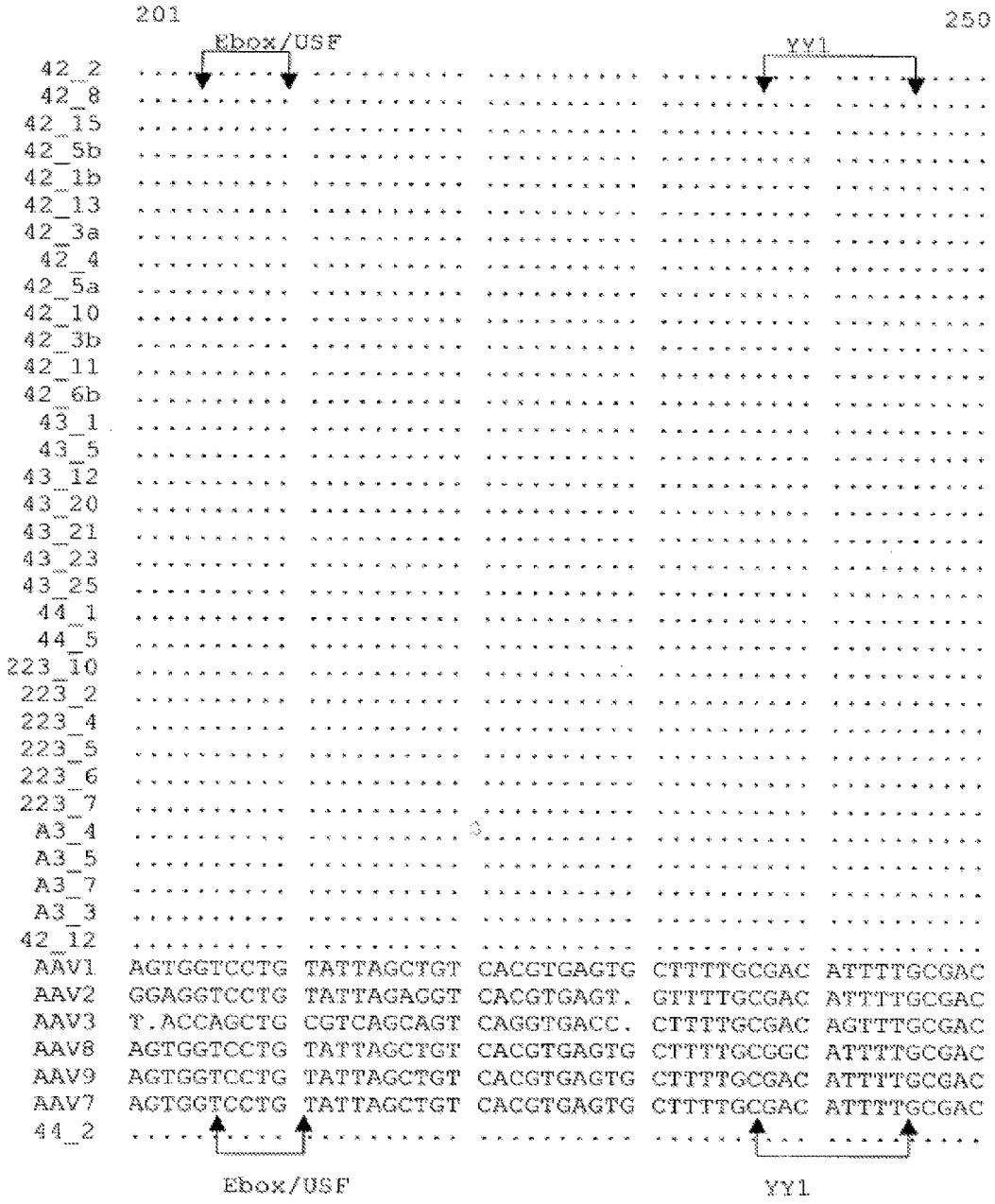
201
250
Ebox/USF
YY1
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 AGTGGTCCTG TATTAGCTGT CACGTGAGTG CTTTTGCGAC ATTTTGCGAC
AAV2 GGAGGTCCTG TATTAGAGGT CACGTGAGT.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

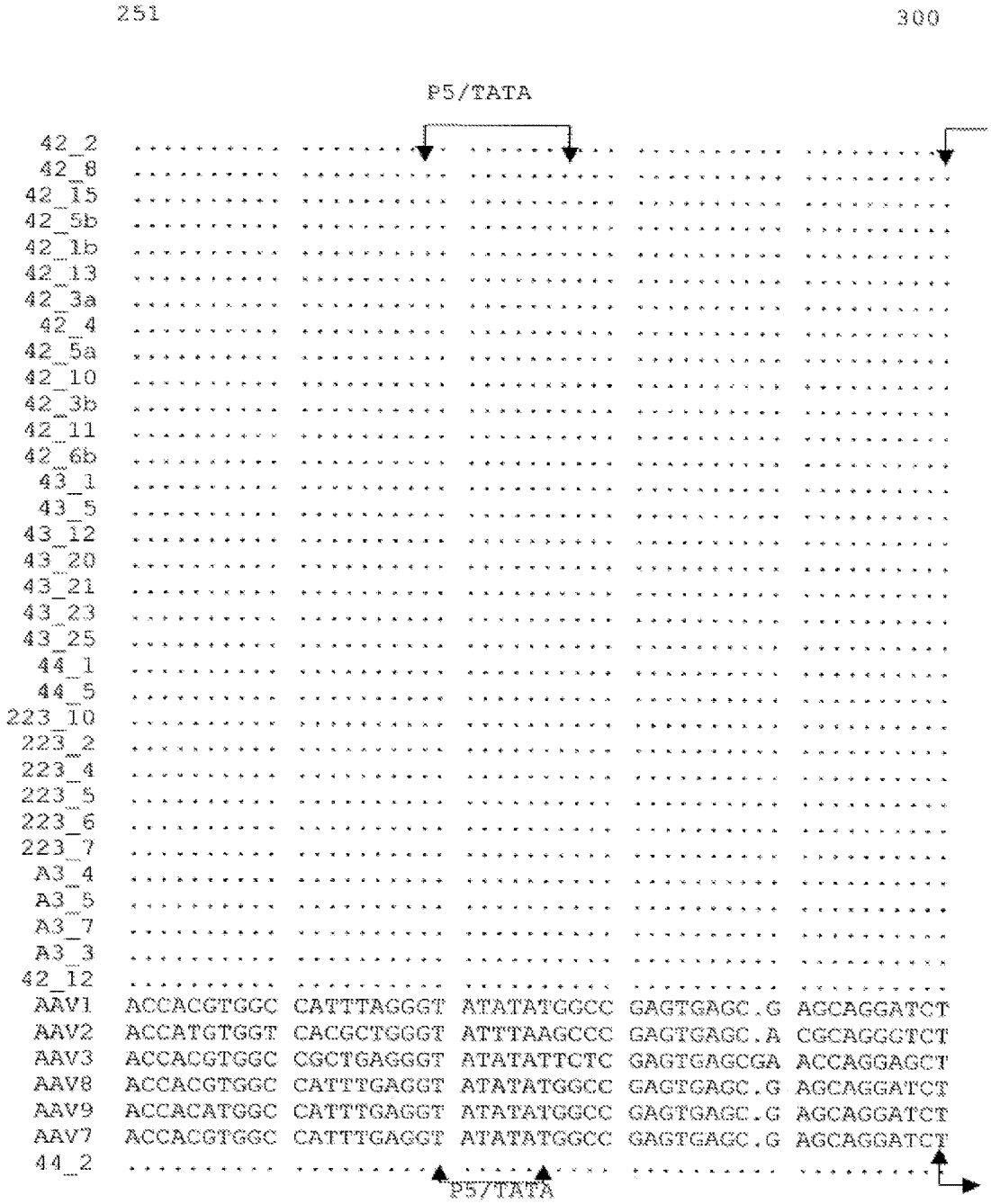
251
300
P5/TATA
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 ACCACGTGGC CATTTAGGGT ATATATGGCC GAGTGAGC.G AGCAGGATCT
AAV2 ACCATGTGGT CACGCTGGGT ATTTAAGCCC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

FIG. 1G

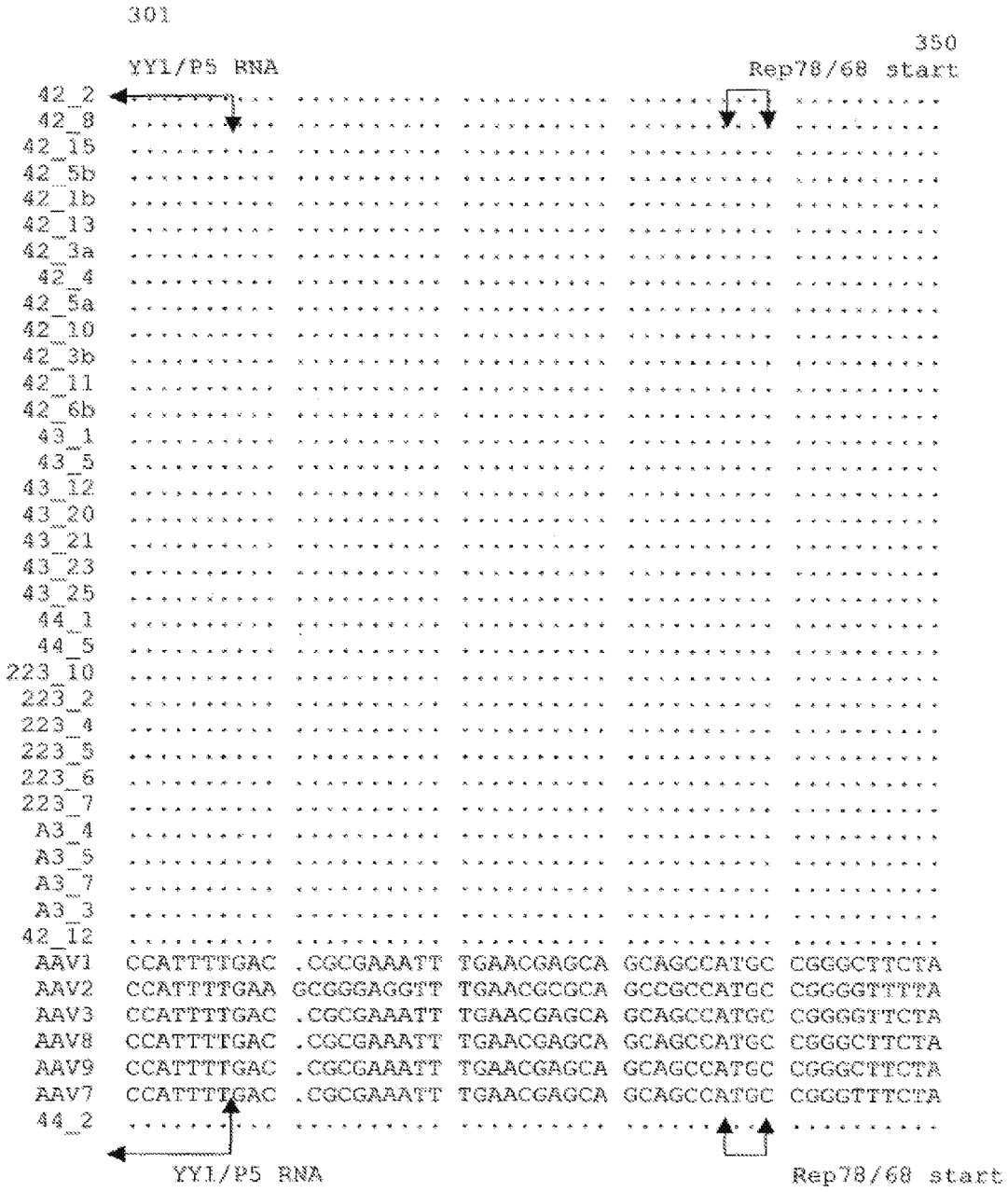
301
350
YY1/P5 RNA
Rep78/68 start
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 CCATTTTGAC .CGCGAAATT TGAACGAGCA GCAGCCATGC CGGGCTTCTA
AAV2 CCATTTTGAA GCGGGAGGTT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

FIG. 1H

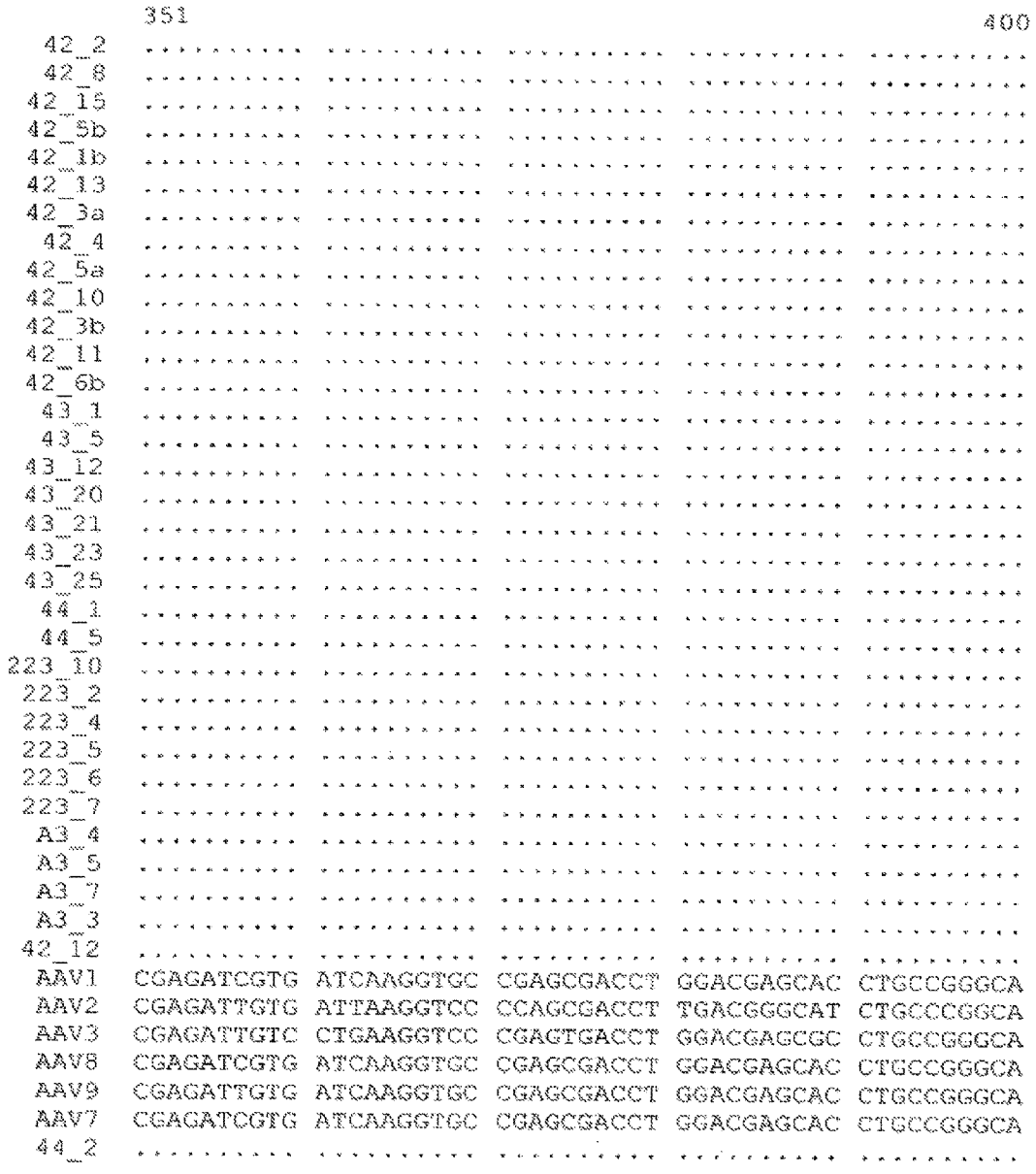
351
400
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 CGAGATCGTG ATCAAGGTGC CGAGCGACCT GGACGAGCAC CTGCCGGGCA
AAV2 CGAGATTGTG ATTAAGGTCC CCAGCGACCT TGACGGGCAT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

FIG. 1I

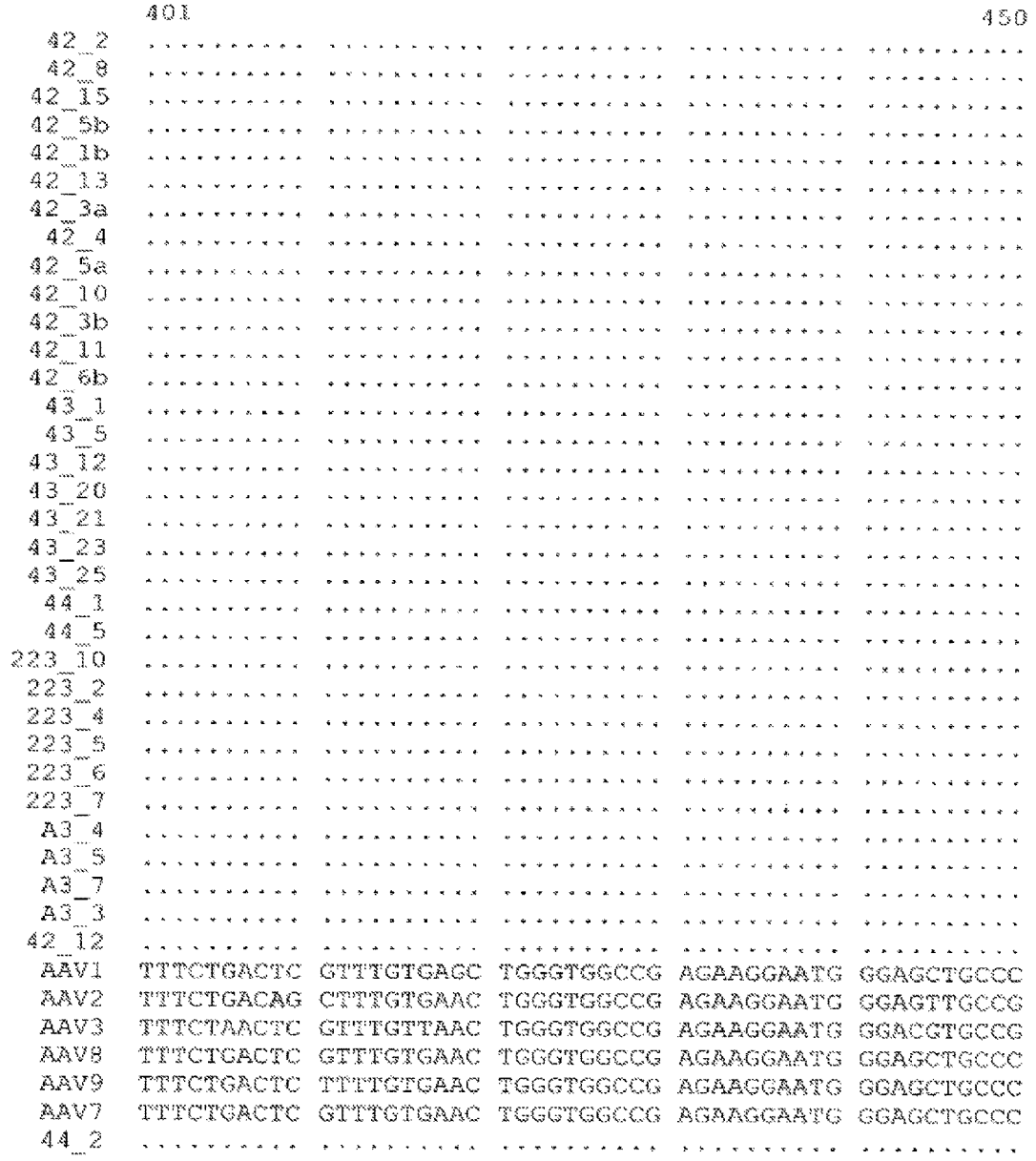
401
450
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 TTTCTGACTC GTTTGTGAGC TGGGTGGCCG AGAAGGAATG GGAGCTGCCC
AAV2 TTTCTGACAG CTTTGTGAAC TGGGTGGCCG AGAAGGAATG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

FIG. 1J

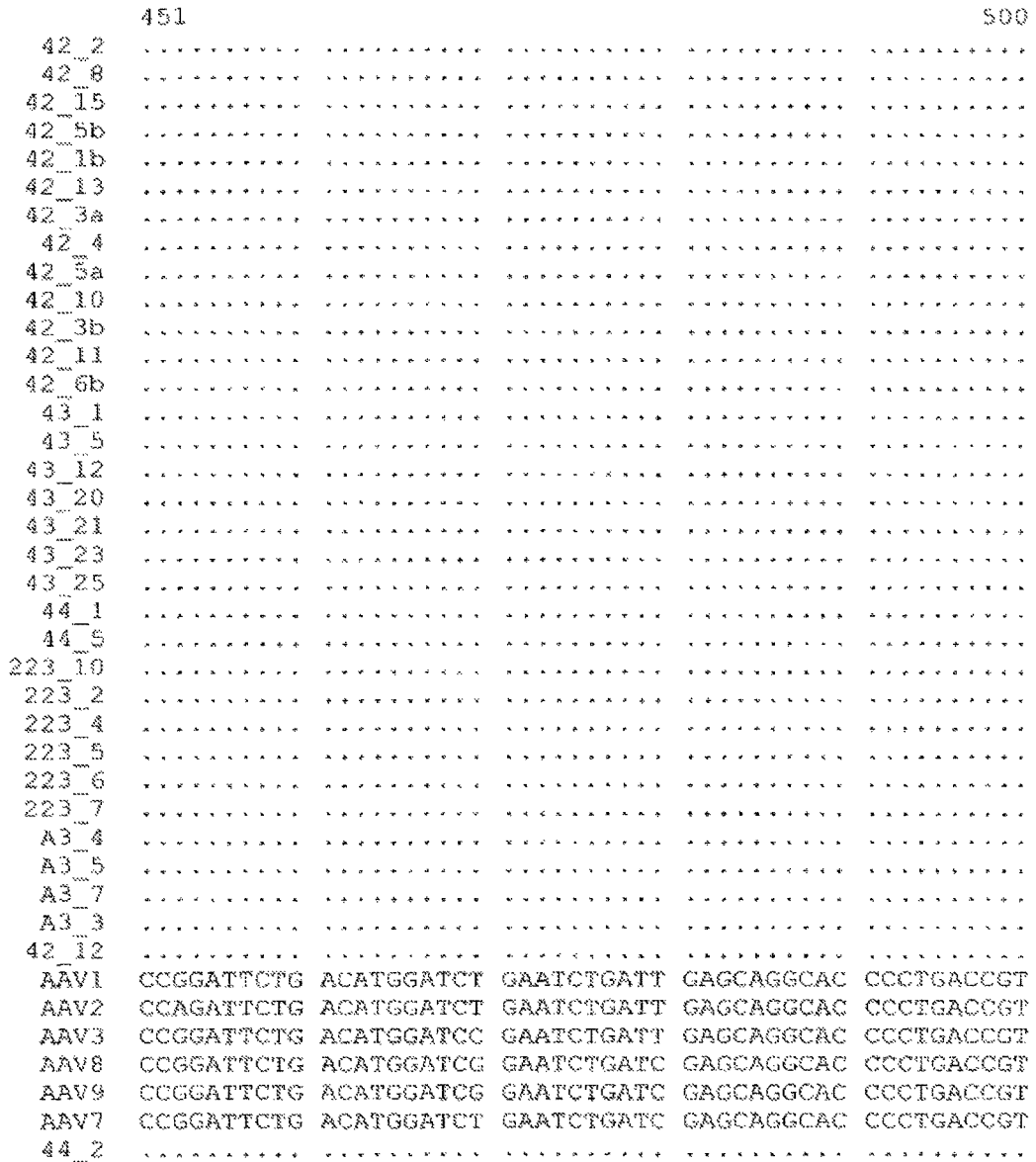
451
500
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 CCGGATTCTG ACATGGATCT GAATCTGATT GAGCAGGCAC CCCTGACCGT
AAV2 CCAGATTCTG ACATGGATCT GAATCTGATT GAGCAGGCAC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

FIG. 1K

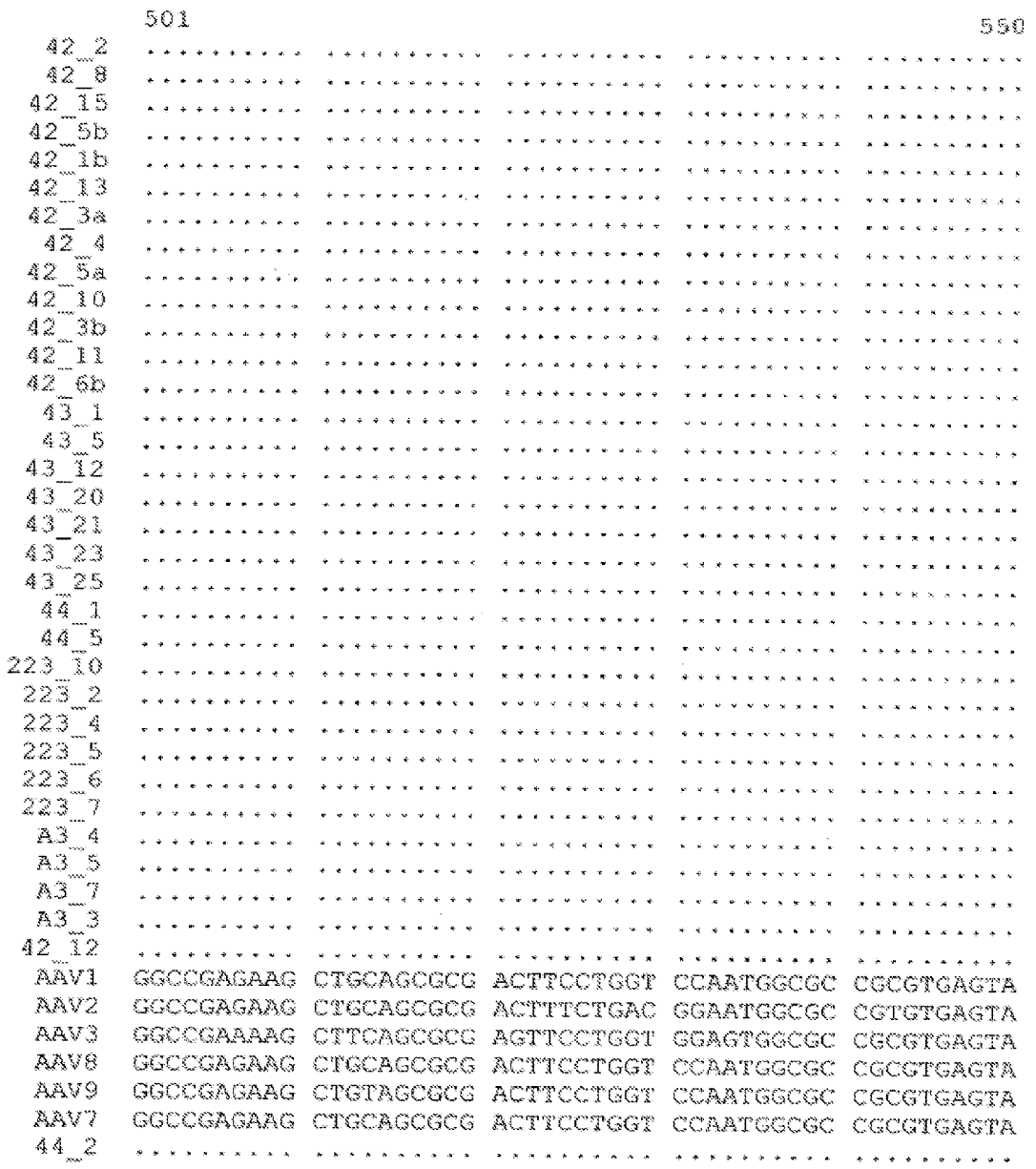
501
550
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 GGCCGAGAAG CTGCAGCGCG ACTTCCTGGT CCAATGGCGC CGCGTGAGTA
AAV2 GGCCGAGAAG CTGCAGCGCG ACTTTCTGAC GGAATGGCGC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

FIG. 1L

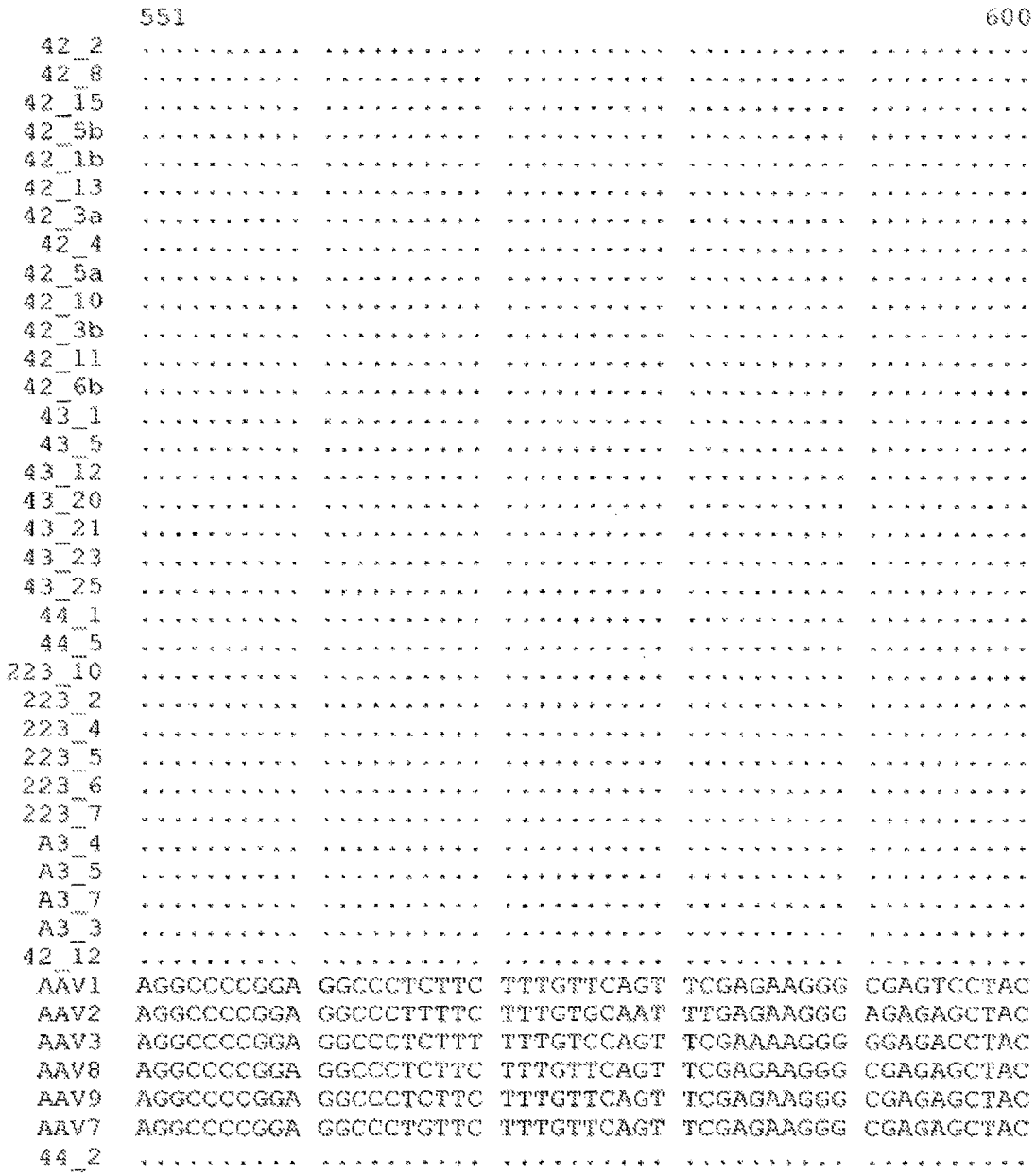
551
600
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 AGGCCCCGGA GGCCCTCTTC TTTGTTCAGT TCGAGAAGGG CGAGTCCTAC
AAV2 AGGCCCCGGA GGCCCTTTTC TTTGTGCAAT TTGAGAAGGG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

FIG. 1M

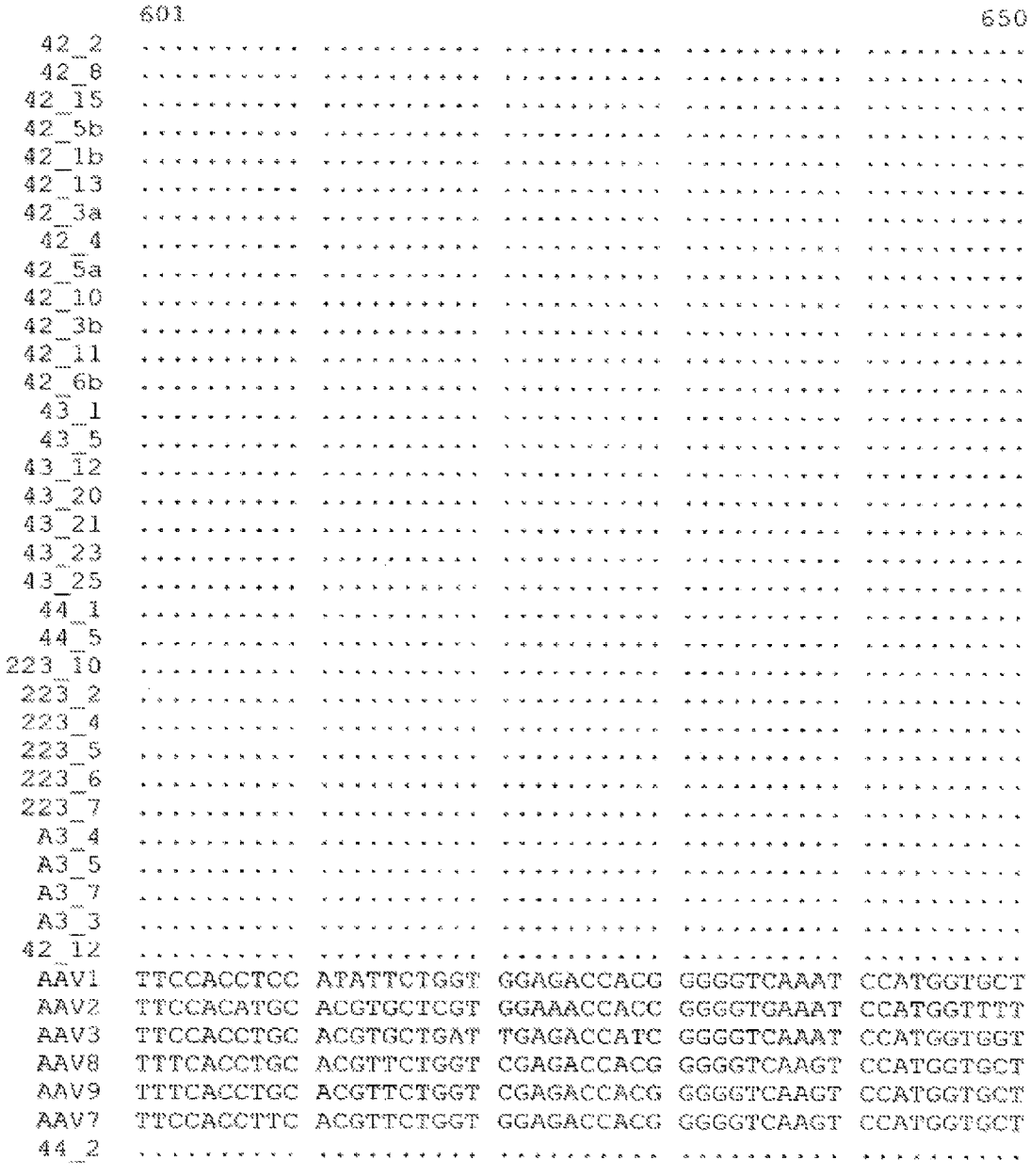
601
650
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 TTCCACCTCC ATATTCTGGT GGAGACCACG GGGGTCAAAT CCATGGTGCT
AAV2 TTCCACATGC ACGTGCTCGT GGAAACCACC GGGGTGAAAT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

FIG. 1N

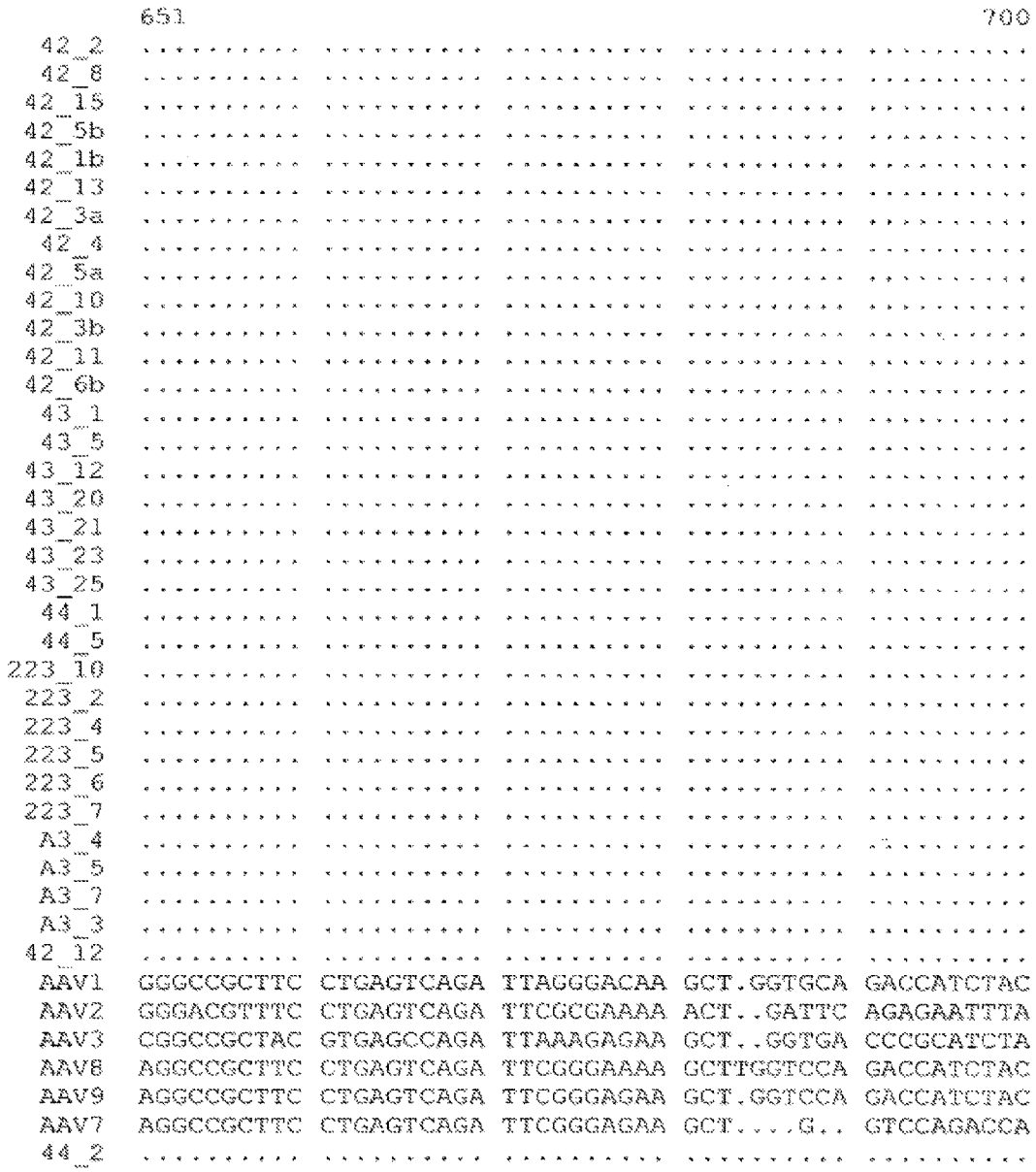
651
700
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 GGGCCGCTTC CTGAGTCAGA TTAGGGACAA GCT.GGTGCA GACCATCTAC
AAV2 GGGACGTTTC CTGAGTCAGA TTCGCGAAAA ACT..GATTC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

FIG. 10

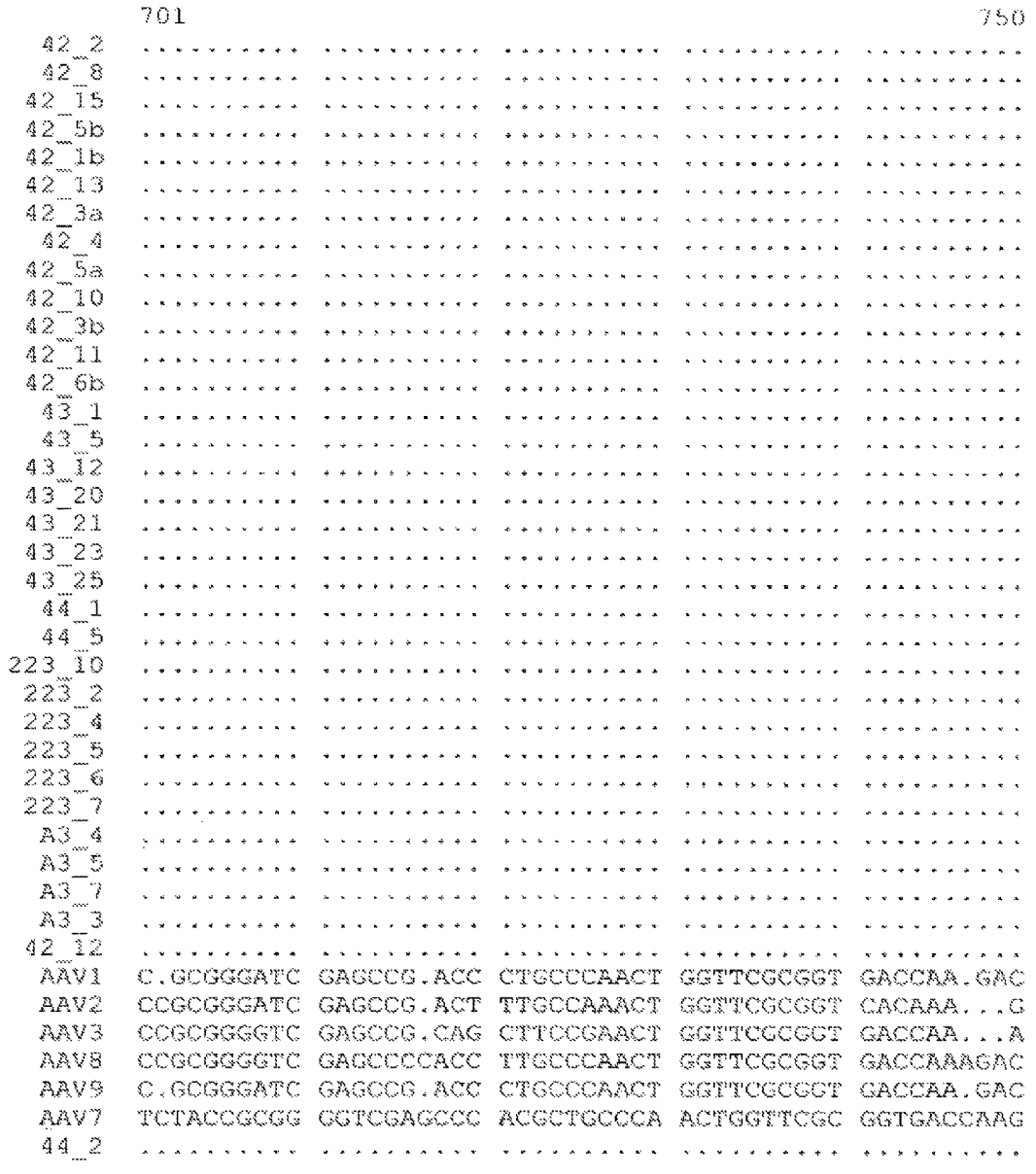
701
750
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 C.GCGGGATC GAGCCG.ACC CTGCCCAACT GGTTCGCGGT GACCAA.GAC
AAV2 CCGCGGGATC GAGCCG.ACT TTGCCAAACT GGTTCGCGGT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

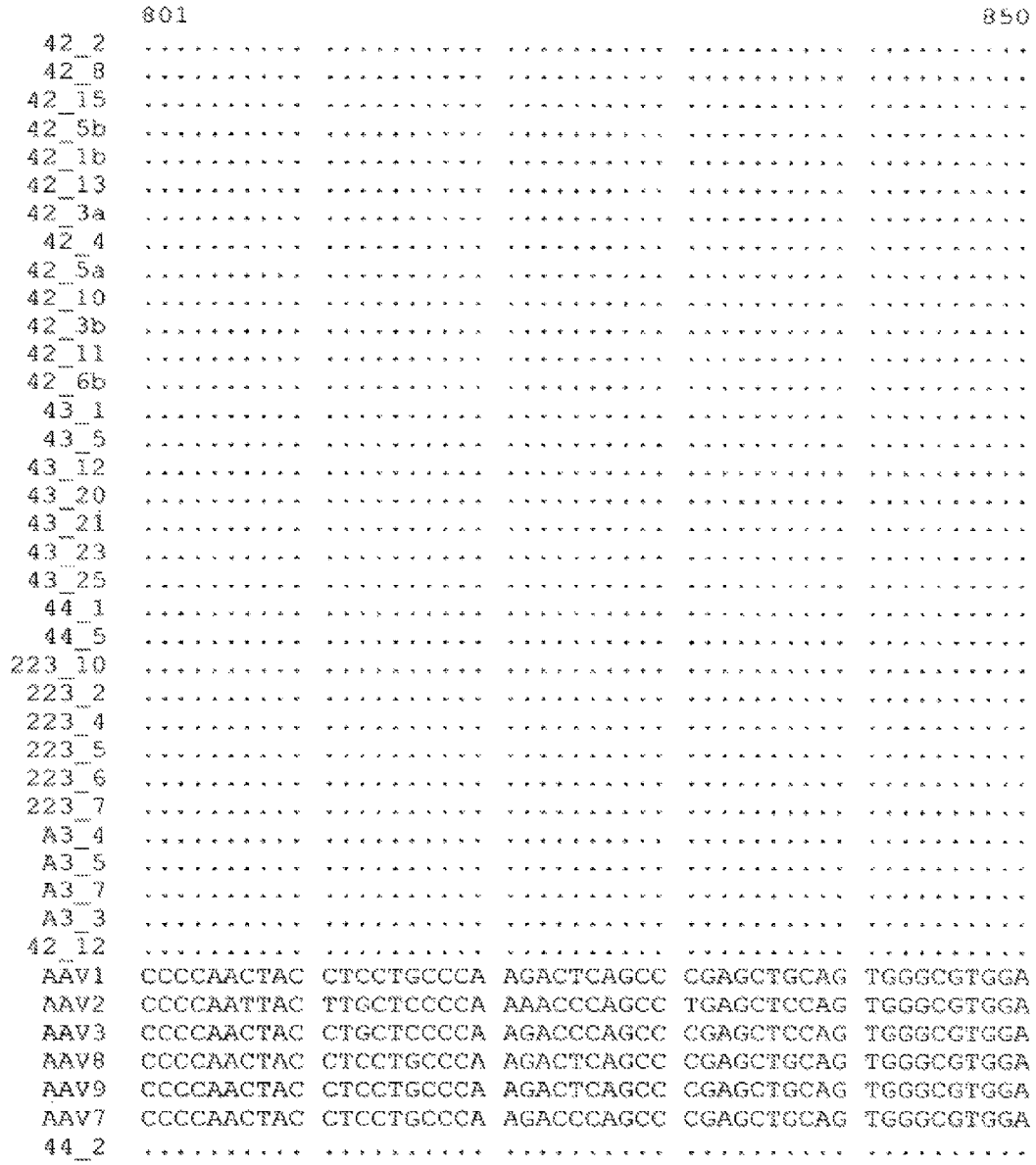
801
850
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 CCCCAACTAC CTCCTGCCCA AGACTCAGCC CGAGCTGCAG TGGGCGTGGA
AAV2 CCCCAATTAC TTGCTCCCCA AAACCCAGCC TGAGCTCCAG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

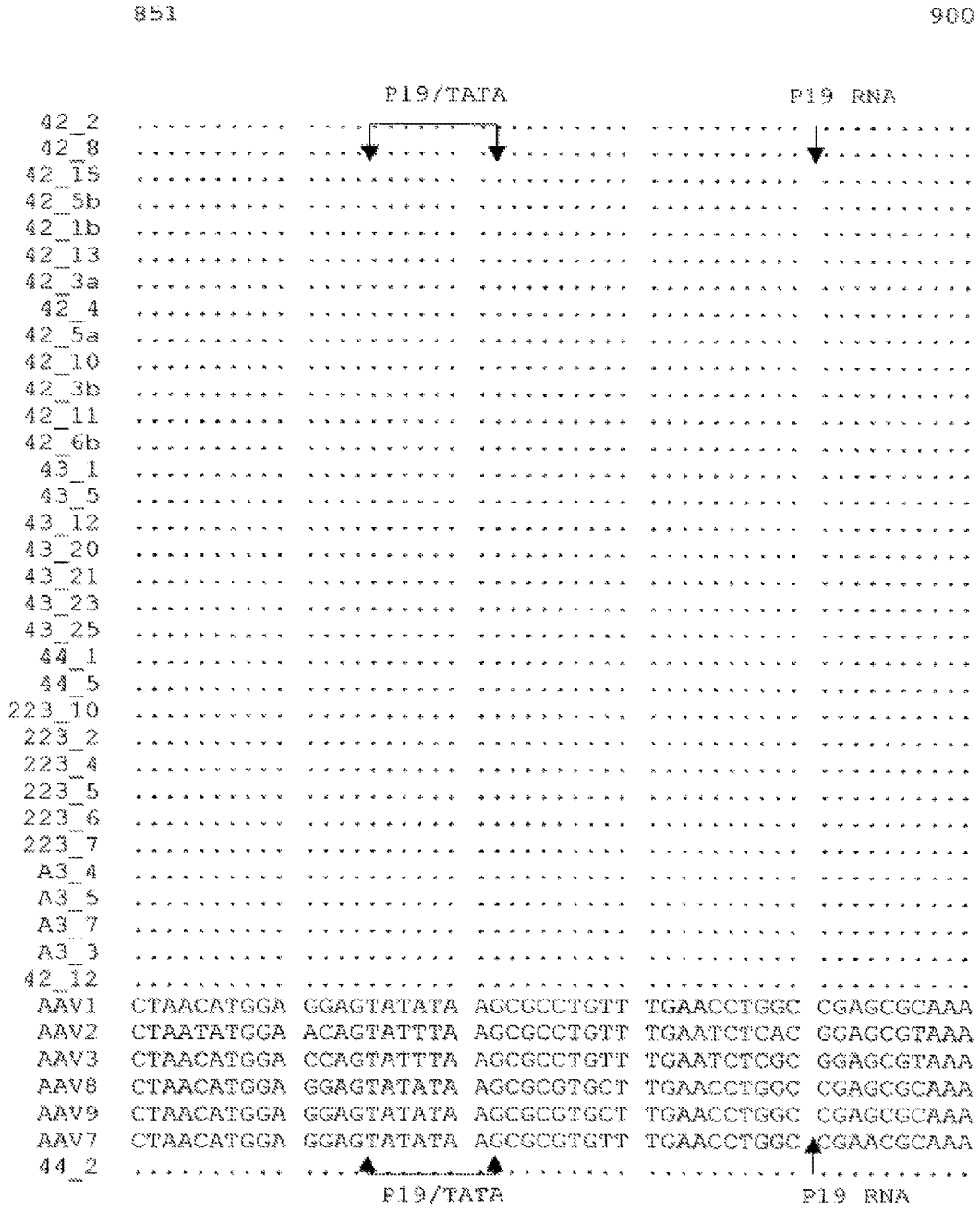
851
900
P19/TATA
P19 RNA
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 CTAACATGGA GGAGTATATA AGCGCCTGTT TGAACCTGGC CGAGCGCAAA
AAV2 CTAATATGGA ACAGTATTTA AGCGCCTGTT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

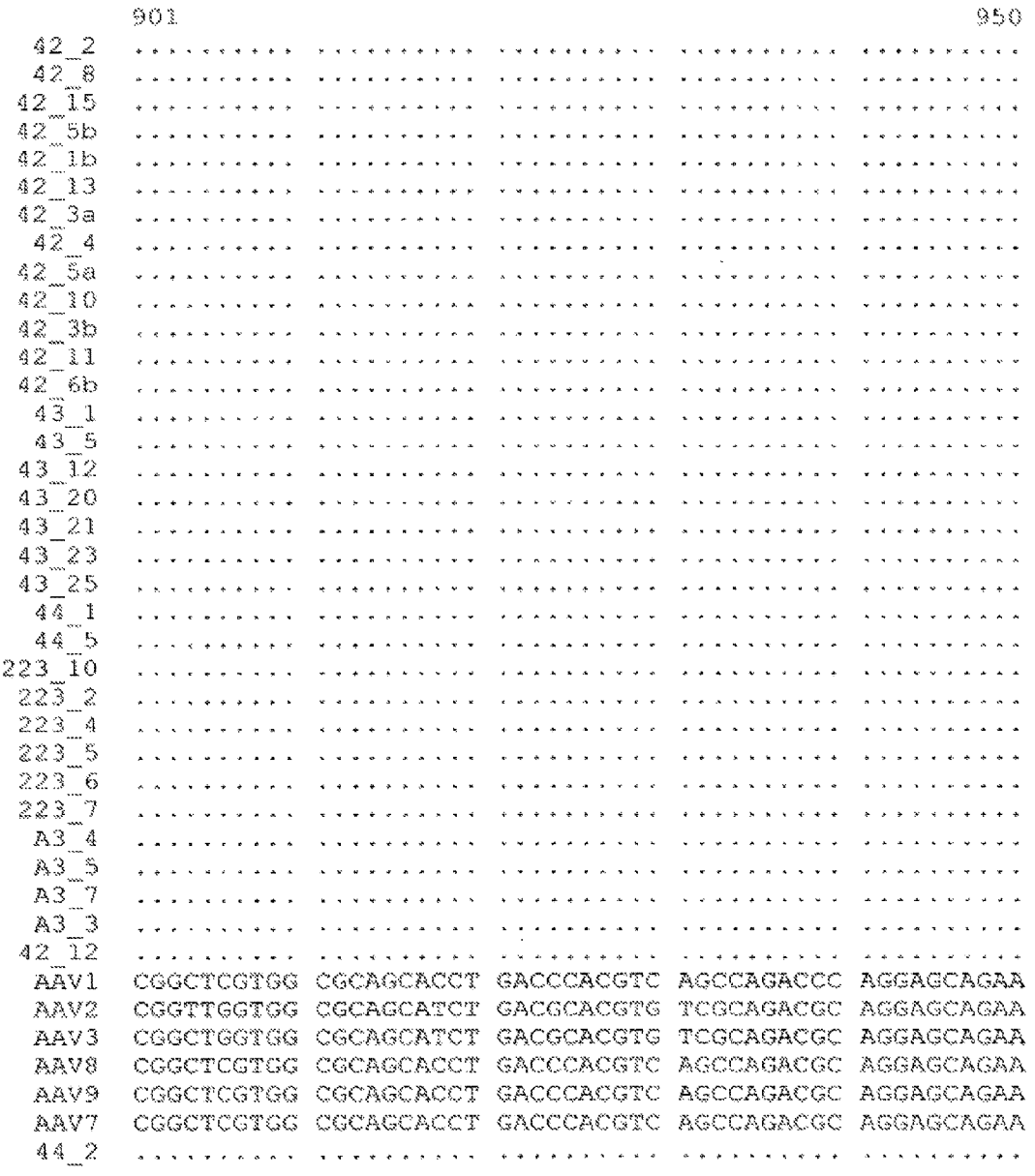
901
950
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 CGGCTCGTGG CGCAGCACCT GACCCACGTC AGCCAGACCC AGGAGCAGAA
AAV2 CGGTTGGTGG CGCAGCATCT GACGCACGTG TCGCAGACGC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

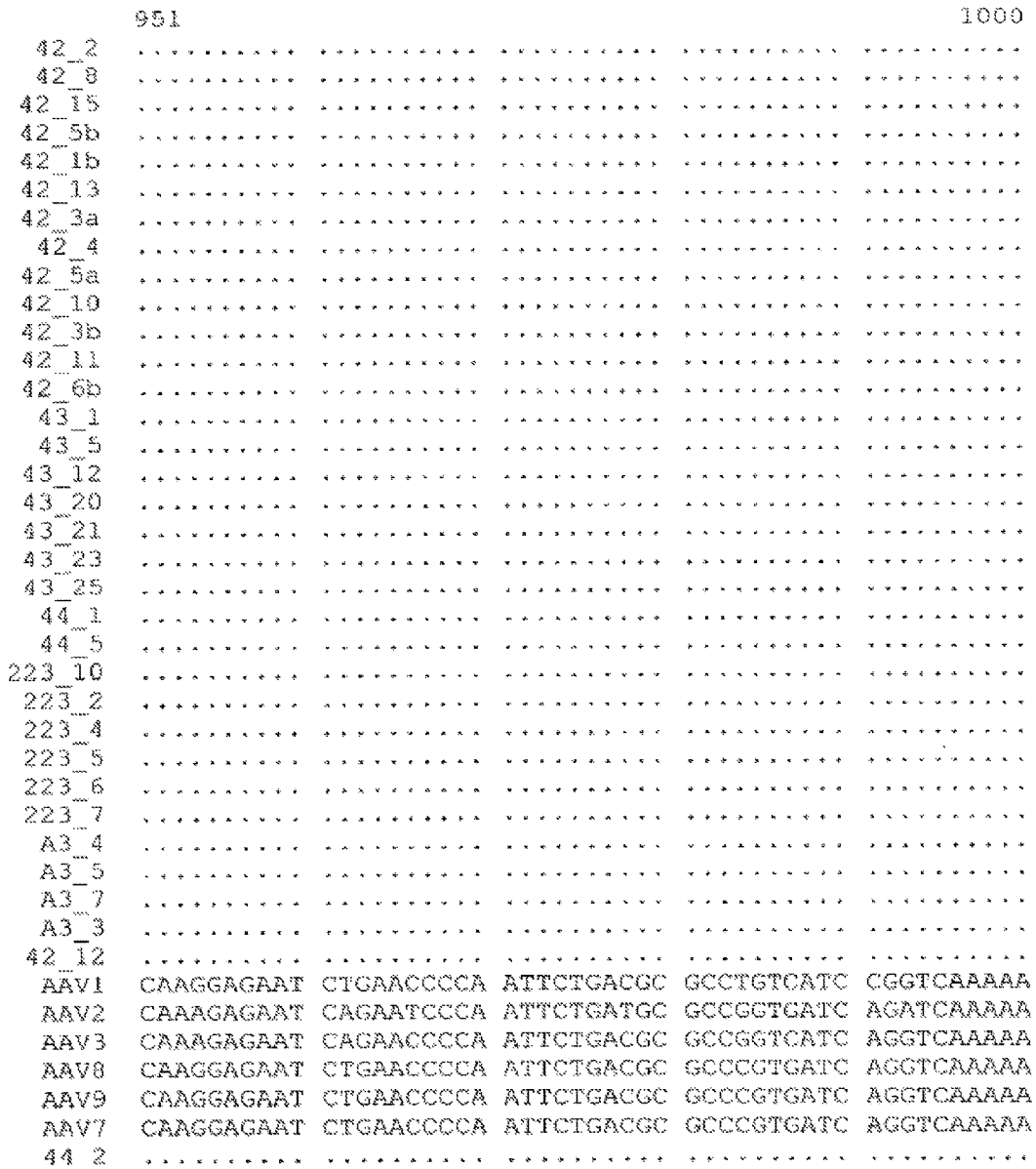
951
1000
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 CAAGGAGAAT CTGAACCCCA ATTCTGACGC GCCTGTCATC CGGTCAAAAA
AAV2 CAAAGAGAAT CAGAATCCCA ATTCTGATGC GCCGGTGATC 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

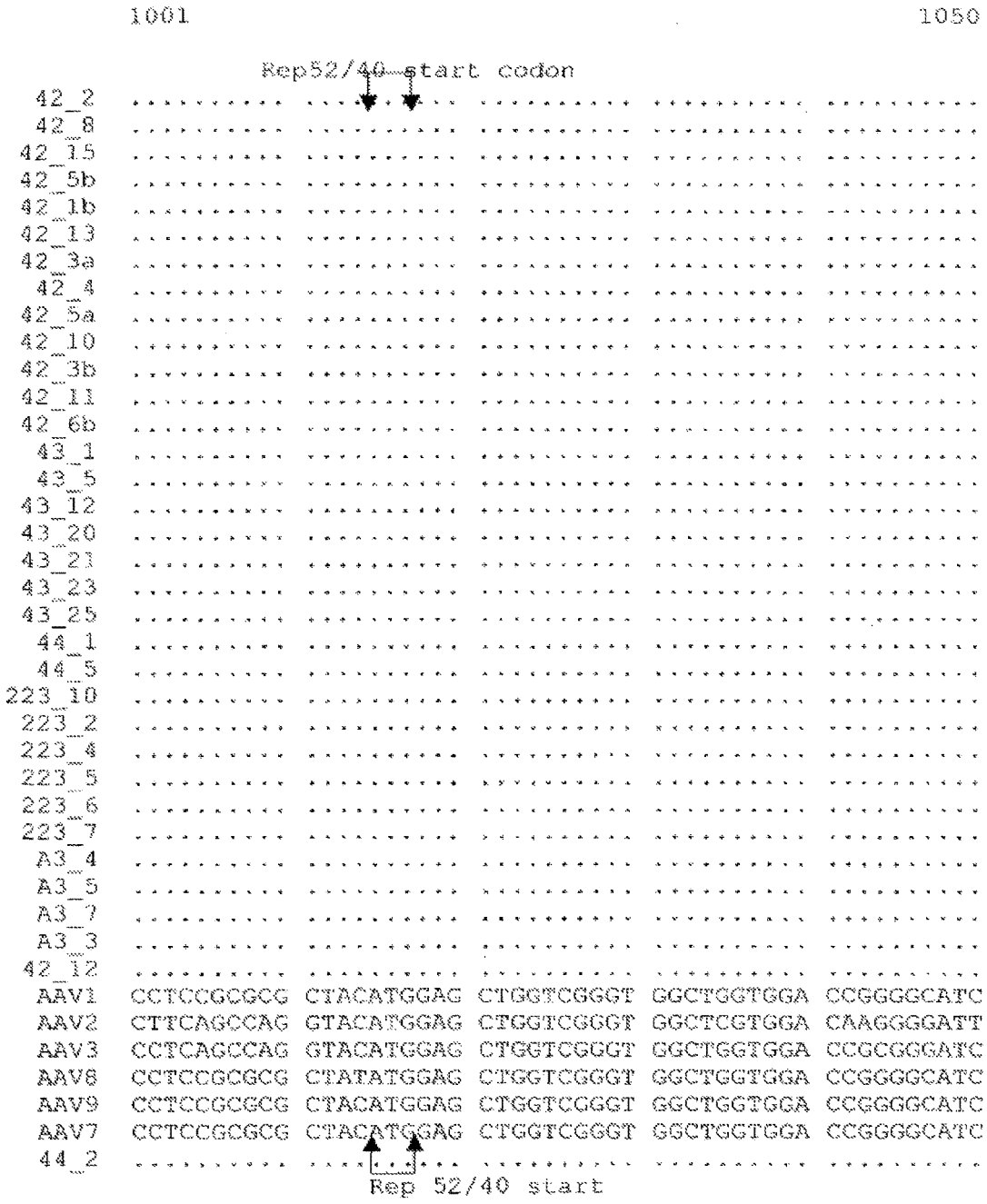
1001
1050
Rep52/40 start codon
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 CCTCCGCGCG CTACATGGAG CTGGTCGGGT GGCTGGTGGA CCGGGGCATC
AAV2 CTTCAGCCAG GTACATGGAG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

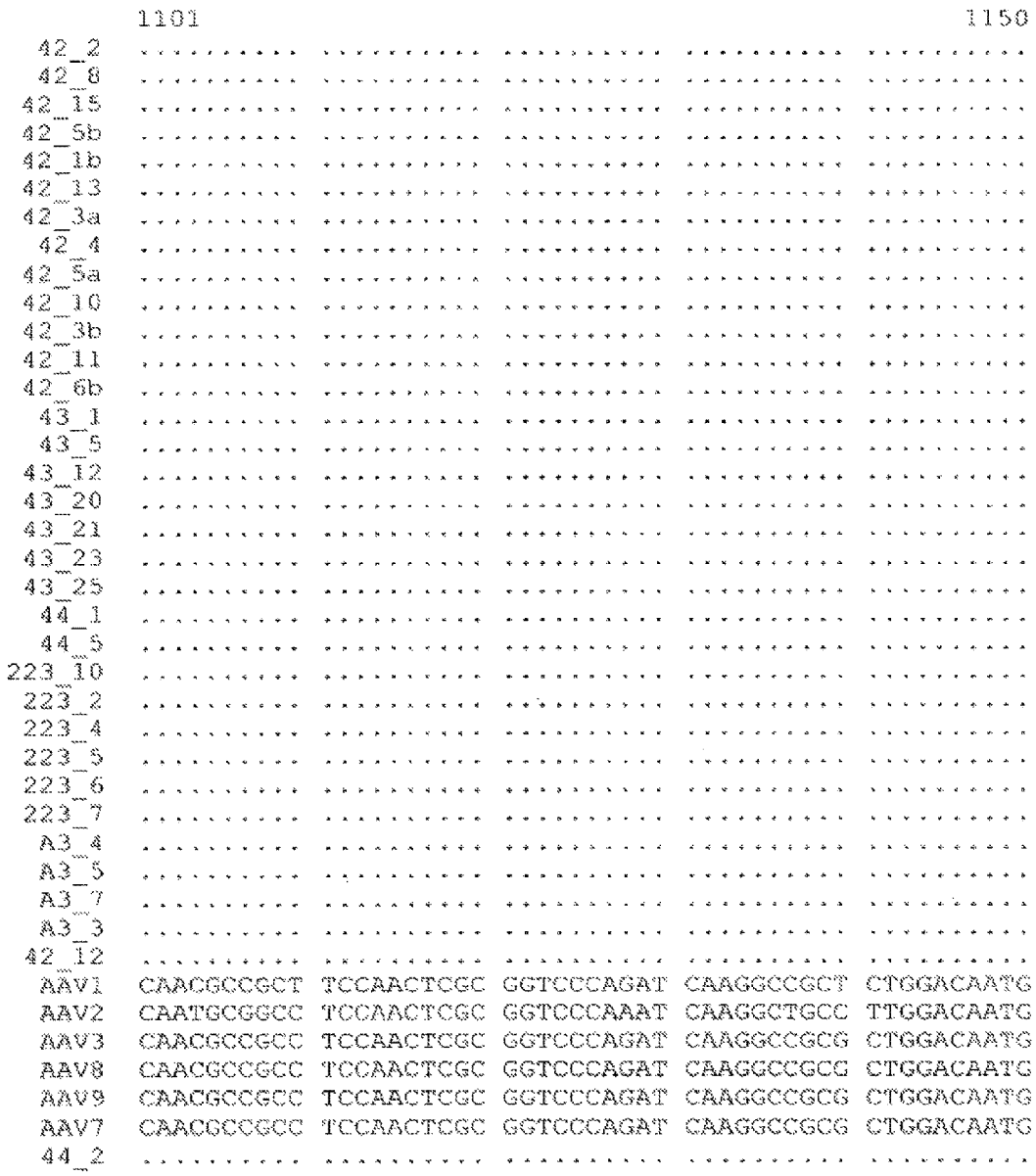
1101
1150
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 CAACGCCGCT TCCAACTCGC GGTCCCAGAT CAAGGCCGCT CTGGACAATG
AAV2 CAATGCGGCC TCCAACTCGC GGTCCCAAAT CAAGGCTGCC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

FIG. 1X

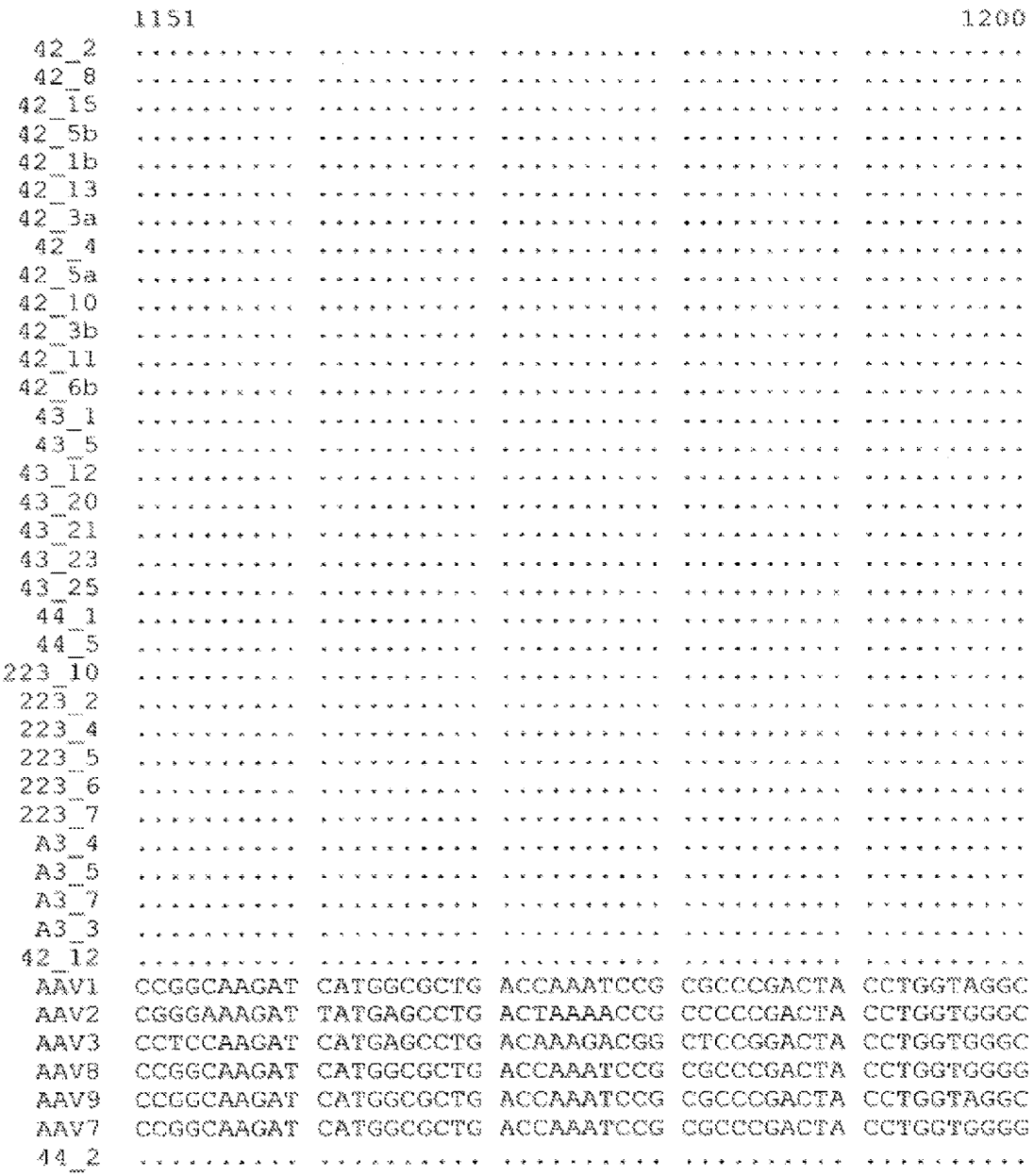
1151
1200
42_2
42_8
42_1S
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 CCGGCAAGAT CATGGCGCTG ACCAAATCCG CGCCCGACTA CCTGGTAGGC
AAV2 CGGGAAAGAT TATGAGCCTG ACTAAAACCG CCCCCGACTA CCTGGTGGGC
AAV3 CCTCCAAGAT CATGAGCCTG ACAAAGACGG CTCCGGACTA CCTGGTGGGC
AAV8 CCGGCAAGAT CATGGCGCTG ACCAAATCCG CGCCCGACTA CCTGGTGGGG
AAV9 CCGGCAAGAT CATGGCGCTG ACCAAATCCG CGCCCGACTA CCTGGTAGGC
AAV7 CCGGCAAGAT CATGGCGCTG ACCAAATCCG CGCCCGACTA CCTGGTGGGG
44_2

FIG 1Y

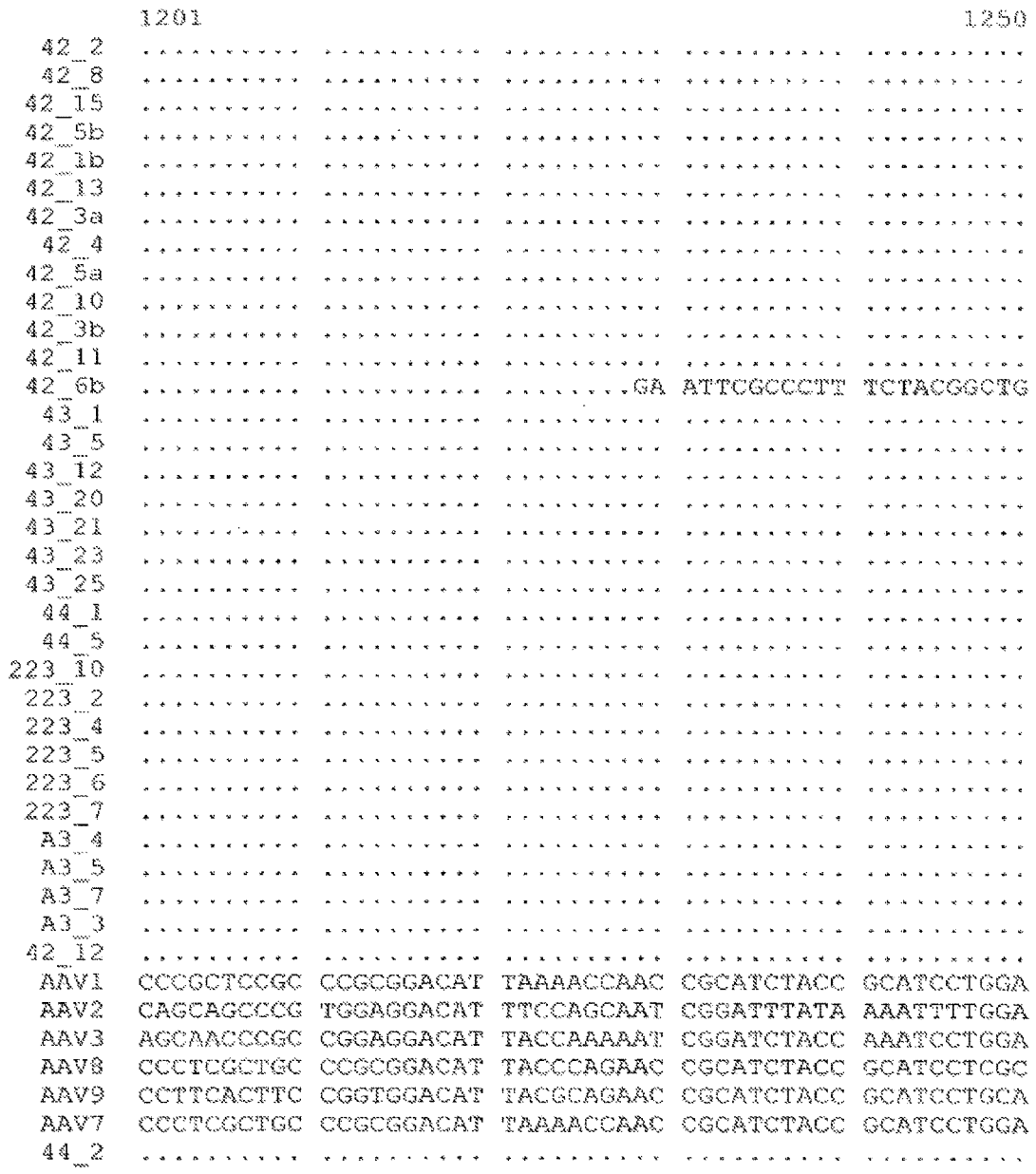
1201
1250
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
GA ATTCGCCCTT TCTACGGCTG
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 CCCGCTCCGC CCGCGGACAT TAAAACCAAC CGCATCTACC GCATCCTGGA
AAV2 CAGCAGCCCG TGGAGGACAT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

FIG. 1Z

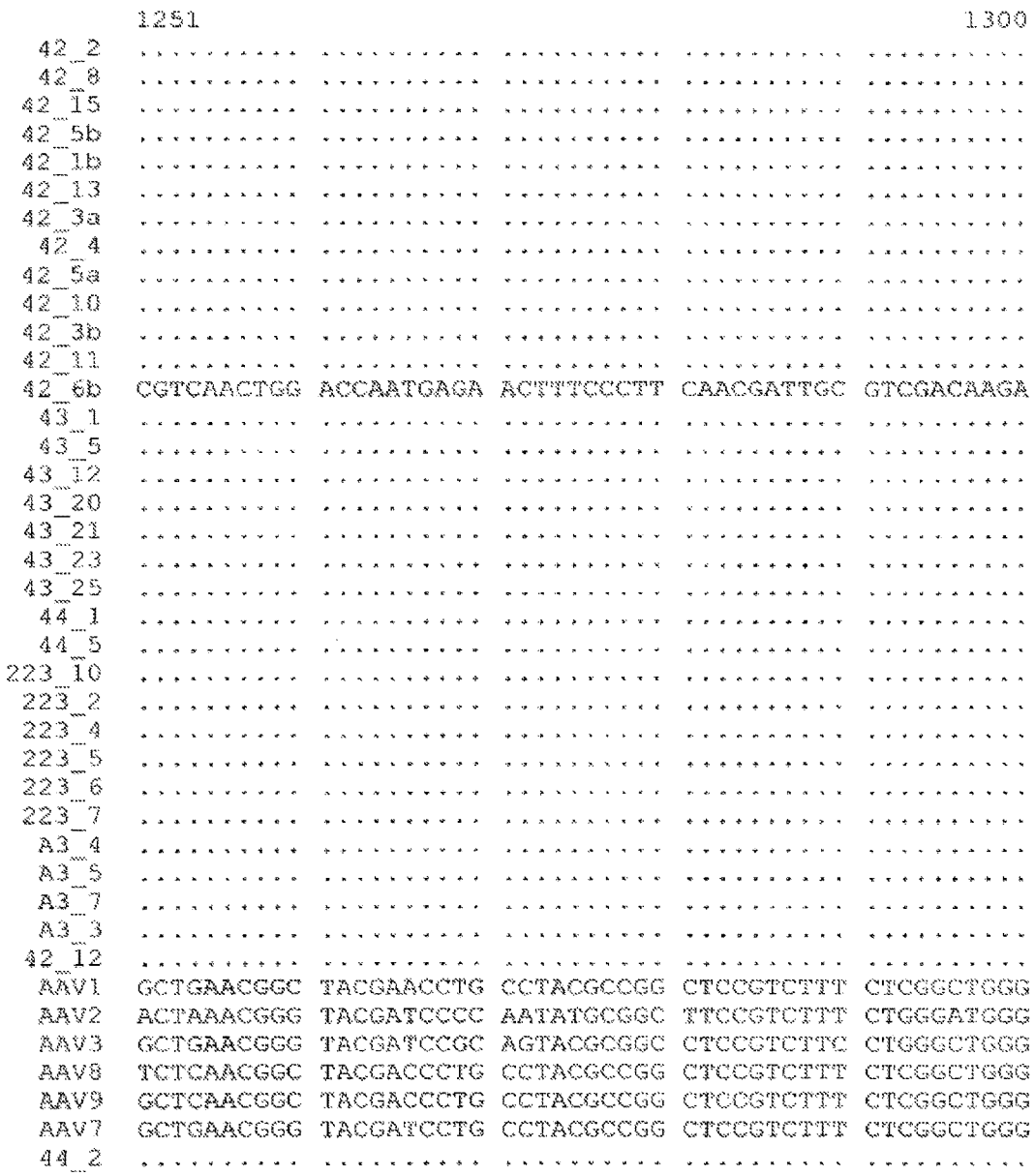
1251
1300
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b CGTCAACTGG ACCAATGAGA ACTTTCCCTT CAACGATTGC GTCGACAAGA
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 GCTGAACGGC TACGAACCTG CCTACGCCGG CTCCGTCTTT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

FIG. 1AA

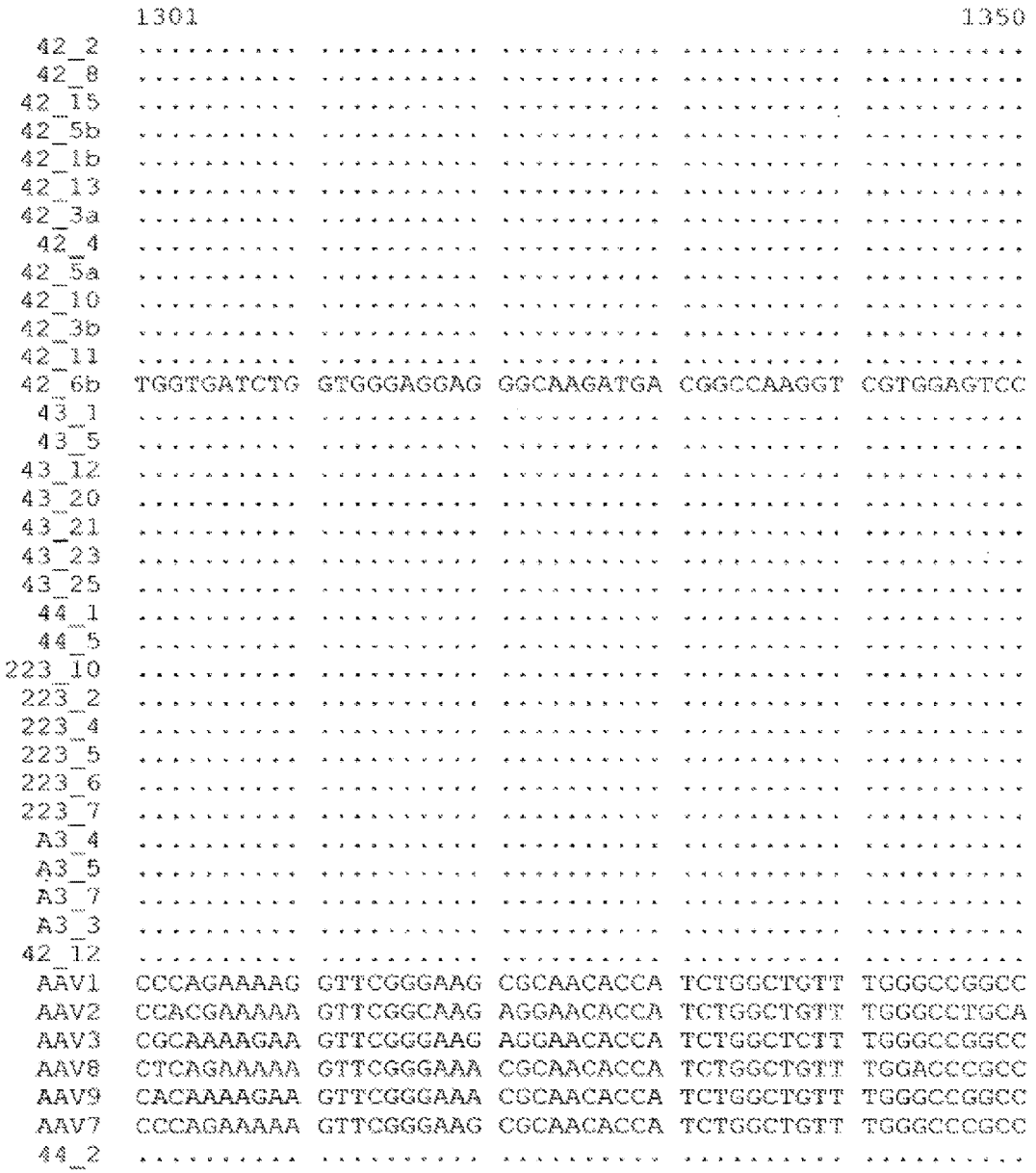
1301
1350
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT CGTGGAGTCC
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 CCCAGAAAAG GTTCGGGAAG CGCAACACCA TCTGGCTGTT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

FIG. 1AB

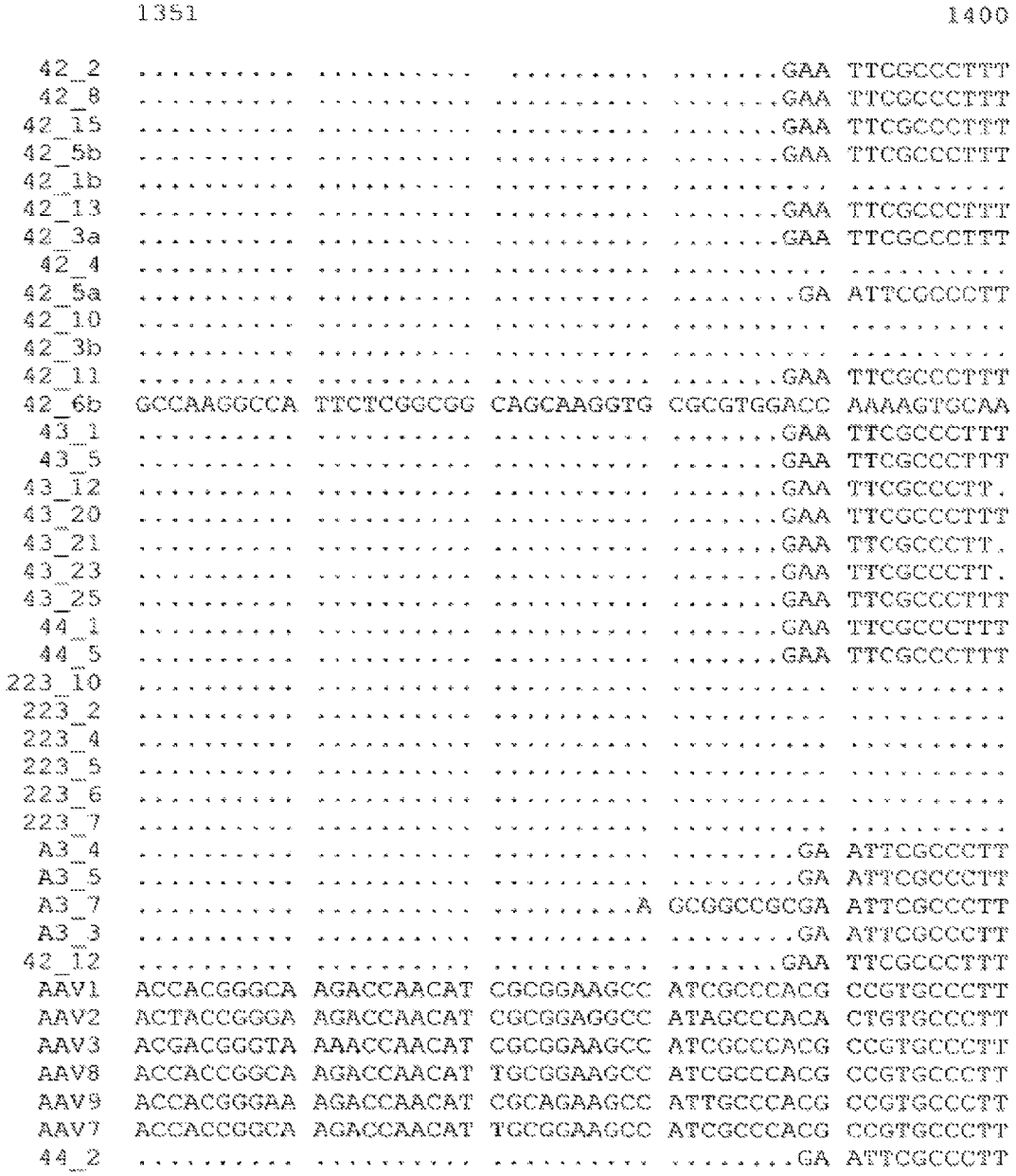
1351
1400
42_2 ....GAA TTCGCCCTTT
42_8 ....GAA TTCGCCCTTT
42_15 ....GAA TTCGCCCTTT
42_5b ....GAA TTCGCCCTTT
42_1b ....
42_13 ....GAA TTCGCCCTTT
42_3a ....GAA TTCGCCCTTT
42_4 ....
42_5a ....GA ATTCGCCCTT
42_10 ....
42_3b ....
42_11 ....GAA TTCGCCCTTT
42_6b GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC AAAAGTGCAA
43_1 ....GAA TTCGCCCTTT
43_5 ....GAA TTCGCCCTTT
43_12 ....GAA TTCGCCCTT.
43_20 ....GAA TTCGCCCTTT
43_21 ....GAA TTCGCCCTT.
43_23 ....GAA TTCGCCCTT.
43_25 ....GAA TTCGCCCTTT
44_1 ....GAA TTCGCCCTTT
44_5 ....GAA TTCGCCCTTT
223_10 ....
223_2 ....
223_4 ....
223_5 ....
223_6 ....
223_7 ....
A3_4 ....GA ATTCGCCCTT
A3_5 ....GA ATTCGCCCTT
A3_7 ....A GCGGCCGCGA ATTCGCCCTT
A3_3 ....GA ATTCGCCCTT
42_12 ....GAA TTCGCCCTTT
AAV1 ACCACGGGCA AGACCAACAT CGCGGAAGCC ATCGCCCACG CCGTGCCCTT
AAV2 ACTACCGGGA AGACCAACAT CGCGGAGGCC ATAGCCCACA CTGTGCCCTT
AAV3 ACGACGGGTA AAACCAACAT CGCGGAAGCC ATCGCCCACG CCGTGCCCTT
AAV8 ACCACCGGCA AGACCAACAT TGCGGAAGCC ATCGCCCACG CCGTGCCCTT
AAV9 ACCACGGGAA AGACCAACAT CGCAGAAGCC ATTGCCCACG CCGTGCCCTT
AAV7 ACCACCGGCA AGACCAACAT TGCGGAAGCC ATCGCCCACG CCGTGCCCTT
44_2 ....GA ATTCGCCCTT

FIG. 1AC

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

FIG. 1AD

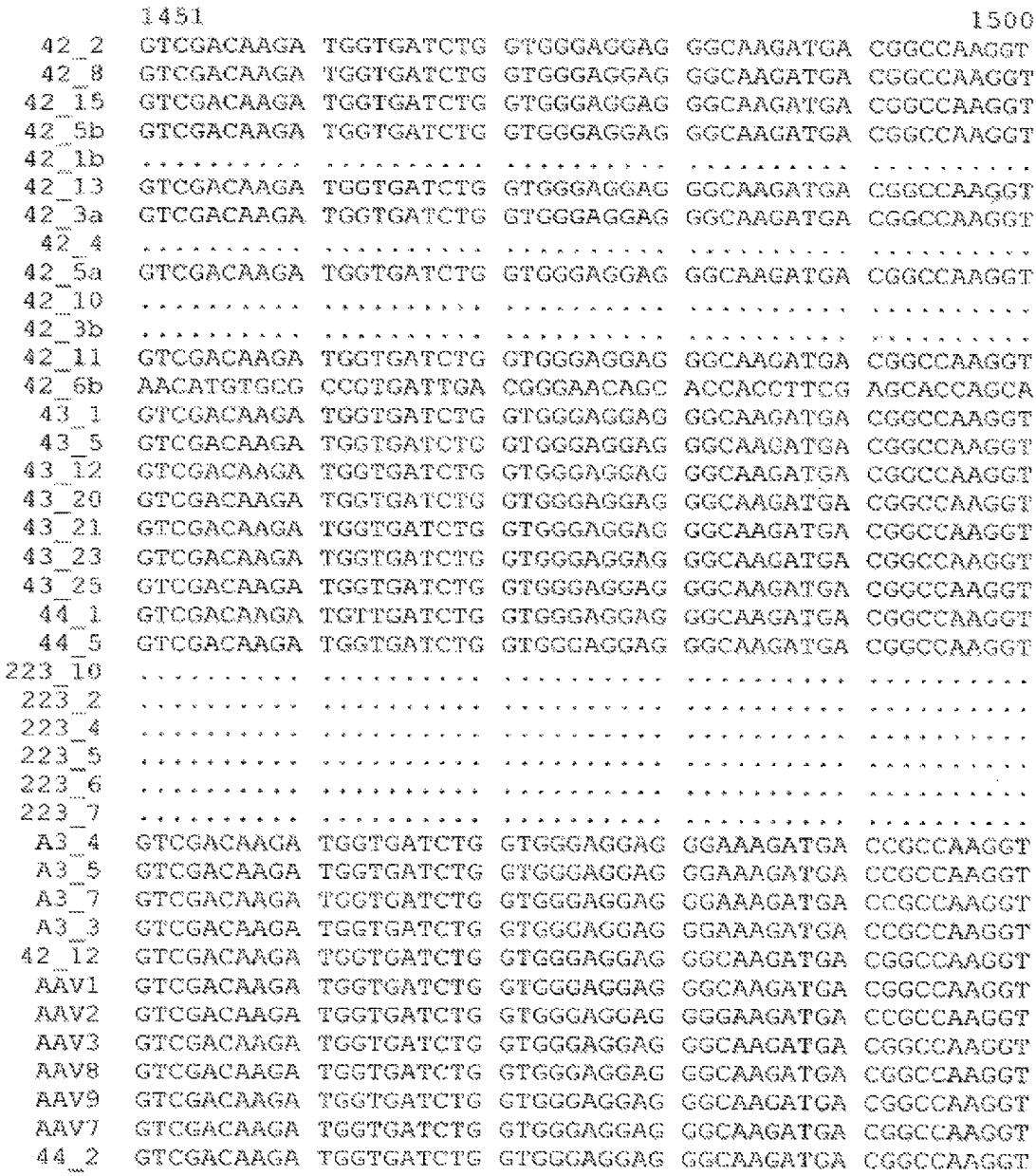
1451
1500
42_2 GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
42_8 GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
42_15 GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
42_5b GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
42_1b ....
42_13 GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
42_3a GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
42_4 ....
42_5a GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
42_10 ....
42_3b ....
42_11 GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
42_6b AACATGTGCG CCGTGATTGA CGGGAACAGC ACCACCTTCG AGCACCAGCA
43_1 GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
43_5 GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
43_12 GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
43_20 GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
43_21 GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
43_23 GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
43_25 GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
44_1 GTCGACAAGA TGTTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
44_5 GTCGACAAGA TGGTGATCTG GTGGCAGGAG 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 GGCAACATGA CGGCCAAGGT
AAV7 GTCGACAAGA TGGTGATCTG GTGGGAGGAG GGCAAGATGA CGGCCAAGGT
44_2 GTCGACAAGA TGGTGATCTG GTGGCAGGAG GGCAAGATGA CGGCCAAGGT

FIG. 1AE

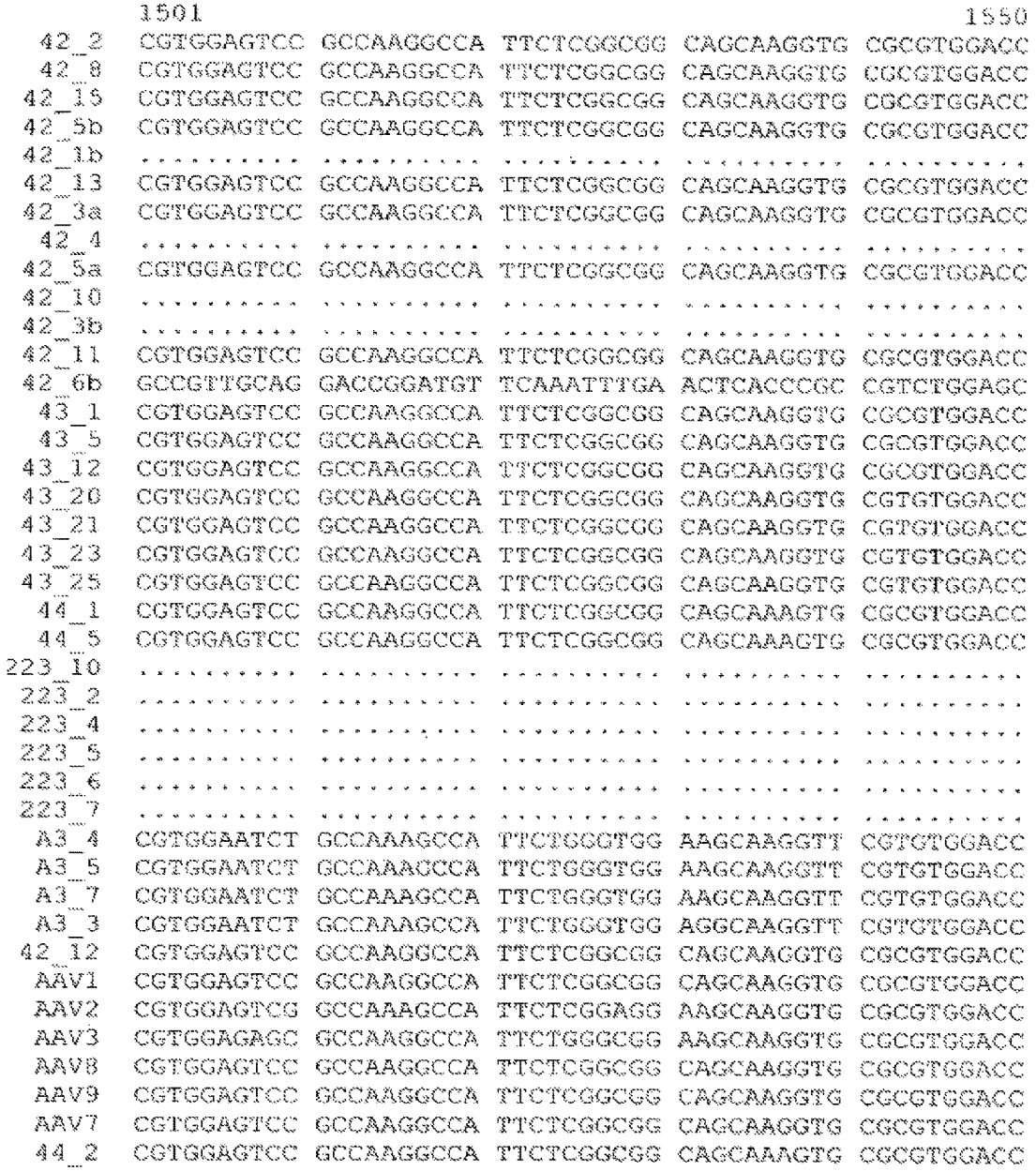
1501 1550
42_2 CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC
42_8 CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC
42_15 CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC
42_5b CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG CAGCAAGGTG CGCGTGGACC
42_1b ....
42_13 CGTGGAGTCC GCCAAGGCCA TTCTCGGCGG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

FIG. 1AF

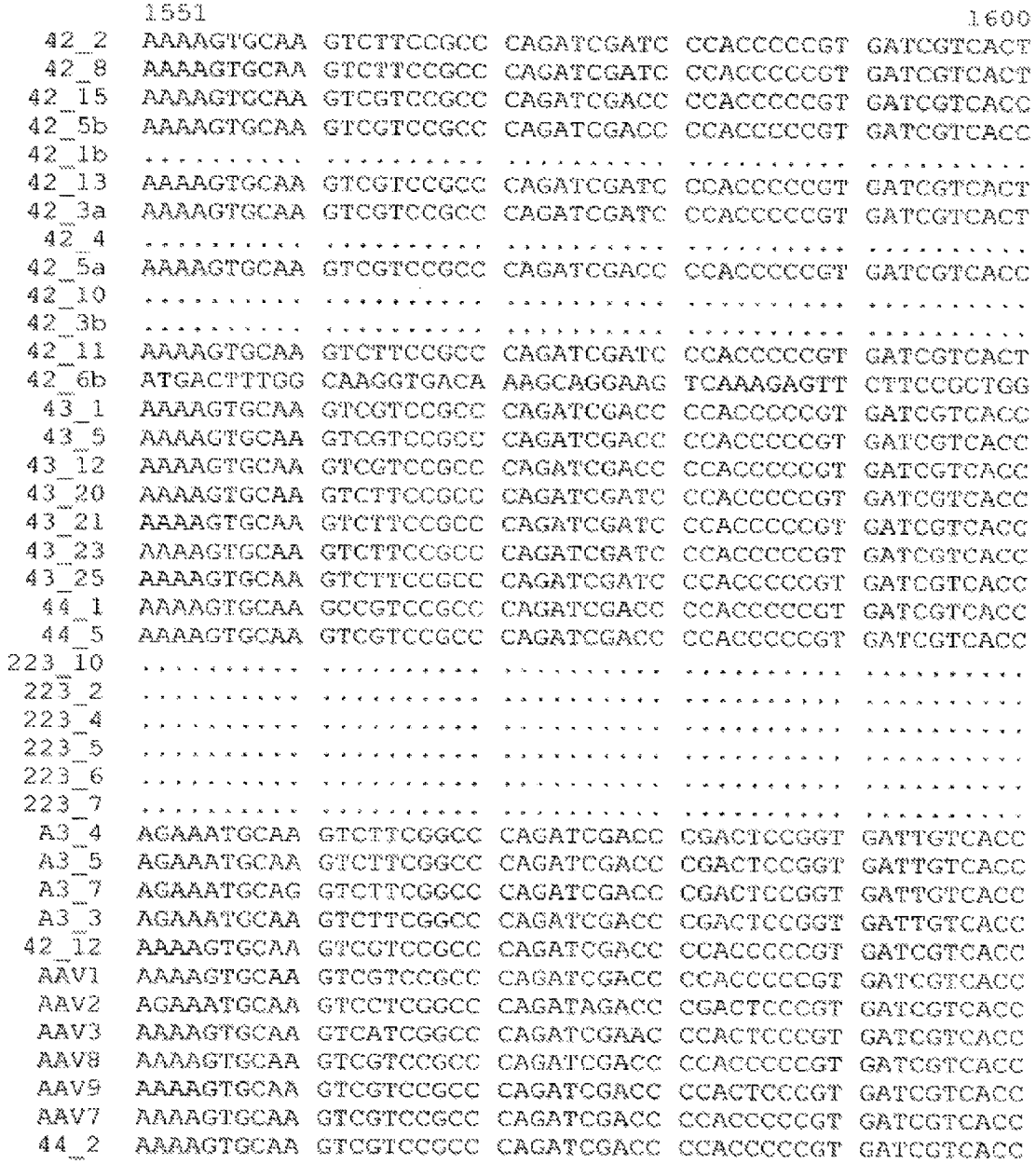
1551
1600
42_2 AAAAGTGCAA GTCTTCCGCC CAGATCGATC CCACCCCCGT GATCGTCACT
42_8 AAAAGTGCAA GTCTTCCGCC CAGATCGATC CCACCCCCGT GATCGTCACT
42_15 AAAAGTGCAA GTCGTCCGCC CAGATCGACC CCACCCCCGT GATCGTCACC
42_5b AAAAGTGCAA GTCGTCCGCC CAGATCGACC CCACCCCCGT GATCGTCACC
42_1b ....
42_13 AAAAGTGCAA GTCGTCCGCC CAGATCGATC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

FIG. 1AG

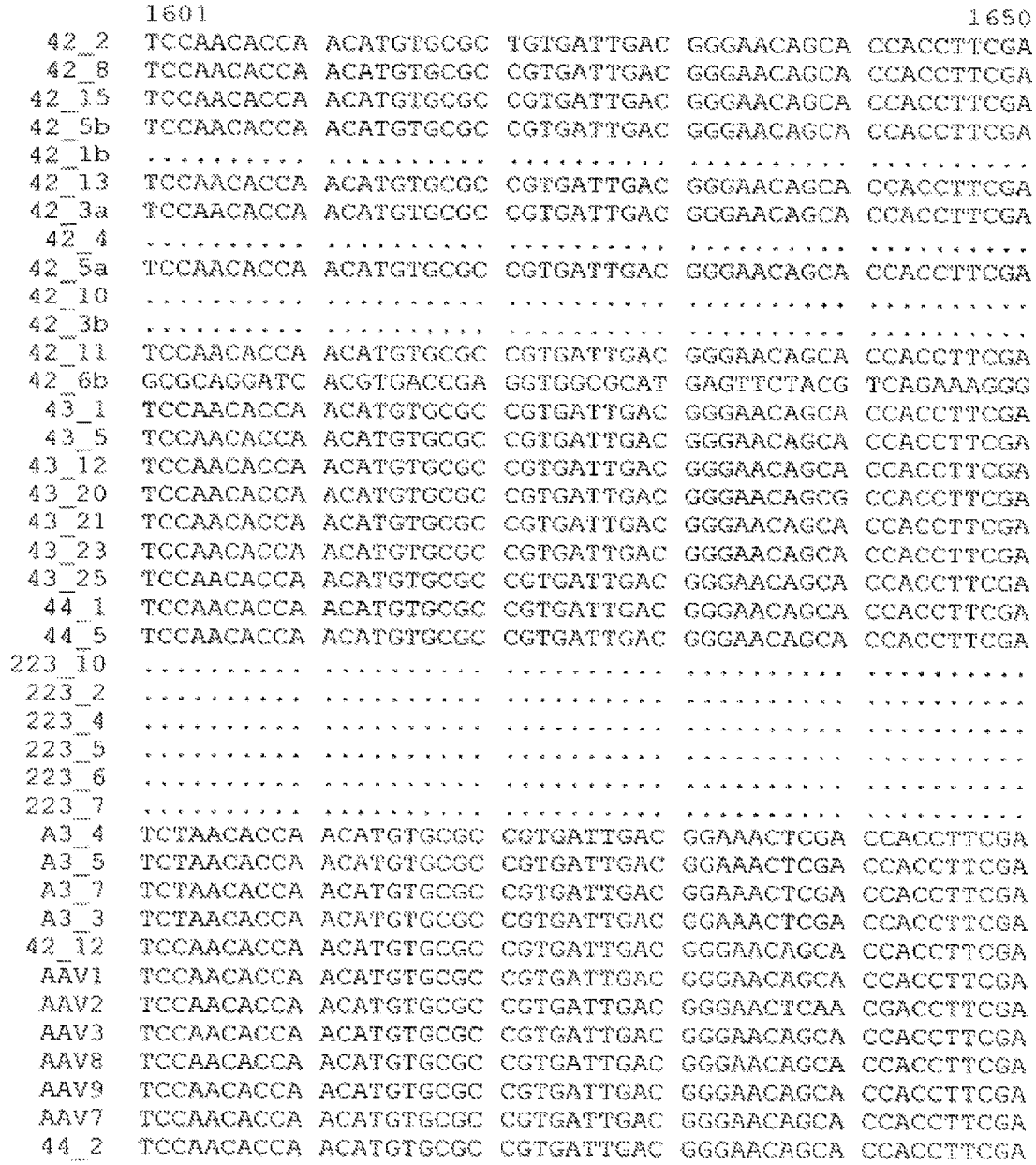
1601
1650
42_2 TCCAACACCA ACATGTGCGC TGTGATTGAC GGGAACAGCA CCACCTTCGA
42_8 TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
42_15 TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
42_5b TCCAACACCA ACATGTGCGC CGTGATTGAC GGGAACAGCA CCACCTTCGA
42_1b .....
42_13 TCCAACACCA ACATGTGCGC CGTGATTGAC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

FIG. 1AH

```
          1651                                                        1700
  42_2    GCACCAGCAG CCGTTACAAG ACCGGATGTT CAAATTTGAA CTCACCCGCC
  42_8    GCACCAGCAG CCGTTACAAG ACCGGATGTT CAAATTTGAA CTCACCCGCC
 42_15    GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAATTTGAA CTCACCCGCC
 42_5b    GCACCAGCAG CCGTTACAAG ACCGGATGTT CAAATTTGAA CTCACCCGCC
 42_1b    .......... .......... .......... .......... ..........
 42_13    GCACCAGCAG CCGTTACAAG ACCGGATGTT CAAATTTGAA CTCACCCGCC
 42_3a    GCACCAGCAG CCGTTACAAG ACCGGATGTT CAAATTTGAA CTCACCCGCC
  42_4    .......... .......... .......... .......... ..........
 42_5a    GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAATTTGAA CTCACCCGCC
 42_10    .......... .......... .......... .......... ..........
 42_3b    .......... .......... .......... .......... ..........
 42_11    GCACCAGCAG CCGTTACAAG ACCGGATGTT CAAATTTGAA CTCACCCGCC
 42_6b    TGGAGCCAAC AAGAGACCCG CCCCCGATGA CGCGGATAAA AGCGAGCCCA
  43_1    GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAGTTCGAA CTCACCCGCC
  43_5    GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAGTTCGAA CTCACCCGCC
 43_12    GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAGTTCGAA CTCACCCGCC
 43_20    GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAATTTGAA CTCACCCGCC
 43_21    GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAATTTGAA CTCACCCGCC
 43_23    GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAATTTGAA CTCACCCGCC
 43_25    GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAATTTGAA CTCACCCGCC
  44_1    GCACCAGCAG CCGTTGCGGG ACCGGATGTT CAAGTTTGAA CTCACCCGCC
  44_5    GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAGTTTGAA CTCACCCGCC
223_10    .......... .......... .......... .......... ..........
 223_2    .......... .......... .......... .......... ..........
 223_4    .......... .......... .......... .......... ..........
 223_5    .......... .......... .......... .......... ..........
 223_6    .......... .......... .......... .......... ..........
 223_7    .......... .......... .......... .......... ..........
  A3_4    GCACCAGCAG CCGTTGCAAG ACCGGATGTT CAAATTTGAA CTTACCCGCC
  A3_5    GCACCAGCAG CCGTTGCAAG ACCGGATGTT CAAATTTGAA CTTACCCGCC
  A3_7    GCACCAGCAG CCGTTGCAAG ACCGGATGTT CAAATTTGAA CTTACCCGCC
  A3_3    GCACCAGCAG CCGTTGCAAG ACCGGATGTT CAAATTTGAA CTTACCCGCC
 42_12    GCACCAGCAG CCGTTACAAG ACCGGATGTT CAAATTTGAA CTCACCCGCC
  AAV1    GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAATTTGAA CTCACCCGCC
  AAV2    ACACCAGCAG CCGTTGCAAG ACCGGATGTT CAAATTTGAA CTCACCCGCC
  AAV3    GCATCAGCAG CCGCTGCAGG ACCGGATGTT TGAATTTGAA CTTACCCGCC
  AAV8    GCACCAGCAG CCTCTCCAGG ACCGGATGTT TAAGTTCGAA CTCACCCGCC
  AAV9    GCACCAGCAG CCTCTCCAGG ACCGGATGTT TAAGTTCGAA CTCACCCGCC
  AAV7    GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAATTTGAA CTCACCCGCC
  44_2    GCACCAGCAG CCGTTGCAGG ACCGGATGTT CAAGTTTGAA CTCACCCGCC
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FIG. 1AI

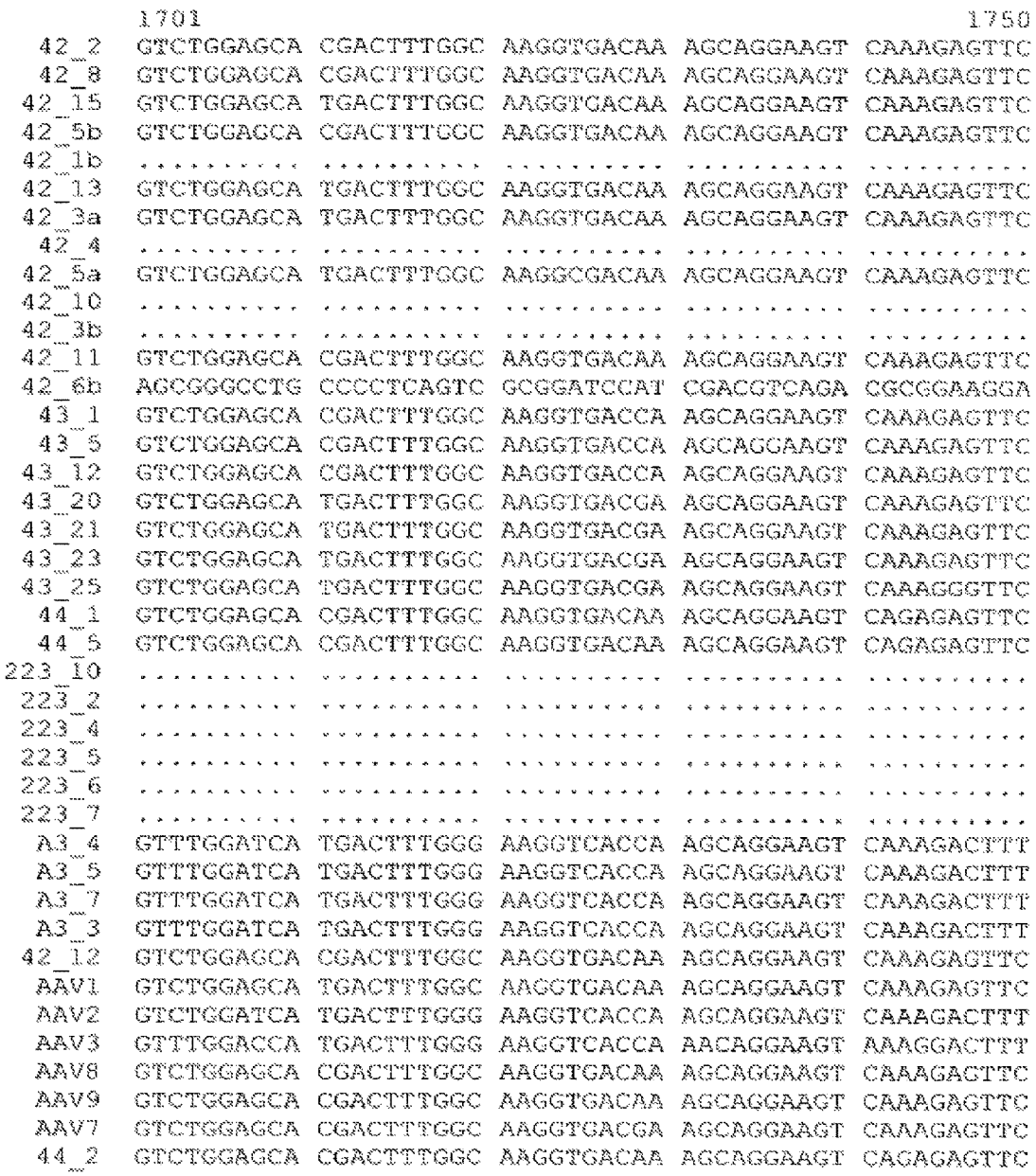

1701
1750
42_2 GTCTGGAGCA CGACTTTGGC AAGGTGACAA AGCAGGAAGT CAAAGAGTTC
42_8 GTCTGGAGCA CGACTTTGGC AAGGTGACAA AGCAGGAAGT CAAAGAGTTC
42_15 GTCTGGAGCA TGACTTTGGC AAGGTGACAA AGCAGGAAGT CAAAGAGTTC
42_5b GTCTGGAGCA CGACTTTGGC AAGGTGACAA AGCAGGAAGT CAAAGAGTTC
42_1b ....
42_13 GTCTGGAGCA TGACTTTGGC AAGGTGACAA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

FIG. 1AJ

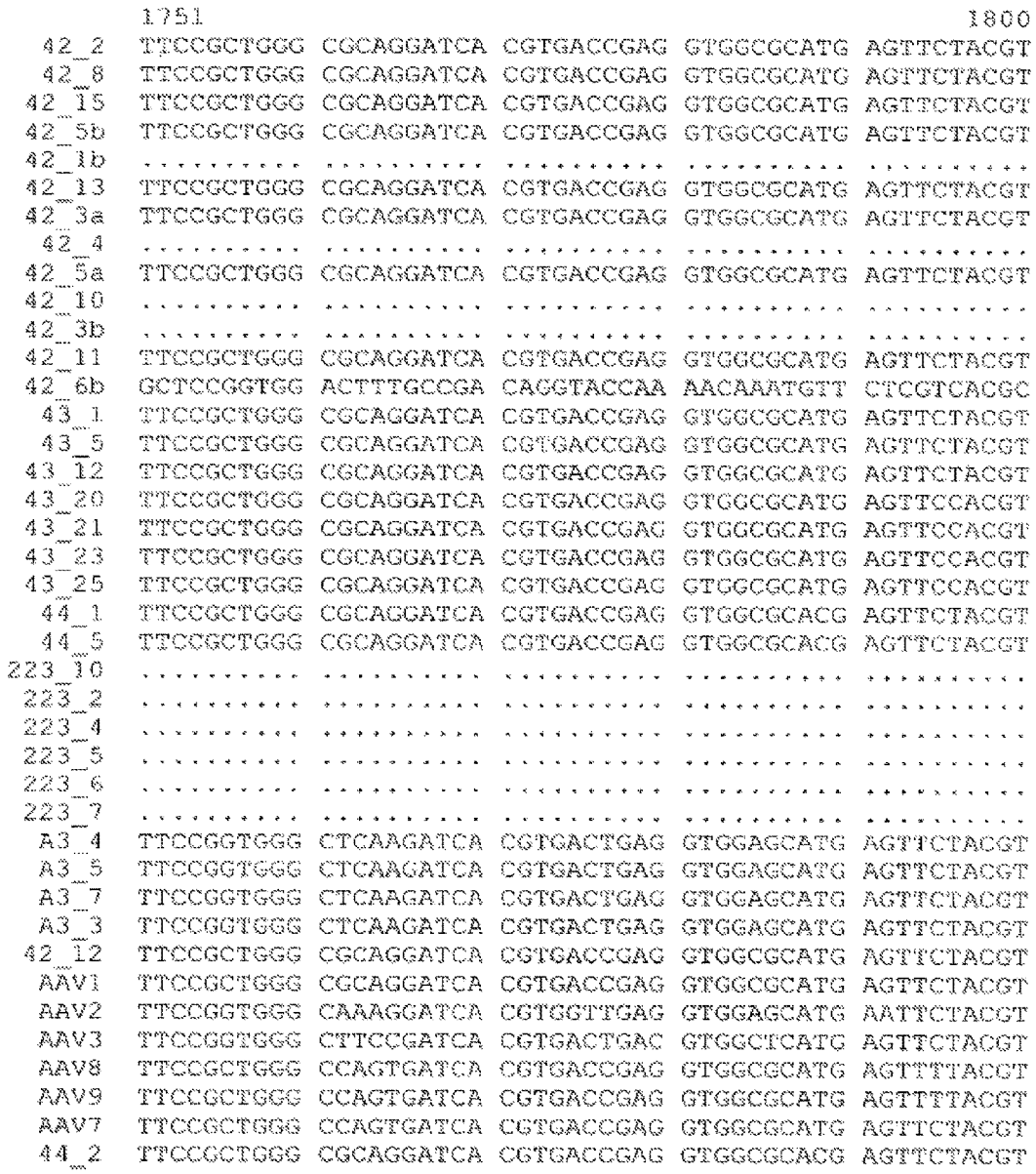
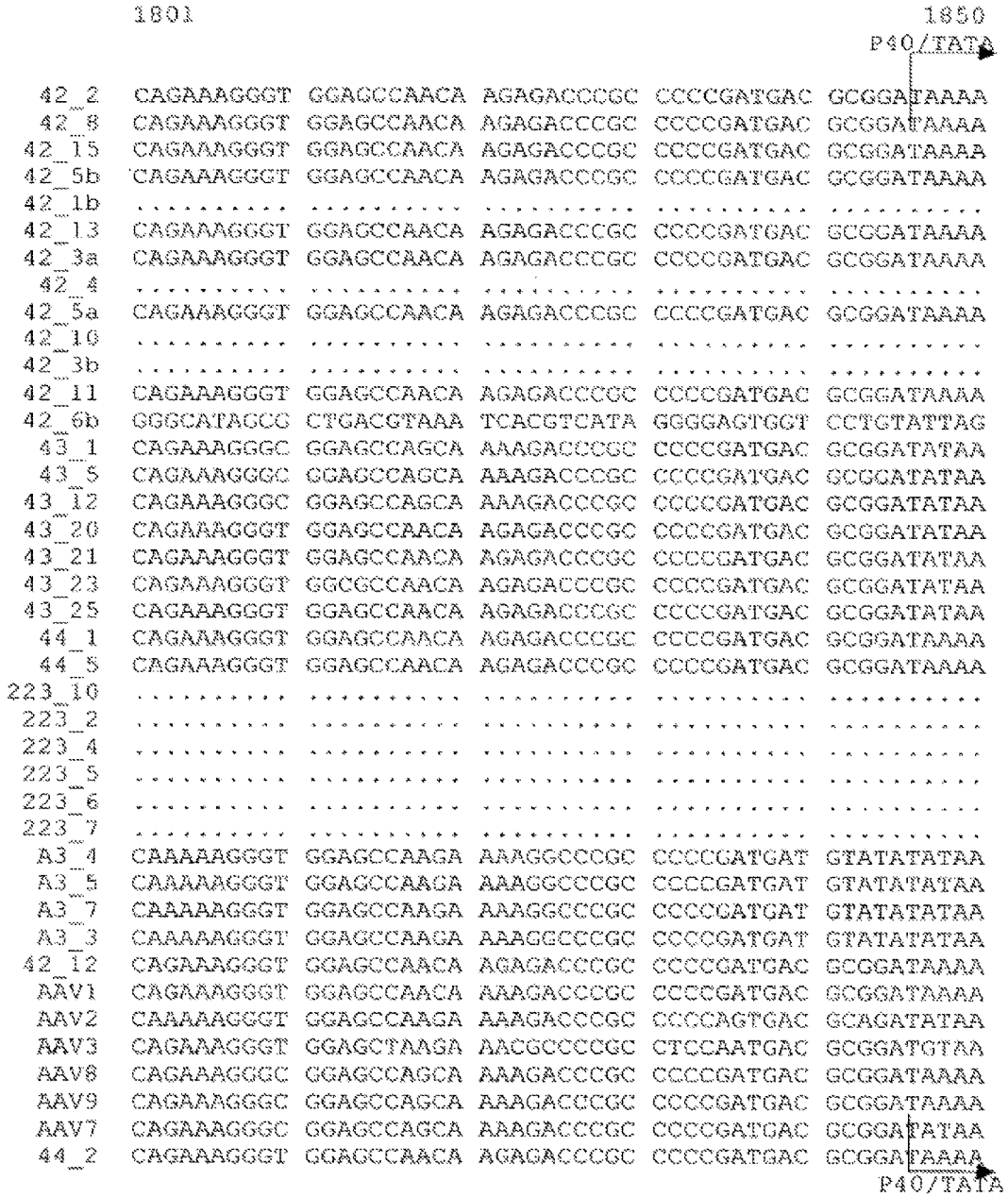

1751
1800
42_2 TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCTACGT
42_8 TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCTACGT
42_15 TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCTACGT
42_5b TTCCGCTGGG CGCAGGATCA CGTGACCGAG GTGGCGCATG AGTTCTACGT
42_1b ....
42_13 TTCCGCTGGG CGCAGGATCA CGTGACCGAG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

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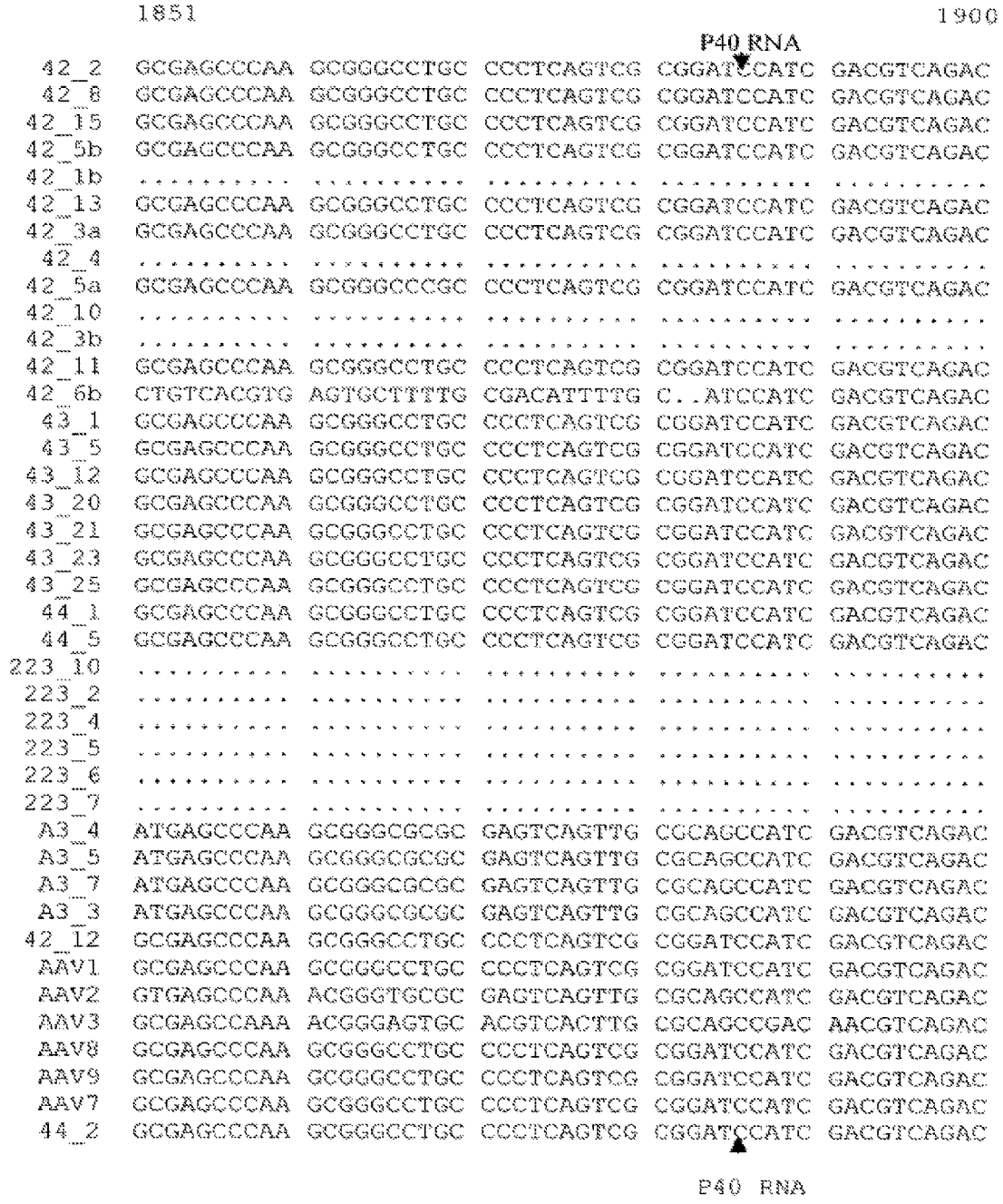
42_15 CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATAAAA
42_5b CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATAAAA
42_1b ....
42_13 CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATAAAA
42_3a CAGAAAGGGT GGAGCCAACA AGAGACCCGC CCCCGATGAC GCGGATAAAA
42_4 ....
42_5a CAGAAAGGGT GGAGCCAACA AGAGACCCGC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

FIG. 1AL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1900
P40 RNA
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42_8 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
42_15 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
42_5b GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
42_1b ....
42_13 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
42_3a GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
42_4 ....
42_5a GCGAGCCCAA GCGGGCCCGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
42_10 ....
42_3b ....
42_11 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
42_6b CTGTCACGTG AGTGCTTTTG CGACATTTTG C..ATCCATC GACGTCAGAC
43_1 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
43_5 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
43_12 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
43_20 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
43_21 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
43_23 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
43_25 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
44_1 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
44_5 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
223_10 ....
223_2 ....
223_4 ....
223_5 ....
223_6 ....
223_7 ....
A3_4 ATGAGCCCAA GCGGGCGCGC GAGTCAGTTG CGCAGCCATC GACGTCAGAC
A3_5 ATGAGCCCAA GCGGGCGCGC GAGTCAGTTG CGCAGCCATC GACGTCAGAC
A3_7 ATGAGCCCAA GCGGGCGCGC GAGTCAGTTG CGCAGCCATC GACGTCAGAC
A3_3 ATGAGCCCAA GCGGGCGCGC GAGTCAGTTG CGCAGCCATC GACGTCAGAC
42_12 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
AAV1 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
AAV2 GTGAGCCCAA ACGGGTGCGC GAGTCAGTTG CGCAGCCATC GACGTCAGAC
AAV3 GCGAGCCAAA ACGGGAGTGC ACGTCACTTG CGCAGCCGAC AACGTCAGAC
AAV8 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
AAV9 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
AAV7 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
44_2 GCGAGCCCAA GCGGGCCTGC CCCTCAGTCG CGGATCCATC GACGTCAGAC
P40 RNA

FIG. 1AM

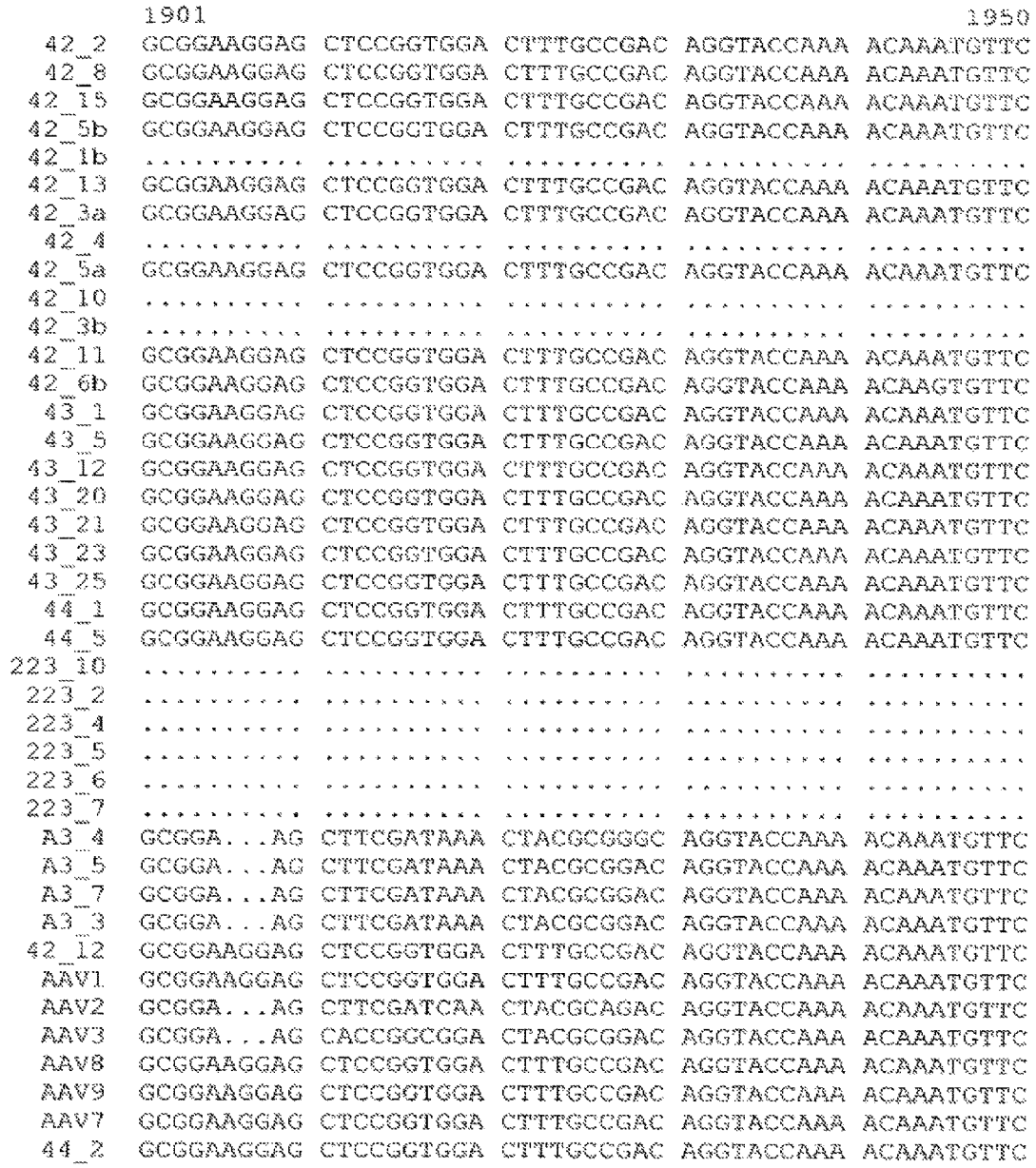
1901
1950
42_2 GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
42_8 GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
42_15 GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
42_5b GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC AGGTACCAAA ACAAATGTTC
42_1b ....
42_13 GCGGAAGGAG CTCCGGTGGA CTTTGCCGAC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

FIG. 1AN

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

FIG. 1AO

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

FIG. 1AP

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

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

FIG. 1AQ

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

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

FIG. 1AR

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

FIG. 1AS

```
          2201                                                                2250

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

FIG. 1AT

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

FIG. 1AU

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

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

FIG. 1AV

```
          2351                                                      2400
  42_2    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
  42_8    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 42_15    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 42_5b    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 42_1b    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 42_13    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 42_3a    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
  42_4    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 42_5a    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 42_10    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 42_3b    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 42_11    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 42_6b    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
  43_1    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
  43_5    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 43_12    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 43_20    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 43_21    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 43_23    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
 43_25    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
  44_1    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
  44_5    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
223_10    .......... .......... .......... .......... ..........
 223_2    .......... .......... .......... .......... ..........
 223_4    .......... .......... .......... .......... ..........
 223_5    .......... .......... .......... .......... ..........
 223_6    .......... .......... .......... .......... ..........
 223_7    .......... .......... .......... .......... ..........
  A3_4    CACCGGGACG ACAGTAGGGG TCTTGTGCTT CCTGGGTACA AGTACCTCGG
  A3_5    CACCGGGACG ACAGTAGGGG TCTTGTGCTT CCTGGGTACA AGTACCTCGG
  A3_7    CACCGGGACG ACAGTAGGGG TCTTGTGCTT CCTGGGTACA AGTACCTCGG
  A3_3    CACCGGGACG ACAGTAGGGG TCTTGTGCTT CCTGGGTACA AGTACCTCGG
 42_12    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
  AAV1    AAGCAGGACG ACGGCCGGGG TCTGGTGCTT CCTGGCTACA AGTACCTCGG
  AAV2    CATAAGGACG ACAGCAGGGG TCTTTGTGCTT 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 CAGCAGCGTC
 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 ACCACGCCGA CGCTGAATTT CAGGAGCGTC
  A3_5    CAACCCGTAC CTCAAATACA ACCACGCCGA CGCTGAATTT CAGGAGCGTC
  A3_7    CAACCCGTAC CTCAAATACA ACCACGCCGA CGCTGAATTT CAGGAGCGTC
  A3_3    CAACCCGTAC CTCAAATACA ACCACGCCGA 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

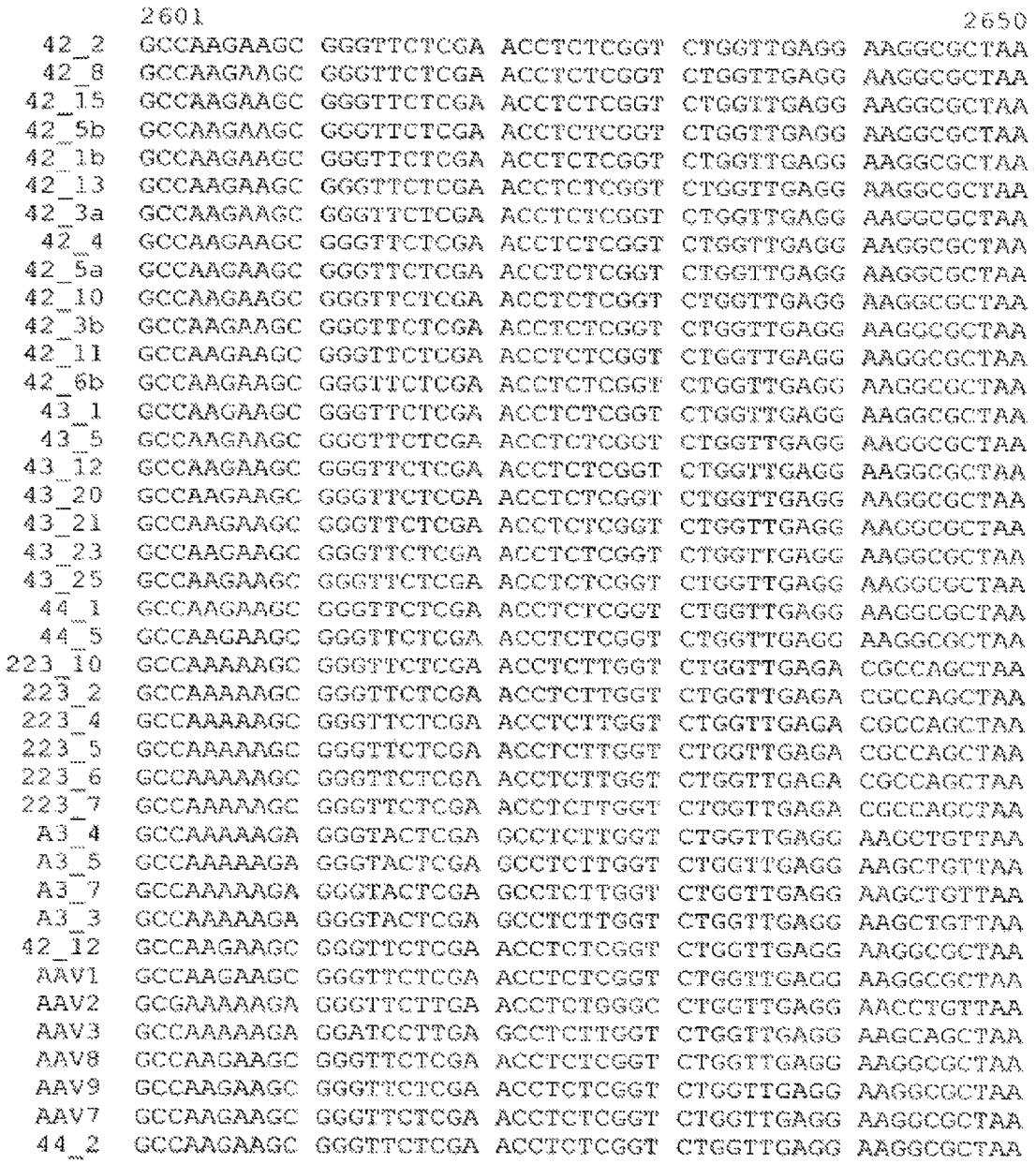
2601
2650
42_2 GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
42_8 GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
42_15 GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
42_5b GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG AAGGCGCTAA
42_1b GCCAAGAAGC GGGTTCTCGA ACCTCTCGGT CTGGTTGAGG 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 GGCTTCTCGA 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 CTGGTTGAGC 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
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FIG. 1AAE

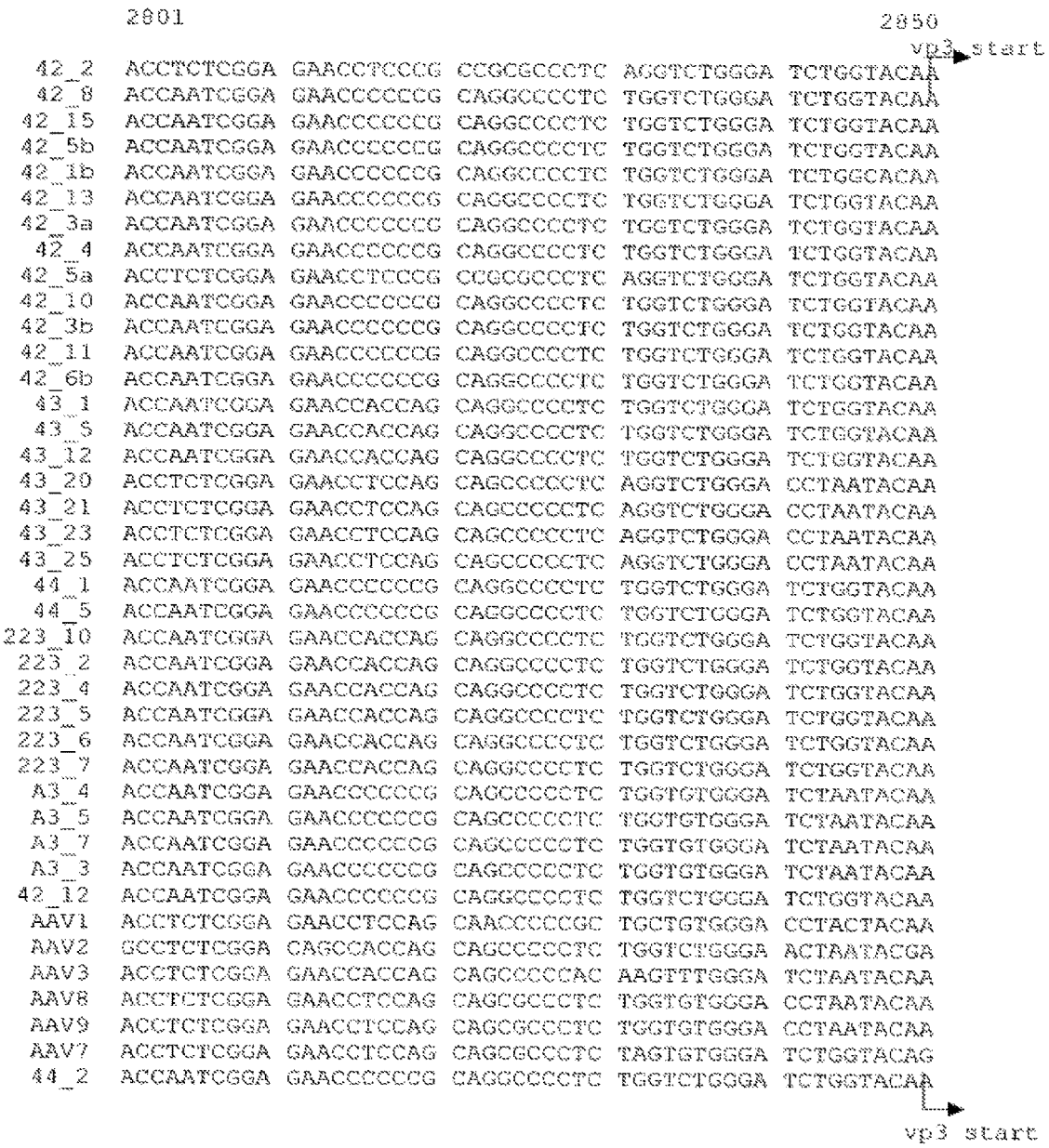
2801
2850
vp3 start
42_2 ACCTCTCGGA GAACCTCCCG CCGCGCCCTC AGGTCTGGGA TCTGGTACAA
42_8 ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
42_15 ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
42_5b ACCAATCGGA GAACCCCCCG CAGGCCCCTC TGGTCTGGGA TCTGGTACAA
42_1b ACCAATCGGA GAACCCCCCG CAGGCCCCTC 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    GCAGTGGGTA 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    GCAGTGGGTA ATGCCTCAGG AAATTGGCAT TGCGATTCCA CATGGCTGGG
 223_4    GGAGTGGGTA ATGCCTCAGG AAATTGGCAT TGCGATTCCA CACGGCTGGG
 223_5    GGAGTGGGTA ATGCCTCAGG AAATTGGCAT TGCGATTCCA CACGGCTGGG
 223_6    GCAGTGGGTA 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 GCACATCGGG 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

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        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
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FIG. 1AAO

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

FIG. 1AAP

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

FIG. 1AAQ

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

FIG. 1AAR

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

FIG. 1AAY

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

FIG. 1AAZ

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

FIG. 1AAAA

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

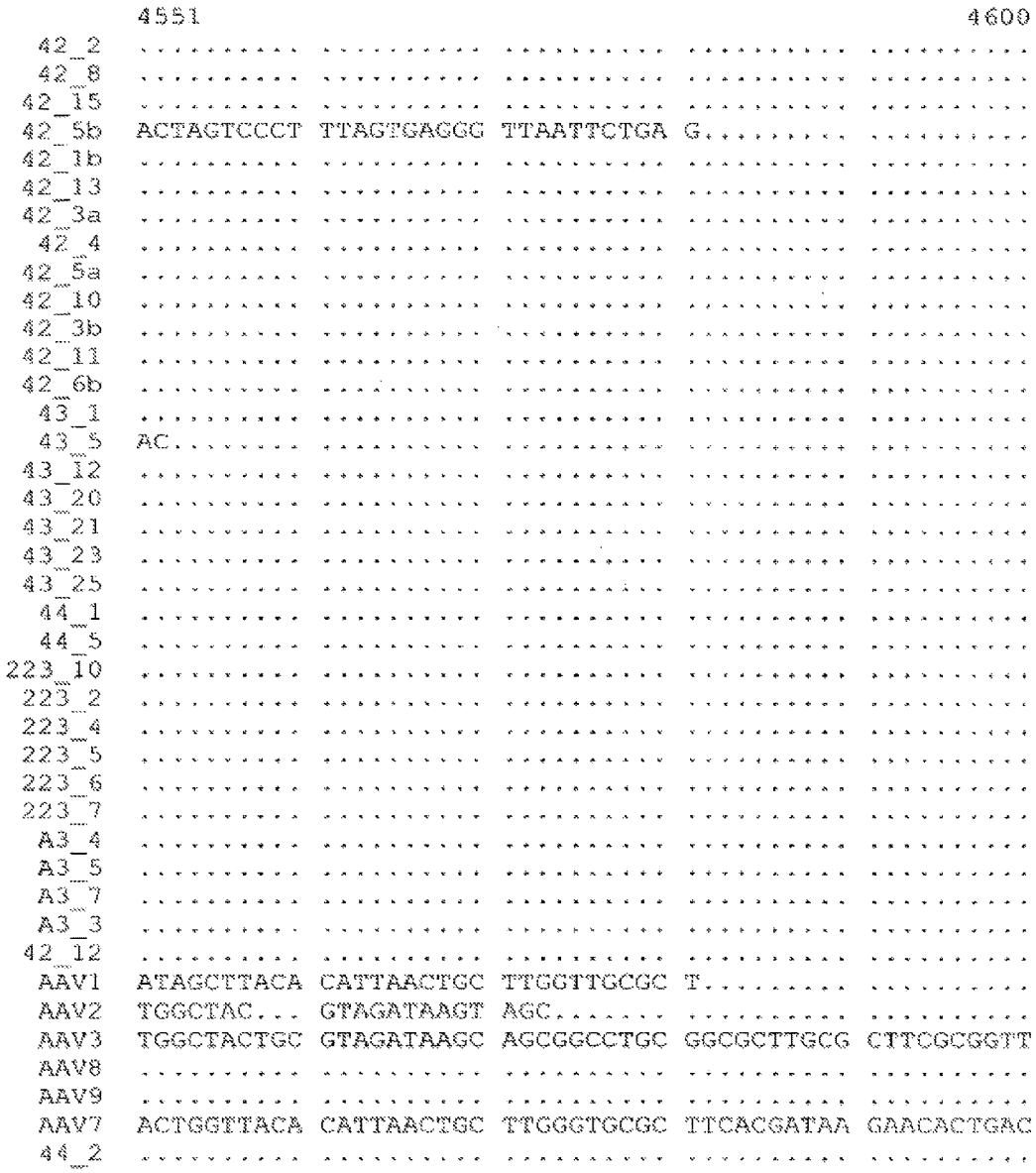

4551
4600
42_2
42_8
42_15
42_5b ACTAGTCCCT TTAGTGAGGG TTAATTCTGA G
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5 AC
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 ATAGCTTACA CATTAACTGC TTGGTTGCGC T
AAV2 TGGCTAC... GTAGATAAGT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

FIG. 1AAAO

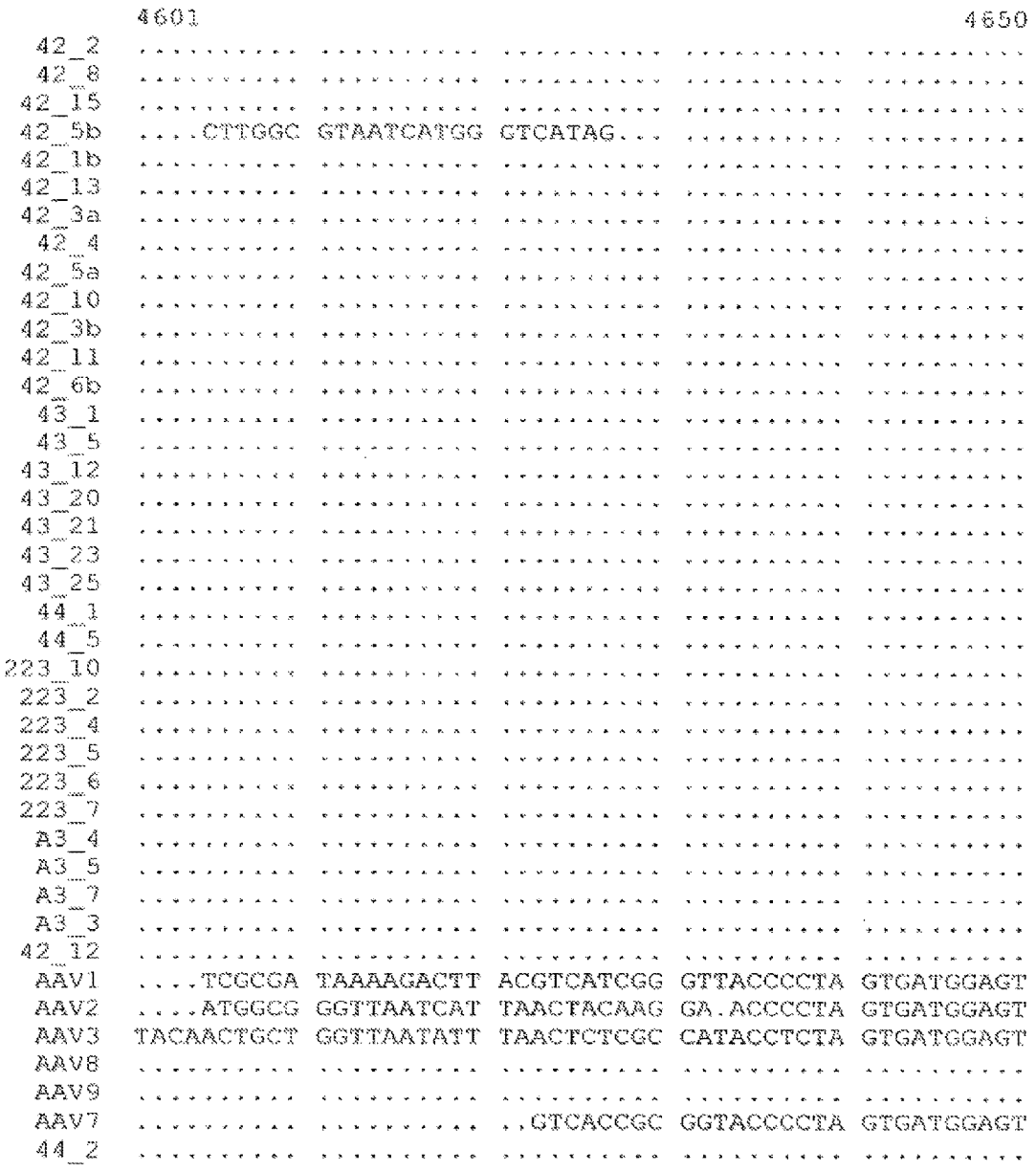

4601
4650
42_2
42_8
42_15
42_5b ....CTTGGC GTAATCATGG GTCATAG...
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 ....TCGCGA TAAAAGACTT ACGTCATCGG GTTACCCCTA GTGATGGAGT
AAV2 ....ATGGCG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

FIG. 1AAAP

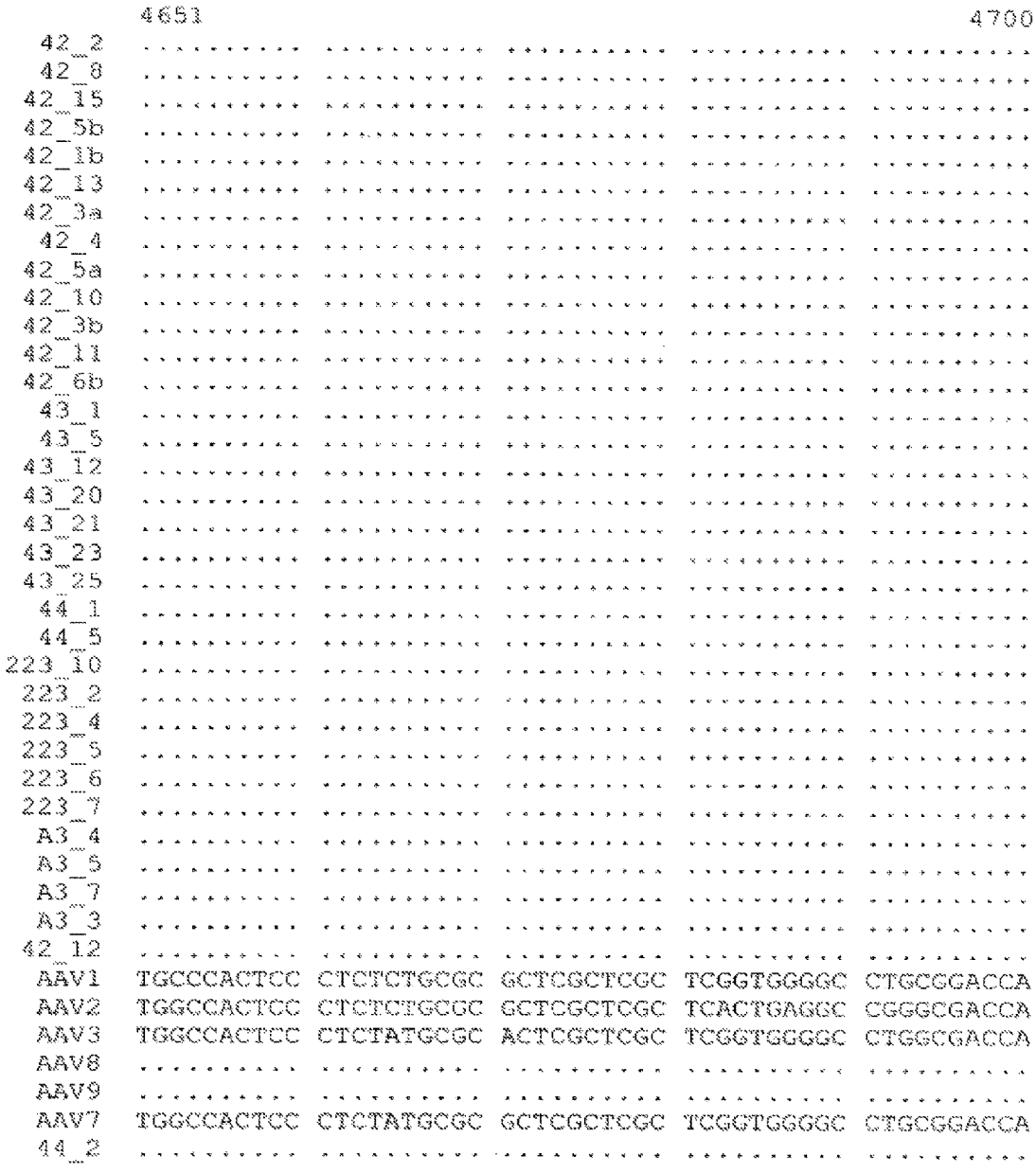

4651
4700
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 TGCCCACTCC CTCTCTGCGC GCTCGCTCGC TCGGTGGGGC CTGCGGACCA
AAV2 TGGCCACTCC CTCTCTGCGC GCTCGCTCGC TCACTGAGGC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

FIG. 1AAAQ

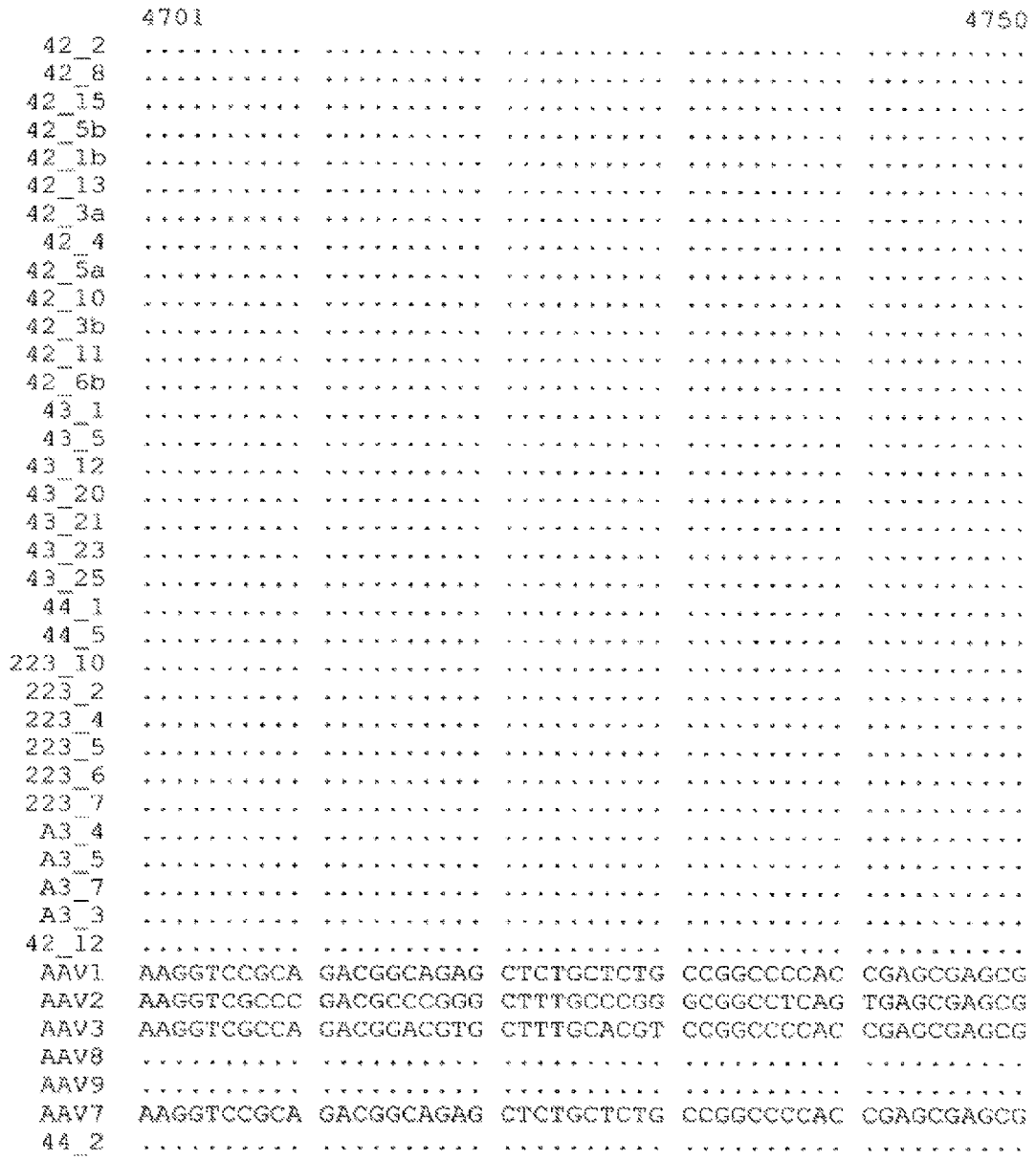
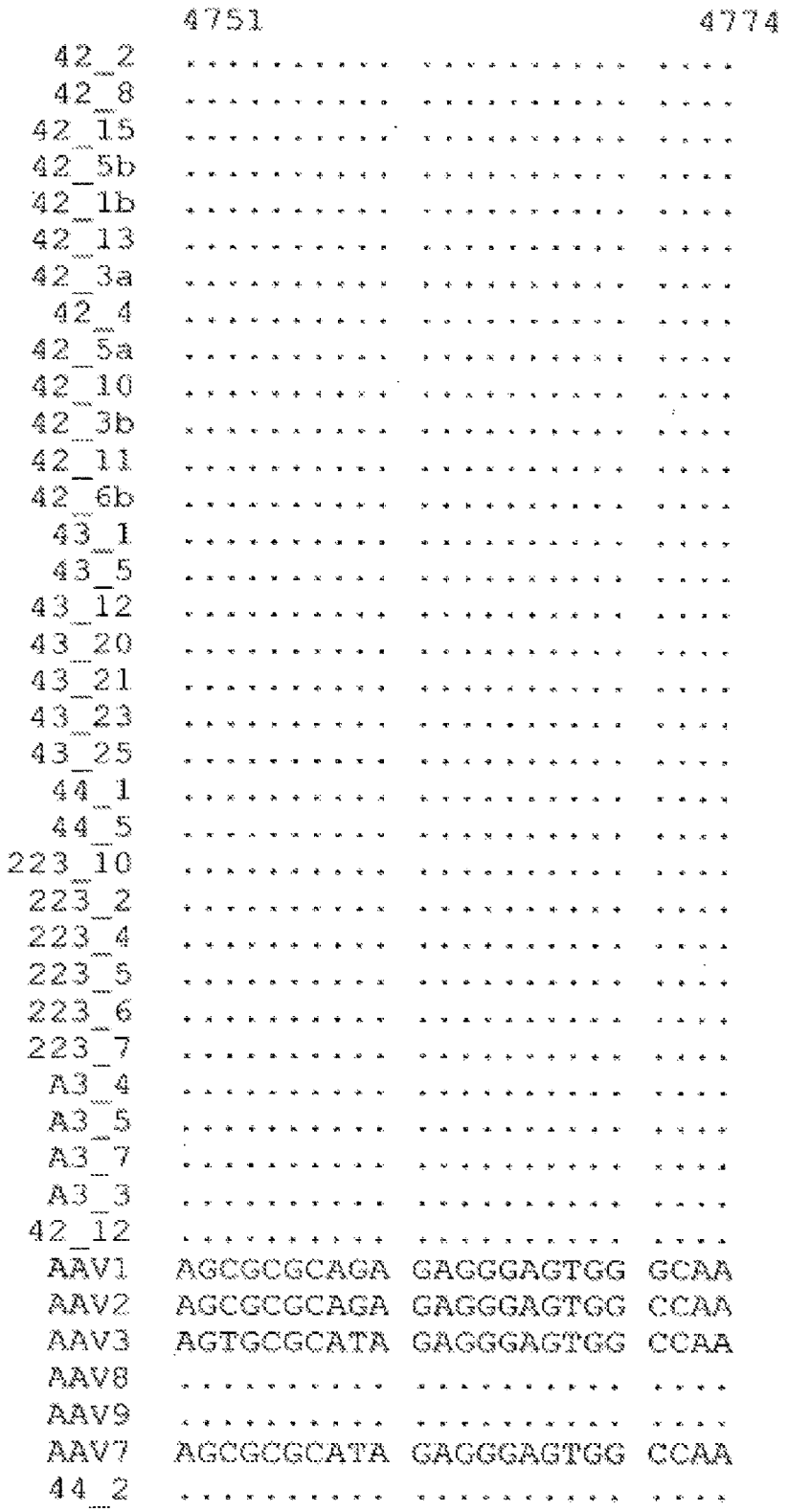

4701
4750
42_2
42_8
42_15
42_5b
42_1b
42_13
42_3a
42_4
42_5a
42_10
42_3b
42_11
42_6b
43_1
43_5
43_12
43_20
43_21
43_23
43_25
44_1
44_5
223_10
223_2
223_4
223_5
223_6
223_7
A3_4
A3_5
A3_7
A3_3
42_12
AAV1 AAGGTCCGCA GACGGCAGAG CTCTGCTCTG CCGGCCCCAC CGAGCGAGCG
AAV2 AAGGTCGCCC GACGCCCGGG CTTTGCCCGG GCGGCCTCAG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

```
                    10         20         30         40         50         60
                    .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
C1\VP1              MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
C2\VP1              MAADGYLPDWLEDNLSEGIREWWDLKPGAPKLKANQQKQDDGRGLVLPGYKYLGPFHGLD
C5\VP1@2            MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYEYLGPFNGLD
AAV4\VP1            -MTDGYLPDWLEDNLSEGVREWWALQPGAPKPKANQQHQDNARGLVLPGYKYLGPGNGLD
AAV1                MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
AAV6\VP1            MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
A3_3                MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPNQQHRDDSRGLVLPGYKYLGPFNGLD
A3_7                MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPNQQHRDDSRGLVLPGYKYLGPFNGLD
A3_4                MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPNQQHRDDSRGLVLPGYKYLGPFNGLD
A3_5                MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPNQQHRDDSRGLVLPGYKYLGPFNGLD
AAV2                MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPFNGLD
AAV3                MAADGYLPDWLEDNLSEGIREWWALKPGVPQPKANQQHQDNRRGLVLPGYKYLGPGNGLD
13.3b\VP1           MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDNGRGLVLPGYKYLGPFNGLD
AAV7                MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDNGRGLVLPGYKYLGPFNGLD
223_4               ------------------------------------------------------------
223_5               ------------------------------------------------------------
223_10              ------------------------------------------------------------
223_2               ------------------------------------------------------------
223_7               ------------------------------------------------------------
223_6               ------------------------------------------------------------
44_1                MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
44_5                MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
44_2                MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
29.3\VP1            MAADGYLPDWLEDNLSEGIREWWALKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
29.5\VP1            MAADGYLPDWLEDNLSEGIREWWALKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
42_15               MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
42_8                MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
42_13               MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
42_3A               MAADGHLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
42_4                MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
42_5A               MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
42_1B               MAADGYLPDWLEDNLSEGIREWWDLRPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
42_5B               MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
43_1                MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
43_12               MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
43_5                MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
AAV8                MAADGYLPDWLEDNLSEGIREWWALKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
43_21               MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
43_25               MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
43_23               MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
43_20               MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
AAV_9               MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
24.1                MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLRPFNGLD
42.2REAL            MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
7.2\VP1             MAADGYLPDWLEGNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYRYLGPFNGLD
27.3\VP1            MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
16.3\VP1            MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
42_10               MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
42_3B               MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
42_11               MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
F1\VP1              MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
F5\VP1@3            MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
F3\VP1              MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
42_6B               MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
42_12               MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
AAV5\CAP            MSFVDHPPDWLEE-VGEGLREFLGLEAGPPKPKPNQQHQDQARGLVLPGYNYLGPGNGLD
```

FIG. 2A

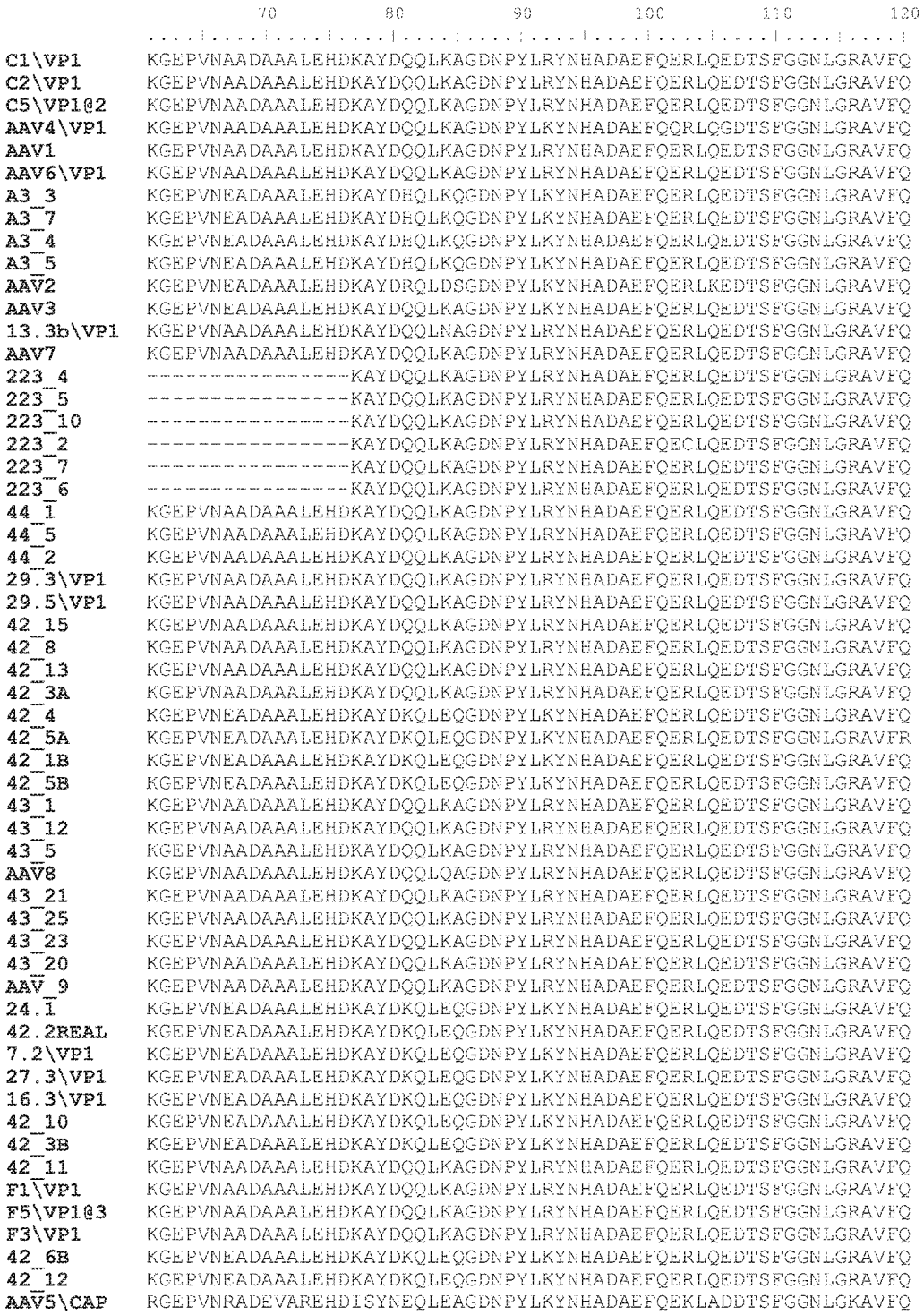

70 80 90 100 110 120
C1\VP1 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
C2\VP1 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
C5\VP1@2 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
AAV4\VP1 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQQRLQGDTSFGGNLGRAVFQ
AAV1 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNEADAEFQERLQEDTSFGGNLGRAVFQ
AAV6\VP1 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
A3_3 KGEPVNEADAAALEHDKAYDHQLKQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQ
A3_7 KGEPVNEADAAALEHDKAYDHQLKQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQ
A3_4 KGEPVNEADAAALEHDKAYDHQLKQGDNPYLKYNEADAEFQERLQEDTSFGGNLGRAVFQ
A3_5 KGEPVNEADAAALEHDKAYDHQLKQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQ
AAV2 KGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQ
AAV3 KGEPVNEADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQ
13.3b\VP1 KGEPVNAADAAALEHDKAYDQQLNAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
AAV7 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
223_4 ----------KAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
223_5 ----------KAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
223_10 ----------KAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
223_2 ----------KAYDQQLKAGDNPYLRYNHADAEFQECLQEDTSFGGNLGRAVFQ
223_7 ----------KAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
223_6 ----------KAYDQQLKAGDNPYLRYNEADAEFQERLQEDTSFGGNLGRAVFQ
44_1 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
44_5 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
44_2 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
29.3\VP1 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNEADAEFQERLQEDTSFGGNLGRAVFQ
29.5\VP1 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
42_15 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
42_8 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
42_13 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
42_3A KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
42_4 KGEPVNEADAAALEHDKAYDKQLEQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQ
42_5A KGEPVNEADAAALEHDKAYDKQLEQGDNPYLKYNEADAEFQERLQEDTSFGGNLGRAVFR
42_1B KGEPVNEADAAALEHDKAYDKQLEQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQ
42_5B KGEPVNEADAAALEHDKAYDKQLEQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQ
43_1 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
43_12 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNEADAEFQERLQEDTSFGGNLGRAVFQ
43_5 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
AAV8 KGEPVNAADAAALEHDKAYDQQLQAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
43_21 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
43_25 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
43_23 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
43_20 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
AAV_9 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
24.1 KGEPVNEADAAALEHDKAYDKQLEQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQ
42.2REAL KGEPVNEADAAALEHDKAYDKQLEQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQ
7.2\VP1 KGEPVNEADAAALEHDKAYDKQLEQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQ
27.3\VP1 KGEPVNEADAAALEHDKAYDKQLEQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQ
16.3\VP1 KGEPVNEADAAALEHDKAYDKQLEQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQ
42_10 KGEPVNEADAAALEHDKAYDKQLEQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQ
42_3B KGEPVNEADAAALEHDKAYDKQLEQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQ
42_11 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNEADAEFQERLQEDTSFGGNLGRAVFQ
F1\VP1 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
F5\VP1@3 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
F3\VP1 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
42_6B KGEPVNEADAAALEHDKAYDKQLEQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQ
42_12 KGEPVNEADAAALEHDKAYDKQLEQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQ
AAV5\CAP RGEPVNRADEVAREHDISYNEQLEAGDNPYLKYNHADAEFQEKLADDTSFGGNLGKAVFQ

FIG. 2B

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                  130         140         150         160         170         180
                  ....|....|....|....|....|....|....|....|....|....|....|....|
C1\VP1            AKKRVLEPLGLVEEGAKTAPGKKRP-LESPQ-EPDSSSGIGKKGKQPAKKRLNFEEDTGA
C2\VP1            AKKRVLEPLGLVEEGAKTAPGKKRP-LESPQ-EPDSSSGIGKKGKQPAKKRLNFEEDTGA
C5\VP1@2          AKKRVLEPLGLVEEGAKTAPGKKRP-LESPQ-EPDSSSGIGKKGKQPAKKRLNFEEDTGA
AAV4\VP1          AKKRVLEPLGLVEQAGETAPGKKRPLIESPQ-QPDSSTGIGKKGKQPAKKKLVFEDETGA
AAV1              AKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQ-EPDSSSGIGKTGQQPAKKRLNFGQTGDS
AAV6\VP1          AKKRVLEPFGLVEEGAKTAPGKKRPVEQSPQ-EPDSSSGIGKTGQQPAKKRLNFGQTGDS
A3_3              AKKRVLEPLGLVEEAVKTAPGKKRPIEQSPA-EPDSSSGIGKSGQQPAKKRLNFGQTGDT
A3_7              AKKRVLEPLGLVEEAVKTAPGKKRPIEQSPA-EPDSSSGIGKSGQQPAKKRLNFGQTGDT
A3_4              AKKRVLEPLGLVEEAVKTAPGKKRPIEQSPA-EPDSSSGIGESGQQPAKKRLNFGQTGDT
A3_5              AKKRVLEPLGLVEEAVKTAPGKKRPIEQSPA-EPDSSSGIGKSGQQPAKKRLNFGQTGDT
AAV2              AKKRVLEPLGLVEEPVKTAPGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDA
AAV3              AKKRILEPLGLVEEAAKTAPGKKGAVDQSPQ-EPDSSSGVGKSGKQPARKRLNFGQTGDS
13.3b\VP1         AKKRVLEPLGLVEEGAKTAPAKKRPVEPSPQRSPDSSTGIGKKGQQPARKRLNFGQTGDS
AAV7              AKKRVLEPLGLVEEGAKTAPAKKRPVEPSPQRSPDSSTGIGKKGQQPARKRLNFGQTGDS
223_4             AKKRVLEPLGLVETPAKTAPGKKRPVD------SPDSTSGIGKKGQQPAKKRLNFGQTGDS
223_5             AKKRVLEPLGLVETPAKTAPGKKRPVD-----SPDSTSGIGKKGQQPAKKRLNFGQTGDS
223_10            AKKRVLEPLGLVETPAKTAPGKKRPVD-----SPDSTSGIGKKGQQPAKKRLNFGQTGDS
223_2             AKKRVLEPLGLVETPAKTAPGKKRPVD-----SPDSTSGIGKKGQQPAKKRLNFGQTGDS
223_7             AKKRVLEPLGLVETPAKTAPGKKRPVD------SPDSTSGIGKKGQQPAKKRLNFGQTGDS
223_6             AKKRVLEPLGLVETPAKTAPGKKRPVD------SPDSTSGIGKKGQQPAKKRLNFGQTGDS
44_1              AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPAKKRLNFGQTGDS
44_5              AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPAKKRLNFGQTGDS
44_2              AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPAKKRLNFGQTGDS
29.3\VP1          AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPDSTTGIGKKGQQPAKKRLNFGQTGDS
29.5\VP1          AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPAKKRLNFGQTGDS
42_15             AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKTGQQPAKKRLNFGQTGDS
42_8              AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKTGQQPAKKRLNFGQTGDS
42_13             AKKRVLEPLGLVEEGAKTAPGKKRPIE------SPDSSTGIGKKGQQPAKKKLNFGQTGDS
42_3A             AKKRVLEPLGLVEEGAKTAPGKKRPIE-----SPDSSTGIGKKGQQPAKKKLNFGQTGDS
42_4              AKKRVLEPLGLVEEGAKTAPGKKRPIE------SPDSSTGIGKKGQQPAKKKLNFGQTGDS
42_5A             AKKRVLEPLGLVEEGAKTAPGKKRPIE-----SPDSSTGIGKKGQQPAKKKLNFGQTGDS
42_1B             AKKRVLEPLGLVEEGAKTAPGKKRPIE------SPDSSTGIGKKGQQPAKKRLNFGQTGDS
42_5B             AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKTGQQPAKKRLNFGQTGDS
43_1              AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKKGHQPARKRLNFGQTGDS
43_12             AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKKGHQPARKRLNFGQTGDS
43_5              AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKKGHQPARKRLNFGQTGDS
AAV8              AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPARKRLNFGQTGDS
43_21             AKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQ-EPDSSSGIGKTGQQPAKKRLNFGQTGDS
43_25             AKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQ-EPDSSSGIGKTGQQPAKKRLNFGQTGDS
43_23             AKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQ-EPDSSSGIGKTGQQPAKKRLNFGQTGDS
43_20             AKKRVLEPLGLVEEGAKTAPGKKRLVEQSPQ-EPDSSSGIGKTGQQPAKKRLNFGQTGDS
AAV_9             AKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQ-EPDSSSGIGKSGQQPAKKRLNFGQTGDS
24.1              AKKRVLEPLGLVEEVAKTAPGKKRPIE------SPDSSTGIGKKGQQPAKKKLNFGQTGDS
42.2REAL          AKKRVLEPLGLVEEGAKTAPGKKRPIE-----SPDSSTGIGKKGQQPAKKKLNFGQTGDS
7.2\VP1           AKKRVLEPLGLVEEGAKTAPGKKRPIE------SPDSSTGIGKNGQPPAKKKLNFGQTGDS
27.3\VP1          AKKRVLEPLGLVEEGAKTASGKKRPIE-----SPDSSTGIGKKGQQPAKKKLNFGQTGDS
16.3\VP1          AKKRVLEPLGLVEEGAKTAPGKKRPIE------SPDSSTGIGKKGQQPAKKKLNFGQTGDS
42_10             AKKRVLEPLGLVEEGAKTAPGKKRPIE------SPDSSTGIGRKGQQPAKKKLNFGQTGDS
42_3B             AKKRVLEPLGLVEEGAKTAPGKKRPIE-----SPDSSTGIGKKGQQPAKKKLNFGQTGDS
42_11             AKKRVLEPLGLVEEGAKTAPGKKRPIE------SPDSSTGIGKKGQQPAKKKLNFGQTGDS
F1\VP1            AKKRVLEPLGLVEEGAKTAPGKKRPID-----SPDSSTGIGKKGQQPAKKKLNFGQTGDS
F5\VP1@3          AKKRVLEPLGLVEEGAKTAPGKKRPID------SPDSSTGIGKKGQQPAKKKLNFGQTGDS
F3\VP1            AKKRVLEPLGLVEEGAKTAPGKKRPIG-----SPDSSTGIGKKGQQPAKKKLNFGQTGDS
42_6B             AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKTGQQPAKKRLNFGQTGDS
42_12             AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKTGQQPAKKRLNFGQTGDS
AAV5\CAP          AKKRVLEPFGLVEEGAKTAPTGKR---------IDDHFPKRKKARTEEDSKP--STSSDA
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FIG. 2C

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                  190         200         210         220         230         240
                  ....|....|....|....|....|....|....|....|....|....|....|....|
C1\VP1            GDGP----PEGSDTSAMS--SDIEMRAAPGGNAVDAGQGSDGVGNASGDWHCDSTWSEGK
C2\VP1            GDGP----PEGSDTSAMS--SDIEMRAAPGGNAVDAGQGSDGVGNASGDWHCDSTWSEGK
C5\VP1@2          GDGP----PEGSDTSAMS--SDIEMRAAPGGNAVDAGQGSDGVGNASGDWHCDSTWSEGK
AAV4\VP1          GDGP----PEGSTSGAMS--DDSEMRAAAGGAAVEGGQGADGVGNASGDWHCDSTWSEGH
AAV1              ESVPD-PQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR
AAV6\VP1          ESVPD-PQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR
A3_3              ESVPG-PQPIGEPPAAPSGVGSNTMASGGGAPMADNNEGADGVGNSSGNWHCDSTWMGDR
A3_7              ESVPD-PQPIGEPPAAPSGVGSNTMASGGGAPMADNNEGADGVGNSSGNWHCDSTWMGDR
A3_4              ESVPD-PQPIGEPPAAPSGVGSNTMASGGGAPMADDNEGADGVGNSSGNWHCDSTWMGDR
A3_5              ESVPD-PQPIGEPPAAPSGVGSNTMASGGGAPMADNNEGADGVGNSSGNWHCDSTWMGDR
AAV2              DSVPD-PQPLGQPPAAPSGLGTNTMATGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDR
AAV3              ESVPD-PQPLGEPPAAPTSLGSNTMASGGGAPMADNNEGADGVGNSSGNWHCDSQWLGDR
13.3b\VP1         ESVPD-PQPLGEPPAAPSSVGSGTVAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR
AAV7              ESVPD-PQPLGEPPAAPSSVGSGTVAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR
223_4             EPVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTRLGDR
223_5             EPVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTRLGDR
223_10            ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR
223_2             ESVPD-PQPIGEPPAGPSGLGSGTMVAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR
223_7             ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR
223_6             ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNSEGADGVGNASGNWHCDSTWLGDR
44_1               ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR
44_5               ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR
44_2               ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR
29.3\VP1          ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR
29.5\VP1          ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDG
42_15             ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR
42_8              ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR
42_13             ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR
42_3A             ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR
42_4              ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR
42_5A             ESVPD-PQPLGEPPAAPSGLGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR
42_1B             ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR
42_5B             ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR
43_1              ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR
43_12             ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR
43_5              ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR
AAV8              ESVPD-PQPLGEPPAAPSGVGPNTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR
43_21             ESVPD-PQPLGEPPAAPSGLGPNTMASGGGAPMADNNEGADGVGNSSGNWHCDSTWLGDR
43_25             ESVPD-PQPLGEPPAAPSGLGPNTMASGGGAPMADNNEGADGVGNSSGNWHCDSTWLGDR
43_23             ESVPD-PQPLGEPPAAPSGLGPNTMASGGGAPMADNNEGADGVGNSSGNWHCDSTWLGDR
43_20             ESVPD-PQPLGEPPAAPSGLGPNTMASGGGAPMADNNEGADGVGNSSGNWHCDSTWLGDR
AAV_9             ESVPD-PQPLGEPPEAPSGLGPNTMASGGGAPMADNNEGADGVGNSSGNWHCDSTWLGDR
24.1               ESVPD-PQPLGEPPAAPSGLGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR
42.2REAL          ESVPD-PQPLGEPPAAPSGLGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR
7.2\VP1           ESVPD-PQPLGEPPAAPSGLGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR
27.3\VP1          ESVPD-PQPLGEPPAAPSGLGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR
16.3\VP1          ESVPD-PQPLGEPPAAPSGLGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR
42_10             ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR
42_3B             ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR
42_11             ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR
F1\VP1            ESVPD-PQPLGEPPAAPSSVGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR
F5\VP1@3          ESVPD-PQPLGEPPAAPSSVGSGTMAAGGGAPTADNNEGADGVGNASGNWHCDSTWLGDR
F3\VP1            ESVPD-PQPLGEPPAAPSSVGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR
42_6B             ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR
42_12             ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR
AAV5\CAP          EAGPSGSQQLQIPAQPASSLGADTMSAGGGGPLGDNNQGADGVGNASGDWHCDSTWMGDR
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FIG. 2D

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                  250        260        270        280        290        300
                  ....|....|....|....|....|....|....|....|....|....|....|....|
C1\VP1            VTTTSTRTWVLPTYNNHLYLRLG-----TTSNSNTYNGFSTPWGYFDFNRFHCHFSPRDW
C2\VP1            VTTTSTRTWVLPTYNNHLYLRLG-----TTSNSNTYNGFSTPWGYFDFNRFHCHFSPRDW
C5\VP1@2          VTTTSTRTWVLPTYNNHLYLRLG-----TTSNSNTYNGFSTPWGYFDFNRFHCHFSPRDW
AAV4\VP1          VTTTSTRTWVLPTYNNHLYKRLG-----ESLQSNTYNGFSTPWGYFDFNRFHCHFSPRDW
AAV1              VITTSTRTWALPTYNNHLYKQIS-SASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDW
AAV6\VP1          VITTSTRTWALPTYNNHLYKQIS-SASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDW
A3_3              VITTSTRTWALPTYNNHLYKQIS--SESGATNDNHYFGYSTPWGYFDFNRFHCHFSPRDW
A3_7              VITTSTRTWALPTYNNRLYKQIS--SESGATNDNHYFGYSTPWGYFDFNRFHCHFSPRDW
A3_4              VITTSTRTWALPTYNNHLYKQIS--SESGATNDNHYFGYSTPWGYFDFNRFHCHFSPRDW
A3_5              VITTSTRTWALPTYNNHLYKQIS--SESGATNDNHYFGYSTPWGYFDFNRFHCHFSPRDW
AAV2              VITTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDW
AAV3              VITTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDW
13.3b\VP1         VITTSTRTWALPTYNNHLYEQIS-SETAGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
AAV7              VITTSTRTWALPTYNNHLYKQIS-SETAGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
223_4             VITTSTRTWALPTYNNHLYKQIS-SQSAGSTNDNVYFGYSTPWGYFDFNRFHCHFSPRDW
223_5             VITTSTRTWALPTYNNHLYKQIS-SQSAGSTNDNVYFGYSTPWGYFDFNRFHCHFSPRDW
223_10            VITTSTRTWALPTYNNHLYKQIS-SQSAGSTNDNVYFGYSTPWGYFDFNRFHCHFSPRDW
223_2             VITTSTRTWALPTYNNHLYKQIS-SQSAGSTNDNVYFGYSTPWGYFDFNRFHCHFSPRDW
223_7             VITTSTRTWALPTYNNHLYKQIS-SQSAGSTNDNVYFGYSTPWGYFDFNRFHCHFSPRDW
223_6             VITTSTRTWALPTYNNHLYKQIS-SQSAGSTNDNVYFGYSTPWGYFDFNRFHCHFSPRDW
44_1              VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
44_5              VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
44_2              VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
29.3\VP1          VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
29.5\VP1          VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
42_15             VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
42_8              VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
42_13             VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
42_3A             VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
42_4              VITTSTRTWALPTYNNHLYKQIS--SQSGATNDNHFFGYSTPWGYFDFNRFHCHFSSRDW
42_5A             VITTSTRTWALPTYNNHLYKQIS--SQSGATNDNHFFGYSTPWGYFDFNRFHCHFSPRDW
42_1B             VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
42_5B             VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
43_1              VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
43_12             VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
43_5              VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
AAV8              VITTSTRTWALPTYNNHLYKQISNGTSGGATNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
43_21             VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
43_25             VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
43_23             VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
43_20             VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
AAV_9             VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
24.1              VITTSTRTWALPTYNNHLYKQIS-SQS-GATNDNHFFSYSTPWGYFDFNRFHCHFSPRDW
42.2REAL          VITTSTRTWALPTYNNHLYKQIS-SQS-GATNDNHFFGYSTPWGYFDFNRFHCHFSPRDW
7.2\VP1           VITTSTRTWALPTYNNHLYKQIS-SQS-GATNDNHFFGYSTPWGYFDFNRFHCHFSPRDW
27.3\VP1          VITTSTRTWALPTYNNHLYKQIS-SQS-GATNDNHFFGYSTPWGYFDFNRFHCHFSPRDW
16.3\VP1          VITTSTRTWALPTYNNHLYKQIS-SQS-GATNDNHFFGYSTPWGYFDFNRFHCHFSPRDW
42_10             VITTSTRTWALPTYNNHLYKQIS-SQS-GATNDNHFFGYSTPWGYFDFNRFHCHFSPRDW
42_3B             VITTSTRTWALPTYNNHLYKQIS-SQS-GATNDNHFFGYSTPWGYFDFNRFHCHFSPRDW
42_11             VITTSTRTWALPTYNNHLYKQIS-SQS-GATNDNHFFGYSTPWGYFDFNRFHCHFSPRDW
F1\VP1            VITTSTRTWALPTYNNHLYKQIS-SSSSGATNDNHYFGYSTPWGYFDFNRFHCHFSPRDW
F5\VP1@3          VITTSTRTWALPTYNNHLYKQIS-SSSSGATNDNHYFGYSTPWGYFDFNRFHCHFSPRDW
F3\VP1            VITTSTRTWALPTYNNHLYKQIS-SSSSGATNDNHYFGYSTPWGYFDFKRFHCHFSPRDW
42_6B             VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
42_12             VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW
AAV5\CAP          VVTKSTRTWVLPSYNNHQYREIK-SGSVDGSNANAYFGYSTPWGYFDFNRFHSHWSPRDW
```

FIG. 2E

```
                    310         320         330         340         350         360
                    ....|....|....|....|....|....|....|....|....|....|....|....|
C1\VP1              QRLINNNWGLRPKAMRVKIFNIQVKEVTTSNGETTVANNLTSTVQIFADSSYELPYVMDA
C2\VP1              QRLINNNWGLRPKAMRVKIFNIQVKEVTTSNGETTVANNLTSTVQIFADSSYELPYVMDA
C5\VP1@2            QRLINNNWGLRPKAMRVKIFNIQVKEVTTSNGETTVANNLTSTVQIFADSSYELPYVMDA
AAV4\VP1            QRLINNNWGMRPKAMRVKIFNIQVKEVTTSNGETTVANNLTSTVQIFADSSYELPYVMDA
AAV1                QRLINNNWGFRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGS
AAV6\VP1            QRLINNNWGFRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGS
A3_3                QRLINNNWGFRPKKLNFKLFNIQVKEVTQNDGTTTIANNLTSAVQVFTDSEYQLPYVLGS
A3_7                QRLINNNWGFRPKKLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGS
A3_4                QRLINNNWGFRPKKLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGS
A3_5                QRLINNNWGFRPKKLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGS
AAV2                QRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGS
AAV3                QRLINNNWGFRPKKLSFKLFNIQVRGVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGS
13.3b\VP1           QRLINNNWGFRPKKLRFKLFNIQVKEVTTNDGVTTIANNLTSTIQVFSDSEYQLPYVLGS
AAV7                QRLINNNWGFRPKKLRFKLFNIQVKEVTTNDGVTTIANNLTSTIQVFSDSEYQLPYVLGS
223_4               QRLINNNWGFRPKKLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGS
223_5               QRLINNNWGFRPKKLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGS
223_10              QRLINNNWGFRPKKLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGS
223_2               QRLINNNWGFRPKKLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGS
223_7               QRLINNNWGFRPKKLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDPEYQLPYVLGS
223_6               QRLINNNWGFRPKKLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGS
44_1                QRLINNNWGFRPKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS
44_5                QRLINNNWGFRPKRPNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS
44_2                QRLINNNWGFRPKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS
29.3\VP1            QRLINNNWGFRPKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS
29.5\VP1            QRLINNNWGFRPKSLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS
42_15               QRLINNNWGFRPKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS
42_8                QRLINNNWGFRPKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS
42_13               QRLINNNWGFRPKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS
42_3A               QRLINNSWGFRPKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS
42_4                QRLINNNWGFRPKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYRLPYVLGS
42_5A               QRLINNNRGFRPRKLRFKLFNIQVKEVTTNDGVTTIANNLTSTIQVFSDSEYQLPYVLGS
42_1B               QRLINNNWGFRPKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS
42_5B               QRLINNNWGFRPKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS
43_1                QRLINNNWGFRPKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVPGS
43_12               QRLINNNWGFRPKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS
43_5                QRLINNNWGFRPKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS
AAV8                QRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS
43_21               QRLINNNWGFRPKRLNFKLFNIQVKEVTTNEGTKTIANNLTSTVRVFTDSEYQLPYVLGS
43_25               QRLINNNWGFRPKRLNFKLFNIQVKEVTTNEGTKTIANNLTSTVQVFTDSEYQLPYVLGS
43_23               QRLINNNWGFRPKRLNFKLFNIQVKEVTTNEGTKTIANNLTSTVQVFTDLEYQLPYVLGS
43_20               QRLINNNWGFRPKRLNFKLFNIQVKEVTTNEGTKTIANNLTSTVQVFTDSEYQLPYVLGS
AAV_9               QRLINNNWGFRPKRLNFKLFNIQVKEVTTNEGTKTIANNLTSTVQVFTDSEYQLPYVLGS
24.1                QRLINNNWGFRPRKLRFKLFNIQVKEVTTNDGVTTIANNLTSTIQVFSDSEYQLPYVLGS
42.2REAL            QRLINNNWGFRPRKLRFKLFNIQVKEVTTNDGVTTIANNLTSTIQVFSDSEYQLPYVLGS
7.2\VP1             QRLINNNWGFRPRKLRFKLFNIQVKEVTTNDGVTTIANNLTSTIQVFSDSEYQLPYVLGS
27.3\VP1            QRLINNNWGFRPRKLRFKLFNIQVKEVTTNDGVTTIANNLTSTIQVFSDSEYQLPYVLGS
16.3\VP1            QRLINNNWGFRPRKLRFKLFNIQVKEVTTNDGVTTIANNLTSTIQVFSDSEYQLPYVLGS
42_10               QRLINNNWGFRPRKLRFKLFNIQVKEVTTNDGVTTIANNLTSTIQVFSDSEYQLPYVLGS
42_3B               QRLINNNWGFRPRKLRFKLFNIQVKEVTTNDGVTTIANNLTSTIQVFSDSEYQLPYVLGS
42_11               QRLINNNWGFRPRKLRFKLFNIQVKEVTTNDGVTTIANNLTSTIQVFSDSEYQLPYVLGS
F1\VP1              QRLINNNWGFRPKKLRFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGS
F5\VP1@3            QRLINNNWGFRPKKLRFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGS
F3\VP1              QRLINNNWGFRPKKLRFKLLNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGS
42_6B               QRLINNNWGFRPRKLRFKLFNIQVKEVTTDDGVTTIANNLTSTIQVFSDSEYQLPYVLGS
42_12               QRLINNNWGFRPKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS
AAV5\CAP            QRLINNYWGFRPRSLRVKIFNIQVKEVTVQDSTTTIANNLTSTVQVFTDDDYQLPYVVGN
```

FIG. 2F

```
                    370         380         390         400         410         420
                    ....|....|....|....|....|....|....|....|....|....|....|....|
C1\VP1              GQEGSLSPFPNDVFMVPQYGYCGIVTG-ENQNQTDRNAFYCLEYFPSQMLRTGNNFEMAY
C2\VP1              GQEGSLPPFPNDVFMVPQYGYCGIVTG-ENQNQTDRNAFYCLEYFPSQMLRTGNNFEMAY
C5\VP1@2            GQEGSLPPFPNDVFMVPQYGYCGIVTG-ENQNQTDRNAFYCLEYFPSQMLRTGNNFETAY
AAV4\VP1            GQEGSLPPFPNDVFMVPQYGYCGLVTGNTSQQQTDRNAFYCLEYFPSQMLRTGNNFEITY
AAV1                AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFTFSY
AAV6\VP1            AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFTFSY
A3_3                AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFTFSY
A3_7                AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFTFSY
A3_4                AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFTFSY
A3_5                AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFTFSY
AAV2                AHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFTFSY
AAV3                AHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFQFSY
13.3b\VP1           AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFEFSY
AAV7                AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFEFSY
223_4               AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFTFSY
223_5               AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFTFSY
223_10              AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFTFSY
223_2               AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFTFSY
223_7               AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFTFSY
223_6               AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFTFSY
44_1                AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY
44_5                AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY
44_2                AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY
29.3\VP1            ARQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY
29.5\VP1            AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY
42_15               AHQGCFPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMRRTGNNFEFSY
42_8                AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY
42_13               AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY
42_3A               AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY
42_4                AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY
42_5A               AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFEFSY
42_1B               AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY
42_5B               AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY
43_1                AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY
43_12               AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY
43_5                AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY
AAV8                AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFQFTY
43_21               AHQGCLPPFPADVFMVPQYGYLTLNNG---SQALGRSSFYCLEYFPSQMLRTGNNFQFSY
43_25               AHQGCLPPFPADVFMVPQYGYLTLNNG---SQALGRSSFYCLEYFPSQMLRTGNNFQFSY
43_23               AHQGCLPPFPADVFMVPQYGYLTLNNG---SQALGRSSFYCLEYFPSQMPRTGNNFQFSY
43_20               AHQGCLPPFPADVFTVPQYGYLTLNNG---SQALGRSSFYCLEYFPSQMLRTGNNFQFSY
AAV_9               AHQGCLPPFPADVFMVPQYGYLTLNNG---SQALGRSSFYCLEYFPSQMLRTGNNFQFSY
24.1                AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFEFSY
42.2REAL            AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFEFSY
7.2\VP1             AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGDNFEFSY
27.3\VP1            AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFCCLEYFPSQMLRTGNNFEFSY
16.3\VP1            AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSMGRSSFYCLEYFPSQMLRTGNNFEFSY
42_10               AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFEFSY
42_3B               AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFEFSY
42_11               AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFEFSY
F1\VP1              AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFEFSY
F5\VP1@3            AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFEFSY
F3\VP1              AHQGCLPPFPADVFMIPQYGYLTLDNG---SQSVGRSSFYCLEYFPSQMLRTGNNFEFSY
42_6B               AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFEFSY
42_12               AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY
AAV5\CAP            GTEGCLPAFPPQVFTLPQYGYATLNRD-NTENPTERSSFFCLEYFPSKMLRTGNNFEFTY
```

FIG. 2G

```
                  430        440        450        460        470        480
                  ....|....|....|....|....|....|....|....|....|....|....|....|
C1\VP1            NFGKVPFHSMYAYSQSPDRLMNPLLDQYLWHLQSTTSGETLNQGNAATTFGKIRSGDFAF
C2\VP1            NFEKVPFHSMYAHSQSLDRLMNPLLDQYLWHLQSTTSGETLNQGNAATTFGKIRSGDFAF
C5\VP1@2          NFEKVPFHSMYAHSQSLDGLMNPLLDQYLWHLQSTTSGETLNQGNAATTFGKIRSGDFAF
AAV4\VP1          SFEKVPFHSMYAHSQSLDRLMNPLIDQYLWGLQSTTTGTTLNAGTATTNFTKLRPTNFSN
AAV1              TFEEVPFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSG-SAQNKDLLFSRGSPAGMSV
AAV6\VP1          TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSG-SAQNKDLLFSRGSPAGMSV
A3_3              TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSKTQ-GTSGTTQQSRLQFSQAGPSSMAQ
A3_7              TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSKTQ-GTSGTTQQSRLQFSQAGPSSMAQ
A3_4              TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSKTQ-GTSGTTQQSRLQFSQAGPSSMAQ
A3_5              TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSKTQ-GTSGTTQQSRLQFNQAGPSSMAQ
AAV2              TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTN-TPSGTTTQSRLQFSQAGASDIRD
AAV3              TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQGTTSGTTNQSRLLFSQAGPQSMSL
13.3b\VP1         SFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQSDPGGTAGNRELQFYQGGPSTMAE
AAV7               SFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQSNPGGTAGNRELQFYQGGPSTMAE
223_4             TFEDVPFHSSYAHSQSLGRLMNPLIDQYLYYLARTQSNAGGTAGNRELQFYQGGPTTMAE
223_5             TFEDVPFHSSYAHSQSLGRLMNPLIDQYLYYLARTQSNAGGTAGNRELQFYQGGPTTMAE
223_10            TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQSNAGGTAGNRELQFYQGGPTTMAE
223_2             TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQSNAGGTAGNRELQFYQGGPTTMAE
223_7             TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQSNAGGTAGNRELQFYQGGPTTMAE
223_6             TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQSNAGGTAGNRELQFYQGGPTTMAE
44_1              QFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTGG-TAGTQQLLFSQAGPNNMSA
44_5              QFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTGG-TAGTQQLLFSQAGPNNMSA
44_2              QFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTGG-TAGTQQLLFSQAGPNNMSA
29.3\VP1          QFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTGG-TAGTQQLLFSQAGPNNMSA
29.5\VP1          QFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTGG-TAGTQQLLFSQAGPNNMSA
42_15             QFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTGG-TAGTQQLLFSQAGPNNMSA
42_8              QFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTGG-TAGTQQLLFSQAGPNNMSA
42_13             QFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTGG-TAGTQQLLFSQAGPNNMSA
42_3A             QFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTGG-TAGTQQLLFSQAGPNNMSA
42_4              QFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTGG-TAGTQQLLFSQAGPNNMSA
42_5A             QFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTGG-TAGTQQLLFSQAGPNNMSA
42_1B             QFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTGG-TAGTQQLLFSQAGPNNMSA
42_5B             QFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTGG-TAGTQQLLFSQAGPNNMSA
43_1              TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTGG-TQGTQQLLFSQAGPANMSA
43_12             TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTGG-TQGTQQLLFSQAGPANMSA
43_5              TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTGG-TQGTQQLLFSQAGPANMSA
AAV8              TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQTTGG-TANTQTLGFSQGGPNTMAN
43_21             TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLVRTQTTG--TGGTQTLAFSQAGPSSMAN
43_25             TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLVRTQTTG--TGGTQTLAFSQAGPSSMAN
43_23             TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLVRTQTTG--TGGTQTLAFSQAGPSSMAN
43_20             TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLVRTQTTG--TGGTQTLAFSQAGPSSMAN
AAV_9             TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLVRTQTTG--TGGTQTLAFSQAGPSSMAN
24.1               TFEEVPFHSSYVHSQSLDRLMNPLIDQYLYYLARTQST---TGSTRELQFHQAGPNTMAE
42.2REAL          TFEEVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQST---TGSTRELQFHQAGPNTMAE
7.2\VP1           TFEEVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQST---TGSTRELQFHQAGPNTMAE
27.3\VP1          TFEEVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQST---TGSTRELQFHQAGPNTVAE
16.3\VP1          TFEEVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQST---TGSTRELQFHQAGPNTMAE
42_10             TFEEVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQST---TGSTRELQFHQAGPNTMAE
42_3B             TFEEVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQST---TGSTRELQFHQAGPNTMAE
42_11             TFEEVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQST---TGSTRELQFHQAGPNTMAE
F1\VP1            SFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQST---TGSTRELQFHQAGPNTMAE
F5\VP1@3          SFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQST---TGSTRELQFHQAGPNTMAE
F3\VP1            SFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQST---TGSTRELQFHQAGPNTMAE
42_6B             TFEEVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQST---TGSTRELQFHQAGPNTMAE
42_12             QFEDVPFHSSYAHSQSLDRLTNPLIDQYLYYLARTQST---TGSTRGLQFHQAGPNTMAE
AAV5\CAP          NFEEVPFHSSFAPSQNLFKLANPLVDQYLYRFVSTNNTGG-------VQFNKNLAGRYAN
```

FIG. 2H

```
                    490         500         510         520         530         540
                    ....|....|....|....|....|....|....|....|....|....|....|....|
C1\VP1              YRKNWLPGPCVKQQRLSKTASQNYKIPASGGNALLKYDTHYTLNNRWSNIAPGPPMATAG
C2\VP1              YRKNWLPGPCVKQQRFSKTASQNYKIPASGGNALLKYDTHYTLNNRWSNIAPGPPMATAG
C5\VP1@2            YRKNWLPGPCVKQQRFSKTASQNYKIPASGGNALLKYDTHYTLNNRWSNIAPGPPMATAG
AAV4\VP1            FKKNWLPGPSIKQQGFSKTANQNYKIPATGSDSLIKYETHSTLDGRWSALTPGPPMATAG
AAV1                QPKNWLPGPCYRQQRVSKTKTDN-----NNSNFTWTGASKYNLNGRESIINPGTAMASHK
AAV6\VP1            QPKNWLPGPCYRQQRVSKTKTDN-----NNSNFTWTGASKYNLNGRESIINPGTAMASHK
A3_3                QAKNWLPGPSYRQQRMSKTANDN-----NNSEFAWTAATKYYLNGRNSLVNPGPPVASHK
A3_7                QAKNWLPGPSYRQQRMSKTANDN-----NNSEFAWTAATKYYLNGRNSLVNPGPPMASHK
A3_4                QAKNWLPGPSYRQQRMSKTANDN-----NNSEFAWTAATKYYLNGRNSLVNPGPPMASHK
A3_5                QAKNWLPGPSYRQQRMSKTANDN-----NNSEFAWTAATKYYPNGRNSLVNPGPPMASHK
AAV2                QSRNWLPGPCYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDSLVNPGPAMASHK
AAV3                QARNWLPGPCYRQQRLSKTANDN-----NNSNFPWTAASKYHLNGRDSLVNPGPAMASHK
13.3b\VP1           QAKNWLPGPCFRQQRVSKTLDQN-----NNSNFAWTGATKYHLNGRNSLVNPGVAMATHK
AAV7                QAKNWLPGPCFRQQRVSKTLDQN-----NNSNFAWTGATKYHLNGRNSLVNPGVAMATHK
223_4               QAKNWLPGPCFRQQRVSKTLDQN-----NNSNFAWTGATKYHLNGRNSLVNPGVAMATHK
223_5               QAKNWLPGPCFRQQRVSKTLDQN-----NNSNFAWTGATKYHLNGRNSLVNPGVAMATHK
223_10              QAKNWLPGPCFRQQRVSKTLDQN-----NNSNFAWTGATKYHLNXRNSLVNPGVAMATHK
223_2               QAKNWLPGPCFRQQRVSKTLDQN-----NNSNFAWTGATKYHLNGRNSLVNPGVAMATHK
223_7               QAKNWLPGPCFRQQRVSKTLDQN-----NNSNFAWTGATKYHLNGRNSLVNPGVAMATHK
223_6               QAKNWLPGPCFRQQRVSKTLDQN-----NNSNFAWTGATKYHLNGRNSLVNPGVAMATHK
44_1                QAKNWLPGPCYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVNPGVAMATHK
44_5                QAKNWLPGPCYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVNPGVAMATHK
44_2                QAKNWLPGPCYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVNPGVAMATHK
29.3\VP1            QAKNWLPGPCYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVNPGVAMATHK
29.5\VP1            QAKNWLPGPCYRQQRVSTTLSQN-----DNSNFAWTGATKYHLNGRDSLVNPGVAMATHK
42_15               QAKNWLPGPCYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVNPGVAMATHK
42_8                QAKNWLPGPCYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVNPGVAMATHK
42_13               QAKNWLPGPCYRQQRVSTTVSQN-----NNSNFAWTGATKYHLNGRDSLVNPGVAMATHK
42_3A               QAKNWLPGPCYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVNPGVAMATHK
42_4                QAKNWLPGPCYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVNPGVAMATHK
42_5A               QAKNWLPGPCYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVNPGVAMATHK
42_1B               QAKNWLPGPCYRQQRVSTTVSQN-----NNSNFAWTGATKYHLNGRDSLVNPGVAMATHK
42_5B               QAKNWLPGPCYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVNPGVAMATHK
43_1                QAKNWLPGPCYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVNPGVAMATHK
43_12               QAKNWLPGPCYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVNPGVAMATHK
43_5                QAKNWLPGPCYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVNPGVAMATHK
AAV8                QAKNWLPGPCYRQQRVSTTTGQN-----NNSNFAWTAGTKYHLNGRNSLANPGIAMATHK
43_21               QARNWVPGPCYRQQRVSTTTNQS-----NNSNFAWTGAAKFKLNGRDSLMNPGVAMASHK
43_25               QARNWVPGPCYRQQRVSTTTNQN-----NNSNFAWTGAAKFKLNGRDSLMNPGVAMASHK
43_23               QARNWVPGPCYRQQRVSTTTNQN-----NNSNFAWTGAAKFKLNGRDSLMNPGVAMASHK
43_20               QARNWVPGPCYRQQRVSTTTNQN-----NNSNFAWTGAAKFKLNGRDSLMNPGVAMASHK
AAV_9               QARNWVPGPCYRQQRVSTTTNQN-----NNSNFAWTGAAKFKLNGRDSLMNPGVAMASHK
24.1                QSKNWLPGPCYRQQRLSKNIDSN-----NNSNFAWTGATKYHLNGRNSLTNPGVAMATNK
42.2REAL            QSKNWLPGPCYRQQRLSKNIDSN-----NNSNFAWTGATKYHLNGRNSLTNPGVAMATNK
7.2\VP1             QSKNWLPGPCYRQQRLSKNIDSN-----NNSNFAWTGATKYHLNGRNSLTNPGVAMATNK
27.3\VP1            QSKNWLPGPCYRQQRLSKNIDSN-----NNSNFAWTGATKYHLNGRNSLTNPGVAMATNK
16.3\VP1            QSKNWLPGPCYRQQRLSKNIDSN-----NNSNFAWTGATKYHLNGRNSLTNPGVAMATNK
42_10               QSKNWLPGPCYRQQRLSKNIDSN-----NNSNFAWTGATKYHLNGRNSLTNPGVAMATNK
42_3B               QSKNWLPGPCYRQQRLSKNIDSN-----NTSNFAWTGATKYHLNGRNSLTNPGVAMATNK
42_11               QSKNWLPGPCYRRQRLSKDIDSN-----NNSNFAWTGATKYHLNGRNSLTNPGVAMATNK
F1\VP1              QSKNWLPGPCYRQQQLSKNLDFN-----NNSNFAWTAATKYHLNGRNSLTNPGIPMATNK
F5\VP1@3            QSKNWLPGPCYRQQRLSKNLDFN-----NNSNFAWTAATKYHLNGRNSLTNPGIPMATNK
F3\VP1              QSKNWLPGPCYRQQRLSKNLDFN-----NNSNFAWTAATKYHLNGRNSLTNPGIPMATNK
42_6B               QSKNWLPGPCYRQQRLSKNIDSN-----NNSNFAWTGATKYHLNGRNSLTNPGVAMATNK
42_12               QSKNWLPGPCYRQQRLSKNIDSN-----NNSNFAWTGATKYHLNGRNSLTNPGVAMATNK
AAV5\CAP            TYKNWFPGPMGRTQGWNLGSGVN-----RASVSAFATTNRMELEGASYQVPPQPNGMTNN
```

FIG. 2I

```
                  550         560         570         580         590         600
                  ....|....|....|....|....|....|....|....|....|....|....|....|
C1\VP1            PSDGDFS-NAQLIFPGPS--VTGNTTTSAN-NLLFTSEEEIAATNPRDTDMFGQIADNNQ
C2\VP1            PSDGDFS-NAQLIFPGPS--VTGNTTTSAN-NLLFTSEGEIAATNPRDTDMFGQIADNNQ
C5\VP1@2          PSDGDFS-NAQLIFPGPS--VTGNTTTSAN-NLLFTSEEEIAATNPRDTDMFGQIADNNQ
AAV4\VP1          PADSKFS-NSQLIFAGPK--QNGNTATVPG-TLIFTSEEELAATNATDTDMWGNLPGGDQ
AAV1              DDEDKFFPMSGVMIFGKE--SAGASNTALD-NVMITDEEEIKATNPVATERFGTVAVNFQ
AAV6\VP1          DDKDKFFPMSGVMIFGKE--SAGASNTALD-NVMITDEEEIKATNPVATERFGTVAVNLQ
A3_3              DDEEKYFPMHGNLIFGKQ--GTGTTNVDIE-SVLITDEEEIRTTNPVATEQYGQVATNHQ
A3_7              DDEEKYFPMHGNLIFGKQ--GTGTTNVDIE-SVLITDEEEIRTTNPVATEQYGQVATNHQ
A3_4              DDEEKYFPMHGNLIFGKQ--GTGTTNVDIE-SVLITDEEEIRTTNPVATEQYGQVATNHQ
A3_5              DDEEKYFPMHGNLIFGKQ--GTGTTNVDIE-SVLITDEEEIRTTNPVATEQYGQVATNRQ
AAV2              DDEEKFFPQSGVLIFGKQ--GSEKTNVDIE-KVMITDEEEIRTTNPVATEQYGSVSTNLQ
AAV3              DDEEKFFPMHGNLIFGKE--GTTASNAELD-NVMITDEEEIRTTNPVATEQYGTVANNLQ
13.3b\VP1         DDEDRFFPSSGVLIFGKT--GATN-KTTLE-NVLMTNEEEIRPTNPVATEEYGIVSSNLQ
AAV7              DDEDRFFPSSGVLIFGKT--GATN-KTTLE-NVLMTNEEEIRPTNPVATEEYGIVSSNLQ
223_4             DDEERFFPSSGVLIFGKT--GAAN-KTTLE-NVLMTNEEEIRPTNPVATEEYGIVSSNLQ
223_5             DDEERFFPSSGVLIFGKT--GAAN-KTTLE-NVLMTNEEEIRPTNPVATEEYGIVSSNLQ
223_10            DDEERFFPSSGVLIFGKT--GAAN-KTTLE-NVLMTNEEEIRPTNPVATEEYGIVSSNLQ
223_2             DDEERFSPSSGVLIFGKT--GAAN-KTTLE-NVLMTNEEEIRPTNPVATEEYGIVSSNLQ
223_7             DDEERFFPSSGVLIFGKT--GAAN-KTTLE-NVLMTNEEEIRPTNPVATEEYGIVSSNLQ
223_6             DDEERFFPSSGVLIFGKT--GAAN-KTTLE-NVLMTNEEEIRPTNPVATEEYGIVSSNLQ
44_1              DDEERFFPSSGVLMFGKQ--GAGKDNVDYS-SVMLTSEEEIKTTNPVATEQYGVVADNLQ
44_5              DDEERFFPSSGVLMFGKQ--GAGKDNVDYS-SVMLTSEEEIKTTNPVATEQYGVVADNLQ
44_2              DDEERFFPSSGVLMFGKQ--GAGKDNVDYS-SVMLTSEEEIKTTNPVATEQYGVVADNLQ
29.3\VP1          DDEERFFPSSGVLMFGKQ--GAGKGNVDYS-SVMLTSEEEIKTTNPVATEQYGVVADNLQ
29.5\VP1          DDEERFFPSSGVLMFGKQ--GAGKDNVDYS-SVMLTSEEEIKTTNPVATEQYGVVADNLQ
42_15             DDEERFFPSSGVLMFGKQ--GAGKDNVDYS-SVMLTSEEEIKTTNPVATEQYGVVADNLQ
42_8              DDEERFFPSSGVLMFGKQ--GAGKDNVDYS-SVMLTSEEEIKTTNPVATEQYGVVADNLQ
42_13             GDEERFFPSSGVLMFGKQ--GAGKDNVDYS-SVMLTSEEEIKTTNPVATEQYGVVADNLQ
42_3A             DDEERFFPSSGVLMFGKQ--GAGKDNVDYS-SVMLTSEEEIKTTNPVATEQYGVVADNLQ
42_4              DDEERFFPSSGVLMFGKQ--GAGKDNVDYS-SVMLTSEEEIKTTNPVATEQYGVVADNLQ
42_5A             DDEERFFPSSGVLMFGKQ--GAGKDNVDYS-SVMLTSEEEIKTTNPVATEQYGVVADNLQ
42_1B             GDEERFFPSSGVLMFGKQ--GAGKDNVDYS-SVMLTSEEEIKTTNPVATEQYGVVADNLQ
42_5B             DDEERFFPSSGVLMFGKQ--GAGKDNVDYS-SVMLTSEEEIKTTNPVATEQYGVVADNLQ
43_1              DDEERFFPSSGVLMFGKQ--GAGKDNVDYS-SVMLTSEEEIKTTNPVATEQYGVVADNLQ
43_12             DDEERFFPSSGVLMFGKQ--GAGKDNVDYS-SVMLTSEEEIKTTNPVATEQYGVVADNLQ
43_5              DDEERFFPSSGVLMFGKQ--GAGKDNVDYS-SVMLTSEEEIKTTNPVATEQYGVVADNLQ
AAV8              DDEERFFPSNGILIFGKQ--NAARDNADYS-DVMLTSEEEIKTTNPVATEEYGIVADNLQ
43_21             DDDDRFFPSSGVLIFGKQ--GAGNDGVDYS-QVLITDEEEIKATNPVATEEYGAVAINNQ
43_25             DDDDRFFPSSGVLIFGKQ--GAGNDGVDYS-QVLITDEEEIKATNPVATEEYGAVAINNQ
43_23             DDDDRFFPSSGVLIFGKQ--GAGNDGVDYS-QVLITDEEEIKATNPVATEEYGAVAINNQ
43_20             DDDDRFFPSSGVLIFGKQ--GAGNDGVDYS-QVLITDEEEIKATNPVATEEYGAVAINNQ
AAV_9             DDEDRFFPSSGVLIFGKQ--GAGNDGVDYS-QVLITDEEEIKATNPVATEEYGAVAINNQ
24.1              DDEDQFFPINGVLVFGKT--GAAN-KTTLE-NVLMTSEEEIKTTNPVATEEYGVVSSNLQ
42.2REAL          DDEDQFFPINGVLVFGET--GAAN-KTTLE-NVLMTSEEEIKTTNPVATEEYGVVSSNLQ
7.2\VP1           DDEDQFFPINGVLVFGKT--GAAN-KTTLE-NVLMTSEEEIKTTNPVATEEYGVVSSNLQ
27.3\VP1          DDEDQFLPINGVLVFGKT--GAAN-KTTLE-NVLMTSEEEIKTTNPVATEEYGVVSSNLQ
16.3\VP1          DDEGQFFPINGVLVFGKT--GAAN-KTTLE-NVLMTSEEEIKTTNPVATEEYGVVSSNLQ
42_10             DDEDQFFPINGVLVFGKT--GAAN-KTTLE-NVLMTSEEEIKTTNPVATEEYGVVSSNLQ
42_3B             DDEDQFFPINGVLVFGKT--GAAN-KTTLE-NVLMTSEEEIKTTNPVATEQYGVVSSNLQ
42_11             DDEDQFFPINGVLVFGKT--GAAN-KTTLE-NVLMTSEEEIKTTNPVATEEYGVVSSNLQ
F1\VP1            DDEDQFFPINGVLVFGKT--GAAN-KTTLE-NVLMTSEEEIKTTNPVATEEYGVVSSNLQ
F5\VP1@3          DDEDQFFPINGVLVFGKT--GAAN-KTTLE-NVLMTSEEEIKTTNPVATEEYGVVSSNLQ
F3\VP1            DDEDQFFPINGVLVFGKT--GAAN-KTTLE-NVLMTSEEEIKTTNPVATEEYGVVSSNLQ
42_6B             DDEDQFFPINGVLVFGKT--GAAN-KTTLE-NVLMTSEEEIKTTNPVATEEYGVVSSNLQ
42_12             DDEDQFFPINGVLVFGKT--GAAN-KTTLE-NVLMTSEEEIKTTNPVATEEYGVVSSNLQ
AAV5\CAP          LQGSNTYALENTMIFNSQPANPGTTATYLEGNMLITSESETQPVNRVAYNVGGQMATNNQ
```

FIG. 2J

```
                    610         620         630         640         650         660
                    ....|....|....|....|....|....|....|....|....|....|....|....|
C1\VP1              NATTAPITGNVTAMGVLPGMVWQNRDIYYQGPIWAKIPHADGHFHPSPLIGGFGLKHPPP
C2\VP1              NATTAPITGNVTAMGVLPGMVWQNRDIYYQGPIWAKIPHADGHFHPSPLIGGFGLKHPPP
C5\VP1@2            NATTAPITGNVTAMGVLPGMVWQNRDIYYQGPIWAKIPHADGHFHPSPLIGGFGLKHPPP
AAV4\VP1            SNSNLPTVDRLTALGAVPGMVWQNRDIYYQGPIWAKIPHTDGHFHPSPLIGGFGLKHPPP
AAV1                SSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKNPPP
AAV6\VP1            SSSTDPATGDVHVMGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPP
A3_3                SQNTTASYGSVDSQGILPGMVWQDRDVYLQGPIWAKTPHTDGHFHPSPLMGGFGLKHPPP
A3_7                SQNTTASYGSVDSQGILPGMVWQDRDVYLQGPIWAKTPHTDGHFHPSPLMGGFGLKHPPP
A3_4                SQDTTASYGSVDSQGILPGMVWQDRDVYLQGPIWAKTPHTDGHFHPSPLMGGFGLKHPPP
A3_5                SQNTTASYGSVDSQGILPGMVWQDRDVYLQGPIWAKTPHTDGHFHPSPLMGGFGLKHPPP
AAV2                RGNRQAATADVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPP
AAV3                SSNTAPTTGTVNHQGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPP
13.3b\VP1           AANTAAQTQVVNNQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
AAV7                AANTAAQTQVVNNQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
223_4               AASTAAQTQVVNNQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
223_5               AASTAAQTQVVNNQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
223_10              AASTAAQTQVVNNQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
223_2               AASTAAQTQVVNNQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
223_7               AASTAAQTQVVNNQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
223_6               AASTAAQTQVVNNQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
44_1                QQNAAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
44_5                QQNAAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
44_2                QQNAAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
29.3\VP1            QQNAAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
29.5\VP1            QQNAAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
42_15               QQNAAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
42_8                QQNAAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
42_13               QQNAAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
42_3A               QQNAAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
42_4                QQNAAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
42_5A               QQNAAPIVGAVNSQGALPGMAWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
42_1B               QQNAAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
42_5B               QQNAAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
43_1                QTNGAPIVGTVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
43_12               QTNGAPIVGTVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
43_5                QTNGAPIVGTVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
AAV8                QQNTAPQIGTVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
43_21               AANTQAQTGLVHNQGVIPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
43_25               AANTQAQTGLVHNQGVIPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
43_23               AANTQAQTGLVHNQGVIPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
43_20               AANTQAQTGLVHNQGVIPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
AAV_9               AANTQAQTGLVHNQGVIPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
24.1                SSTAGPQTQTVNSQGALPGMVWQNRDVCLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
42.2REAL            SSTAGPQTQTVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
7.2\VP1             SSTAGPQTQTVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
27.3\VP1            SSTAGPRTQTVNSQGALPGMVWQNRDVYLQGPIWAEIPHTDGNFHPSPLMGGFGLKHPPP
16.3\VP1            SSTAGPQTQTVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
42_10               SSTAGPQTQTVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
42_3B               SSTAGPQTQTVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
42_11               SSTAGPQTQTVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
F1\VP1              PSTAGPQSQTINSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
F5\VP1@3            SSTAGPQSQTINSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLEHPPP
F3\VP1              SSTAGPQSQTINSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
42_6B               SSTAGPQTQTVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMDGFGLKHPPP
42_12               SSTAGPQTQTVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP
AAV5\CAP            SSTTAPATGTYNLQEIVPGSVWMERDVYLQGPIWAKIPETGAHFHPSPAMGGFGLKHPPP
```

FIG. 2K

```
                    670         680         690         700         710         720
                    ....|....|....|....|....|....|....|....|....|....|....|....|
C1\VP1              QIFIKNTPVPANPATTFTAARVDSFITQYSTGQVAVQIEWEIEKERSKRWNPEVQFTSNY
C2\VP1              QIFIKNTPVPANPATTFTAARVDSFITQYSTGQVAVQIEWEIEKERSKRRNPEVQFTSNY
C5\VP1@2            QIFIKNTPVPAYPATTFTAARVDSFITQYSTGQVAVQIEWEIEKERSKRWNPEVQFTSNC
AAV4\VP1            QIFIKNTPVPANPATTFSSTPVNSFITQYSTGQVSVQIDWEIQKERSKRWNPEVQFTSNY
AAV1                QILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNY
AAV6\VP1            QILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNY
A3_3                QILIKNTPVPANPATTFTPGKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
A3_7                QILIKNTPVPANPATTFTPGKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
A3_4                QILIKNTPVPANPATTFTPGKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
A3_5                QILIKNTPVPANPATTFTPGKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
AAV2                QILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
AAV3                QIMIKNTPVPANPPTTFSPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
13.3b\VP1           QILIKNTPVPANPPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWDPEIQYTSNF
AAV7                QILIKNTPVPANPPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNF
223_4               QILIKNTPVPANPPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNF
223_5               QILIKNTPVPANPPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNF
223_10              QILIKNTPVPANPPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNF
223_2               QILIKNTPVPANPPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNF
223_7               QILIKNTPVPANPPEVFTPAKIASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNF
223_6               QILIKNTPVPANPPEVFTPAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNF
44_1                QILIKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
44_5                QILIKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
44_2                QILIKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
29.3\VP1            QILIKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
29.5\VP1            QILIKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
42_15               QILIKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
42_8                QILIKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
42_13               QILIKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
42_3A               QILIKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
42_4                QILIKNTPVPADPPTTFSQAKPASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
42_5A               QILIKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
42_1B               QILIKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
42_5B               QILIKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
43_1                QILVKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
43_12               QILVKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
43_5                QILVKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
AAV8                QILIKNTPVPADPPTTFNQSKLNSFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
43_21               QILIKNTPVPADPPLTFNQAKLNSFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
43_25               QILIKNTPVPADPPLTFNQAKLNSFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
43_23               QILIKNTPVPADPPLTFNQAKLNSFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
43_20               QILIKNTPVPADPPLTFNQAKLNSFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
AAV_9               QILIKNTPVPADPPLTFNQAKLNSFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
24.1                QILIKNTPVPANPPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
42.2REAL            QILIKNTPVPANPPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
7.2\VP1             QILIKNTPVPANPPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
27.3\VP1            QILIKNTPVPANPPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
16.3\VP1            QILIKNTPVPANPPGVFTPALFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
42_10               QILIKNTPVPANPPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
42_3B               QILIKNTPVPANPPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
42_11               QILIKNTPVPANPPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
F1\VP1              QILIKNTPVPANPPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
F5\VP1@3            QILIKNTPVPANPPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
F3\VP1              QILIKNTPVPANPPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
42_6B               QILIKNTPVPANPPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY
42_12               QILIK----------------------------------------------------YTSNY
AAV5\CAP            MMLIKNTPVPGN-ITSFSDVPVSSFITQYSTGQVTVEMEWELKKENSKRWNPEIQYTNNY
```

FIG. 2L

```
                    730         740         750
            ....|....|....|....|....|....|.
C1\VP1      GNQSSMLWAPDTTGKYTEPRVIGSRYLTNHL
C2\VP1      GNQSSMLWAPDTTGKYTEPRVIGSRYLTNHL
C5\VP1@2    GNQSSMLWAPDTTGKYTEPRVIGSRYLTNHL
AAV4\VP1    GQQNSLLWAPDAAGKYTEPRAIGTRYLTHHL
AAV1        AKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
AAV6\VP1    AKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
A3_3        NKSVNVEFTVDANGVYSEPRPIGTRYLTRNL
A3_7        NKSVNVEFTVDANGVYSEPRPIGTRYLTRNL
A3_4        NKSVNVEFTVDANGVYSEPRPIGTRYLTRNL
A3_5        NKSVNVEFTVDANGVYSEPRPIGTRYLTRNL
AAV2        NKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL
AAV3        NKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL
13.3b\VP1   EKQTGVDFAVDSQGVYSEPRPIGTRYLTRNL
AAV7        EKQTGVDFAVDSQGVYSEPRPIGTRYLTRNL
223_4       DKQTGVDFAVDSQGVYSEP------------
223_5       DKQTGVDFAVDSQGVYSEP------------
223_10      DKQTGVDFAVDSQGVYSEP------------
223_2       DKQTGVDFAVDSQGVYSEP------------
223_7       DKQTGVDFAVDSQGVYSEP------------
223_6       DKQTGVDFAVDSQGVYSEP------------
44_1        YKSTNVDFAVNTDGTYSEPRPIGTRYLTRNL
44_5        YKSTNVDFAVNTDGTYSEPRPIGTRYLTRNL
44_2        YKSTNVDFAVNTDGTYSEPRPIGTRYLTRNL
29.3\VP1    YKSTNVDFAVNTDGTYSEPRPIGTRYLTRNL
29.5\VP1    YKSTNVDFAVNTDGTYSEPRPIGTRYLTRNL
42_15       YKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL
42_8        YKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL
42_13       YKSTNVDFAVNTEGTYSEPRPIGTRYLTRSL
42_3A       YKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL
42_4        YKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL
42_5A       YKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL
42_1B       YKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL
42_5B       YKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL
43_1        YKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL
43_12       YKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL
43_5        YKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL
AAV8        YKSTSVDFAVNTEGVYSEPRPIGTRYLTRNL
43_21       YKSTNVDFAVNTEGVYSEPRPIGTRYLTRNL
43_25       YKSTNVDFAVNTEGVYSEPRPIGTRYLTRNL
43_23       YKSTNVDFAVNTEGVYSEPRPIGTRYLTRNL
43_20       YKSTNVDFAVNTEGVYSEPRPIGTRYLTRNL
AAV_9       YKSTNVDFAVNTEGVYSEPRPIGTRYLTRNL
24.1        AKSNNVEFAVNNEGVYTEPRPIGTRYLTRNL
42.2REAL    AKSNNVEFAVNNEGVYTEPRPIGTRYLTRNL
7.2\VP1     AKSNNVEFAVNNEGVYTEPRPIGTRYLTRNL
27.3\VP1    AKSNNVEFAVNNEGVYTEPRPIGTRYLTRNL
16.3\VP1    AKSNNVEFAVNNEGVYTEPRPIGTRYLTRNL
42_10       AKSNNVEFAVNNEGVYTEPRPIGTRYLTRNL
42_3B       AKSNNVEFAVNNEGVYTEPRPIGTRYLTRNL
42_11       AKSNNVEFAVNNEGVYTEPRPIGTRYLTRNL
F1\VP1      AKSNNVEFAVNPDGVYTEPRPIGTRYLPRNL
F5\VP1@3    AKSNNVEFAVNPDGVYTEPRPIGTRYLTRNL
F3\VP1      AKSNNVEFAVNPDGVYTEPRPIGTRYLTRNL
42_6B       AKSNNVEFAVNNEGVYTEPRPIGTRYLTRNL
42_12       YKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL
AAV5\CAP    NDPQFVDFAPDSTGEYRTTRPIGTRYLTRPL
```

FIG. 2M

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
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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
```

METHOD OF DETECTING AND/OR IDENTIFYING ADENO-ASSOCIATED VIRUS (AAV) SEQUENCES AND ISOLATING NOVEL SEQUENCES IDENTIFIED THEREBY

CROSS-REFERENCE TO RELATED APPLICATIONS

This is a divisional of U.S. patent application Ser. No. 13/633,971, filed Oct. 3, 2012, which is a divisional of U.S. patent application Ser. No. 12/962,793, filed Dec. 8, 2010, now U.S. Pat. No. 8,524,446, issued Sep. 3, 2013, which is a continuation of U.S. patent application Ser. No. 10/291,583, filed Nov. 12, 2002, now abandoned, which claims the benefit under 35 USC 119(e) of U.S. Provisional Patent Application No. 60/386,675, filed Jun. 5, 2002, U.S. Provisional Patent Application No. 60/377,066, filed May 1, 2002, U.S. Provisional Patent Application No. 60/341,117, filed Dec. 17, 2001, and U.S. Provisional Patent Application No. 60/350,607, filed Nov. 13, 2001. These applications are incorporated by reference herein.

BACKGROUND OF THE INVENTION

Adeno-associated virus (AAV), a member of the Parvovirus family, is a small nonenveloped, icosahedral virus with single-stranded linear DNA genomes of 4.7 kilobases (kb) to 6 kb. AAV is assigned to the genus, Dependovirus, because the virus was discovered as a contaminant in purified adenovirus stocks. AAV's life cycle includes a latent phase at which AAV genomes, after infection, are site specifically integrated into host chromosomes and an infectious phase in which, following either adenovirus or herpes simplex virus infection, the integrated genomes are subsequently rescued, replicated, and packaged into infectious viruses. The properties of non-pathogenicity, broad host range of infectivity, including non-dividing cells, and potential site-specific chromosomal integration make AAV an attractive tool for gene transfer.

Recent studies suggest that AAV vectors may be the preferred vehicle for gene therapy. To date, there have been 6 different serotypes of AAVs isolated from human or non-human primates (NHP) and well characterized. Among them, human serotype 2 is the first AAV that was developed as a gene transfer vector; it has been widely used for efficient gene transfer experiments in different target tissues and animal models. Clinical trials of the experimental application of AAV2 based vectors to some human disease models are in progress, and include such diseases as cystic fibrosis and hemophilia B.

What are desirable are AAV-based constructs for gene delivery.

SUMMARY OF THE INVENTION

In one aspect, the invention provides a novel method of detecting and identifying AAV sequences from cellular DNAs of various human and non-human primate (NHP) tissues using bioinformatics analysis, PCR based gene amplification and cloning technology, based on the nature of latency and integration of AAVs in the absence of helper virus co-infection.

In another aspect, the invention provides method of isolating novel AAV sequences detected using the above described method of the invention. The invention further comprises methods of generating vectors based upon these novel AAV serotypes, for serology and gene transfer studies solely based on availability of capsid gene sequences and structure of rep/cap gene junctions.

In still another aspect, the invention provides a novel method for performing studies of serology, epidemiology, biodistribution and mode of transmission, using reagents according to the invention, which include generic sets of primers/probes and quantitative real time PCR.

In yet another aspect, the invention provides a method of isolating complete and infectious genomes of novel AAV serotypes from cellular DNA of different origins using RACE and other molecular techniques.

In a further aspect, the invention provides a method of rescuing novel serotypes of AAV genomes from human and NHP cell lines using adenovirus helpers of different origins.

In still a further aspect, the invention provides novel AAV serotypes, vectors containing same, and methods of using same.

These and other aspects of the invention will be readily apparent from the following detailed description of the invention.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGS. **1**A through **1**AAAR provide an alignment of the nucleic acid sequences encoding at least the cap proteins for the AAV serotypes. The full-length sequences including the ITRs, the rep region, and the capsid region are provided for novel AAV serotype 7 [SEQ ID NO: 1], and for previously published AAV1 [SEQ IN NO:6], AAV2 [SEQ ID NO:7]; and AAV3 [SEQ ID NO:8]. Novel AAV serotypes AAV8 [SEQ ID NO:4] and AAV9 [SEQ ID NO:5] are the subject of co-filed applications. The other novel clones of the invention provided in this alignment include: 42-2 [SEQ ID NO:9], 42-8 [SEQ ID NO:27], 42-15 [SEQ ID NO:28], 42-5b [SEQ ID NO: 29], 42-1b [SEQ ID NO:30]; 42-13 [SEQ ID NO: 31], 42-3a [SEQ ID NO: 32], 42-4 [SEQ ID NO:33], 42-5a [SEQ ID NO: 34], 42-10 [SEQ ID NO:35], 42-3b [SEQ ID NO: 36], 42-11 [SEQ ID NO: 37], 42-6b [SEQ ID NO:38], 43-1 [SEQ ID NO: 39], 43-5 [SEQ ID NO: 40], 43-12 [SEQ ID NO:41], 43-20 [SEQ ID NO:42], 43-21 [SEQ ID NO: 43], 43-23 [SEQ ID NO:44], 43-25 [SEQ ID NO: 45], 44.1 [SEQ ID NO:47], 44.5 [SEQ ID NO:47], 223.10 [SEQ ID NO:48], 223.2 [SEQ ID NO:49], 223.4 [SEQ ID NO:50], 223.5 [SEQ ID NO: 51], 223.6 [SEQ ID NO: 52], 223.7 [SEQ ID NO: 53], A3.4 [SEQ ID NO: 54], A3.5 [SEQ ID NO:55], A3.7 [SEQ ID NO: 56], A3.3 [SEQ ID NO:57], 42.12 [SEQ ID NO: 58], 44.2 [SEQ ID NO: 59]. The nucleotide sequences of the signature regions of AAV10 [SEQ ID NO: 117], AAV11 [SEQ ID NO: 118] and AAV12 [SEQ ID NO: 119] are provided in this figure. Critical landmarks in the structures of AAV genomes are shown. Gaps are demonstrated by dots. The 3' ITR of AAV1 [SEQ ID NO:6] is shown in the same configuration as in the published sequences. TRS represents terminal resolution site. Notice that AAV7 is the only AAV reported that uses GTG as the initiation codon for VP3.

FIGS. **2**A through **2**M are an alignment of the amino acid sequences of the proteins of the vp1 capsid proteins of previously published AAV serotypes 1 [SEQ ID NO:64], AAV2 [SEQ ID NO:70], AAV3 [SEQ ID NO: 71], AAV4 [SEQ ID NO:63], AAV5 [SEQ ID NO: 114], and AAV6 [SEQ ID NO:65] and novel AAV sequences of the invention, including: C1 [SEQ ID NO:60], C2 [SEQ ID NO:61], C5 [SEQ ID NO:62], A3-3 [SEQ ID NO:66], A3-7 [SEQ ID NO:67], A3-4 [SEQ ID NO:68], A3-5 [SEQ ID NO: 69], 3.3b [SEQ ID NO: 62], 223.4 [SEQ ID NO: 73], 223-5 [SEQ

ID NO:74], 223-10 [SEQ ID NO:75], 223-2 [SEQ ID NO:76], 223-7 [SEQ ID NO: 77], 223-6 [SEQ ID NO: 78], 44-1 [SEQ ID NO: 79], 44-5 [SEQ ID NO:80], 44-2 [SEQ ID NO:81], 42-15 [SEQ ID NO: 84], 42-8 [SEQ ID NO: 85], 42-13 [SEQ ID NO:86], 42-3A [SEQ ID NO:87], 42-4 [SEQ ID NO:88], 42-5A [SEQ ID NO:89], 42-1B [SEQ ID NO:90], 42-5B [SEQ ID NO:91], 43-1 [SEQ ID NO: 92], 43-12 [SEQ ID NO: 93], 43-5 [SEQ ID NO:94], 43-21 [SEQ ID NO:96], 43-25 [SEQ ID NO: 97], 43-20 [SEQ ID NO:99], 24.1 [SEQ ID NO: 101], 42.2 [SEQ ID NO: 102], 7.2 [SEQ ID NO: 103], 27.3 [SEQ ID NO: 104], 16.3 [SEQ ID NO: 105], 42.10 [SEQ ID NO: 106], 42-3B [SEQ ID NO: 107], 42-11 [SEQ ID NO: 108], F1 [SEQ ID NO: 109], F5 [SEQ ID NO: 110], F3 [SEQ ID NO: 111], 42-6B [SEQ ID NO: 112], 42-12 [SEQ ID NO: 113]. Novel serotypes AAV8 [SEQ ID NO:95] and AAV9 [SEQ ID NO: 100] are the subject of co-filed patent applications.

FIGS. **3**A through **3**C provide the amino acid sequences of the AAV7 rep proteins [SEQ ID NO:3].

DETAILED DESCRIPTION OF THE INVENTION

In the present invention, the inventors have found a method which takes advantage of the ability of adeno-associated virus (AAV) to penetrate the nucleus, and, in the absence of a helper virus co-infection, to integrate into cellular DNA and establish a latent infection. This method utilizes a polymerase chain reaction (PCR)-based strategy for detection, identification and/or isolation of sequences of AAVs from DNAs from tissues of human and non-human primate origin as well as from other sources. Advantageously, this method is also suitable for detection, identification and/or isolation of other integrated viral and non-viral sequences, as described below.

The invention further provides nucleic acid sequences identified according to the methods of the invention. One such adeno-associated virus is of a novel serotype, termed herein serotype 7 (AAV7). Other novel adeno-associated virus serotypes provided herein include AAV10, AAV11, and AAV12. Still other novel AAV serotypes identified according to the methods of the invention are provided in the present specification. See, Figures and Sequence Listing, which is incorporated by reference.

Also provided are fragments of these AAV sequences. Among particularly desirable AAV fragments are the cap proteins, including the vp1, vp2, vp3, the hypervariable regions, the rep proteins, including rep 78, rep 68, rep 52, and rep 40, and the sequences encoding these proteins. Each of these fragments may be readily utilized in a variety of vector systems and host cells. Such fragments may be used alone, in combination with other AAV sequences or fragments, or in combination with elements from other AAV or non-AAV viral sequences. In one particularly desirable embodiment, a vector contains the AAV cap and/or rep sequences of the invention.

As described herein, alignments are performed using any of a variety of publicly or commercially available Multiple Sequence Alignment Programs, such as AClustal W≅, accessible through Web Servers on the internet. Alternatively, Vector NTI utilities are also used. There are also a number of algorithms known in the art which can be used to measure nucleotide sequence identity, including those contained in the programs described above. As another example, polynucleotide sequences can be compared using Fasta, a program in GCG Version 6.1. Fasta provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences. For instance, percent sequence identity between nucleic acid sequences can be determined using Fasta with its default parameters (a word size of 6 and the NOPAM factor for the scoring matrix) as provided in GCG Version 6.1, herein incorporated by reference. Similar programs are available for amino acid sequences, e.g., the "Clustal X" program. Generally, any of these programs are used at default settings, although one of skill in the art can alter these settings as needed. Alternatively, one of skill in the art can utilize another algorithm or computer program which provides at least the level of identity or alignment as that provided by the referenced algorithms and programs.

The term "substantial homology" or "substantial similarity," when referring to a nucleic acid, or fragment thereof, indicates that, when optimally aligned with appropriate nucleotide insertions or deletions with another nucleic acid (or its complementary strand), there is nucleotide sequence identity in at least about 95 to 99% of the aligned sequences. Preferably, the homology is over full-length sequence, or an open reading frame thereof, or another suitable fragment which is at least 15 nucleotides in length. Examples of suitable fragments are described herein.

The term "substantial homology" or "substantial similarity," when referring to amino acids or fragments thereof, indicates that, when optimally aligned with appropriate amino acid insertions or deletions with another amino acid, there is amino acid sequence identity in at least about 95 to 99% of the aligned sequences. Preferably, the homology is over full-length sequence, or a protein thereof, e.g., a cap protein, a rep protein, or a fragment thereof which is at least 8 amino acids, or more desirably, at least 15 amino acids in length. Examples of suitable fragments are described herein.

By the term "highly conserved" is meant at least 80% identity, preferably at least 90% identity, and more preferably, over 97% identity. Identity is readily determined by one of skill in the art by resort to algorithms and computer programs known by those of skill in the art.

The term "percent sequence identity" or "identical" in the context of nucleic acid sequences refers to the residues in the two sequences which are the same when aligned for maximum correspondence. The length of sequence identity comparison may be over the full-length of the genome, the full-length of a gene coding sequence, or a fragment of at least about 500 to 5000 nucleotides, is desired. However, identity among smaller fragments, e.g. of at least about nine nucleotides, usually at least about 20 to 24 nucleotides, at least about 28 to 32 nucleotides, at least about 36 or more nucleotides, may also be desired. Similarly, "percent sequence identity" may be readily determined for amino acid sequences, over the full-length of a protein, or a fragment thereof. Suitably, a fragment is at least about 8 amino acids in length, and may be up to about 700 amino acids. Examples of suitable fragments are described herein.

The AAV sequences and fragments thereof are useful in production of rAAV, and are also useful as antisense delivery vectors, gene therapy vectors, or vaccine vectors. The invention further provides nucleic acid molecules, gene delivery vectors, and host cells which contain the AAV sequences of the invention.

As described herein, the vectors of the invention containing the AAV capsid proteins of the invention are particularly well suited for use in applications in which the neutralizing antibodies diminish the effectiveness of other AAV serotype based vectors, as well as other viral vectors. The rAAV vectors of the invention are particularly advantageous in rAAV readministration and repeat gene therapy.

These and other embodiments and advantages of the invention are described in more detail below. As used throughout this specification and the claims, the terms Acomprising≅ and "including" and their variants are inclusive of other components, elements, integers, steps and the like. Conversely, the term "consisting" and its variants is exclusive of other components, elements, integers, steps and the like.

I. Methods of the Invention

A. Detection of Sequences Via Molecular Cloning

In one aspect, the invention provides a method of detecting and/or identifying target nucleic acid sequences in a sample. This method is particularly well suited for detection of viral sequences which are integrated into the chromosome of a cell, e.g., adeno-associated viruses (AAV) and retroviruses, among others. The specification makes reference to AAV, which is exemplified herein. However, based on this information, one of skill in the art may readily perform the methods of the invention on retroviruses [e.g., feline leukemia virus (FeLV), HTLVI and HTLVII], and lentivirinae [e.g., human immunodeficiency virus (HIV), simian immunodeficiency virus (SIV), feline immunodeficiency virus (FIV), equine infectious anemia virus, and spumavirinal)], among others. Further, the method of the invention may also be used for detection of other viral and non-viral sequences, whether integrated or non-integrated into the genome of the host cell.

As used herein, a sample is any source containing nucleic acids, e.g., tissue, tissue culture, cells, cell culture, and biological fluids including, without limitation, urine and blood. These nucleic acid sequences may be DNA or RNA from plasmids, natural DNA or RNA from any source, including bacteria, yeast, viruses, and higher organisms such as plants or animals. DNA or RNA is extracted from the sample by a variety of techniques known to those of skill in the art, such as those described by Sambrook, Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory). The origin of the sample and the method by which the nucleic acids are obtained for application of the method of the invention is not a limitation of the present invention. Optionally, the method of the invention can be performed directly on the source of DNA, or on nucleic acids obtained (e.g., extracted) from a source.

The method of the invention involves subjecting a sample containing DNA to amplification via polymerase chain reaction (PCR) using a first set of primers specific for a first region of double-stranded nucleic acid sequences, thereby obtaining amplified sequences.

As used herein, each of the Aregions≅ is predetermined based upon the alignment of the nucleic acid sequences of at least two serotypes (e.g., AAV) or strains (e.g., lentiviruses), and wherein each of said regions is composed of sequences having a 5' end which is highly conserved, a middle which is preferably, but necessarily, variable, and a 3' end which is highly conserved, each of these being conserved or variable relative to the sequences of the at least two aligned AAV serotypes. Preferably, the 5' and/or 3' end is highly conserved over at least about 9, and more preferably, at least 18 base pairs (bp). However, one or both of the sequences at the 5= or 3=end may be conserved over more than 18 bp, more than 25 bp, more than 30 bp, or more than 50 bp at the 5' end. With respect to the variable region, there is no requirement for conserved sequences, these sequences may be relatively conserved, or may have less than 90, 80, or 70% identity among the aligned serotypes or strains.

Each of the regions may span about 100 bp to about 10 kilobase pairs in length. However, it is particularly desirable that one of the regions is a Asignature region≅, i.e., a region which is sufficiently unique to positively identify the amplified sequence as being from the target source. For example, in one embodiment, the first region is about 250 bp in length, and is sufficiently unique among known AAV sequences, that it positively identifies the amplified region as being of AAV origin. Further, the variable sequences within this region are sufficiently unique that can be used to identify the serotype from which the amplified sequences originate. Once amplified (and thereby detected), the sequences can be identified by performing conventional restriction digestion and comparison to restriction digestion patterns for this region in any of AAV1, AAV2, AAV3, AAV4, AAV5, or AAV6, or that of AAV7, AAV10, AAV11, AAV12, or any of the other novel serotypes identified by the invention, which is predetermined and provided by the present invention.

Given the guidance provided herein, one of skill in the art can readily identify such regions among other integrated viruses to permit ready detection and identification of these sequences. Thereafter, an optimal set of generic primers located within the highly conserved ends can be designed and tested for efficient amplification of the selected region from samples. This aspect of the invention is readily adapted to a diagnostic kit for detecting the presence of the target sequence (e.g., AAV) and for identifying the AAV serotype, using standards which include the restriction patterns for the AAV serotypes described herein or isolated using the techniques described herein. For example, quick identification or molecular serotyping of PCR products can be accomplished by digesting the PCR products and comparing restriction patterns.

Thus, in one embodiment, the "signature region" for AAV spans about bp 2800 to about 3200 of AAV 1 [SEQ ID NO:6], and corresponding base pairs in AAV 2, AAV3, AAV4, AAV5, and AAV6. More desirably, the region is about 250 bp, located within bp 2886 to about 3143 bp of AAV 1 [SEQ ID NO:6], and corresponding base pairs in AAV 2 [SEQ ID NO:7], AAV3 [SEQ ID NO8], and other AAV serotypes. See, FIG. **1**. To permit rapid detection of AAV in the sample, primers which specifically amplify this signature region are utilized. However, the present invention is not limited to the exact sequences identified herein for the AAV signature region, as one of skill in the art may readily alter this region to encompass a shorter fragment, or a larger fragment of this signature region.

The PCR primers are generated using techniques known to those of skill in the art. Each of the PCR primer sets is composed of a 5' primer and a 3' primer. See, e.g., Sambrook et al, cited herein. The term "primer" refers to an oligonucleotide which acts as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product which is complementary to a nucleic acid strand is induced. The primer is preferably single stranded. However, if a double stranded primer is utilized, it is treated to separate its strands before being used to prepare extension products. The primers may be about 15 to 25 or more nucleotides, and preferably at least 18 nucleotides. However, for certain applications shorter nucleotides, e.g., 7 to 15 nucleotides are utilized.

The primers are selected to be sufficiently complementary to the different strands of each specific sequence to be amplified to hybridize with their respective strands. Therefore, the primer sequence need not reflect the exact sequence of the region being amplified. For example, a non-complementary nucleotide fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being completely complementary to the strand. Alterna-

tively, non-complementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence of the strand to be amplified to hybridize therewith and form a template for synthesis of the extension product of the other primer.

The PCR primers for the signature region according to the invention are based upon the highly conserved sequences of two or more aligned sequences (e.g., two or more AAV serotypes). The primers can accommodate less than exact identity among the two or more aligned AAV serotypes at the 5' end or in the middle. However, the sequences at the 3' end of the primers correspond to a region of two or more aligned AAV serotypes in which there is exact identity over at least five, preferably, over at least nine base pairs, and more preferably, over at least 18 base pairs at the 3' end of the primers. Thus, the 3' end of the primers is composed of sequences with 100% identity to the aligned sequences over at least five nucleotides. However, one can optionally utilize one, two, or more degenerate nucleotides at the 3' end of the primer.

For example, the primer set for the signature region of AAV was designed based upon a unique region within the AAV capsid, as follows. The 5' primer was based upon nt 2867-2891 of AAV2 [SEQ ID NO:7], 5'-GGTAATTCCTC-CGGAAATTGGCATT3'. See, FIG. **1**. The 3' primer was designed based upon nt 3096-3122 of AAV2 [SEQ ID NO:7], 5'-GACTCATCAACAACAACTGGGGATTC-3'. However, one of skill in the art may have readily designed the primer set based upon the corresponding regions of AAV 1, AAV3, AAV4, AAV5, AAV6, or based upon the information provided herein, AAV7, AAV10, AAV11, AAV12, or another novel AAV of the invention. In addition, still other primer sets can be readily designed to amplify this signature region, using techniques known to those of skill in the art.

B. Isolation of Target Sequences

As described herein, the present invention provides a first primer set which specifically amplifies the signature region of the target sequence, e.g., an AAV serotype, in order to permit detection of the target. In a situation in which further sequences are desired, e.g., if a novel AAV serotype is identified, the signature region may be extended. Thus, the invention may further utilize one or more additional primer sets.

Suitably, these primer sets are designed to include either the 5' or 3' primer of the first primer set and a second primer unique to the primer set, such that the primer set amplifies a region 5' or 3' to the signature region which anneals to either the 5' end or the 3' end of the signature region. For example, a first primer set is composed of a 5' primer, P1 and a 3' primer P2 to amplify the signature region. In order to extend the signature region on its 3' end, a second primer set is composed of primer P1 and a 3' primer P4, which amplifies the signature region and contiguous sequences downstream of the signature region. In order to extend the signature region on its 5' end, a third primer set is composed of a 5' primer, P5, and primer P2, such that the signature region and contiguous sequences upstream of the signature region are amplified. These extension steps are repeated (or performed at the same time), as needed or desired. Thereafter, the products results from these amplification steps are fused using conventional steps to produce an isolated sequence of the desired length.

The second and third primer sets are designed, as with the primer set for the signature region, to amplify a region having highly conserved sequences among the aligned sequences. Reference herein to the term "second" or "third" primer set is for each of discussion only, and without regard to the order in which these primers are added to the reaction mixture, or used for amplification. The region amplified by the second primer set is selected so that upon amplification it anneals at its 5' end to the 3' end of the signature region. Similarly, the region amplified by the third primer set is selected so that upon amplification it anneals at its 3' end anneals to the 5' end of the signature region. Additional primer sets can be designed such that the regions which they amplify anneal to the either the 5' end or the 3' end of the extension products formed by the second or third primer sets, or by subsequent primer sets.

For example, where AAV is the target sequence, a first set of primers (P 1 and P2) are used to amplify the signature region from the sample. In one desirable embodiment, this signature region is located within the AAV capsid. A second set of primers (P1 and P4) is used to extend the 3' end of the signature region to a location in the AAV sequence which is just before the AAV 3' ITR, i.e., providing an extension product containing the entire 3' end of the AAV capsid when using the signature region as an anchor. In one embodiment, the P4 primer corresponds to nt 4435 to 4462 of AAV2 [SEQ ID NO:7], and corresponding sequences in the other AAV serotypes. This results in amplification of a region of about 1.6 kb, which contains the 0.25 kb signature region. A third set of primers (P3 and P2) is used to extend the 5' end of signature region to a location in the AAV sequences which is in the 3' end of the rep genes, i.e., providing an extension product containing the entire 5' end of the AAV capsid when using the signature region as an anchor. In one embodiment, the P3 primer corresponds to nt 1384 to 1409 of AAV2 [SEQ ID NO:7], and corresponding sequences in the other AAV serotypes. This results in amplification of a region of about 1.7 kb, which contains the 0.25 kb signature region. Optionally, a fourth set of primers are used to further extend the extension product containing the entire 5' end of the AAV capsid to also include the rep sequences. In one embodiment, the primer designated P5 corresponds to nt 108 to 133 of AAV2 [SEQ ID NO:7], and corresponding sequences in the other AAV serotypes and is used in conjunction with the P2 primer.

Following completion of the desired number of extension steps, the various extension products are fused, making use of the signature region as an anchor or marker, to construct an intact sequence. In the example provided herein, AAV sequences containing, at a minimum, an intact AAV cap gene are obtained. Larger sequences may be obtained, depending upon the number of extension steps performed.

Suitably, the extension products are assembled into an intact AAV sequence using methods known to those of skill in the art. For example, the extension products may be digested with DraIII, which cleaves at the DraIII site located within the signature region, to provide restriction fragments which are re-ligated to provide products containing (at a minimum) an intact AAV cap gene. However, other suitable techniques for assembling the extension products into an intact sequence may be utilized. See, generally, Sambrook et al, cited herein.

As an alternative to the multiple extension steps described above, another embodiment of the invention provides for direct amplification of a 3.1 kb fragment which allows isolation of full-length cap sequences. To directly amplify a 3.1 kb full-length cap fragment from NHP tissue and blood DNAs, two other highly conserved regions were identified in AAV genomes for use in PCR amplification of large fragments. A primer within a conserved region located in the middle of the rep gene is utilized (AV1ns: 5' GCTGCGT-

CAACTGGACCAATGAGAAC 3', nt of SEQ ID NO:6) in combination with the 3' primer located in another conserved region downstream of the Cap gene (AV2cas: 5' CGCAGAGACCAAAGTTCAACTGAAACGA 3', SEQ ID NO: 7) for amplification of AAV sequences including the full-length AAV cap. Typically, following amplification, the products are cloned and sequence analysis is performed with an accuracy of ≥99.9%. Using this method, the inventors have isolated at least 50 capsid clones which have subsequently been characterized. Among them, 37 clones were derived from Rhesus macaque tissues (rh.1-rh.37), 6 clones from cynomologous macaques (cy.1-cy.6), 2 clones from Baboons (bb.1 and bb.2) and 5 clones from Chimps (ch.1-ch.5). These clones are identified elsewhere in the specification, together with the species of animal from which they were identified and the tissues in that animal these novel sequences have been located.

C. Alternative Method for Isolating Novel AAV

In another aspect, the invention provides an alternative method for isolating novel AAV from a cell. This method involves infecting the cell with a vector which provides helper functions to the AAV; isolating infectious clones containing AAV; sequencing the isolated AAV; and comparing the sequences of the isolated AAV to known AAV serotypes, whereby differences in the sequences of the isolated AAV and known AAV serotypes indicates the presence of a novel AAV.

In one embodiment, the vector providing helper functions provides essential adenovirus functions, including, e.g., E1a, E1b, E2a, E4ORF6. In one embodiment, the helper functions are provided by an adenovirus. The adenovirus may be a wild-type adenovirus, and may be of human or non-human origin, preferably non-human primate (NHP) origin. The DNA sequences of a number of adenovirus types are available from Genbank, including type Ad5 [Genbank Accession No. M73260]. The adenovirus sequences may be obtained from any known adenovirus serotype, such as serotypes 2, 3, 4, 7, 12 and 40, and further including any of the presently identified human types [see, e.g., Horwitz, cited above]. Similarly adenoviruses known to infect non-human animals (e.g., chimpanzees) may also be employed in the vector constructs of this invention. See, e.g., U.S. Pat. No. 6,083,716. In addition to wild-type adenoviruses, recombinant viruses or non-viral vectors (e.g., plasmids, episomes, etc.) carrying the necessary helper functions may be utilized. Such recombinant viruses are known in the art and may be prepared according to published techniques. See, e.g., U.S. Pat. Nos. 5,871,982 and 6,251,677, which describe a hybrid Ad/AAV virus. The selection of the adenovirus type is not anticipated to limit the following invention. A variety of adenovirus strains are available from the American Type Culture Collection, Manassas, Va., or available by request from a variety of commercial and institutional sources. Further, the sequences of many such strains are available from a variety of databases including, e.g., PubMed and GenBank.

In another alternative, infectious AAV may be isolated using genome walking technology (Siebert et al., 1995, *Nucleic Acid Research,* 23:1087-1088, Friezner-Degen et al., 1986, *J. Biol. Chem.* 261:6972-6985, BD Biosciences Clontech, Palo Alto, Calif.). Genome walking is particularly well suited for identifying and isolating the sequences adjacent to the novel sequences identified according to the method of the invention. For example, this technique may be useful for isolating inverted terminal repeat (ITRs) of the novel AAV serotype, based upon the novel AAV capsid and/or rep sequences identified using the methods of the invention. This technique is also useful for isolating sequences adjacent to other AAV and non-AAV sequences identified and isolated according to the present invention. See, Examples 3 and 4.

The methods of the invention may be readily used for a variety of epidemiology studies, studies of biodistribution, monitoring of gene therapy via AAV vectors and vector derived from other integrated viruses. Thus, the methods are well suited for use in pre-packaged kits for use by clinicians, researchers, and epidemiologists.

II. Diagnostic Kit

In another aspect, the invention provides a diagnostic kit for detecting the presence of a known or unknown adeno-associated virus (AAV) in a sample. Such a kit may contain a first set of 5' and 3' PCR primers specific for a signature region of the AAV nucleic acid sequence. Alternatively, or additionally, such a kit can contain a first set of 5' and 3' PCR primers specific for the 3.1 kb fragment which includes the full-length AAV capsid nucleic acid sequence identified herein (e.g., the AV1ns and AV2cas primers.) Optionally, a kit of the invention may further contain two or more additional sets of 5' and 3' primers, as described herein, and/or PCR probes. These primers and probes are used according to the present invention amplify signature regions of each AAV serotype, e.g., using quantitative PCR.

The invention further provides a kit useful for identifying an AAV serotype detected according to the method of the invention and/or for distinguishing novel AAV from known AAV. Such a kit may further include one or more restriction enzymes, standards for AAV serotypes providing their "signature restriction enzyme digestions analyses", and/or other means for determining the serotype of the AAV detected.

In addition, kits of the invention may include, instructions, a negative and/or positive control, containers, diluents and buffers for the sample, indicator charts for signature comparisons, disposable gloves, decontamination instructions, applicator sticks or containers, and sample preparator cups, as well as any desired reagents, including media, wash reagents and concentration reagents. Such reagents may be readily selected from among the reagents described herein, and from among conventional concentration reagents. In one desirable embodiment, the wash reagent is an isotonic saline solution which has been buffered to physiologic pH, such as phosphate buffered saline (PBS); the elution reagent is PBS containing 0.4 M NaCl, and the concentration reagents and devices. For example, one of skill in the art will recognize that reagents such as polyethylene glycol (PEG), or NH_4SO_4 may be useful, or that devices such as filter devices. For example, a filter device with a 100 K membrane would concentrate rAAV.

The kits provided by the present invention are useful for performing the methods described herein, and for study of biodistribution, epidemiology, mode of transmission of novel AAV serotypes in human and NHPs.

Thus, the methods and kits of the invention permit detection, identification, and isolation of target viral sequences, particularly integrated viral sequences. The methods and kits are particularly well suited for use in detection, identification and isolation of AAV sequences, which may include novel AAV serotypes.

In one notable example, the method of the invention facilitated analysis of cloned AAV sequences by the inventors, which revealed heterogeneity of proviral sequences between cloned fragments from different animals, all of which were distinct from the known six AAV serotypes, with the majority of the variation localized to hypervariable regions of the capsid protein. Surprising divergence of AAV

sequences was noted in clones isolated from single tissue sources, such as lymph node, from an individual rhesus monkey. This heterogeneity is best explained by apparent evolution of AAV sequence within individual animals due, in part, to extensive homologous recombination between a limited number of co-infecting parenteral viruses. These studies suggest sequence evolution of widely disseminated virus during the course of a natural AAV infection that presumably leads to the formation of swarms of quasispecies which differ from one another in the array of capsid hypervariable regions. This is the first example of rapid molecular evolution of a DNA virus in a way that formerly was thought to be restricted to RNA viruses.

Sequences of several novel AAV serotypes identified by the method of the invention and characterization of these serotypes is provided.

III. Novel AAV Serotypes

A. Nucleic Acid Sequences

Nucleic acid sequences of novel AAV serotypes identified by the methods of the invention are provided. See, SEQ ID NO: 1, 9-59, and 117-120, which are incorporated by reference herein. See also, FIG. **1** and the sequence listing.

For novel serotype AAV7, the full-length sequences, including the AAV 5' ITRs, capsid, rep, and AAV 3' ITRs are provided in SEQ ID NO: 1.

For other novel AAV serotypes of the invention, the approximately 3.1 kb fragment isolated according to the method of the invention is provided. This fragment contains sequences encoding full-length capsid protein and all or part of the sequences encoding the rep protein. These sequences include the clones identified below.

For still other novel AAV serotypes, the signature region encoding the capsid protein is provided. For example, the AAV10 nucleic acid sequences of the invention include those illustrated in FIG. **1** [See, SEQ ID NO: 117, which spans 255 bases]. The AAV11 nucleic acid sequences of the invention include the DNA sequences illustrated in FIG. **1** [See, SEQ ID NO: 118 which spans 258 bases]. The AAV12 nucleic acid sequences of the invention include the DNA sequences illustrated in FIG. **1** [See, SEQ ID NO: 119, which consists of 255 bases]. Using the methodology described above, further AAV10, AAV11 and AAV12 sequences can be readily identified and used for a variety of purposes, including those described for AAV7 and the other novel serotypes herein.

FIG. **1** provides the non-human primate (NHP) AAV nucleic acid sequences of the invention in an alignment with the previously published AAV serotypes, AAV 1 [SEQ ID NO:6], AAV2 [SEQ ID NO:7], and AAV3 [SEQ ID NO:8]. These novel NHP sequences include those provided in the following Table I, which are identified by clone number:

TABLE 1

AAV Cap Sequence	Clone Number	Source Species	Tissue	SEQ ID NO (DNA)
Rh.1	Clone 9 (AAV9)	Rhesus	Heart	5
Rh.2	Clone 43.1	Rhesus	MLN	39
Rh.3	Clone 43.5	Rhesus	MLN	40
Rh.4	Clone 43.12	Rhesus	MLN	41
Rh.5	Clone 43.20	Rhesus	MLN	42
Rh.6	Clone 43.21	Rhesus	MLN	43
Rh.7	Clone 43.23	Rhesus	MLN	44
Rh.8	Clone 43.25	Rhesus	MLN	45
Rh.9	Clone 44.1	Rhesus	Liver	46
Rh.10	Clone 44.2	Rhesus	Liver	59
Rh.11	Clone 44.5	Rhesus	Liver	47

TABLE 1-continued

AAV Cap Sequence	Clone Number	Source Species	Tissue	SEQ ID NO (DNA)
Rh.12	Clone 42.1B	Rhesus	MLN	30
Rh.13	42.2	Rhesus	MLN	9
Rh.14	Clone 42.3A	Rhesus	MLN	32
Rh.15	Clone 42.3B	Rhesus	MLN	36
Rh.16	Clone 42.4	Rhesus	MLN	33
Rh.17	Clone 42.5A	Rhesus	MLN	34
Rh.18	Clone 42.5B	Rhesus	MLN	29
Rh.19	Clone 42.6B	Rhesus	MLN	38
Rh.20	Clone 42.8	Rhesus	MLN	27
Rh.21	Clone 42.10	Rhesus	MLN	35
Rh.22	Clone 42.11	Rhesus	MLN	37
Rh.23	Clone 42.12	Rhesus	MLN	58
Rh.24	Clone 42.13	Rhesus	MLN	31
Rh.25	Clone 42.15	Rhesus	MLN	28
Rh.26	Clone 223.2	Rhesus	Liver	49
Rh.27	Clone 223.4	Rhesus	Liver	50
Rh.28	Clone 223.5	Rhesus	Liver	51
Rh.29	Clone 223.6	Rhesus	Liver	52
Rh.30	Clone 223.7	Rhesus	Liver	53
Rh.31	Clone 223.10	Rhesus	Liver	48
Rh.32	Clone C1	Rhesus	Spleen, Duo, Kid & Liver	19
Rh.33	Clone C3	Rhesus		20
Rh.34	Clone C5	Rhesus		21
Rh.35	Clone F1	Rhesus	Liver	22
Rh.36	Clone F3	Rhesus		23
Rh.37	Clone F5	Rhesus		24
Cy.1	Clone 1.3	Cyno	Blood	14
Cy.2	Clone 13.3B	Cyno	Blood	15
Cy.3	Clone 24.1	Cyno	Blood	16
Cy.4	Clone 27.3	Cyno	Blood	17
Cy.5	Clone 7.2	Cyno	Blood	18
Cy.6	Clone 16.3	Cyno	Blood	10
bb.1	Clone 29.3	Baboon	Blood	11
bb.2	Clone 29.5	Baboon	Blood	13
Ch.1	Clone A3.3	Chimp	Blood	57
Ch.2	Clone A3.4	Chimp	Blood	54
Ch.3	Clone A3.5	Chimp	Blood	55
Ch.4	Clone A3.7	Chimp	Blood	56

A novel NHP clone was made by splicing capsids fragments of two chimp adenoviruses into an AAV2 rep construct. This new clone, A3. 1, is also termed Ch.5 [SEQ ID NO:20]. Additionally, the present invention includes two human AAV sequences, termed H6 [SEQ ID NO:25] and H2 [SEQ ID NO:26].

The AAV nucleic acid sequences of the invention further encompass the strand which is complementary to the strands provided in the sequences provided in FIG. **1** and the Sequence Listing [SEQ ID NO: 1, 9-59, 117-120], nucleic acid sequences, as well as the RNA and cDNA sequences corresponding to the sequences provided in FIG. **1** and the Sequence Listing [SEQ ID NO: 1, 9-59, 117-120], and their complementary strands. Also included in the nucleic acid sequences of the invention are natural variants and engineered modifications of the sequences of FIG. **1** and the Sequence Listing [SEQ ID NO:1, 9-59, 117-120], and their complementary strands. Such modifications include, for example, labels which are known in the art, methylation, and substitution of one or more of the naturally occurring nucleotides with a degenerate nucleotide.

Further included in this invention are nucleic acid sequences which are greater than 85%, preferably at least

about 90%, more preferably at least about 95%, and most preferably at least about 98 to 99% identical or homologous to the sequences of the invention, including FIG. **1** and the Sequence Listing [SEQ ID NO: 1, 9-59, 117-120]. These terms are as defined herein.

Also included within the invention are fragments of the novel AAV sequences identified by the method described herein. Suitable fragments are at least 15 nucleotides in length, and encompass functional fragments, i.e., fragments which are of biological interest. In one embodiment, these fragments are fragments of the novel sequences of FIG. **1** and the Sequence Listing [SEQ ID NO: 1, 9-59, 117-120], their complementary strands, cDNA and RNA complementary thereto.

Examples of suitable fragments are provided with respect to the location of these fragments on AAV1, AAV2, or AAV7. However, using the alignment provided herein (obtained using the Clustal W program at default settings), or similar techniques for generating an alignment with other novel serotypes of the invention, one of skill in the art can readily identify the precise nucleotide start and stop codons for desired fragments.

Examples of suitable fragments include the sequences encoding the three variable proteins (vp) of the AAV capsid which are alternative splice variants: vp1 [e.g., nt 825 to 3049 of AAV7, SEQ ID NO: 1]; vp2 [e.g., nt 1234-3049 of AAV7, SEQ ID NO: 1]; and vp3 [e.g., nt 1434-3049 of AAV7, SEQ ID NO: 1]. It is notable that AAV7 has an unusual GTG start codon. With the exception of a few house-keeping genes, such a start codon has not previously been reported in DNA viruses. The start codons for vp1, vp2 and vp3 for other AAV serotypes have been believed to be such that they permit the cellular mechanism of the host cell in which they reside to produce vp1, vp2 and vp3 in a ratio of 10%:10%:80%, respectively, in order to permit efficient assembly of the virion. However, the AAV7 virion has been found to assemble efficiently even with this rare GTG start codon. Thus, the inventors anticipate this it is desirable to alter the start codon of the vp3 of other AAV serotypes to contain this rare GTG start codon, in order to improve packaging efficiency, to alter the virion structure and/or to alter location of epitopes (e.g., neutralizing antibody epitopes) of other AAV serotypes. The start codons may be altered using conventional techniques including, e.g., site directed mutagenesis. Thus, the present invention encompasses altered AAV virions of any selected serotype, composed of a vp3, and/or optionally, vp1 and/or vp2 having start codons altered to GTG.

Other suitable fragments of AAV, include a fragment containing the start codon for the AAV capsid protein [e.g., nt 468 to 3090 of AAV7, SEQ ID NO: 1, nt 725 to 3090 of AAV7, SEQ ID NO: 1, and corresponding regions of the other AAV serotypes]. Still other fragments of AAV7 and the other novel AAV serotypes identified using the methods described herein include those encoding the rep proteins, including rep 78 [e.g., initiation codon 334 of FIG. **1** for AAV7], rep 68 [initiation codon nt 334 of FIG. **1** for AAV7], rep 52 [initiation codon 1006 of FIG. **1** for AAV7], and rep 40 [initiation codon 1006 of FIG. **1** for AAV7] Other fragments of interest may include the AAV 5' inverted terminal repeats ITRs, [nt 1 to 107 of FIG. **1** for AAV7]; the AAV 3' ITRs [nt 4704 to 4721 of FIG. **1** for AAV7], P19 sequences, AAV P40 sequences, the rep binding site, and the terminal resolute site (TRS). Still other suitable fragments will be readily apparent to those of skill in the art. The corresponding regions in the other novel serotypes of the invention can be readily determined by reference to FIG. **1**, or by utilizing conventional alignment techniques with the sequences provided herein.

In addition to including the nucleic acid sequences provided in the figures and Sequence Listing, the present invention includes nucleic acid molecules and sequences which are designed to express the amino acid sequences, proteins and peptides of the AAV serotypes of the invention. Thus, the invention includes nucleic acid sequences which encode the following novel AAV amino acid sequences: C1 [SEQ ID NO:60], C2 [SEQ ID NO:61], C5 [SEQ ID NO:62], A3-3 [SEQ ID NO:66], A3-7 [SEQ ID NO:67], A3-4 [SEQ ID NO:68], A3-5 [SEQ ID NO: 69], 3.3b [SEQ ID NO: 62], 223.4 [SEQ ID NO: 73], 223-5 [SEQ ID NO:74], 223-10 [SEQ ID NO:75], 223-2 [SEQ ID NO:76], 223-7 [SEQ ID NO: 77], 223-6 [SEQ ID NO: 78], 44-1 [SEQ ID NO: 79], 44-5 [SEQ ID NO:80], 44-2 [SEQ ID NO:81], 42-15 [SEQ ID NO: 84], 42-8 [SEQ ID NO: 85], 42-13 [SEQ ID NO:86], 42-3A [SEQ ID NO:87], 42-4 [SEQ ID NO:88], 42-5A [SEQ ID NO:89], 42-1B [SEQ ID NO:90], 42-5B [SEQ ID NO:91], 43-1 [SEQ ID NO: 92], 43-12 [SEQ ID NO: 93], 43-5 [SEQ ID NO:94], 43-21 [SEQ ID NO:96], 43-25 [SEQ ID NO: 97], 43-20 [SEQ ID NO:99], 24.1 [SEQ ID NO: 101], 42.2 [SEQ ID NO: 102], 7.2 [SEQ ID NO: 103], 27.3 [SEQ ID NO: 104], 16.3 [SEQ ID NO: 105], 42.10 [SEQ ID NO: 106], 42-3B [SEQ ID NO: 107], 42-11 [SEQ ID NO: 108], F1 [SEQ ID NO: 109], F5 [SEQ ID NO: 110], F3 [SEQ ID NO:111], 42-6B [SEQ ID NO: 112], and/or 42-12 [SEQ ID NO: 113], and artificial AAV serotypes generated using these sequences and/or unique fragments thereof.

As used herein, artificial AAV serotypes include, without limitation, AAV with a non-naturally occurring capsid protein. Such an artificial capsid may be generated by any suitable technique, using a novel AAV sequence of the invention (e.g., a fragment of a vp1 capsid protein) in combination with heterologous sequences which may be obtained from another AAV serotype (known or novel), non-contiguous portions of the same AAV serotype, from a non-AAV viral source, or from a non-viral source. An artificial AAV serotype may be, without limitation, a chimeric AAV capsid, a recombinant AAV capsid, or a "humanized" AAV capsid.

B. AAV Amino Acid Sequences, Proteins and Peptides

The invention provides proteins and fragments thereof which are encoded by the nucleic acid sequences of the novel AAV serotypes identified herein, including, e.g., AAV7 [nt 825 to 3049 of AAV7, SEQ ID NO: 1] the other novel serotypes provided herein. Thus, the capsid proteins of the novel serotypes of the invention, including: H6 [SEQ ID NO: 25], H2 [SEQ ID NO: 26], 42-2 [SEQ ID NO:9], 42-8 [SEQ ID NO:27], 42-15 [SEQ ID NO:28], 42-5b [SEQ ID NO: 29], 42-1b [SEQ ID NO:30]; 42-13 [SEQ ID NO: 31], 42-3a [SEQ ID NO: 32], 42-4 [SEQ ID NO:33], 42-5a [SEQ ID NO: 34], 42-10 [SEQ ID NO:35], 42-3b [SEQ ID NO: 36], 42-11 [SEQ ID NO: 37], 42-6b [SEQ ID NO:38], 43-1 [SEQ ID NO: 39], 43-5 [SEQ ID NO: 40], 43-12 [SEQ ID NO:41], 43-20 [SEQ ID NO:42], 43-21 [SEQ ID NO: 43], 43-23 [SEQ ID NO:44], 43-25 [SEQ ID NO: 45], 44.1 [SEQ ID NO:47], 44.5 [SEQ ID NO:47], 223.10 [SEQ ID NO:48], 223.2 [SEQ ID NO:49], 223.4 [SEQ ID NO:50], 223.5 [SEQ ID NO: 51], 223.6 [SEQ ID NO: 52], 223.7 [SEQ ID NO: 53], A3.4 [SEQ ID NO: 54], A3.5 [SEQ ID NO:55], A3.7 [SEQ ID NO: 56], A3.3 [SEQ ID NO:57], 42.12 [SEQ ID NO: 58], and 44.2 [SEQ ID NO: 59], can be readily generated using conventional techniques from the open reading frames provided for the above-listed clones.

The invention further encompasses AAV serotypes generated using sequences of the novel AAV serotypes of the invention, which are generated using synthetic, recombinant or other techniques known to those of skill in the art. The invention is not limited to novel AAV amino acid sequences, peptides and proteins expressed from the novel AAV nucleic acid sequences of the invention and encompasses amino acid sequences, peptides and proteins generated by other methods known in the art, including, e.g., by chemical synthesis, by other synthetic techniques, or by other methods. For example, the sequences of any of C1 [SEQ ID NO:60], C2 [SEQ ID NO:61], C5 [SEQ ID NO:62], A3-3 [SEQ ID NO:66], A3-7 [SEQ ID NO:67], A3-4 [SEQ ID NO:68], A3-5 [SEQ ID NO: 69], 3.3b [SEQ ID NO: 62], 223.4 [SEQ ID NO: 73], 223-5 [SEQ ID NO:74], 223-10 [SEQ ID NO:75], 223-2 [SEQ ID NO:76], 223-7 [SEQ ID NO: 77], 223-6 [SEQ ID NO: 78], 44-1 [SEQ ID NO: 79], 44-5 [SEQ ID NO:80], 44-2 [SEQ ID NO:81], 42-15 [SEQ ID NO: 84], 42-8 [SEQ ID NO: 85], 42-13 [SEQ ID NO:86], 42-3A [SEQ ID NO:87], 42-4 [SEQ ID NO:88], 42-5A [SEQ ID NO:89], 42-1B [SEQ ID NO:90], 42-5B [SEQ ID NO:91], 43-1 [SEQ ID NO: 92], 43-12 [SEQ ID NO: 93], 43-5 [SEQ ID NO:94], 43-21 [SEQ ID NO:96], 43-25 [SEQ ID NO: 97], 43-20 [SEQ ID NO:99], 24.1 [SEQ ID NO: 101], 42.2 [SEQ ID NO: 102], 7.2 [SEQ ID NO: 103], 27.3 [SEQ ID NO: 104], 16.3 [SEQ ID NO: 105], 42.10 [SEQ ID NO: 106], 42-3B [SEQ ID NO: 107], 42-11 [SEQ ID NO: 108], F1 [SEQ ID NO: 109], F5 [SEQ ID NO: 110], F3 [SEQ ID NO: 111], 42-6B [SEQ ID NO: 112], and/or 42-12 [SEQ ID NO: 113] by be readily generated using a variety of techniques.

Suitable production techniques are well known to those of skill in the art. See, e.g., Sambrook et al, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press (Cold Spring Harbor, N.Y.). Alternatively, peptides can also be synthesized by the well known solid phase peptide synthesis methods (Merrifield, *J. Am. Chem. Soc.,* 85:2149 (1962); Stewart and Young, Solid Phase Peptide Synthesis (Freeman, San Francisco, 1969) pp. 27-62). These and other suitable production methods are within the knowledge of those of skill in the art and are not a limitation of the present invention.

Particularly desirable proteins include the AAV capsid proteins, which are encoded by the nucleotide sequences identified above. The sequences of many of the capsid proteins of the invention are provided in an alignment in FIG. **2** and/or in the Sequence Listing, SEQ ID NO: 2 and 60 to 115, which is incorporated by reference herein. The AAV capsid is composed of three proteins, vp1, vp2 and vp3, which are alternative splice variants. The full-length sequence provided in these figures is that of vp1. Based on the numbering of the AAV7 capsid [SEQ ID NO:2], the sequences of vp2 span amino acid 138-737 of AAV7 and the sequences of vp3 span amino acids 203-737 of AAV7. With this information, one of skill in the art can readily determine the location of the vp2 and vp3 proteins for the other novel serotypes of the invention.

Other desirable proteins and fragments of the capsid protein include the constant and variable regions, located between hypervariable regions (HPV) and the sequences of the HPV regions themselves. An algorithm developed to determine areas of sequence divergence in AAV2 has yielded 12 hypervariable regions (HVR) of which 5 overlap or are part of the four previously described variable regions. [Chiorini et al, *J. Virol,* 73:1309-19 (1999); Rutledge et al, *J. Virol.,* 72:309-319] Using this algorithm and/or the alignment techniques described herein, the HVR of the novel AAV serotypes are determined. For example, with respect to the number of the AAV2 vp11 [SEQ ID NO:70], the HVR are located as follows: HVR1, aa 146-152; HVR2, aa 182-186; HVR3, aa 262-264; HVR4, aa 381-383; HVR5, aa 450-474; HVR6, aa 490-495; HVR7, aa500-504; HVR8, aa 514-522; HVR9, aa 534-555; HVR10, aa 581-594; HVR11, aa 658-667; and HVR12, aa 705-719. Utilizing an alignment prepared in accordance with conventional methods and the novel sequences provided herein [See, e.g., FIG. **2**], one can readily determine the location of the HVR in the novel AAV serotypes of the invention. For example, utilizing FIG. **2**, one can readily determine that for AAV7 [SEQ ID NO:2]. HVR1 is located at aa 146-152; HVR2 is located at 182-187; HVR3 is located at aa 263-266, HVR4 is located at aa 383-385, HVR5 is located at aa 451-475; HVR6 is located at aa 491-496 of AAV7; HVR7 is located at aa 501-505; HVR8 is located at aa 513-521; HVR9 is located at 533-554; HVR10 is located at aa 583-596; HVR11 is located at aa 660-669; HVR12 is located at aa 707-721. Using the information provided herein, the HVRs for the other novel serotypes of the invention can be readily determined.

In addition, within the capsid, amino acid cassettes of identity have been identified. These cassettes are of particular interest, as they are useful in constructing artificial serotypes, e.g., by replacing a HVR1 cassette of a selected serotype with an HVR1 cassette of another serotype. Certain of these cassettes of identity are noted in FIG. **2**. See, FIG. **2**, providing the Clustal X alignment, which has a ruler is displayed below the sequences, starting at 1 for the first residue position. The line above the ruler is used to mark strongly conserved positions. Three characters (*, : , .) are used. "*" indicates positions which have a single, fully conserved residue. ":" indicates that a "strong" group is fully conserved "." Indicates that a "weaker" group is fully conserved. These are all the positively scoring groups that occur in the Gonnet Pam250 matrix. The strong groups are defined as a strong score >0.5 and the weak groups are defined as weak score <0.5.

Additionally, examples of other suitable fragments of AAV capsids include, with respect to the numbering of AAV2 [SEQ ID NO:70], aa 24-42, aa 25-28; aa 81-85; aa133-165; aa 134-165; aa 137-143; aa 154-156; aa 194-208; aa 261-274; aa 262-274; aa 171-173; aa 413-417; aa 449-478; aa 494-525; aa 534-571; aa 581-601; aa 660-671; aa 709-723. Still other desirable fragments include, for example, in AAV7, amino acids 1 to 184 of SEQ ID NO:2, amino acids 199 to 259; amino acids 274 to 446; amino acids 603 to 659; amino acids 670 to 706; amino acids 724 to 736; aa 185 to 198; aa 260 to 273; aa447 to 477; aa495 to 602; aa660 to 669; and aa707 to 723. Still other desirable regions, based on the numbering of AAV7 [SEQ ID NO:2], are selected from among the group consisting of aa 185 to 198; aa 260 to 273; aa447 to 477;aa495 to 602; aa660 to 669; and aa707 to 723. Using the alignment provided herein performed using the Clustal X program at default settings, or using other commercially or publicly available alignment programs at default settings, one of skill in the art can readily determine corresponding fragments of the novel AAV capsids of the invention.

Other desirable proteins are the AAV rep proteins [aa 1 to 623 of SEQ ID NO:3 for AAV7] and functional fragments thereof, including, e.g., aa 1 to 171, aa 172 to 372, aa 373 to 444, aa 445 to 623 of SEQ ID NO:3, among others. Suitably, such fragments are at least 8 amino acids in length. See, FIG. **3**. Comparable regions can be identified in the proteins of the other novel AAV of the invention, using the techniques described herein and those which are known in

the art. In addition, fragments of other desired lengths may be readily utilized. Such fragments may be produced recombinantly or by other suitable means, e.g., chemical synthesis.

The sequences, proteins, and fragments of the invention may be produced by any suitable means, including recombinant production, chemical synthesis, or other synthetic means. Such production methods are within the knowledge of those of skill in the art and are not a limitation of the present invention.

IV. Production of rAAV with Novel AAV Capsids

The invention encompasses novel, wild-type AAV serotypes identified by the invention, the sequences of which wild-type AAV serotypes are free of DNA and/or cellular material with these viruses are associated in nature. In another aspect, the present invention provides molecules which utilize the novel AAV sequences of the invention, including fragments thereof, for production of molecules useful in delivery of a heterologous gene or other nucleic acid sequences to a target cell.

The molecules of the invention which contain sequences of a novel AAV serotype of the invention include any genetic element (vector) which may be delivered to a host cell, e.g., naked DNA, a plasmid, phage, transposon, cosmid, episome, a protein in a non-viral delivery vehicle (e.g., a lipid-based carrier), virus, etc. which transfer the sequences carried thereon. The selected vector may be delivered by any suitable method, including transfection, electroporation, liposome delivery, membrane fusion techniques, high velocity DNA-coated pellets, viral infection and protoplast fusion. The methods used to construct any embodiment of this invention are known to those with skill in nucleic acid manipulation and include genetic engineering, recombinant engineering, and synthetic techniques. See, e.g., Sambrook et al, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor, N.Y.

In one embodiment, the vectors of the invention contain sequences encoding a novel AAV capsid of the invention (e.g., AAV7 capsid, AAV 44-2 (rh.10), an AAV10 capsid, an AAV11 capsid, an AAV12 capsid), or a fragment of one or more of these AAV capsids. Alternatively, the vectors may contain the capsid protein, or a fragment thereof, itself.

Optionally, vectors of the invention may contain sequences encoding AAV rep proteins. Such rep sequences may be from the same AAV serotype which is providing the cap sequences. Alternatively, the present invention provides vectors in which the rep sequences are from an AAV serotype which differs from that which is providing the cap sequences. In one embodiment, the rep and cap sequences are expressed from separate sources (e.g., separate vectors, or a host cell and a vector). In another embodiment, these rep sequences are expressed from the same source as the cap sequences. In this embodiment, the rep sequences may be fused in frame to cap sequences of a different AAV serotype to form a chimeric AAV vector. Optionally, the vectors of the invention further contain a minigene comprising a selected transgene which is flanked by AAV 5' ITR and AAV 3' ITR.

Thus, in one embodiment, the vectors described herein contain nucleic acid sequences encoding an intact AAV capsid which may be from a single AAV serotype (e.g., AAV7 or another novel AAV). Alternatively, these vectors contain sequences encoding artificial capsids which contain one or more fragments of the AAV7 (or another novel AAV) capsid fused to heterologous AAV or non-AAV capsid proteins (or fragments thereof). These artificial capsid proteins are selected from non-contiguous portions of the AAV7 (or another novel AAV) capsid or from capsids of other AAV serotypes. For example, it may be desirable to modify the coding regions of one or more of the AAV vp1, e.g., in one or more of the hypervariable regions (i.e., HPV1-12), or vp2, and/or vp3. In another example, it may be desirable to alter the start codon of the vp3 protein to GTG. These modifications may be to increase expression, yield, and/or to improve purification in the selected expression systems, or for another desired purpose (e.g., to change tropism or alter neutralizing antibody epitopes).

The vectors described herein, e.g., a plasmid, are useful for a variety of purposes, but are particularly well suited for use in production of a rAAV containing a capsid comprising AAV sequences or a fragment thereof. These vectors, including rAAV, their elements, construction, and uses are described in detail herein.

In one aspect, the invention provides a method of generating a recombinant adeno-associated virus (AAV) having an AAV serotype 7 (or another novel AAV) capsid, or a portion thereof. Such a method involves culturing a host cell which contains a nucleic acid sequence encoding an adeno-associated virus (AAV) serotype 7 (or another novel AAV) capsid protein, or fragment thereof, as defined herein; a functional rep gene; a minigene composed of, at a minimum, AAV inverted terminal repeats (ITRs) and a transgene; and sufficient helper functions to permit packaging of the minigene into the AAV7 (or another novel AAV) capsid protein.

The components required to be cultured in the host cell to package an AAV minigene in an AAV capsid may be provided to the host cell in trans. Alternatively, any one or more of the required components (e.g., minigene, rep sequences, cap sequences, and/or helper functions) may be provided by a stable host cell which has been engineered to contain one or more of the required components using methods known to those of skill in the art. Most suitably, such a stable host cell will contain the required component(s) under the control of an inducible promoter. However, the required component(s) may be under the control of a constitutive promoter. Examples of suitable inducible and constitutive promoters are provided herein, in the discussion of regulatory elements suitable for use with the transgene. In still another alternative, a selected stable host cell may contain selected component(s) under the control of a constitutive promoter and other selected component(s) under the control of one or more inducible promoters. For example, a stable host cell may be generated which is derived from 293 cells (which contain E1 helper functions under the control of a constitutive promoter), but which contains the rep and/or cap proteins under the control of inducible promoters. Still other stable host cells may be generated by one of skill in the art.

The minigene, rep sequences, cap sequences, and helper functions required for producing the rAAV of the invention may be delivered to the packaging host cell in the form of any genetic element which transfer the sequences carried thereon. The selected genetic element may be delivered by any suitable method, including those described herein. The methods used to construct any embodiment of this invention are known to those with skill in nucleic acid manipulation and include genetic engineering, recombinant engineering, and synthetic techniques. See, e.g., Sambrook et al, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor, N.Y. Similarly, methods of generating rAAV virions are well known and the selection of a suitable method is not a limitation on the present invention. See, e.g., K. Fisher et al, *J. Virol.*, 70:520-532 (1993) and U.S. Pat. No. 5,478,745.

A. The Minigene

The minigene is composed of, at a minimum, a transgene and its regulatory sequences, and 5= and 3=AAV inverted terminal repeats (ITRs). It is this minigene which is packaged into a capsid protein and delivered to a selected host cell.

1. The Transgene

The transgene is a nucleic acid sequence, heterologous to the vector sequences flanking the transgene, which encodes a polypeptide, protein, or other product, of interest. The nucleic acid coding sequence is operatively linked to regulatory components in a manner which permits transgene transcription, translation, and/or expression in a host cell.

The composition of the transgene sequence will depend upon the use to which the resulting vector will be put. For example, one type of transgene sequence includes a reporter sequence, which upon expression produces a detectable signal. Such reporter sequences include, without limitation, DNA sequences encoding β-lactamase, β-galactosidase (LacZ), alkaline phosphatase, thymidine kinase, green fluorescent protein (GFP), chloramphenicol acetyltransferase (CAT), luciferase, membrane bound proteins including, for example, CD2, CD4, CD8, the influenza hemagglutinin protein, and others well known in the art, to which high affinity antibodies directed thereto exist or can be produced by conventional means, and fusion proteins comprising a membrane bound protein appropriately fused to an antigen tag domain from, among others, hemagglutinin or Myc.

These coding sequences, when associated with regulatory elements which drive their expression, provide signals detectable by conventional means, including enzymatic, radiographic, colorimetric, fluorescence or other spectrographic assays, fluorescent activating cell sorting assays and immunological assays, including enzyme linked immunosorbent assay (ELISA), radioimmunoassay (RIA) and immunohistochemistry. For example, where the marker sequence is the LacZ gene, the presence of the vector carrying the signal is detected by assays for beta-galactosidase activity. Where the transgene is green fluorescent protein or luciferase, the vector carrying the signal may be measured visually by color or light production in a luminometer.

However, desirably, the transgene is a non-marker sequence encoding a product which is useful in biology and medicine, such as proteins, peptides, RNA, enzymes, or catalytic RNAs. Desirable RNA molecules include tRNA, dsRNA, ribosomal RNA, catalytic RNAs, and antisense RNAs. One example of a useful RNA sequence is a sequence which extinguishes expression of a targeted nucleic acid sequence in the treated animal.

The transgene may be used to correct or ameliorate gene deficiencies, which may include deficiencies in which normal genes are expressed at less than normal levels or deficiencies in which the functional gene product is not expressed. A preferred type of transgene sequence encodes a therapeutic protein or polypeptide which is expressed in a host cell. The invention further includes using multiple transgenes, e.g., to correct or ameliorate a gene defect caused by a multi-subunit protein. In certain situations, a different transgene may be used to encode each subunit of a protein, or to encode different peptides or proteins. This is desirable when the size of the DNA encoding the protein subunit is large, e.g., for an immunoglobulin, the platelet-derived growth factor, or a dystrophin protein. In order for the cell to produce the multi-subunit protein, a cell is infected with the recombinant virus containing each of the different subunits. Alternatively, different subunits of a protein may be encoded by the same transgene. In this case, a single transgene includes the DNA encoding each of the subunits, with the DNA for each subunit separated by an internal ribozyme entry site (IRES). This is desirable when the size of the DNA encoding each of the subunits is small, e.g., the total size of the DNA encoding the subunits and the IRES is less than five kilobases. As an alternative to an IRES, the DNA may be separated by sequences encoding a 2A peptide, which self-cleaves in a post-translational event. See, e.g., M. L. Donnelly, et al, *J. Gen. Virol.,* 78(Pt 1):13-21 (January 1997); Furler, S., et al, *Gene Ther.,* 8(11):864-873 (June 2001); Klump H., et al., *Gene Ther.,* 8(10):811-817 (May 2001). This 2A peptide is significantly smaller than an IRES, making it well suited for use when space is a limiting factor. However, the selected transgene may encode any biologically active product or other product, e.g., a product desirable for study.

Suitable transgenes may be readily selected by one of skill in the art. The selection of the transgene is not considered to be a limitation of this invention.

2. Regulatory Elements

In addition to the major elements identified above for the minigene, the vector also includes conventional control elements necessary which are operably linked to the transgene in a manner which permits its transcription, translation and/or expression in a cell transfected with the plasmid vector or infected with the virus produced by the invention. As used herein, Aoperably linked≅ sequences include both expression control sequences that are contiguous with the gene of interest and expression control sequences that act in trans or at a distance to control the gene of interest.

Expression control sequences include appropriate transcription initiation, termination, promoter and enhancer sequences; efficient RNA processing signals such as splicing and polyadenylation (polyA) signals; sequences that stabilize cytoplasmic mRNA; sequences that enhance translation efficiency (i.e., Kozak consensus sequence); sequences that enhance protein stability; and when desired, sequences that enhance secretion of the encoded product. A great number of expression control sequences, including promoters which are native, constitutive, inducible and/or tissue-specific, are known in the art and may be utilized.

Examples of constitutive promoters include, without limitation, the retroviral Rous sarcoma virus (RSV) LTR promoter (optionally with the RSV enhancer), the cytomegalovirus (CMV) promoter (optionally with the CMV enhancer) [see, e.g., Boshart et al, *Cell,* 41:521-530 (1985)], the SV40 promoter, the dihydrofolate reductase promoter, the β-actin promoter, the phosphoglycerol kinase (PGK) promoter, and the EF1α promoter [Invitrogen].

Inducible promoters allow regulation of gene expression and can be regulated by exogenously supplied compounds, environmental factors such as temperature, or the presence of a specific physiological state, e.g., acute phase, a particular differentiation state of the cell, or in replicating cells only. Inducible promoters and inducible systems are available from a variety of commercial sources, including, without limitation, Invitrogen, Clontech and Ariad. Many other systems have been described and can be readily selected by one of skill in the art. Examples of inducible promoters regulated by exogenously supplied promoters include the zinc-inducible sheep metallothionine (MT) promoter, the dexamethasone (Dex)-inducible mouse mammary tumor virus (MMTV) promoter, the T7 polymerase promoter system [WO 98/10088]; the ecdysone insect promoter [No et al, *Proc. Natl. Acad. Sci. USA,* 93:3346-3351 (1996)], the tetracycline-repressible system [Gossen et al, *Proc. Natl. Acad. Sci. USA,* 89:5547-5551 (1992)], the tetracycline-

inducible system [Gossen et al, *Science,* 268:1766-1769 (1995), see also Harvey et al, *Curr. Opin. Chem. Biol.,* 2:512-518 (1998)], the RU486-inducible system [Wang et al, *Nat. Biotech.,* 15:239-243 (1997) and Wang et al, *Gene Ther.,* 4:432-441 (1997)] and the rapamycin-inducible system [Magari et al, *J. Clin. Invest.,* 100:2865-2872 (1997)]. Still other types of inducible promoters which may be useful in this context are those which are regulated by a specific physiological state, e.g., temperature, acute phase, a particular differentiation state of the cell, or in replicating cells only.

In another embodiment, the native promoter for the transgene will be used. The native promoter may be preferred when it is desired that expression of the transgene should mimic the native expression. The native promoter may be used when expression of the transgene must be regulated temporally or developmentally, or in a tissue-specific manner, or in response to specific transcriptional stimuli. In a further embodiment, other native expression control elements, such as enhancer elements, polyadenylation sites or Kozak consensus sequences may also be used to mimic the native expression.

Another embodiment of the transgene includes a transgene operably linked to a tissue-specific promoter. For instance, if expression in skeletal muscle is desired, a promoter active in muscle should be used. These include the promoters from genes encoding skeletal β-actin, myosin light chain 2A, dystrophin, muscle creatine kinase, as well as synthetic muscle promoters with activities higher than naturally-occurring promoters (see Li et al., *Nat. Biotech.,* 17:241-245 (1999)). Examples of promoters that are tissue-specific are known for liver (albumin, Miyatake et al., *J. Virol.,* 71:5124-32 (1997); hepatitis B virus core promoter, Sandig et al., *Gene Ther.,* 3:1002-9 (1996); alpha-fetoprotein (AFP), Arbuthnot et al., *Hum. Gene Ther.,* 7:1503-14 (1996)), bone osteocalcin (Stein et al., *Mol. Biol. Rep.,* 24:185-96 (1997)); bone sialoprotein (Chen et al., *J. Bone Miner. Res.,* 11:654-64 (1996)), lymphocytes (CD2, Hansal et al., *J. Immunol.,* 161:1063-8 (1998); immunoglobulin heavy chain; T cell receptor a chain), neuronal such as neuron-specific enolase (NSE) promoter (Andersen et al., *Cell. Mol. Neurobiol.,* 13:503-15 (1993)), neurofilament light-chain gene (Piccioli et al., *Proc. Natl. Acad. Sci. USA,* 88:5611-5 (1991)), and the neuron-specific vgf gene (Piccioli et al., *Neuron,* 15:373-84 (1995)), among others.

Optionally, plasmids carrying therapeutically useful transgenes may also include selectable markers or reporter genes may include sequences encoding geneticin, hygromicin or purimycin resistance, among others. Such selectable reporters or marker genes (preferably located outside the viral genome to be rescued by the method of the invention) can be used to signal the presence of the plasmids in bacterial cells, such as ampicillin resistance. Other components of the plasmid may include an origin of replication. Selection of these and other promoters and vector elements are conventional and many such sequences are available [see, e.g., Sambrook et al, and references cited therein].

The combination of the transgene, promoter/enhancer, and 5= and 3=ITRs is referred to as a "minigene" for ease of reference herein. Provided with the teachings of this invention, the design of such a minigene can be made by resort to conventional techniques.

3. Delivery of the Minigene to a Packaging Host Cell

The minigene can be carried on any suitable vector, e.g., a plasmid, which is delivered to a host cell. The plasmids useful in this invention may be engineered such that they are suitable for replication and, optionally, integration in prokaryotic cells, mammalian cells, or both. These plasmids (or other vectors carrying the 5' AAV ITR-heterologous molecule-3'ITR) contain sequences permitting replication of the minigene in eukaryotes and/or prokaryotes and selection markers for these systems. Selectable markers or reporter genes may include sequences encoding geneticin, hygromicin or purimycin resistance, among others. The plasmids may also contain certain selectable reporters or marker genes that can be used to signal the presence of the vector in bacterial cells, such as ampicillin resistance. Other components of the plasmid may include an origin of replication and an amplicon, such as the amplicon system employing the Epstein Barr virus nuclear antigen. This amplicon system, or other similar amplicon components permit high copy episomal replication in the cells. Preferably, the molecule carrying the minigene is transfected into the cell, where it may exist transiently. Alternatively, the minigene (carrying the 5' AAV ITR-heterologous molecule-3' ITR) may be stably integrated into the genome of the host cell, either chromosomally or as an episome. In certain embodiments, the minigene may be present in multiple copies, optionally in head-to-head, head-to-tail, or tail-to-tail concatamers. Suitable transfection techniques are known and may readily be utilized to deliver the minigene to the host cell.

Generally, when delivering the vector comprising the minigene by transfection, the vector is delivered in an amount from about 5 μg to about 100 μg DNA, and preferably about 10 to about 50 μg DNA to about 1×10^4 cells to about 1×10^{13} cells, and preferably about 10^5 cells. However, the relative amounts of vector DNA to host cells may be adjusted, taking into consideration such factors as the selected vector, the delivery method and the host cells selected.

B. Rep and Cap Sequences

In addition to the minigene, the host cell contains the sequences which drive expression of the novel AAV capsid protein (e.g., AAV7 or other novel AAV capsid or an artificial capsid protein comprising a fragment of one or more of these capsids) in the host cell and rep sequences of the same serotype as the serotype of the AAV ITRs found in the minigene. The AAV cap and rep sequences may be independently obtained from an AAV source as described above and may be introduced into the host cell in any manner known to one in the art as described above. Additionally, when pseudotyping a novel AAV capsid of the invention, the sequences encoding each of the essential rep proteins may be supplied by the same AAV serotype, or the sequences encoding the rep proteins may be supplied by different AAV serotypes (e.g., AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, or one of the novel serotypes identified herein). For example, the rep78/68 sequences may be from AAV2, whereas the rep52/40 sequences may from AAV1.

In one embodiment, the host cell stably contains the capsid protein under the control of a suitable promoter, such as those described above. Most desirably, in this embodiment, the capsid protein is expressed under the control of an inducible promoter. In another embodiment, the capsid protein is supplied to the host cell in trans. When delivered to the host cell in trans, the capsid protein may be delivered via a plasmid which contains the sequences necessary to direct expression of the selected capsid protein in the host cell. Most desirably, when delivered to the host cell in trans, the plasmid carrying the capsid protein also carries other sequences required for packaging the rAAV, e.g., the rep sequences.

In another embodiment, the host cell stably contains the rep sequences under the control of a suitable promoter, such as those described above. Most desirably, in this embodi-

ment, the essential rep proteins are expressed under the control of an inducible promoter. In another embodiment, the rep proteins are supplied to the host cell in trans. When delivered to the host cell in trans, the rep proteins may be delivered via a plasmid which contains the sequences necessary to direct expression of the selected rep proteins in the host cell. Most desirably, when delivered to the host cell in trans, the plasmid carrying the capsid protein also carries other sequences required for packaging the rAAV, e.g., the rep and cap sequences.

Thus, in one embodiment, the rep and cap sequences may be transfected into the host cell on a single nucleic acid molecule and exist stably in the cell as an episome. In another embodiment, the rep and cap sequences are stably integrated into the genome of the cell. Another embodiment has the rep and cap sequences transiently expressed in the host cell. For example, a useful nucleic acid molecule for such transfection comprises, from 5' to 3', a promoter, an optional spacer interposed between the promoter and the start site of the rep gene sequence, an AAV rep gene sequence, and an AAV cap gene sequence.

Optionally, the rep and/or cap sequences may be supplied on a vector that contains other DNA sequences that are to be introduced into the host cells. For instance, the vector may contain the rAAV construct comprising the minigene. The vector may comprise one or more of the genes encoding the helper functions, e.g., the adenoviral proteins E1, E2a, and E4ORF6, and the gene for VAI RNA.

Preferably, the promoter used in this construct may be any of the constitutive, inducible or native promoters known to one of skill in the art or as discussed above. In one embodiment, an AAV P5 promoter sequence is employed. The selection of the AAV to provide any of these sequences does not limit the invention.

In another preferred embodiment, the promoter for rep is an inducible promoter, as are discussed above in connection with the transgene regulatory elements. One preferred promoter for rep expression is the T7 promoter. The vector comprising the rep gene regulated by the T7 promoter and the cap gene, is transfected or transformed into a cell which either constitutively or inducibly expresses the T7 polymerase. See WO 98/10088, published Mar. 12, 1998.

The spacer is an optional element in the design of the vector. The spacer is a DNA sequence interposed between the promoter and the rep gene ATG start site. The spacer may have any desired design; that is, it may be a random sequence of nucleotides, or alternatively, it may encode a gene product, such as a marker gene. The spacer may contain genes which typically incorporate start/stop and polyA sites. The spacer may be a non-coding DNA sequence from a prokaryote or eukaryote, a repetitive non-coding sequence, a coding sequence without transcriptional controls or a coding sequence with transcriptional controls. Two exemplary sources of spacer sequences are the λ phage ladder sequences or yeast ladder sequences, which are available commercially, e.g., from Gibco or Invitrogen, among others. The spacer may be of any size sufficient to reduce expression of the rep78 and rep68 gene products, leaving the rep52, rep40 and cap gene products expressed at normal levels. The length of the spacer may therefore range from about 10 bp to about 10.0 kbp, preferably in the range of about 100 bp to about 8.0 kbp. To reduce the possibility of recombination, the spacer is preferably less than 2 kbp in length; however, the invention is not so limited.

Although the molecule(s) providing rep and cap may exist in the host cell transiently (i.e., through transfection), it is preferred that one or both of the rep and cap proteins and the promoter(s) controlling their expression be stably expressed in the host cell, e.g., as an episome or by integration into the chromosome of the host cell. The methods employed for constructing embodiments of this invention are conventional genetic engineering or recombinant engineering techniques such as those described in the references above. While this specification provides illustrative examples of specific constructs, using the information provided herein, one of skill in the art may select and design other suitable constructs, using a choice of spacers, P5 promoters, and other elements, including at least one translational start and stop signal, and the optional addition of polyadenylation sites.

In another embodiment of this invention, the rep or cap protein may be provided stably by a host cell.

C. The Helper Functions

The packaging host cell also requires helper functions in order to package the rAAV of the invention. Optionally, these functions may be supplied by a herpesvirus. Most desirably, the necessary helper functions are each provided from a human or non-human primate adenovirus source, such as those described above and/or are available from a variety of sources, including the American Type Culture Collection (ATCC), Manassas, Va. (US). In one currently preferred embodiment, the host cell is provided with and/or contains an E1a gene product, an E1b gene product, an E2a gene product, and/or an E4 ORF6 gene product. The host cell may contain other adenoviral genes such as VAI RNA, but these genes are not required. In a preferred embodiment, no other adenovirus genes or gene functions are present in the host cell.

By Aadenoviral DNA which expresses the E1a gene product≅, it is meant any adenovirus sequence encoding E1a or any functional E1a portion. Adenoviral DNA which expresses the E2a gene product and adenoviral DNA which expresses the E4 ORF6 gene products are defined similarly. Also included are any alleles or other modifications of the adenoviral gene or functional portion thereof. Such modifications may be deliberately introduced by resort to conventional genetic engineering or mutagenic techniques to enhance the adenoviral function in some manner, as well as naturally occurring allelic variants thereof. Such modifications and methods for manipulating DNA to achieve these adenovirus gene functions are known to those of skill in the art.

The adenovirus E1a, E1b, E2a, and/or E4ORF6 gene products, as well as any other desired helper functions, can be provided using any means that allows their expression in a cell. Each of the sequences encoding these products may be on a separate vector, or one or more genes may be on the same vector. The vector may be any vector known in the art or disclosed above, including plasmids, cosmids and viruses. Introduction into the host cell of the vector may be achieved by any means known in the art or as disclosed above, including transfection, infection, electroporation, liposome delivery, membrane fusion techniques, high velocity DNA-coated pellets, viral infection and protoplast fusion, among others. One or more of the adenoviral genes may be stably integrated into the genome of the host cell, stably expressed as episomes, or expressed transiently. The gene products may all be expressed transiently, on an episome or stably integrated, or some of the gene products may be expressed stably while others are expressed transiently. Furthermore, the promoters for each of the adenoviral genes may be selected independently from a constitutive promoter, an inducible promoter or a native adenoviral promoter. The promoters may be regulated by a specific physiological state

of the organism or cell (i.e., by the differentiation state or in replicating or quiescent cells) or by exogenously-added factors, for example.

D. Host Cells and Packaging Cell Lines

The host cell itself may be selected from any biological organism, including prokaryotic (e.g., bacterial) cells, and eukaryotic cells, including, insect cells, yeast cells and mammalian cells. Particularly desirable host cells are selected from among any mammalian species, including, without limitation, cells such as A549, WEHI, 3T3, 10T 1/2, BHK, MDCK, COS 1, COS 7, BSC 1, BSC 40, BMT 10, VERO, WI38, HeLa, 293 cells (which express functional adenoviral E1), Saos, C2C12, L cells, HT1080, HepG2 and primary fibroblast, hepatocyte and myoblast cells derived from mammals including human, monkey, mouse, rat, rabbit, and hamster. The selection of the mammalian species providing the cells is not a limitation of this invention; nor is the type of mammalian cell, i.e., fibroblast, hepatocyte, tumor cell, etc. The most desirable cells do not carry any adenovirus gene other than E1, E2a and/or E4 ORF6; nor do they contain any other virus gene which could result in homologous recombination of a contaminating virus during the production of rAAV; and it is capable of infection or transfection of DNA and expression of the transfected DNA. In a preferred embodiment, the host cell is one that has rep and cap stably transfected in the cell.

One host cell useful in the present invention is a host cell stably transformed with the sequences encoding rep and cap, and which is transfected with the adenovirus E1, E2a, and E4ORF6 DNA and a construct carrying the minigene as described above. Stable rep and/or cap expressing cell lines, such as B-50 (PCT/US98/19463), or those described in U.S. Pat. No. 5,658,785, may also be similarly employed. Another desirable host cell contains the minimum adenoviral DNA which is sufficient to express E4 ORF6. Yet other cell lines can be constructed using the novel AAV rep and/or novel AAV cap sequences of the invention.

The preparation of a host cell according to this invention involves techniques such as assembly of selected DNA sequences. This assembly may be accomplished utilizing conventional techniques. Such techniques include cDNA and genomic cloning, which are well known and are described in Sambrook et al., cited above, use of overlapping oligonucleotide sequences of the adenovirus and AAV genomes, combined with polymerase chain reaction, synthetic methods, and any other suitable methods which provide the desired nucleotide sequence.

Introduction of the molecules (as plasmids or viruses) into the host cell may also be accomplished using techniques known to the skilled artisan and as discussed throughout the specification. In preferred embodiment, standard transfection techniques are used, e.g., $CaPO_4$ transfection or electroporation, and/or infection by hybrid adenovirus/AAV vectors into cell lines such as the human embryonic kidney cell line HEK 293 (a human kidney cell line containing functional adenovirus E1 genes which provides trans-acting E1 proteins).

These novel AAV-based vectors which are generated by one of skill in the art are beneficial for gene delivery to selected host cells and gene therapy patients since no neutralization antibodies to AAV7 have been found in the human population. Further, early studies show no neutralizing antibodies in cyno monkey and chimpanzee populations, and less than 15% cross-reactivity of AAV7 in rhesus monkeys, the species from which the serotype was isolated. One of skill in the art may readily prepare other rAAV viral vectors containing the AAV7 capsid proteins provided herein using a variety of techniques known to those of skill in the art. One may similarly prepare still other rAAV viral vectors containing AAV7 sequence and AAV capsids of another serotype. Similar advantages are conferred by the vectors based on the other novel AAV of the invention.

Thus, one of skill in the art will readily understand that the AAV7 sequences of the invention can be readily adapted for use in these and other viral vector systems for in vitro, ex vivo or in vivo gene delivery. Similarly, one of skill in the art can readily select other fragments of the novel AAV genome of the invention for use in a variety of rAAV and non-rAAV vector systems. Such vectors systems may include, e.g., lentiviruses, retroviruses, poxviruses, vaccinia viruses, and adenoviral systems, among others. Selection of these vector systems is not a limitation of the present invention.

Thus, the invention further provides vectors generated using the nucleic acid and amino acid sequences of the novel AAV of the invention. Such vectors are useful for a variety of purposes, including for delivery of therapeutic molecules and for use in vaccine regimens. Particularly desirable for delivery of therapeutic molecules are recombinant AAV containing capsids of the novel AAV of the invention. These, or other vector constructs containing novel AAV sequences of the invention may be used in vaccine regimens, e.g., for co-delivery of a cytokine, or for delivery of the immunogen itself.

V. Recombinant Viruses and Uses Thereof

Using the techniques described herein, one of skill in the art may generate a rAAV having a capsid of a novel serotype of the invention, or a novel capsid containing one or more novel fragments of an AAV serotype identified by the method of the invention. In one embodiment, a full-length capsid from a single serotype, e.g., AAV7 [SEQ ID NO: 2] can be utilized. In another embodiment, a full-length capsid may be generated which contains one or more fragments of a novel serotype of the invention fused in frame with sequences from another selected AAV serotype. For example, a rAAV may contain one or more of the novel hypervariable region sequences of an AAV serotype of the invention. Alternatively, the unique AAV serotypes of the invention may be used in constructs containing other viral or non-viral sequences.

It will be readily apparent to one of skill in the art one embodiment, that certain serotypes of the invention will be particularly well suited for certain uses. For example, vectors based on AAV7 capsids of the invention are particularly well suited for use in muscle; whereas vectors based on rh.10 (44-2) capsids of the invention are particularly well suited for use in lung. Uses of such vectors are not so limited and one of skill in the art may utilize these vectors for delivery to other cell types, tissues or organs. Further, vectors based upon other capsids of the invention may be used for delivery to these or other cells, tissues or organs.

A. Delivery of Transgene

In another aspect, the present invention provides a method for delivery of a transgene to a host which involves transfecting or infecting a selected host cell with a vector generated with the sequences of the AAV of the invention. Methods for delivery are well known to those of skill in the art and are not a limitation of the present invention.

In one desirable embodiment, the invention provides a method for AAV-mediated delivery of a transgene to a host. This method involves transfecting or infecting a selected host cell with a recombinant viral vector containing a selected transgene under the control of sequences which direct expression thereof and AAV capsid proteins.

Optionally, a sample from the host may be first assayed for the presence of antibodies to a selected AAV serotype. A variety of assay formats for detecting neutralizing antibodies are well known to those of skill in the art. The selection of such an assay is not a limitation of the present invention. See, e.g., Fisher et al, *Nature Med.*, 3(3):306-312 (March 1997) and W. C. Manning et al, *Human Gene Therapy*, 9:477-485 (Mar. 1, 1998). The results of this assay may be used to determine which AAV vector containing capsid proteins of a particular serotype are preferred for delivery, e.g., by the absence of neutralizing antibodies specific for that capsid serotype.

In one aspect of this method, the delivery of vector with a selected AAV capsid proteins may precede or follow delivery of a gene via a vector with a different serotype AAV capsid protein. Similarly, the delivery of vector with other novel AAV capsid proteins of the invention may precede or follow delivery of a gene via a vector with a different serotype AAV capsid protein. Thus, gene delivery via rAAV vectors may be used for repeat gene delivery to a selected host cell. Desirably, subsequently administered rAAV vectors carry the same transgene as the first rAAV vector, but the subsequently administered vectors contain capsid proteins of serotypes which differ from the first vector. For example, if a first vector has AAV7 capsid proteins [SEQ ID NO:2], subsequently administered vectors may have capsid proteins selected from among the other serotypes, including AAV1, AAV2, AAV3A, AAV3B, AAV4, AAV6, AAV10, AAV11, and AAV12, or any of the other novel AAV capsids identified herein including, without limitation: A3.1, H2, H6, C1, C2, C5, A3-3, A3-7, A3-4, A3-5, 3.3b, 223.4, 223-5, 223-10, 223-2, 223-7, 223-6, 44-1, 44-5, 44-2, 42-15, 42-8, 42-13, 42-3A, 42-4, 42-5A, 42-1B, 42-5B, 43-1, 43-12, 43-5, 43-21, 43-25, 43-20, 24.1, 42.2, 7.2, 27.3, 16.3, 42.10, 42-3B, 42-11, F1, F5, F3, 42-6B, and/or 42-12.

The above-described recombinant vectors may be delivered to host cells according to published methods. The rAAV, preferably suspended in a physiologically compatible carrier, may be administered to a human or non-human mammalian patient. Suitable carriers may be readily selected by one of skill in the art in view of the indication for which the transfer virus is directed. For example, one suitable carrier includes saline, which may be formulated with a variety of buffering solutions (e.g., phosphate buffered saline). Other exemplary carriers include sterile saline, lactose, sucrose, calcium phosphate, gelatin, dextran, agar, pectin, peanut oil, sesame oil, and water. The selection of the carrier is not a limitation of the present invention.

Optionally, the compositions of the invention may contain, in addition to the rAAV and carrier(s), other conventional pharmaceutical ingredients, such as preservatives, or chemical stabilizers. Suitable exemplary preservatives include chlorobutanol, potassium sorbate, sorbic acid, sulfur dioxide, propyl gallate, the parabens, ethyl vanillin, glycerin, phenol, and parachlorophenol. Suitable chemical stabilizers include gelatin and albumin.

The viral vectors are administered in sufficient amounts to transfect the cells and to provide sufficient levels of gene transfer and expression to provide a therapeutic benefit without undue adverse effects, or with medically acceptable physiological effects, which can be determined by those skilled in the medical arts. Conventional and pharmaceutically acceptable routes of administration include, but are not limited to, direct delivery to the selected organ (e.g., intraportal delivery to the liver), oral, inhalation (including intranasal and intratracheal delivery), intraocular, intravenous, intramuscular, subcutaneous, intradermal, and other parental routes of administration. Routes of administration may be combined, if desired.

Dosages of the viral vector will depend primarily on factors such as the condition being treated, the age, weight and health of the patient, and may thus vary among patients. For example, a therapeutically effective human dosage of the viral vector is generally in the range of from about 1 ml to about 100 ml of solution containing concentrations of from about 1×10^9 to 1×10^{16} genomes virus vector. A preferred human dosage may be about 1×10^{13} to 1×10^{16} AAV genomes. The dosage will be adjusted to balance the therapeutic benefit against any side effects and such dosages may vary depending upon the therapeutic application for which the recombinant vector is employed. The levels of expression of the transgene can be monitored to determine the frequency of dosage resulting in viral vectors, preferably AAV vectors containing the minigene. Optionally, dosage regimens similar to those described for therapeutic purposes may be utilized for immunization using the compositions of the invention.

Examples of therapeutic products and immunogenic products for delivery by the AAV-containing vectors of the invention are provided below. These vectors may be used for a variety of therapeutic or vaccinal regimens, as described herein. Additionally, these vectors may be delivered in combination with one or more other vectors or active ingredients in a desired therapeutic and/or vaccinal regimen.

B. Therapeutic Transgenes

Useful therapeutic products encoded by the transgene include hormones and growth and differentiation factors including, without limitation, insulin, glucagon, growth hormone (GH), parathyroid hormone (PTH), growth hormone releasing factor (GRF), follicle stimulating hormone (FSH), luteinizing hormone (LH), human chorionic gonadotropin (hCG), vascular endothelial growth factor (VEGF), angiopoietins, angiostatin, granulocyte colony stimulating factor (GCSF), erythropoietin (EPO), connective tissue growth factor (CTGF), basic fibroblast growth factor (bFGF), acidic fibroblast growth factor (aFGF), epidermal growth factor (EGF), transforming growth factor α (TGFα), platelet-derived growth factor (PDGF), insulin growth factors I and II (IGF-I and IGF-II), any one of the transforming growth factor β superfamily, including TGF β, activins, inhibins, or any of the bone morphogenic proteins (BMP) BMPs 1-15, any one of the heregluin/neuregulin/ARIA/neu differentiation factor (NDF) family of growth factors, nerve growth factor (NGF), brain-derived neurotrophic factor (BDNF), neurotrophins NT-3 and NT-4/5, ciliary neurotrophic factor (CNTF), glial cell line derived neurotrophic factor (GDNF), neurturin, agrin, any one of the family of semaphorins/collapsins, netrin-1 and netrin-2, hepatocyte growth factor (HGF), ephrins, noggin, sonic hedgehog and tyrosine hydroxylase.

Other useful transgene products include proteins that regulate the immune system including, without limitation, cytokines and lymphokines such as thrombopoietin (TPO), interleukins (IL) IL-1 through IL-25 (including, IL-2, IL-4, IL-12, and IL-18), monocyte chemoattractant protein, leukemia inhibitory factor, granulocyte-macrophage colony stimulating factor, Fas ligand, tumor necrosis factors α and β, interferons α, β, and γ, stem cell factor, flk-2/flt3 ligand. Gene products produced by the immune system are also useful in the invention. These include, without limitations, immunoglobulins IgG, IgM, IgA, IgD and IgE, chimeric immunoglobulins, humanized antibodies, single chain antibodies, T cell receptors, chimeric T cell receptors, single

chain T cell receptors, class I and class II MHC molecules, as well as engineered immunoglobulins and MHC molecules. Useful gene products also include complement regulatory proteins such as complement regulatory proteins, membrane cofactor protein (MCP), decay accelerating factor (DAF), CR1, CF2 and CD59.

Still other useful gene products include any one of the receptors for the hormones, growth factors, cytokines, lymphokines, regulatory proteins and immune system proteins. The invention encompasses receptors for cholesterol regulation, including the low density lipoprotein (LDL) receptor, high density lipoprotein (HDL) receptor, the very low density lipoprotein (VLDL) receptor, and the scavenger receptor. The invention also encompasses gene products such as members of the steroid hormone receptor superfamily including glucocorticoid receptors and estrogen receptors, Vitamin D receptors and other nuclear receptors. In addition, useful gene products include transcription factors such asjun, fos, max, mad, serum response factor (SRF), AP-1, AP2, myb, MyoD and myogenin, ETS-box containing proteins, TFE3, E2F, ATF1, ATF2, ATF3, ATF4, ZF5, NFAT, CREB, HNF-4, C/EBP, SP1, CCAAT-box binding proteins, interferon regulation factor (IRF-1), Wilms tumor protein, ETS-binding protein, STAT, GATA-box binding proteins, e.g., GATA-3, and the forkhead family of winged helix proteins.

Other useful gene products include, carbamoyl synthetase I, ornithine transcarbamylase, arginosuccinate synthetase, arginosuccinate lyase, arginase, fumarylacetacetate hydrolase, phenylalanine hydroxylase, alpha-1 antitrypsin, glucose-6-phosphatase, porphobilinogen deaminase, factor VIII, factor IX, cystathione beta-synthase, branched chain ketoacid decarboxylase, albumin, isovaleryl-coA dehydrogenase, propionyl CoA carboxylase, methyl malonyl CoA mutase, glutaryl CoA dehydrogenase, insulin, beta-glucosidase, pyruvate carboxylate, hepatic phosphorylase, phosphorylase kinase, glycine decarboxylase, H-protein, T-protein, a cystic fibrosis transmembrane regulator (CFTR) sequence, and a dystrophin cDNA sequence. Still other useful gene products include enzymes such as may be useful in enzyme replacement therapy, which is useful in a variety of conditions resulting from deficient activity of enzyme. For example, enzymes that contain mannose-6-phosphate may be utilized in therapies for lysosomal storage diseases (e.g., a suitable gene includes that encoding β-glucuronidase (GUSB)).

Other useful gene products include non-naturally occurring polypeptides, such as chimeric or hybrid polypeptides having a non-naturally occurring amino acid sequence containing insertions, deletions or amino acid substitutions. For example, single-chain engineered immunoglobulins could be useful in certain immunocompromised patients. Other types of non-naturally occurring gene sequences include antisense molecules and catalytic nucleic acids, such as ribozymes, which could be used to reduce overexpression of a target.

Reduction and/or modulation of expression of a gene is particularly desirable for treatment of hyperproliferative conditions characterized by hyperproliferating cells, as are cancers and psoriasis. Target polypeptides include those polypeptides which are produced exclusively or at higher levels in hyperproliferative cells as compared to normal cells. Target antigens include polypeptides encoded by oncogenes such as myb, myc, fyn, and the translocation gene bcr/abl, ras, src, P53, neu, trk and EGRF. In addition to oncogene products as target antigens, target polypeptides for anti-cancer treatments and protective regimens include variable regions of antibodies made by B cell lymphomas and variable regions of T cell receptors of T cell lymphomas which, in some embodiments, are also used as target antigens for autoimmune disease. Other tumor-associated polypeptides can be used as target polypeptides such as polypeptides which are found at higher levels in tumor cells including the polypeptide recognized by monoclonal antibody 17-1A and folate binding polypeptides.

Other suitable therapeutic polypeptides and proteins include those which may be useful for treating individuals suffering from autoimmune diseases and disorders by conferring a broad based protective immune response against targets that are associated with autoimmunity including cell receptors and cells which produce Aself≅-directed antibodies. T cell mediated autoimmune diseases include Rheumatoid arthritis (RA), multiple sclerosis (MS), Sjögren's syndrome, sarcoidosis, insulin dependent diabetes mellitus (IDDM), autoimmune thyroiditis, reactive arthritis, ankylosing spondylitis, scleroderma, polymyositis, dermatomyositis, psoriasis, vasculitis, Wegener's granulomatosis, Crohn's disease and ulcerative colitis. Each of these diseases is characterized by T cell receptors (TCRs) that bind to endogenous antigens and initiate the inflammatory cascade associated with autoimmune diseases.

C. Immunogenic Transgenes

Alternatively, or in addition, the vectors of the invention may contain AAV sequences of the invention and a transgene encoding a peptide, polypeptide or protein which induces an immune response to a selected immunogen. For example, immunogens may be selected from a variety of viral families. Example of desirable viral families against which an immune response would be desirable include, the picornavirus family, which includes the genera rhinoviruses, which are responsible for about 50% of cases of the common cold; the genera enteroviruses, which include polioviruses, coxsackieviruses, echoviruses, and human enteroviruses such as hepatitis A virus; and the genera apthoviruses, which are responsible for foot and mouth diseases, primarily in non-human animals. Within the picornavirus family of viruses, target antigens include the VP1, VP2, VP3, VP4, and VPG. Another viral family includes the calcivirus family, which encompasses the Norwalk group of viruses, which are an important causative agent of epidemic gastroenteritis. Still another viral family desirable for use in targeting antigens for inducing immune responses in humans and non-human animals is the togavirus family, which includes the genera alphavirus, which include Sindbis viruses, Ross-River virus, and Venezuelan, Eastern & Western Equine encephalitis, and rubivirus, including Rubella virus. The flaviviridae family includes dengue, yellow fever, Japanese encephalitis, St. Louis encephalitis and tick borne encephalitis viruses. Other target antigens may be generated from the Hepatitis C or the coronavirus family, which includes a number of non-human viruses such as infectious bronchitis virus (poultry), porcine transmissible gastroenteric virus (pig), porcine hemagglutinating encephalomyelitis virus (pig), feline infectious peritonitis virus (cats), feline enteric coronavirus (cat), canine coronavirus (dog), and human respiratory coronaviruses, which may cause the common cold and/or non-A, B or C hepatitis. Within the coronavirus family, target antigens include the E1 (also called M or matrix protein), E2 (also called S or Spike protein), E3 (also called HE or hemagglutin-elterose) glycoprotein (not present in all coronaviruses), or N (nucleocapsid). Still other antigens may be targeted against the rhabdovirus family, which includes the genera vesiculovirus (e.g., Vesicular Stomatitis Virus), and the general lyssavirus (e.g., rabies).

Within the rhabdovirus family, suitable antigens may be derived from the G protein or the N protein. The family filoviridae, which includes hemorrhagic fever viruses such as Marburg and Ebola virus may be a suitable source of antigens. The paramyxovirus family includes parainfluenza Virus Type 1, parainfluenza Virus Type 3, bovine parainfluenza Virus Type 3, rubulavirus (mumps virus, parainfluenza Virus Type 2, parainfluenza virus Type 4, Newcastle disease virus (chickens), rinderpest, morbillivirus, which includes measles and canine distemper, and pneumovirus, which includes respiratory syncytial virus. The influenza virus is classified within the family orthomyxovirus and is a suitable source of antigen (e.g., the HA protein, the N1 protein). The bunyavirus family includes the genera bunyavirus (California encephalitis, La Crosse), phlebovirus (Rift Valley Fever), hantavirus (puremala is a hemahagin fever virus), nairovirus (Nairobi sheep disease) and various unassigned bungaviruses. The arenavirus family provides a source of antigens against LCM and Lassa fever virus. The reovirus family includes the genera reovirus, rotavirus (which causes acute gastroenteritis in children), orbiviruses, and cultivirus (Colorado Tick fever, Lebombo (humans), equine encephalosis, blue tongue).

The retrovirus family includes the sub-family oncorivirinal which encompasses such human and veterinary diseases as feline leukemia virus, HTLVI and HTLVII, lentivirinal (which includes human immunodeficiency virus (HIV), simian immunodeficiency virus (SIV), feline immunodeficiency virus (FIV), equine infectious anemia virus, and spumavirinal). Between the HIV and SIV, many suitable antigens have been described and can readily be selected. Examples of suitable HIV and SIV antigens include, without limitation the gag, pol, Vif, Vpx, VPR, Env, Tat and Rev proteins, as well as various fragments thereof. In addition, a variety of modifications to these antigens have been described. Suitable antigens for this purpose are known to those of skill in the art. For example, one may select a sequence encoding the gag, pol, Vif, and Vpr, Env, Tat and Rev, amongst other proteins. See, e.g., the modified gag protein which is described in U.S. Pat. No. 5,972,596. See, also, the HIV and SIV proteins described in D. H. Barouch et al, J. Virol., 75(5):2462-2467 (March 2001), and R. R. Amara, et al, Science, 292:69-74 (6 Apr. 2001). These proteins or subunits thereof may be delivered alone, or in combination via separate vectors or from a single vector.

The papovavirus family includes the sub-family polyomaviruses (BKU and JCU viruses) and the sub-family papillomavirus (associated with cancers or malignant progression of papilloma). The adenovirus family includes viruses (EX, AD7, ARD, O.B.) which cause respiratory disease and/or enteritis. The parvovirus family feline parvovirus (feline enteritis), feline panleucopeniavirus, canine parvovirus, and porcine parvovirus. The herpesvirus family includes the sub-family alphaherpesvirinae, which encompasses the genera simplexvirus (HSVI, HSVII), varicellovirus (pseudorabies, varicella zoster) and the sub-family betaherpesvirinae, which includes the genera cytomegalovirus (HCMV, muromegalovirus) and the sub-family gammaherpesvirinae, which includes the genera lymphocryptovirus, EBV (Burkitts lymphoma), infectious rhinotracheitis, Marek=s disease virus, and rhadinovirus. The poxvirus family includes the sub-family chordopoxvirinae, which encompasses the genera orthopoxvirus (Variola (Smallpox) and Vaccinia (Cowpox)), parapoxvirus, avipoxvirus, capripoxvirus, leporipoxvirus, suipoxvirus, and the sub-family entomopoxvirinae. The hepadnavirus family includes the Hepatitis B virus. One unclassified virus which may be suitable source of antigens is the Hepatitis delta virus. Still other viral sources may include avian infectious bursal disease virus and porcine respiratory and reproductive syndrome virus. The alphavirus family includes equine arteritis virus and various Encephalitis viruses.

The present invention may also encompass immunogens which are useful to immunize a human or non-human animal against other pathogens including bacteria, fungi, parasitic microorganisms or multicellular parasites which infect human and non-human vertebrates, or from a cancer cell or tumor cell. Examples of bacterial pathogens include pathogenic gram-positive cocci include pneumococci; staphylococci; and streptococci. Pathogenic gram-negative cocci include meningococcus; gonococcus. Pathogenic enteric gram-negative bacilli include enterobacteriaceae; pseudomonas, acinetobacteria and eikenella; melioidosis; salmonella; shigella; haemophilus; moraxella; *H. ducreyi* (which causes chancroid); brucella; *Franisella tularensis* (which causes tularemia); yersinia (pasteurella); streptobacillus moniliformis and spirillum; Gram-positive bacilli include listeria monocytogenes; erysipelothrix rhusiopathiae; *Corynebacterium diphtheria* (diphtheria); cholera; *B. anthracis* (anthrax); donovanosis (granuloma inguinale); and bartonellosis. Diseases caused by pathogenic anaerobic bacteria include tetanus; botulism; other clostridia; tuberculosis; leprosy; and other mycobacteria. Pathogenic spirochetal diseases include syphilis; treponematoses: yaws, pinta and endemic syphilis; and leptospirosis. Other infections caused by higher pathogen bacteria and pathogenic fungi include actinomycosis; nocardiosis; cryptococcosis, blastomycosis, histoplasmosis and coccidioidomycosis; candidiasis, aspergillosis, and mucormycosis; sporotrichosis; paracoccidiodomycosis, petriellidiosis, torulopsosis, mycetoma and chromomycosis; and dermatophytosis. Rickettsial infections include Typhus fever, Rocky Mountain spotted fever, Q fever, and Rickettsialpox. Examples of mycoplasma and chlamydial infections include: mycoplasma pneumoniae; lymphogranuloma venereum; psittacosis; and perinatal chlamydial infections. Pathogenic eukaryotes encompass pathogenic protozoans and helminths and infections produced thereby include: amebiasis; malaria; leishmaniasis; trypanosomiasis; toxoplasmosis; *Pneumocystis carinii; Trichans; Toxoplasma gondii*; babesiosis; giardiasis; trichinosis; filariasis; schistosomiasis; nematodes; trematodes or flukes; and cestode (tapeworm) infections.

Many of these organisms and/or toxins produced thereby have been identified by the Centers for Disease Control [(CDC), Department of Heath and Human Services, USA], as agents which have potential for use in biological attacks. For example, some of these biological agents, include, *Bacillus anthracis* (anthrax), *Clostridium botulinum* and its toxin (botulism), *Yersinia pestis* (plague), variola major (smallpox), *Francisella tularensis* (tularemia), and viral hemorrhagic fever, all of which are currently classified as Category A agents; *Coxiella burnetti* (Q fever); *Brucella* species (brucellosis), *Burkholderia mallei* (glanders), *Ricinus communis* and its toxin (ricin toxin), *Clostridium perfringens* and its toxin (epsilon toxin), *Staphylococcus* species and their toxins (enterotoxin B), all of which are currently classified as Category B agents; and Nipan virus and hantaviruses, which are currently classified as Category C agents. In addition, other organisms, which are so classified or differently classified, may be identified and/or used for such a purpose in the future. It will be readily understood that the viral vectors and other constructs described herein are useful to deliver antigens from these organisms, viruses,

their toxins or other by-products, which will prevent and/or treat infection or other adverse reactions with these biological agents.

Administration of the vectors of the invention to deliver immunogens against the variable region of the T cells elicit an immune response including CTLs to eliminate those T cells. In rheumatoid arthritis (RA), several specific variable regions of T cell receptors (TCRs) which are involved in the disease have been characterized. These TCRs include V-3, V-14, V-17 and Vα-17. Thus, delivery of a nucleic acid sequence that encodes at least one of these polypeptides will elicit an immune response that will target T cells involved in RA. In multiple sclerosis (MS), several specific variable regions of TCRs which are involved in the disease have been characterized. These TCRs include V-7 and Vα-10. Thus, delivery of a nucleic acid sequence that encodes at least one of these polypeptides will elicit an immune response that will target T cells involved in MS. In scleroderma, several specific variable regions of TCRs which are involved in the disease have been characterized. These TCRs include V-6, V-8, V-14 and Vα-16, Vα-3C, Vα-7, Vα-14, Vα-15, Vα-16, Vα-28 and Vα-12. Thus, delivery of a nucleic acid molecule that encodes at least one of these polypeptides will elicit an immune response that will target T cells involved in scleroderma.

Optionally, vectors containing AAV sequences of the invention may be delivered using a prime-boost regimen. A variety of such regimens have been described in the art and may be readily selected. See, e.g., WO 00/11140, published Mar. 2, 2000, incorporated by reference.

Such prime-boost regimens typically involve the administration of a DNA (e.g., plasmid) based vector to prime the immune system to second, booster, administration with a traditional antigen, such as a protein or a recombinant virus carrying the sequences encoding such an antigen. In one embodiment, the invention provides a method of priming and boosting an immune response to a selected antigen by delivering a plasmid DNA vector carrying said antigen, followed by boosting, e.g., with a vector containing AAV sequences of the invention.

In one embodiment, the prime-boost regimen involves the expression of multiproteins from the prime and/or the boost vehicle. See, e.g., R. R. Amara, Science, 292:69-74 (6 Apr. 2001) which describes a multiprotein regimen for expression of protein subunits useful for generating an immune response against HIV and SIV. For example, a DNA prime may deliver the Gag, Pol, Vif, VPX and Vpr and Env, Tat, and Rev from a single transcript. Alternatively, the SIV Gag, Pol and HIV-1 Env is delivered.

However, the prime-boost regimens are not limited to immunization for HIV or to delivery of these antigens. For example, priming may involve delivering with a first chimp vector of the invention followed by boosting with a second chimp vector, or with a composition containing the antigen itself in protein form. In one or example, the prime-boost regimen can provide a protective immune response to the virus, bacteria or other organism from which the antigen is derived. In another desired embodiment, the prime-boost regimen provides a therapeutic effect that can be measured using convention assays for detection of the presence of the condition for which therapy is being administered.

The priming vaccine may be administered at various sites in the body in a dose dependent manner, which depends on the antigen to which the desired immune response is being targeted. The invention is not limited to the amount or situs of injection(s) or to the pharmaceutical carrier. Rather, the priming step encompasses treatment regimens which include a single dose or dosage which is administered hourly, daily, weekly or monthly, or yearly. As an example, the mammals may receive one or two priming injection containing between about 10 μg to about 50 μg of plasmid in carrier. A desirable priming amount or dosage of the priming DNA vaccine composition ranges between about 1 μg to about 10,000 μg of the DNA vaccine. Dosages may vary from about 1 μg to 1000 μg DNA per kg of subject body weight. The amount or site of injection is desirably selected based upon the identity and condition of the mammal being vaccinated.

The dosage unit of the DNA vaccine suitable for delivery of the antigen to the mammal is described herein. The DNA vaccine is prepared for administration by being suspended or dissolved in a pharmaceutically or physiologically acceptable carrier such as isotonic saline, isotonic salts solution or other formulations which will be apparent to those skilled in such administration. The appropriate carrier will be evident to those skilled in the art and will depend in large part upon the route of administration. The compositions of the invention may be administered to a mammal according to the routes described above, in a sustained release formulation using a biodegradable biocompatible polymer, or by on-site delivery using micelles, gels and liposomes.

Optionally, the priming step of this invention also includes administering with the priming DNA vaccine composition, a suitable amount of an adjuvant, such as are defined herein.

Preferably, a boosting composition is administered about 2 to about 27 weeks after administering the priming DNA vaccine to the mammalian subject. The administration of the boosting composition is accomplished using an effective amount of a boosting vaccine composition containing or capable of delivering the same antigen as administered by the priming DNA vaccine. The boosting composition may be composed of a recombinant viral vector derived from the same viral source or from another source. Alternatively, the "boosting composition" can be a composition containing the same antigen as encoded in the priming DNA vaccine, but in the form of a protein or peptide, which composition induces an immune response in the host. In another embodiment, the boosting vaccine composition includes a composition containing a DNA sequence encoding the antigen under the control of a regulatory sequence directing its expression in a mammalian cell, e.g., vectors such as well-known bacterial or viral vectors. The primary requirements of the boosting vaccine composition are that the antigen of the vaccine composition is the same antigen, or a cross-reactive antigen, as that encoded by the DNA vaccine.

Suitably, the vectors of the invention are also well suited for use in regimens which use non-AAV vectors as well as proteins, peptides, and/or other biologically useful therapeutic or immunogenic compounds. These regimens are particularly well suited to gene delivery for therapeutic poses and for immunization, including inducing protective immunity. Such uses will be readily apparent to one of skill in the art.

Further, a vector of the invention provides an efficient gene transfer vehicle which can deliver a selected transgene to a selected host cell in vivo or ex vivo even where the organism has neutralizing antibodies to one or more AAV serotypes. In one embodiment, the vector (e.g., an rAAV) and the cells are mixed ex vivo; the infected cells are cultured using conventional methodologies; and the transduced cells are re-infused into the patient. Further, the vectors of the invention may also be used for production of a desired gene product in vitro. For in vitro production, a

desired product (e.g., a protein) may be obtained from a desired culture following transfection of host cells with a rAAV containing the molecule encoding the desired product and culturing the cell culture under conditions which permit expression. The expressed product may then be purified and isolated, as desired. Suitable techniques for transfection, cell culturing, purification, and isolation are known to those of skill in the art.

The following examples illustrate several aspects and embodiments of the invention.

EXAMPLES

Example 1

PCR Amplification, Cloning and Characterization of Novel AAV Sequences

Tissues from nonhuman primates were screened for AAV sequences using a PCR method based on oligonucleotides to highly conserved regions of known AAVs. A stretch of AAV sequence spanning 2886 to 3143 bp of AAV1 [SEQ ID NO:6] was selected as a PCR amplicon in which a hypervariable region of the capsid protein (Cap) that is unique to each known AAV serotype, which is termed herein a "signature region," is flanked by conserved sequences. In later analysis, this signature region was shown to be located between conserved residues spanning hypervariable region 3.

An initial survey of peripheral blood of a number of nonhuman primate species revealed detectable AAV in a subset of animals from species such as rhesus macaques, cynomologous macaques, chimpanzees and baboons. However, there were no AAV sequences detected in some other species tested, including Japanese macaques, pig-tailed macaques and squirrel monkeys. A more extensive analysis of vector distribution was conducted in tissues of rhesus monkeys of the University of Pennsylvania and Tulane colonies recovered at necropsy. This revealed AAV sequence throughout a wide array of tissues.

A. Amplification of an AAV Signature Region

DNA sequences of AAV1-6 and AAVs isolated from Goose and Duck were aligned to each other using "Clustal W" at default settings. The alignment for AAV1-6, and including the information for the novel AAV7, is provided in FIG. **1**. Sequence similarities among AAVs were compared.

In the line of study, a 257 bp region spanning 2886 bp to 3143 bp of AAV 1 [SEQ ID NO: 6], and the corresponding region in the genomes of AAV 2-6 genomes [See, FIG. **1**], was identified by the inventors. This region is located with the AAV capsid gene and has highly conserved sequences among at both 5' and 3' ends and is relatively variable sequence in the middle. In addition, this region contains a DraIII restriction enzyme site (CACCACGTC, SEQ ID NO: 15). The inventors have found that this region serves as specific signature for each known type of AAV DNA. In other words, following PCR reactions, digestion with endonucleases that are specific to each known serotypes and gel electrophoresis analysis, this regions can be used to definitively identify amplified DNA as being from serotype 1, 2, 3, 4, 5, 6, or another serotype.

The primers were designed, validated and PCR conditions optimized with AAV1, 2 and 5 DNA controls. The primers were based upon the sequences of AAV2: 5' primer, 1S: bp 2867-2891 of AAV2 (SEQ ID NO:7) and 3' primer, 18as, bp 3095-3121 of AAV2 (SEQ ID NO:7).

Cellular DNAs from different tissues including blood, brain, liver, lung, testis, etc. of different rhesus monkeys were studied utilizing the strategy described above. The results revealed that DNAs from different tissues of these monkeys gave rise to strong PCR amplifications. Further restriction analyses of PCR products indicated that they were amplified from AAV sequences different from any published AAV sequences.

PCR products (about 255 bp in size) from DNAs of a variety of monkey tissues have been cloned and sequenced. Bioinformatics study of these novel AAV sequences indicated that they are novel AAV sequences of capsid gene and distinct from each other. FIG. **1** includes in the alignment the novel AAV signature regions for AAV10-12 [SEQ ID NO: 117, 118 and 119, respectively]. Multiple sequence alignment analysis was performed using the Clustal W (1.81) program. The percentage of sequence identity between the signature regions of AAV 1-7 and AAV 10-12 genomes is provided below.

TABLE 2

Sequences for Analysis

Sequence #	AAV Serotype	Size (bp)
1	AAV1	258
2	AAV2	255
3	AAV3	255
4	AAV4	246
5	AAV5	258
6	AAV6	258
7	AAV7	258
10	AAV10	255
11	AAV11	258
12	AAV12	255

TABLE 3

Pairwise Alignment (Percentage of Identity)

	AAV2	AAV3	AAV4	AAV5	AAV6	AAV7	AAV10	AAV11	AAV12
AAV1	90	90	81	76	97	91	93	94	93
AAV2		93	79	78	90	90	93	93	92
AAV3			80	76	90	92	92	92	92
AAV4				76	81	84	82	81	79
AAV5					75	78	79	79	76
AAV6						91	92	94	94
AAV7							94	92	92
AAV10								95	93
AAV11									94

Over 300 clones containing novel AAV serotype sequences that span the selected 257 bp region were isolated and sequenced. Bioinformatics analysis of these 300+ clones suggests that this 257 bp region is critical in serving as a good land marker or signature sequence for quick isolation and identification of novel AAV serotype.

B. Use of the Signature Region for PCR Amplification.

The 257 bp signature region was used as a PCR anchor to extend PCR amplifications to 5' of the genome to cover the junction region of rep and cap genes (1398 bp-3143 bp, SEQ ID NO:6) and 3' of the genome to obtain the entire cap gene sequence (2866 bp-4600 bp, SEQ ID NO:6). PCR amplifications were carried out using the standard conditions, including denaturing at 95° C. for 0.5-1 min, annealing at 60-65° C. for 0.5-1 min and extension at 72° C. for 1 min per kb with a total number of amplification cycles ranging from 28 to 42.

Using the aligned sequences as described in "A", two other relative conserved regions were identified in the sequence located in 3' end of rep genes and 5' to the 257 bp region and in the sequence down stream of the 257 bp fragment but before the AAV' 3 ITR. Two sets of new primers were designed and PCR conditions optimized for recovery of entire capsid and a part of rep sequences of novel AAV serotypes. More specifically, for the 5' amplification, the 5' primer, AV1Ns, was GCTGCGTCAACTGGACCAATGAGAAC [nt 1398-1423 of AAV1, SEQ ID NO:6] and the 3' primer was 18as, identified above. For the 3' amplification, the 5' primer was is, identified above, and the 3' primer was AV2Las, TCGTTTCAGTTGAACTTTGGTCTCTGCG [nt 4435-4462 of AAV2, SEQ ID NO:7].

In these PCR amplifications, the 257 bp region was used as a PCR anchor and land marker to generate overlapping fragments to construct a complete capsid gene by fusion at the DraIII site in the signature region following amplification of the 5' and 3' extension fragments obtained as described herein. More particularly, to generate the intact AAV7 cap gene, the three amplification products (a) the sequences of the signature region; (b) the sequences of the 5' extension; and (c) the sequences of the 3' extension were cloned into a pCR4-Topo [Invitrogen] plasmid backbone according to manufacturer's instructions. Thereafter, the plasmids were digested with DraIII and recombined to form an intact cap gene.

In this line of work, about 80% of capsid sequences of AAV7 and AAV 8 were isolated and analyzed. Another novel serotype, AAV9, was also discovered from Monkey #2.

Using the PCR conditions described above, the remaining portion of the rep gene sequence for AAV7 is isolated and cloned using the primers that amplify 108 bp to 1461 bp of AAV genome (calculated based on the numbering of AAV2, SEQ ID NO:7). This clone is sequenced for construction of a complete AAV7 genome without ITRs.

C. Direct Amplification of 3.1 kb Cap Fragment

To directly amplify a 3.1 kb full-length Cap fragment from NHP tissue and blood DNAs, two other highly conserved regions were identified in AAV genomes for use in PCR amplification of large fragments. A primer within a conserved region located in the middle of the rep gene was selected (AV1ns: 5' GCTGCGTCAACTGGACCAATGAGAAC 3', nt 1398-1423 of SEQ ID NO:6) in combination with the 3' primer located in another conserved region downstream of the Cap gene (AV2cas: 5' CGCAGAGACCAAAGTTCAACTGAAACGA 3', SEQ ID NO:7) for amplification of full-length cap fragments. The PCR products were Topo-cloned according to manufacturer's directions (Invitrogen) and sequence analysis was performed by Qiagengenomics (Qiagengenomics, Seattle, Wash.) with an accuracy of ≥99.9%. A total of 50 capsid clones were isolated and characterized. Among them, 37 clones were derived from Rhesus macaque tissues (rh.1-rh.37), 6 clones from cynomologous macaques (cy.1-cy.6), 2 clones from Baboons (bb.1 and bb.2) and 5 clones from Chimps (ch.1-ch.5).

To rule out the possibility that sequence diversity within the novel AAV family was not an artifact of the PCR, such as PCR-mediated gene splicing by overlap extension between different partial DNA templates with homologous sequences, or the result of recombination process in bacteria, a series of experiments were performed under identical conditions for VP1 amplification using total cellular DNAs. First, intact AAV7 and AAV8 plasmids were mixed at an equal molar ratio followed by serial dilutions. The serially diluted mixtures were used as templates for PCR amplification of 3.1 kb VP1 fragments using universal primers and identical PCR conditions to that were used for DNA amplifications to see whether any hybrid PCR products were generated. The mixture was transformed into bacteria and isolated transformants to look for hybrid clones possibly derived from recombination process in bacterial cells. In a different experiment, we restricted AAV7 and AAV8 plasmids with Msp I, Ava I and HaeI, all of which cut both genomes multiple times at different positions, mixed the digestions in different combinations and used them for PCR amplification of VP1 fragments under the same conditions to test whether any PCR products could be generated through overlap sequence extension of partial AAV sequences. In another experiment, a mixture of gel purified 5' 1.5 kb AAV7 VP1 fragment and 3' 1.7 kb AAV8 VP1 fragment with overlap in the signature region was serially diluted and used for PCR amplification in the presence and absence of 200 ng cellular DNA extracted from a monkey cell line that was free of AAV sequences by TaqMan analysis. None of these experiments demonstrated efficient PCR-mediated overlap sequence production under the conditions of the genomic DNA Cap amplification (data not shown). As a further confirmation, 3 pairs of primers were designed, which were located at different HVRs, and were sequence specific to the variants of clone 42s from Rhesus macaque F953, in different combinations to amplify shorter fragments from mesenteric lymph node (MLN) DNA from F953 from which clone 42s were isolated. All sequence variations identified in full-length Cap clones were found in these short fragments (data not shown).

Example 2

Adeno-Associated Viruses Undergo Substantial Evolution in Primates During Natural Infections

Sequence analysis of selected AAV isolates revealed divergence throughout the genome that is most concentrated in hypervariable regions of the capsid proteins. Epidemiologic data indicate that all known serotypes are endemic to primates, although isolation of clinical isolates has been restricted to AAV2 and AAV3 from anal and throat swabs of human infants and AAV5 from a human condylomatous wart. No known clinical sequalae have been associated with AAV infection.

In an attempt to better understand the biology of AAV, nonhuman primates were used as models to characterize the sequlae of natural infections. Tissues from nonhuman primates were screened for AAV sequences using the PCR method of the invention based on oligonucleotides to highly

conserved regions of known AAVs (see Example 1). A stretch of AAV sequence spanning 2886 to 3143 bp of AAV1 [SEQ ID NO:6] was selected as a PCR amplicon in which conserved sequences are flanked by a hypervariable region that is unique to each known AAV serotype, termed herein a "signature region."

An initial survey of peripheral blood of a number of nonhuman primate species including rhesus monkeys, cynomologous monkeys, chimpanzees, and baboons revealed detectable AAV in a subset of animals from all species. A more extensive analysis of vector distribution was conducted in tissues of rhesus monkeys of the University of Pennsylvania and Tulane colonies recovered at necropsy. This revealed AAV sequence throughout a wide array of tissues.

The amplified signature sequences were subcloned into plasmids and individual transformants were subjected to sequence analysis. This revealed substantial variation in nucleotide sequence of clones derived from different animals. Variation in the signature sequence was also noted in clones obtained within individual animals. Tissues harvested from two animals in which unique signature sequences were identified (i.e., colon from 98E044 and heart from 98E056) were further characterized by expanding the sequence amplified by PCR using oligonucleotides to highly conserved sequences. In this way, complete proviral structures were reconstructed for viral genomes from both tissues as described herein. These proviruses differ from the other known AAVs with the greatest sequence divergence noted in regions of the Cap gene.

Additional experiments were performed to confirm that AAV sequences resident to the nonhuman primate tissue represented proviral genomes of infectious virus that is capable of being rescued and form virions. Genomic DNA from liver tissue of animal 98E056, from which AAV8 signature sequence was detected, was digested with an endonuclease that does not have a site within the AAV sequence and transfected into 293 cells with a plasmid containing an E1 deleted genome of human adenovirus serotype 5 as a source of helper functions. The resulting lysate was passaged on 293 cells once and the lysate was recovered and analyzed for the presence of AAV Cap proteins using a broadly reacting polyclonal antibody to Cap proteins and for the presence and abundance of DNA sequences from the PCR amplified AAV provirus from which AAV8 was derived. Transfection of endonuclease restricted heart DNA and the adenovirus helper plasmid yielded high quantities of AAV8 virus as demonstrated by the detection of Cap proteins by Western blot analysis and the presence of 10^4 AAV8 vector genomes per 293 cell. Lysates were generated from a large-scale preparation and the AAV was purified by cesium sedimentation. The purified preparation demonstrated 26 nm icosohedral structures that look identical to those of AAV serotype 2. Transfection with the adenovirus helper alone did not yield AAV proteins or genomes, ruling out contamination as a source of the rescued AAV.

To further characterize the inter and intra animal variation of AAV signature sequence, selected tissues were subjected to extended PCR to amplify entire Cap open reading frames.

The resulting fragments were cloned into bacterial plasmids and individual transformants were isolated and fully sequenced. This analysis involved mesenteric lymph nodes from three rhesus monkeys (Tulane/V223—6 clones; Tulane/T612—7 clones; Tulane/F953—14 clones), liver from two rhesus monkeys (Tulane/V251—3 clones; Penn/00E033—3 clones), spleen from one rhesus monkey (Penn/97E043—3 clones), heart from one rhesus monkey (IHGT/98E046—1 clone) and peripheral blood from one chimpanzee (New Iberia/X133—5 clones), six cynomologous macaques (Charles River/A 1378, A3099, A3388, A3442, A2821, A3242—6 clones total) and one Baboon (SFRB/8644—2 clones). Of the 50 clones that were sequenced from 15 different animals, 30 were considered non-redundant based on the finding of at least 7 amino acid differences from one another. The non-redundant VP1 clones are numbered sequentially as they were isolated, with a prefix indicating the species of non-human primate from which they were derived. The structural relationships between these 30 non-redundant clones and the previously described 8 AAV serotypes were determined using the SplitsTree program [Huson, D. H. SplitsTree: analyzing and visualizing evolutionary data. Bioinformatics 14, 68-73 (1998)] with implementation of the method of split decomposition. The analysis depicts homoplasy between a set of sequences in a tree-like network rather than a bifurcating tree. The advantage is to enable detection of groupings that are the result of convergence and to exhibit phylogenetic relationships even when they are distorted by parallel events. Extensive phylogenetic research will be required in order to elucidate the AAV evolution, whereas the intention here only is to group the different clones as to their sequence similarity.

To confirm that the novel VP1 sequences were derived from infectious viral genomes, cellular DNA from tissues with high abundance of viral DNA was restricted with an endonuclease that should not cleave within AAV and transfected into 293 cells, followed by infection with adenovirus. This resulted in rescue and amplification of AAV genomes from DNA of tissues from two different animals (data not shown).

VP1 sequences of the novel AAVs were further characterized with respect to the nature and location of amino acid sequence variation. All 30 VP1 clones that were shown to differ from one another by greater than 1% amino acid sequence were aligned and scored for variation at each residue. An algorithm developed to determine areas of sequence divergence yielded 12 hypervariable regions (HVR) of which 5 overlap or are part of the 4 previously described variable regions [Kotin, cited above; Rutledge, cited above]. The three-fold-proximal peaks contain most of the variability (HVR5-10). Interestingly the loops located at the 2 and 5 fold axis show intense variation as well. The HVRs 1 and 2 occur in the N-terminal portion of the capsid protein that is not resolved in the X-ray structure suggesting that the N-terminus of the VP1 protein is exposed on the surface of the virion.

Real-time PCR was used to quantify AAV sequences from tissues of 21 rhesus monkeys using primers and probes to highly conserved regions of Rep (one set) and Cap (two sets) of known AAVs. Each data point represents analysis from tissue DNA from an individual animal. This confirmed the wide distribution of AAV sequences, although the quantitative distribution differed between individual animals. The source of animals and previous history or treatments did not appear to influence distribution of AAV sequences in rhesus macaques. The three different sets of primers and probes used to quantify AAV yielded consistent results. The highest levels of AAV were found consistently in mesenteric lymph nodes at an average of 0.01 copies per diploid genome for 13 animals that were positive. Liver and spleen also contained high abundance of virus DNA. There were examples of very high AAV, such as in heart of rhesus macaque 98E056, spleen of rhesus macaque 97E043 and liver of

rhesus macaque RQ4407, which demonstrated 1.5, 3 and 20 copies of AAV sequence per diploid genome respectively. Relatively low levels of virus DNA were noted in peripheral blood mononuclear cells, suggesting the data in tissue are not due to resident blood components (data not shown). It should be noted that this method would not necessarily capture all AAVs resident to the nonhuman primates since detection requires high homology to both the oligonucleotides and the real time PCR probe. Tissues from animals with high abundance AAV DNA was further analyzed for the molecular state of the DNA, by DNA hybridization techniques, and its cellular distribution, by in situ hybridization.

The kind of sequence variation revealed in AAV proviral fragments isolated from different animals and within tissues of the same animals is reminiscent of the evolution that occurs for many RNA viruses during pandemics or even within the infection of an individual. In some situations the notion of a wild-type virus has been replaced by the existence of swarms of quasispecies that evolve as a result of rapid replication and mutations in the presence of selective pressure. One example is infection by HIV, which evolves in response to immunologic and pharmacologic pressure. Several mechanisms contribute to the high rate of mutations in RNA viruses, including low fidelity and lack of proof reading capacity of reverse transcriptase and non-homologous and homologous recombination.

Evidence for the formation of quasispecies of AAV was illustrated in this study by the systematic sequencing of multiple cloned proviral fragments. In fact, identical sequences could not be found within any extended clones isolated between or within animals. An important mechanism for this evolution of sequence appears to be a high rate of homologous recombination between a more limited number of parenteral viruses. The net result is extensive swapping of hypervariable regions of the Cap protein leading to an array of chimeras that could have different tropisms and serologic specificities (i.e., the ability to escape immunologic responses especially as it relates to neutralizing antibodies). Mechanisms by which homologous recombination could occur are unclear. One possibility is that + and − strands of different single stranded AAV genomes anneal during replication as has been described during high multiplicity of infections with AAV recombinants. It is unclear if other mechanisms contribute to sequence evolution in AAV infections. The overall rate of mutation that occurs during AAV replication appears to be relatively low and the data do not suggest high frequencies of replication errors. However, substantial rearrangements of the AAV genome have been described during lytic infection leading to the formation of defective interfering particles. Irrespective of the mechanisms that lead to sequence divergence, with few exceptions, vp1 structures of the quasispecies remained intact without frameshifts or nonsense mutations suggesting that competitive selection of viruses with the most favorable profile of fitness contribute to the population dynamics.

These studies have implications in several areas of biology and medicine. The concept of rapid virus evolution, formerly thought to be a property restricted to RNA viruses, should be considered in DNA viruses, which classically have been characterized by serologic assays. It will be important in terms of parvoviruses to develop a new method for describing virus isolates that captures the complexity of its structure and biology, such as with HIV, which are categorized as general families of similar structure and function called Clades. An alternative strategy is to continue to categorize isolates with respect to serologic specificity and develop criteria for describing variants within serologic groups.

Example 3

Vectorology of Recombinant AAV Genomes Equipped with AAV2 ITRs Using Chimeric Plasmids Containing AAV2 Rep and Novel AAV Cap Genes for Serological and Gene Transfer Studies in Different Animal Models

Chimeric packaging constructs are generated by fusing AAV2 rep with cap sequences of novel AAV serotypes. These chimeric packaging constructs are used, initially, for pseudotyping recombinant AAV genomes carrying AAV2 ITRs by triple transfection in 293 cell using Ad5 helper plasmid. These pseudotyped vectors are used to evaluate performance in transduction-based serological studies and evaluate gene transfer efficiency of novel AAV serotypes in different animal models including NHP and rodents, before intact and infectious viruses of these novel serotypes are isolated.

A. pAAV2GFP

The AAV2 plasmid which contains the AAV2 ITRs and green fluorescent protein expressed under the control of a constitutitive promoter. This plasmid contains the following elements: the AAV2 ITRs, a CMV promoter, and the GFP coding sequences.

B. Cloning of Trans Plasmid

To construct the chimeric trans-plasmid for production of recombinant pseudotyped AAV7 vectors, p5E18 plasmid (Xiao et al., 1999, *J. Virol* 73:3994-4003) was partially digested with Xho I to linearize the plasmid at the Xho I site at the position of 3169 bp only. The Xho I cut ends were then filled in and ligated back. This modified p5E18 plasmid was restricted with Xba I and Xho I in a complete digestion to remove the AAV2 cap gene sequence and replaced with a 2267 bp Spe I/Xho I fragment containing the AAV7 cap gene which was isolated from pCRAAV7 6-5+15-4 plasmid.

The resulting plasmid contains the AAV2 rep sequences for Rep78/68 under the control of the AAV2 P5 promoter, and the AAV2 rep sequences for Rep52/40 under the control of the AAV2 P19 promoter. The AAV7 capsid sequences are under the control of the AAV2 P40 promoter, which is located within the Rep sequences. This plasmid further contains a spacer 5' of the rep ORF.

C. Production of Pseudotyped rAAV

The rAAV particles (AAV2 vector in AAV7 capsid) are generated using an adenovirus-free method. Briefly, the cis plasmid (pAAV2.1 lacZ plasmid containing AAV2 ITRs), and the trans plasmid pCRAAV7 6-5+15-4 (containing the AAV2 rep and AAV7 cap) and a helper plasmid, respectively, were simultaneously co-transfected into 293 cells in a ratio of 1:1:2 by calcium phosphate precipitation.

For the construction of the pAd helper plasmids, pBG10 plasmid was purchased from Microbix (Canada). A RsrII fragment containing L2 and L3 was deleted from pBHG10, resulting in the first helper plasmid, pAdΔF13. Plasmid AdΔF1 was constructed by cloning Asp700/SalI fragment with a PmeI/SgfI deletion, isolating from pBHG10, into Bluescript. MLP, L2, L2 and L3 were deleted in the pAdΔF1. Further deletions of a 2.3 kb NruI fragment and, subsequently, a 0.5 kb RsrII/NruI fragment generated helper plasmids pAdΔF5 and pAdΔF6, respectively. The helper plasmid, termed pΔF6, provides the essential helper functions of E2a and E4

ORF6 not provided by the E1-expressing helper cell, but is deleted of adenoviral capsid proteins and functional E1 regions).

Typically, 50 μg of DNA (cis:trans:helper) was transfected onto a 150 mm tissue culture dish. The 293 cells were harvested 72 hours post-transfection, sonicated and treated with 0.5% sodium deoxycholate (37EC for 10 min.) Cell lysates were then subjected to two rounds of a CsCl gradient. Peak fractions containing rAAV vector are collected, pooled and dialyzed against PBS.

Example 4

Creation of Infectious Clones Carrying Intact Novel AAV Serotypes for Study of Basic Virology in Human and NHP Derived Cell Lines and Evaluation of Pathogenesis of Novel AAV Serotypes in NHP and Other Animal Models

To achieve this goal, the genome walker system is employed to obtain 5' and 3' terminal sequences (ITRs) and complete construction of clones containing intact novel AAV serotype genomes.

Briefly, utilizing a commercially available Universal Genome Walker Kit [Clontech], genomic DNAs from monkey tissues or cell lines that are identified as positive for the presence of AAV7 sequence are digested with Dra I, EcoR V, Pvu II and Stu I endonucleases and ligated to Genome Walker Adaptor to generate 4 individual Genome Walker Libraries (GWLs). Using DNAs from GWLs as templates, AAV7 and adjacent genomic sequences will be PCR-amplified by the adaptor primer 1 (AP 1, provided in the kit) and an AAV7 specific primer 1, followed by a nested PCR using the adaptor primer 2 (AP2) and another AAV7 specific primer 2, both of which are internal to the first set of primers. The major PCR products from the nested PCR are cloned and characterized by sequencing analysis.

In this experiment, the primers covering the 257 bp or other signature fragment of a generic AAV genome are used for PCR amplification of cellular DNAs extracted from Human and NHP derived cell lines to identify and characterize latent AAV sequences. The identified latent AAV genomes are rescued from the positive cell lines using adenovirus helpers of different species and strains.

To isolate infectious AAV clones from NHP derived cell lines, a desired cell line is obtained from ATCC and screened by PCR to identify the 257 bp amplicon, i.e., signature region of the invention. The 257 bp PCR product is cloned and serotyped by sequencing analysis. For these cell lines containing the AAV7 sequence, the cells are infected with SV-15, a simian adenovirus purchased from ATCC, human Ad5 or transfected with plasmid construct housing the human Ad genes that are responsible for AAV helper functions. At 48 hour post infection or transfection, the cells are harvested and Hirt DNA is prepared for cloning of AAV7 genome following Xiao et al., 1999, J. Virol, 73:3994-4003.

Example 5

Production of AAV Vectors

A pseudotyping strategy similar to that of Example 3 for AAV1/7 was employed to produce AAV2 vectors packaged with AAV1, AAV5 and AAV8 capsid proteins. Briefly, recombinant AAV genomes equipped with AAV2 ITRs were packaged by triple transfection of 293 cells with cis-plasmid, adenovirus helper plasmid and a chimeric packaging construct where the AAV2 rep gene is fused with cap genes of novel AAV serotypes. To create the chimeric packaging constructs, the Xho I site of p5E18 plasmid at 3169 bp was ablated and the modified plasmid was restricted with Xba I and Xho I in a complete digestion to remove the AAV2 cap gene and replace it with a 2267 bp Spe I/Xho I fragment containing the AAV8 cap gene [Xiao, W., et al., (1999) *J Virol* 73, 3994-4003]. A similar cloning strategy was used for creation of chimeric packaging plasmids of AAV2/1 and AAV2/5. All recombinant vectors were purified by the standard $CsCl_2$ sedimentation method except for AAV2/2, which was purified by single step heparin chromatography.

Genome copy (GC) titers of AAV vectors were determined by TaqMan analysis using probes and primers targeting SV40 poly A region as described previously [Gao, G., et al., (2000) *Hum Gene Ther* 11, 2079-91].

Vectors were constructed for each serotype for a number of in vitro and in vivo studies. Eight different transgene cassettes were incorporated into the vectors and recombinant virions were produced for each serotype. The recovery of virus, based on genome copies, is summarized in Table 4 below. The yields of vector were high for each serotype with no consistent differences between serotypes. Data presented in the table are average genome copy yields with standard deviation $\times 10^{13}$ of multiple production lots of 50 plate (150 mm) transfections.

TABLE 4

Production of Recombinant Vectors

	AAV2/1	AAV2/2	AAV2/5	AAV2/7	AAV2/8
CMV LacZ	7.30 ± 4.33 (n = 9)	4.49 ± 2.89 (n = 6)	5.19 ± 5.19 (n = 8)	3.42 (n = 1)	0.87 (n = 1)
CMV EGFP	6.43 ± 2.42 (n = 2)	3.39 ± 2.42 (n = 2)	5.55 ± 6.49 (n = 4)	2.98 ± 2.66 (n = 2)	3.74 ± 3.88 (n = 2)
TBG LacZ	4.18 (n = 1)	0.23 (n = 1)	0.704 ± 0.43 (n = 2)	2.16 (n = 1)	0.532 (n = 1)
Alb A1AT	4.67 ± 0.75 (n = 2)	4.77 (n = 1)	4.09 (n = 1)	5.04 (n = 1)	2.02 (n = 1)
CB A1AT	0.567 (n = 1)	0.438 (n = 1)	2.82 (n = 1)	2.78 (n = 1)	0.816 ± 0.679 (n = 2)
TBG rhCG	8.51 ± 6.65 (n = 6)	3.47 ± 2.09 (n = 5)	5.26 ± 3.85 (n = 4)	6.52 ± 3.08 (n = 4)	1.83 ± 0.98 (n = 5)
TBG cFIX	1.24 ± 1.29 (n = 3)	0.63 ± 0.394 (n = 6)	3.74 ± 2.48 (n = 7)	4.05 (n = 1)	15.8 ± 15.0 (n = 5)

Example 6

Serologic Analysis of Pseudotyped Vectors

C57BL/6 mice were injected with vectors of different serotypes of AAVCBA1AT vectors intramuscularly (5×10^{11} GC) and serum samples were collected 34 days later. To test neutralizing and cross-neutralizing activity of sera to each serotype of AAV, sera was analyzed in a transduction based neutralizing antibody assay [Gao, G. P., et al., (1996) *J Virol* 70, 8934-43]. More specifically, the presence of neutralizing antibodies was determined by assessing the ability of serum to inhibit transduction of 84-31 cells by reporter viruses (AAVCMVEGFP) of different serotypes. Specifically, the reporter virus AAVCMVEGFP of each serotype [at multiplicity of infection (MOI) that led to a transduction of 90% of indicator cells] was pre-incubated with heat-inactivated serum from animals that received different serotypes of AAV or from naïve mice. After 1-hour incubation at 37° C., viruses were added to 84-31 cells in 96 well plates for 48 or 72-hour, depending on the virus serotype. Expression of GFP was measured by Fluorolmagin (Molecular Dynamics) and quantified by Image Quant Software. Neutralizing antibody titers were reported as the highest serum dilution that inhibited transduction to less than 50%.

The availability of GFP expressing vectors simplified the development of an assay for neutralizing antibodies that was based on inhibition of transduction in a permissive cell line (i.e., 293 cells stably expressing E4 from Ad5). Sera to selected AAV serotypes were generated by intramuscular injection of the recombinant viruses. Neutralization of AAV transduction by 1:20 and 1:80 dilutions of the antisera was evaluated (See Table 5 below). Antisera to AAV1, AAV2, AAV5 and AAV8 neutralized transduction of the serotype to which the antiserum was generated (AAV5 and AAV8 to a lesser extent than AAV1 and AAV2) but not to the other serotype (i.e., there was no evidence of cross neutralization suggesting that AAV 8 is a truly unique serotype).

Example 7

In Vivo Evaluation of Different Serotypes of AAV Vectors

In this study, 7 recombinant AAV genomes, AAV2CBhA1AT, AAV2AlbhA1AT, AAV2CMVrhCG, AAV2TBGrhCG, AAV2TBGcFIX, AAV2CMVLacZ and AAV2TBGLacZ were packaged with capsid proteins of different serotypes. In all 7 constructs, minigene cassettes were flanked with AAV2 ITRs. cDNAs of human α-antitrypsin (A1AT) [Xiao, W., et al., (1999) J Virol 73, 3994-4003] β-subunit of rhesus monkey choriogonadotropic hormone (CG) [Zoltick, P. W. & Wilson, J. M. (2000) *Mol Ther* 2, 657-9] canine factor IX [Wang, L., et al., (1997) *Proc Natl Acad Sci USA* 94, 11563-6] and bacterial β-glactosidase (i.e., Lac Z) genes were used as reporter genes. For liver-directed gene transfer, either mouse albumin gene promoter (Alb) [Xiao, W. (1999), cited above] or human thyroid hormone binding globulin gene promoter (TBG) [Wang (1997), cited above] was used to drive liver specific expression of reporter genes. In muscle-directed gene transfer experiments, either cytomegalovirus early promoter (CMV) or chicken β-actin promoter with CMV enhancer (CB) was employed to direct expression of reporters.

For muscle-directed gene transfer, vectors were injected into the right tibialis anterior of 4-6 week old NCR nude or C57BL/6 mice (Taconic, Germantown, N.Y.). In liver-directed gene transfer studies, vectors were infused intraportally into 7-9 week old NCR nude or C57BL/6 mice (Taconic, Germantown, N.Y.). Serum samples were collected intraorbitally at different time points after vector administration. Muscle and liver tissues were harvested at different time points for cryosectioning and Xgal histochemical staining from animals that received the lacZ vectors. For the re-administration experiment, C56BL/6 mice initially received AAV2/1, 2/2, 2/5, 2/7 and 2/8CBA1AT vectors intramuscularly and followed for A1AT gene expression for 7 weeks. Animals were then treated with AAV2/8TBGcFIX intraportally and studied for cFIX gene expression.

TABLE 5

Serological Analysis of New AAV Serotypes.

		% Infection on 84-31 cells with AAVCMVEGFP virus:									
	Immunization	AAV2/1 Serum dilution:		AAV2/2 Serum dilution:		AAV2/5 Serum dilution:		AAV2/7 Serum dilution:		AAV2/8 Serum dilution:	
Sera:	Vector	1/20	1/80	1/20	1/80	1/20	1/80	1/20	1/80	1/20	1/80
Group 1	AAV2/1	0	0	100	100	100	100	100	100	100	100
Group 2	AAV2/2	100	100	0	0	100	100	100	100	100	100
Group 3	AAV2/5	100	100	100	100	16.5	16.5	100	100	100	100
Group 4	AAV2/7	100	100	100	100	100	100	61.5	100	100	100
Group 5	AAV2/8	100	100	100	100	100	100	100	100	26.3	60

Human sera from 52 normal subjects were screened for neutralization against selected serotypes. No serum sample was found to neutralize AAV2/7 and AAV2/8 while AAV2/2 and AAV2/1 vectors were neutralized in 20% and 10% of sera, respectively. A fraction of human pooled IgG representing a collection of 60,000 individual samples did not neutralize AAV2/7 and AAV2/8, whereas AAV2/2 and AAV2/1 vectors were neutralized at titers of serum equal to 1/1280 and 1/640, respectively.

ELISA based assays were performed to quantify serum levels of hA1AT, rhCG and cFIX proteins as described previously [Gao, G. P., et al., (1996) *J Virol* 70, 8934-43; Zoltick, P. W. & Wilson, J. M. (2000) *Mol Ther* 2, 657-9; Wang, L., et al., *Proc Natl Acad Sci USA* 94, 11563-6]. The experiments were completed when animals were sacrificed for harvest of muscle and liver tissues for DNA extraction and quantitative analysis of genome copies of vectors present in target tissues by TaqMan using the same set of primers

and probe as in titration of vector preparations [Zhang, Y., et al., (2001) *Mol Ther* 3, 697-707].

The performance of vectors base on the new serotypes were evaluated in murine models of muscle and liver-directed gene transfer and compared to vectors based on the known serotypes AAV1, AAV2 and AAV5. Vectors expressing secreted proteins (alpha-antitrypsin (A1AT) and chorionic gonadotropin (CG)) were used to quantitate relative transduction efficiencies between different serotypes through ELISA analysis of sera. The cellular distribution of transduction within the target organ was evaluated using lacZ expressing vectors and X-gal histochemistry.

The performance of AAV vectors in skeletal muscle was analyzed following direct injection into the tibialis anterior muscles. Vectors contained the same AAV2 based genome with the immediate early gene of CMV or a CMV enhanced β-actin promoter driving expression of the transgene. Previous studies indicated that immune competent C57BL/6 mice elicit limited humoral responses to the human A1AT protein when expressed from AAV vectors [Xiao, W., et al., (1999) *J Virol* 73, 3994-4003].

In each strain, AAV2/1 vector produced the highest levels of A1AT and AAV2/2 vector the lowest, with AAV2/7 and AAV2/8 vectors showing intermediate levels of expression. Peak levels of CG at 28 days following injection of nu/nu NCR mice showed the highest levels from AAV2/7 and the lowest from AAV2/2 with AAV2/8 and AAV2/1 in between. Injection of AAV2/1 and AAV2/7 lacZ vectors yielded gene expression at the injection sites in all muscle fibers with substantially fewer lacZ positive fibers observed with AAV2/2 and AAV 2/8 vectors. These data indicate that the efficiency of transduction with AAV2/7 vectors in skeletal muscle is similar to that obtained with AAV2/1, which is the most efficient in skeletal muscle of the previously described serotypes [Xiao, W. (1999), cited above; Chao, H., et al., (2001) *Mol Ther* 4, 217-22; Chao, H., et al., (2000) *Mol Ther* 2, 619-23].

Similar murine models were used to evaluate liver-directed gene transfer. Identical doses of vector based on genome copies were infused into the portal veins of mice that were analyzed subsequently for expression of the transgene. Each vector contained an AAV2 based genome using previously described liver-specific promoters (i.e., albumin or thyroid hormone binding globulin) to drive expression of the transgene. More particularly, CMVCG and TBGCG minigene cassettes were used for muscle and liver-directed gene transfer, respectively. Levels of rhCG were defined as relative units ($RUs \times 10^3$). The data were from assaying serum samples collected at day 28, post vector administration (4 animals per group). As shown in Table 3, the impact of capsid proteins on the efficiency of transduction of A1AT vectors in nu/nu and C57BL/6 mice and CG vectors in C57BL/6 mice was consistent (See Table 6).

TABLE 6

Expression of β-unit of Rhesus Monkey Chorionic Gonadotropin (rhCG)

Vector	Muscle	Liver
AAV2/1	4.5 ± 2.1	1.6 ± 1.0
AAV2	0.5 ± 0.1	0.7 ± 0.3
AAV2/5	ND*	4.8 ± 0.8
AAV2/7	14.2 ± 2.4	8.2 ± 4.3
AAV2/8	4.0 ± 0.7	76.0 ± 22.8

*Not determined in this experiment.

In all cases, AAV2/8 vectors yielded the highest levels of transgene expression that ranged from 16 to 110 greater than what was obtained with AAV2/2 vectors; expression from AAV2/5 and AAV2/7 vectors was intermediate with AAV2/7 higher than AAV2/5. Analysis of X-Gal stained liver sections of animals that received the corresponding lacZ vectors showed a correlation between the number of transduced cells and overall levels of transgene expression. DNAs extracted from livers of C57BL/6 mice who received the A1AT vectors were analyzed for abundance of vector DNA using real time PCR technology.

The amount of vector DNA found in liver 56 days after injection correlated with the levels of transgene expression (See Table 7). For this experiment, a set of probe and primers targeting the SV40 polyA region of the vector genome was used for TaqMan PCR. Values shown are means of three individual animals with standard deviations. The animals were sacrificed at day 56 to harvest liver tissues for DNA extraction. These studies indicate that AAV8 is the most efficient vector for liver-directed gene transfer due to increased numbers of transduced hepatocytes.

TABLE 7

Real Time PCR Analysis for Abundance of AAV Vectors in nu/nu Mouse Liver Following Injection of 1×10^{11} Genome Copies of Vector.

AAV vectors/Dose	Genome Copies per Cell
AAV2/1AlbA1AT	0.6 ± 0.36
AAV2AlbA1AT	0.003 ± 0.001
AAV2/5AlbA1AT	0.83 ± 0.64
AAV2/7AlbA1AT	2.2 ± 1.7
AAV2/8AlbA1AT	18 ± 11

The serologic data described above suggest that AAV2/8 vector should not be neutralized in vivo following immunization with the other serotypes. C57BL/6 mice received intraportal injections of AAV2/8 vector expressing canine factor IX (10^{11} genome copies) 56 days after they received intramuscular injections of A1AT vectors of different serotypes. High levels of factor IX expression were obtained 14 days following infusion of AAV2/8 into naïve animals (17±2 μg/ml, n=4) which were not significantly different that what was observed in animals immunized with AAV2/1 (31±23 μg/ml, n=4), AAV2/2 (16 μg/ml, n=2), and AAV2/7 (12 μg/ml, n=2). This contrasts to what was observed in AAV2/8 immunized animals that were infused with the AAV2/8 factor IX vector in which no detectable factor IX was observed (<0.1 μg/ml, n=4).

Oligonucleotides to conserved regions of the cap gene did amplify sequences from rhesus monkeys that represented unique AAVs. Identical cap signature sequences were found in multiple tissues from rhesus monkeys derived from at least two different colonies. Full-length rep and cap open reading frames were isolated and sequenced from single sources. Only the cap open reading frames of the novel AAVs were necessary to evaluate their potential as vectors because vectors with the AAV7 or AAV8 capsids were generated using the ITRs and rep from AAV2. This also simplified the comparison of different vectors since the actual vector genome is identical between different vector serotypes. In fact, the yields of recombinant vectors generated using this approach did not differ between serotypes.

Vectors based on AAV7 and AAV8 appear to be immunologically distinct (i.e., they are not neutralized by antibodies generated against other serotypes). Furthermore, sera from humans do not neutralize transduction by AAV7 and

AAV8 vectors, which is a substantial advantage over the human derived AAVs currently under development for which a significant proportion of the human population has pre-existing immunity that is neutralizing [Chirmule, N., et al., (1999) *Gene Ther* 6, 1574-83].

The tropism of each new vector is favorable for in vivo applications. AAV2/7 vectors appear to transduce skeletal muscle as efficiently as AAV2/1, which is the serotype that confers the highest level of transduction in skeletal muscle of the primate AAVs tested to date [Xiao, W., cited above; Chou (2001), cited above, and Chou (2000), cited above]. Importantly, AAV2/8 provides a substantial advantage over the other serotypes in terms of efficiency of gene transfer to liver that until now has been relatively disappointing in terms of the numbers of hepatocytes stably transduced. AAV2/8 consistently achieved a 10 to 100-fold improvement in gene transfer efficiency as compared to the other vectors. The basis for the improved efficiency of AAV2/8 is unclear, although it presumably is due to uptake via a different receptor that is more active on the basolateral surface of hepatocytes. This improved efficiency will be quite useful in the development of liver-directed gene transfer where the number of transduced cells is critical, such as in urea cycle disorders and familial hypercholesterolemia.

Thus, the present invention provides a novel approach for isolating new AAVs based on PCR retrieval of genomic sequences. The amplified sequences were easily incorporated into vectors and tested in animals. The lack of pre-existing immunity to AAV7 and the favorable tropism of the vectors for muscle indicates that AAV7 is suitable for use as a vector in human gene therapy and other in vivo applications. Similarly, the lack of pre-existing immunity to the AAV serotypes of the invention, and their tropisms, renders them useful in delivery of therapeutic molecules and other useful molecules.

Example 9

Tissue Tropism Studies

In the design of a high throughput functional screening scheme for novel AAV constructs, a non-tissue specific and highly active promoter, CB promoter (CMV enhanced chicken β actin promoter) was selected to drive an easily detectable and quantifiable reporter gene, human α antitrypsin gene. Thus only one vector for each new AAV clone needs to be made for gene transfer studies targeting 3 different tissues, liver, lung and muscle to screen for tissue tropism of a particular AAV construct. The following table summarizes data generated from 4 novel AAV vectors in the tissue tropism studies (AAVCBA1AT), from which a novel AAV capsid clone, 44.2, was found to be a very potent gene transfer vehicle in all 3 tissues with a big lead in the lung tissue particularly. Table 8 reports data obtained (in μg A1AT/mL serum) at day 14 of the study.

TABLE 8

	Target Tissue		
Vector	Lung	Liver	Muscle
AAV2/1	ND	ND	45 ± 11
AAV2/5	0.6 ± 0.2	ND	ND
AAV2/8	ND	84 ± 30	ND
AAV2/rh.2 (43.1)	14 ± 7	25 ± 7.4	35 ± 14
AAV2/rh.10 (44.2)	23 ± 6	53 ± 19	46 ± 11
AAV2/rh.13 (42.2)	3.5 ± 2	2 ± 0.8	3.5 ± 1.7
AAV2/rh.21 (42.10)	3.1 ± 2	2 ± 1.4	4.3 ± 2

A couple of other experiments were then performed to confirm the superior tropism of AAV 44.2 in lung tissue. First, AAV vector carried CC10hA1AT minigene for lung specific expression were pseudotyped with capsids of novel AAVs were given to Immune deficient animals (NCR nude) in equal volume (50 μl each of the original preps without dilution) via intratracheal injections as provided in the following table. In Table 9, 50 μl of each original prep per mouse, NCR Nude, detection limit ≥0.033 μg/ml, Day 28

TABLE 9

Vector	Total GC in 50 μl vector	μg of A1AT/ml with 50 μl vector	μg of A1AT/ml with 1×10^{11} vector	Relative Gene transfer as compared to rh.10 (clone 44.2)
2/1	3×10^{12}	2.6 ± 0.5	0.09 ± 0.02	2.2
2/2	5.5×10^{11}	<0.03	<0.005	<0.1
2/5	3.6×10^{12}	0.65 ± 0.16	0.02 ± 0.004	0.5
2/7	4.2×10^{12}	1 ± 0.53	0.02 ± 0.01	0.5
2/8	7.5×10^{11}	0.9 ± 0.7	0.12 ± 0.09	2.9
2/ch.5 (A.3.1)	9×10^{12}	1 ± 0.7	0.01 ± 0.008	0.24
2/rh.8 (43.25)	4.6×10^{12}	26 ± 21	0.56 ± 0.46	13.7
2/rh.10 (44.2)	2.8×10^{12}	115 ± 38	4.1 ± 1.4	100
2/rh.13 (42.2)	6×10^{12}	7.3 ± 0.8	0.12 ± 0.01	2.9
2/rh.21 (42.10)	2.4×10^{12}	9 ± 0.9	0.38 ± 0.04	9.3
2/rh.22 (42.11)	2.6×10^{12}	6 ± 0.4	0.23 ± 0.02	5.6
2/rh.24 (42.13)	1.1×10^{11}	0.4 ± 0.3	0.4 ± 0.3	1

The vectors were also administered to immune competent animals (C57BL/6) in equal 5 genome copies (1×10^{11} GC) as shown in the Table 10. (1×10^{11} GC per animal, C57BL/6, day 14, detection limit ≥0.033 g/ml)

TABLE 10

AAV Vector	μg of A1AT/ml with 1×10^{11} vector	Relative Gene transfer as compared to rh.10 (clone 44.2)
2/1	0.076 ± 0.031	2.6
2/2	0.1 ± 0.09	3.4
2/5	0.0840.033	2.9
2/7	0.33 ± 0.01	11
2/8	1.92 ± 1.3	2.9
2/ch.5 (A.3.1)	0.048 ± 0.004	1.6
2/rh.8 (43.25)	1.7 ± 0.7	58
2/rh.10 (44.2)	2.93 ± 1.7	100
2/rh.13 (42.2)	0.45 ± 0.15	15
2/rh.21 (42.10)	0.86 ± 0.32	29
2/rh.22 (42.11)	0.38 ± 0.18	13
2/rh.24 (42.13)	0.3 ± 0.19	10

The data from both experiments confirmed the superb tropism of clone 44.2 in lung-directed gene transfer.

Interestingly, performance of clone 44.2 in liver and muscle directed gene transfer was also outstanding, close to that of the best liver transducer, AAV8 and the best muscle transducer AAV1, suggesting that this novel AAV has some intriguing biological significance.

To study serological properties of those novel AAVs, pseudotyped AAVGFP vectors were created for immunization of rabbits and in vitro transduction of 84-31 cells in the

presence and absence of antisera against different capsids. The data are summarized below:

TABLE 11a

	Cross-NAB assay in 8431 cells and adenovirus (Adv) coinfection Infection in 8431 cells (coinfected with Adv) with: Serum from rabbit immunized with:			
	10^9 GC rh.13 AAV2/42.2	10^9 GC rh.21 AAV2/42.10	10^9 GC rh.22 AAV2/42.11	10^{10} GC rh.24 AAV2/42.13
AAV2/1	1/20	1/20	1/20	No NAB
AAV2/2	1/640	1/1280	1/5120	No NAB
AAV2/5	No NAB	1/40	1/160	No NAB
AAV2/7	1/81920	1/81920	1/40960	1/640
AAV2/8	1/640	1/640	1/320	1/5120
Ch.5 AAV2/A3	1/20	1/160	1/640	1/640
rh.8 AAV2/43.25	1/20	1/20	1/20	1/320

TABLE 11a-continued

	Cross-NAB assay in 8431 cells and adenovirus (Adv) coinfection Infection in 8431 cells (coinfected with Adv) with: Serum from rabbit immunized with:			
	10^9 GC rh.13 AAV2/42.2	10^9 GC rh.21 AAV2/42.10	10^9 GC rh.22 AAV2/42.11	10^{10} GC rh.24 AAV2/42.13
rh.10 AAV2/44.2	No NAB	No NAB	No NAB	1/5120
rh.13 AAV2/42.2	1/5120	1/5120	1/5120	No NAB
rh.21 AAV2/42.10	1/5120	1/10240	1/5120	1/20
rh.22 AAV2/42.11	1/20480	1/20480	1/40960	No NAB
rh.24 AAV2/42.13	No NAB	1/20	1/20	1/5120

TABLE 11b

	Cross-NAB assay in 8431 cells and Adv coinfection Infection in 8431 cells (coinfected with Adv) with: Serum from rabbit immunized with:				
	10^9 GC rh.12 AAV2/42.1B	10^{10} GC ch.5 AAV2/A3	10^{10}GC rh.8 AAV2/43.25	10^9 GC rh.10 AAV2/44.2	10^9 GC rh.20 AAV2/42.8.2
AAV2/1	No NAB	1/20480	No NAB	1/80	ND
AAV2/2	1/20	No NAB	No NAB	No NAB	ND
AAV2/5	No NAB	1/320	No NAB	No NAB	ND
AAV2/7	1/2560	1/640	1/160	1/81920	ND
AAV2/8	1/10240	1/2560	1/2560	1/81920	ND
ch.5 AAV2/A3	1/1280	1/10240	ND	1/5120	1/320
rh.8 AAV2/43.25	1/1280	ND	1/20400	1/5120	1/2560
rh.10 AAV2/44.2	1/5120	ND	ND	1/5120	1/5120
rh.13 AAV2/42.2	1/20	ND	ND	No NAB	1/320
rh.21 AAV2/42.10	1/20	ND	ND	1/40	1/80
rh.22 AAV2/42.11	No NAB	ND	ND	ND	No NAB
rh.24 AAV2/42.13	1/5120	ND	ND	ND	1/2560

TABLE 12

	Titer of rabbit sera		Titer after
	Vector	Titer d21	Boosting
ch.5	AAV2/A3	1/10,240	1/40,960
rh.8	AAV2/43.25	1/20,400	1/163,840
rh.10	AAV2/44.2	1/10,240	1/527,680
rh.13	AAV2/42.2	1/5,120	1/20,960
rh.21	AAV2/42.10	1/20,400	1/81,920
rh.22	AAV2/42.11	1/40,960	ND
rh.24	AAV2/42.13	1/5,120	ND

TABLE 13 a

	Infection in 8431 cells (coinfected with Adv) with GFP					
	10^9 GC/well AAV2/1	10^9 GC/well AAV2/2	10^9 GC/well AAV2/5	10^9 GC/well AAV2/7	10^9 GC/well AAV2/8	10^9 GC/well ch.5 AAV2/A3
# GFU/field	128	>200	95	56	13	1
	83	>200	65	54	11	1

TABLE 13b

Infection in 8431 cells (coinfected with Adv) with GFP							
	10^9 GC/well rh.8 AAV2/43.25	10^9 GC/well rh.10 AAV2/44.2	10^9 GC/well rh.13 AAV2/42.2	10^9 GC/well rh.21 AAV2/42.10	10^9 GC/well rh.22 AAV2/42.11	10^9 GC/well rh.24 AAV2/42.13	10^9 GC/well rh.12 AAV2/42.1B
# GFU/field	3	13	54	62	10	3	18
	2	12	71	60	14	2	20
			48	47	16	3	12

Example 10

Mouse Model of Familial Hypercholesterolemia

The following experiment demonstrates that the AAV2/7 construct of the invention delivers the LDL receptor and express LDL receptor in an amount sufficient to reduce the levels of plasma cholesterol and triglycerides in animal models of familial hypercholesterolemia.

A. Vector Construction

AAV vectors packaged with AAV7 or AAV8 capsid proteins were constructed using a pseudotyping strategy [Hildinger M, et al., *J. Virol* 2001; 75:6199-6203]. Recombinant AAV genomes with AAV2 inverted terminal repeats (ITR) were packaged by triple transfection of 293 cells with the cis-plasmid, the adenovirus helper plasmid and a chimeric packaging construct, a fusion of the capsids of the novel AAV serotypes with the rep gene of AAV2. The chimeric packaging plasmid was constructed as previously described [Hildinger et al, cited above]. The recombinant vectors were purified by the standard $CsCl_2$ sedimentation method. To determine the yield TaqMan (Applied Biosystems) analysis was performed using probes and primers targeting the SV40 poly(A) region of the vectors [Gao G P, et al., *Hum Gene Ther.* 2000 Oct. 10; 11(15):2079-91]. The resulting vectors express the transgene under the control of the human thyroid hormone binding globulin gene promoter (TBG).

B. Animals

LDL receptor deficient mice on the C57Bl/6 background were purchased from the Jackson Laboratory (Bar Harbor, Me., USA) and maintained as a breeding colony. Mice were given unrestricted access to water and obtained a high fat Western Diet (high % cholesterol) starting three weeks prior vector injection. At day −7 as well at day 0, blood was obtained via retroorbital bleeds and the lipid profile evaluated. The mice were randomly divided into seven groups. The vector was injected via an intraportal injection as previously described ([Chen S J et al., *Mol Therapy* 2000; 2(3), 256-261]. Briefly, the mice were anaesthetized with ketamine and xylazine. A laparotomy was performed and the portal vein exposed. Using a 30 g needle the appropriate dose of vector diluted in 100 ul PBS was directly injected into the portal vein. Pressure was applied to the injection site to ensure a stop of the bleeding. The skin wound was closed and draped and the mice carefully monitored for the following day. Weekly bleeds were performed starting at day 14 after liver directed gene transfer to measure blood lipids. Two animals of each group were sacrificed at the time points week 6 and week 12 after vector injection to examine atherosclerotic plaque size as well as receptor expression. The remaining mice were sacrificed at week 20 for plaque measurement and determination of transgene expression.

TABLE 14

	Vector	dose	n
Group 1	AAV2/7-TBG-hLDLr	1×10^{12} gc	12
Group 2	AAV2/7-TBG-hLDLr	3×10^{11} gc	12
Group 3	AAV2/7-TBG-hLDLr	1×10^{11} gc	12
Group 4	AAV2/8-TBG-hLDLr	1×10^{12} gc	12
Group 5	AAV2/8-TBG-hLDLr	3×10^{11} gc	12
Group 6	AAV2/8-TBG-hLDLr	1×10^{11} gc	12
Group 7	AAV2/7-TBG-LacZ	1×10^{11} gc	16

C. Serum Lipoprotein and Liver Function Analysis

Blood samples were obtained from the retroorbital plexus after a 6 hour fasting period. The serum was separated from the plasma by centrifugation. The amount of plasma lipoproteins and liver transaminases in the serum were detected using an automatized clinical chemistry analyzer (ACE, Schiapparelli Biosystems, Alpha Wassermann)

D. Detection of Transgene Expression

LDL receptor expression was evaluated by immunofluorescence staining and Western blotting. For Western Blot frozen liver tissue was homogenized with lysis buffer (20 mM Tris, pH7.4, 130 mM NaCl, 1% Triton X 100, proteinase inhibitor (complete, EDTA-free, Roche, Mannheim, Germany). Protein concentration was determined using the Micro BCA Protein Assay Reagent Kit (Pierce, Rockford, Ill.). 40 μg of protein was resolved on 4-15% Tris-HCl Ready Gels (Biorad, Hercules, Calif.) and transferred to a nitrocellulose membrane (Invitrogen,). To generate Anti-hLDL receptor antibodies a rabbit was injected intravenously with an AdhLDLr prep (1×10^{13} GC). Four weeks later the rabbit serum was obtained and used for Western Blot. A 1:100 dilution of the serum was used as a primary antibody followed by a HRP-conjugated anti-rabbit IgG and ECL chemiluminescent detection (ECL Western Blot Detection Kit, Amersham, Arlington Heights, Ill.).

E. Immunocytochemistry

For determination of LDL receptor expression in frozen liver sections immunohistochemistry analyses were performed. 10 um cryostat sections were either fixed in acetone for 5 minutes, or unfixed. Blocking was obtained via a 1 hour incubation period with 10% of goat serum. Sections were then incubated for one hour with the primary antibody at room temperature. A rabbit polyclonal antibody anti-human LDL (Biomedical Technologies Inc., Stoughton, Mass.) was used diluted accordingly to the instructions of the manufacturer. The sections were washed with PBS, and incubated with 1:100 diluted fluorescein goat anti-rabbit IgG (Sigma, St Louis, Mo.). Specimens were finally examined under fluorescence microscope Nikon Microphot-FXA. In all cases, each incubation was followed by extensive washing with PBS. Negative controls consisted of preincubation with PBS, omission of the primary antibody, and substitution of the primary antibody by an isotype-matched non-

immune control antibody. The three types of controls mentioned above were performed for each experiment on the same day.

F. Gene Transfer Efficiency

Liver tissue was obtained after sacrificing the mice at the designated time points. The tissue was shock frozen in liquid nitrogen and stored at −80° C. until further processing. DNA was extracted from the liver tissue using a QIAamp DNA Mini Kit (QIAGEN GmbH, Germany) according to the manufacturers protocol. Genome copies of AAV vectors in the liver tissue were evaluated using Taqman analysis using probes and primers against the SV40 poly(A) tail as described above.

G. Atherosclerotic Plaque Measurement

For the quantification of the atherosclerotic plaques in the mouse aorta the mice were anaesthetized (10% ketamine and xylazine, ip), the chest opened and the arterial system perfused with ice-cold phosphate buffered saline through the left ventricle. The aorta was then carefully harvested, slit down along the ventral midline from the aortic arch down to the femoral arteries and fixed in formalin. The lipid-rich atherosclerotic plaques were stained with Sudan IV (Sigma, Germany) and the aorta pinned out flat on a black wax surface. The image was captured with a Sony DXC-960 MD color video camera. The area of the plaque as well as of the complete aortic surface was determined using Phase 3 Imaging Systems (Media Cybernetics).

H. Clearance of I^{125} LDL

Two animals per experimental group were tested. A bolus of I^{125}-labeled LDL (generously provided by Dan Rader, U Penn) was infused slowly through the tail vein over a period of 30 sec (1,000,000 counts of [I^{125}]-LDL diluted in 100 μl sterile PBS/animal). At time points 3 min, 30 min, 1.5 hr, 3 hr, 6 hr after injection a blood sample was obtained via the retro-orbital plexus. The plasma was separated off from the whole blood and 10 μl plasma counted in the gamma counter. Finally the fractional catabolic rate was calculated from the lipoprotein clearance data.

I. Evaluation of Liver Lipid Accumulation

Oil Red Staining of frozen liver sections was performed to determine lipid accumulation. The frozen liver sections were briefly rinsed in distilled water followed by a 2 minute incubation in absolute propylene glycol. The sections were then stained in oil red solution (0.5% in propylene glycol) for 16 hours followed by counterstaining with Mayer's hematoxylin solution for 30 seconds and mounting in warmed glycerin jelly solution.

For quantification of the liver cholesterol and triglyceride content liver sections were homogenized and incubated in chloroform/methanol (2:1) overnight. After adding of 0.05% H_2SO_4 and centrifugation for 10 minutes, the lower layer of each sample was collected, divided in two aliquots and dried under nitrogen. For the cholesterol measurement the dried lipids of the first aliquot were dissolved in 1% Triton X-100 in chloroform. Once dissolved, the solution was dried under nitrogen. After dissolving the lipids in ddH_20 and incubation for 30 minutes at 37° C. the total cholesterol concentration was measured using a Total Cholesterol Kit (Wako Diagnostics). For the second aliquot the dried lipids were dissolved in alcoholic KOH and incubated at 60° C. for 30 minutes. Then 1M MgCl2 was added, followed by incubation on ice for 10 minutes and centrifugation at 14,000 rpm for 30 minutes. The supernatant was finally evaluated for triglycerides (Wako Diagnostics).

All of the vectors pseudotyped in an AAV2/8 or AAV2/7 capsid lowered total cholesterol, LDL and triglycerides as compared to the control. These test vectors also corrected phenotype of hypercholesterolemia in a dose-dependent manner. A reduction in plaque area for the AAV2/8 and AAV2/7 mice was observed in treated mice at the first test (2 months), and the effect was observed to persist over the length of the experiment (6 months).

Example 10

Functional Factor IX Expression and Correction of Hemophilia

A. Knock-Out Mice

Functional canine factor IX (FIX) expression was assessed in hemophilia B mice. Vectors with capsids of AAV1, AAV2, AAV5, AAV7 or AAV8 were constructed to deliver AAV2 5' ITR—liver-specific promoter [LSP]—canine FIX—woodchuck hepatitis post-regulatory element (WPRE)—AAV2 3' ITR. The vectors were constructed as described in Wang et al, 2000, *Molecular Therapy* 2: 154-158), using the appropriate capsids.

Knock-out mice were generated as described in Wang et al, 1997. *Proc. Natl. Acad. Sci. USA* 94: 11563-11566. This model closely mimic the phenotypes of hemophilia B in human.

Vectors of different serotypes (AAV1, AAV2, AAV5, AAV7 and AAV8) were delivered as a single intraportal injection into the liver of adult hemophiliac C57Bl/6 mice in a dose of 1×10^{11} GC/mouse for the five different serotypes and one group received an AAV8 vector at a lower dose, 1×10^{10} GC/mouse. Control group was injected with 1×10^{11} GC of AAV2/8 TBG LacZ3. Each group contains 5-10 male and female mice. Mice were bled bi-weekly after vector administration.

1. ELISA

The canine FIX concentration in the mouse plasma was determined by an ELISA assay specific for canine factor IX, performed essentially as described by Axelrod et al, 1990, *Proc. Natl. Acad. Sci. USA,* 87:5173-5177 with modifications. Sheep anti-canine factor IX (Enzyme Research Laboratories) was used as primary antibody and rabbit anti-canine factor IX ((Enzyme Research Laboratories) was used as secondary antibody. Beginning at two weeks following injection, increased plasma levels of cFIX were detected for all test vectors. The increased levels were sustained at therapeutic levels throughout the length of the experiment, i.e., to 12 weeks. Therapeutic levels are considered to be 5% of normal levels, i.e., at about 250 ng/mL.

The highest levels of expression were observed for the AAV2/8 (at 101) and AAV2/7 constructs, with sustained superphysiology levels cFIX levels (ten-fold higher than the normal level). Expression levels for AAV2/8 (10^{11}) were approximately 10 fold higher than those observed for AAV2/2 and AAV2/8 (10^{10}). The lowest expression levels, although still above the therapeutic range, were observed for AAV2/5.

2. In Vitro Activated Partial Thromboplastin Time (aPTT) Assay

Functional factor IX activity in plasma of the FIX knock-out mice was determined by an in vitro activated partial thromboplastin time (aPTT) assay-Mouse blood samples were collected from the retro-orbital plexus into 1/10 volume of citrate buffer. The aPTT assay was performed as described by Wang et al, 1997, *Proc. Natl. Acad. Sci. USA* 94: 11563-11566.

Clotting times by aPTT on plasma samples of all vector injected mice were within the normal range (approximately 60 sec) when measured at two weeks post-injection, and

sustained clotting times in the normal or shorter than normal range throughout the study period (12 weeks).

Lowest sustained clotting times were observed in the animals receiving AAV2/8 (10^{11}) and AAV2/7. By week 12, AAV2/2 also induced clotting times similar to those for AAV2/8 and AAV2/7. However, this lowered clotting time was not observed for AAV2/2 until week 12, whereas lowered clotting times (in the 25-40 sec range) were observed for AAV2/8 and AAV2/7 beginning at week two.

Immuno-histochemistry staining on the liver tissues harvested from some of the treated mice is currently being performed. About 70-80% of hepatocytes are stained positive for canine FIX in the mouse injected with AAV2/8.cFIX vector.

B. Hemophilia B Dogs

Dogs that have a point mutation in the catalytic domain of the F.IX gene, which, based on modeling studies, appears to render the protein unstable, suffer from hemophilia B [Evans et al, 1989, Proc. Natl. Acad. Sci. USA, 86:10095-10099). A colony of such dogs has been maintained for more than two decades at the University of North Carolina, Chapel Hill. The homeostatic parameters of these dogs are well described and include the absence of plasma F.IX antigen, whole blood clotting times in excess of 60 minutes, whereas normal dogs are 6-8 minutes, and prolonged activated partial thromboplastin time of 50-80 seconds, whereas normal dogs are 13-28 seconds. These dogs experience recurrent spontaneous hemorrhages. Typically, significant bleeding episodes are successfully managed by the single intravenous infusion of 10 ml/kg of normal canine plasma; occasionally, repeat infusions are required to control bleeding.

Four dogs are injected intraportally with AAV.cFIX according to the schedule below. A first dog receives a single injection with AAV2/2.cFIX at a dose of 3.7×10^{11} genome copies (GC)/kg. A second dog receives a first injection of AAV2/2.cFIX (2.8×10^{11} GC/kg), followed by a second injection with AAV2/7.cFIX (2.3×10^{13} GC/kg) at day 1180. A third dog receives a single injection with AAV2/2.cFIX at a dose of 4.6×10^{12} GC/kg. The fourth dog receives an injection with AAV2/2.cFIX (2.8×10^{12} GC/kg) and an injection at day 995 with AAV2/7.cFIX (5×10^{12} GC/kg).

The abdomen of hemophilia dogs are aseptically and surgically opened under general anesthesia and a single infusion of vector is administered into the portal vein. The animals are protected from hemorrhage in the peri-operative period by intravenous administration of normal canine plasma. The dog is sedated, intubated to induce general anesthesia, and the abdomen shaved and prepped. After the abdomen is opened, the spleen is moved into the operative field. The splenic vein is located and a suture is loosely placed proximal to a small distal incision in the vein. A needle is rapidly inserted into the vein, then the suture loosened and a 5 F cannula is threaded to an intravenous location near the portal vein threaded to an intravenous location near the portal vein bifurcation. After hemostasis is secured and the catheter balloon inflated, approximately 5.0 ml of vector diluted in PBS is infused into the portal vein over a 5 minute interval. The vector infusion is followed by a 5.0 ml infusion of saline. The balloon is then deflated, the callula removed and venous hemostasis is secured. The spleen is then replaced, bleeding vessels are cauterized and the operative wound is closed. The animal is extubated having tolerated the surgical procedure well. Blood samples are analyzed as described. [Wang et al, 2000, *Molecular Therapy* 2: 154-158]

Results showing correction or partial correction are anticipated for AAV2/7.

All publications cited in this specification including priority applications, U.S. patent application Ser. Nos. 13/633,971, 12/962,793, 10/291,583, and U.S. provisional patent application Nos. 60/386,675, 60/377,066, 60/341,117, and 60/350,607, are incorporated herein by reference. While the invention has been described with reference to particularly preferred embodiments, it will be appreciated that modifications can be made without departing from the spirit of the invention. Such modifications are intended to fall within the scope of the claims.

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Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
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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
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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
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<210> SEQ ID NO 3
<211> LENGTH: 623
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: rep protein of adeno-associated virus serotype 7

<400> SEQUENCE: 3

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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
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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
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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> SEQ ID NO 4
<211> LENGTH: 4393
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: adeno-associated virus serotype 8

<400> SEQUENCE: 4

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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

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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

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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
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ggccaaggtc gtggagtccg ccaaggccat tctcggcggc agcaaggtgc gcgtggacca 1440

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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

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acctctctga gggcattcgc gagtggtggg cgctgaaacc tggagccccg aagcccaaag 2220

ccaaccagca aaagcaggac gacggccggg gtctggtgct tcctggctac aagtacctcg 2280

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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> SEQ ID NO 5
<211> LENGTH: 4385
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: adeno-associated virus serotype 9

<400> SEQUENCE: 5

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gtgcttttgc gacattttgc gacaccacat ggccatttga ggtatatatg gccgagtgag 180

cgagcaggat ctccattttg accgcgaaat ttgaacgagc agcagccatg ccgggcttct 240

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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

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gcaaacggct cgtggcgcag cacctgaccc acgtcagcca gacgcaggag cagaacaagg 840

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tggagctggt cgggtggctg gtggaccggg gcatcacctc cgagaagcag tggatccagg 960

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aagccattgc ccacgccgtg cccttctacg gctgcgtcaa ctggaccaat gagaactttc 1320

ccttcaacga ttgcgtcgac aagatggtga tctggtggga ggagggcaag atgacggcca 1380

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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

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tggaatccag agatccagta tacttcaaac tactacaaat ctacaaatgt ggactttgct 4260

gtcaatacca aaggtgttta ctctgagcct cgccccattg gtactcgtta cctcacccgt 4320

aatttgtaat tgcctgttaa tcaataaacc ggttaattcg tttcagttga actttggtct 4380

ctgcg 4385

<210> SEQ ID NO 6
<211> LENGTH: 4718
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: adeno-associated virus serotype 1

<400> SEQUENCE: 6

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attttgcgac accacgtggc catttagggt atatatggcc gagtgagcga gcaggatctc 300

cattttgacc gcgaaatttg aacgagcagc agccatgccg ggcttctacg agatcgtgat 360

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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> SEQ ID NO 9
<211> LENGTH: 3098
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 42.2

<400> SEQUENCE: 9

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gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcttccg 180

cccagatcga tcccaccccc 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

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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

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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

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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

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ggcacccgtt acctcacccg taacctgtaa ttgcctgtta atcaataaac cggttaattc 3060

gtttcagttg aactttggtc tctgcgaagg gcgaattc 3098

<210> SEQ ID NO 10
<211> LENGTH: 3098
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 16.3

<400> SEQUENCE: 10

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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

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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

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accagaccga gaggttcgag aacccgcttc ttggcctgga agactgctcg cccgaggttg 1920

cccccaaaag acgtatcttc ttgaagacgc tcctgaaact cagcgtcggc gtggttgtac 1980

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gccgcggcgt ctgcctcgtt gaccggctct cccttgtcga gtccgttgaa gggtccgagg 2100

tacttgtagc caggaagcac cagaccccgg ccgtcgtcct gcttttgctg gttggctttg 2160

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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

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cttgccctcc tcccaccaga tcaccatctt gtcgacgcaa tcgttgaagg gaaagttctc 3060

attggtccag ttgacgcagc cgtagaaagg gcgaattc 3098

<210> SEQ ID NO 11
<211> LENGTH: 3121
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 29.3

<400> SEQUENCE: 11

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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 tcgctctttcg tcgtccttgt gggttgccat agcgacaccg 720

ggatttacca gagagtctct gccattcaga tgatacttgg tggcaccggt ccaggcaaag 780

ttgctgttgt tattttgcga cagtgtcgtg gagacgcgtt gctgccggta gcagggcccg 840

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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

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agtcgctgcc agtcacgtgg tgagaagtgg cagtggaatc tgttaaagtc aaaatacccc 1440

caggggggtgc tgtagccgaa gtaggtgttg tcgttggtgc ttcctcccga agtcccgttg 1500

gagatttgct tgtagaggtg gttgttgtag gtggggaggg cccaggttcg ggtgctggtg 1560

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actccgtcgg cgccttcgtt attgtctgcc attggagcgc caccgcctgc agccattgta 1680

ccagatccca gaccagaggg gcctgcgggg ggttctccga ttggttgagg gtcgggcact 1740

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acccttttttg acgtagaatt catgctccac ctcaaccacg tgatcctttg cccaccggaa 2760

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cgactccacg accttggcgg tcatcttccc ctcctcccac cagatcacca tcttgtcgac 3060

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c 3121

<210> SEQ ID NO 12
<211> LENGTH: 3121

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<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 29.4

<400> SEQUENCE: 12

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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

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agaagagacc ggtagagcca tcaccccagc gttctccaga ctcctctacg ggcatcggca 1320

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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

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agggctgcct gcctccgttc ccggcggacg tcttcatgat tcctcagtac gggtacctga 1980

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agttgctatt ttctcaggcc gggcctaata acatgtcggc tcaggccaaa aactggctac 2280

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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

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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

c 3121

<210> SEQ ID NO 13
<211> LENGTH: 3121
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 29.5

<400> SEQUENCE: 13

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caagcaatta cagattacgg gtgaggtaac gggtgccgat ggggcgaggc tcagaataag 120

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c 3121

<210> SEQ ID NO 14
<211> LENGTH: 3131
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 1-3

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<400> SEQUENCE: 14

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agtccgccaa ggccattctc ggcggcagca aggtgcgcgt ggaccaaaag tgcaagtcgt 180

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cctgcccctc agtcgcggat ccatcgacgt cagacgcgga aggagctccg gtggactttg 540

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gcaaaacgtg cgagagaatg aatcggaatt tcaacatttg cttcacacac ggggtcagag 660

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agggcgaatt c 3131

<210> SEQ ID NO 15
<211> LENGTH: 3127
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 13-3b

<400> SEQUENCE: 15

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cagagtaaac accctggctg tcaacggcaa agtccacacc agtctgcttt tcaaagttgg 180

aggtgtactg aatctccggg tcccagcgct tgctgttttc cttctgcagc tcccactcga 240

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taaacacctc cggaggatta gcgggaacgg gagtgttctt gatcaggatc tgaggaggcg 360

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cgaattc 3127

<210> SEQ ID NO 16
<211> LENGTH: 3106
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 24-1

<400> SEQUENCE: 16

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attgattaac aagtaattac aggttacggg tgaggtaacg ggtgccaatg gggcgaggct 120

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gaattttggc ccagatggga ccctgcaggc acacgtcccg gttctgccag accatgccgg 480

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<210> SEQ ID NO 17
<211> LENGTH: 3102
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 27-3

<400> SEQUENCE: 17

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cagtataaac cccttcgttg ttgacagcaa attccacatt attagacttg gcataatttg 180

aggtgtactg aatctctgga ttccagcgtt tgctgttttc tttctgcagt tcccactcga 240

tctccacgct gacctggccg gtgctgtact gcgtgataaa tgaggcaaac ttggcaggag 300

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gccgtcatct tgccctcctc ccaccagatc accatcttgt cgacgcaatc gttgaaggga 3060

aagttctcat tggtccagtt gacgcagccg aagggcgaat tc 3102

<210> SEQ ID NO 18
<211> LENGTH: 3106
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 7-2

<400> SEQUENCE: 18

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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

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gcagagcccc ctggctgttg acagtctgtg tctggggtcc ggccgtagac gattgcaggt 540

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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

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aactcatacg ccacctcggt cacgtgatcc tgcgcccagc ggaagaactc tttgacttcc 2760

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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
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<210> SEQ ID NO 19
<211> LENGTH: 3105
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone C1

<400> SEQUENCE: 19

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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 gcctgcccct    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

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gttattggct ctcgttattt gactaatcat ttgtaactgc ctagttaatc aataaaccgt 3060

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<210> SEQ ID NO 20
<211> LENGTH: 3105
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone C3

<400> SEQUENCE: 20

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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 gcctgccct 480

cagttgcgga gccatcgacg tcagacgcgg aagcaccggt ggactttgcg gacaggtacc 540

aaaacaaatg ttctcgtcac gcgggcatgc ttcagatgct gtttccctgc aagacatgcg 600

agagaatgaa tcagaatttc aacgtctgct tcacgcacgg ggtcagagac tgctcagagt 660

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<210> SEQ ID NO 21
<211> LENGTH: 3105
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone C5

<400> SEQUENCE: 21

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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

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ggggaaagga ggcagacttc cctcttgtcc agcgtccatc acgtacggga gctcatacga 1260

cgagtccgca aatatctgaa ccgtgctggt aaggttatta gcgaccgtag tctcgccgtt 1320

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cttgtcgtgc tcgagggccg ctgcgtccgc cgcgttgacg ggctcccccc tgtcgagtcc 2100

gttgaagggt ccgaggtact cgtagccagg aagcaccaga ccccggccgt cgtcctgctt 2160

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ctcagagagg ttgtcctcga gccaatctgg aagataaccg tcagcagcca tacctggttt 2280

aagtcattta ttgctcagaa acacagtcat ccaagtccac gttgacgaga tcgcaggccg 2340

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gaaacagcat ctgaagcatg cccgcgtgac gagaacattt gttttggtac ctgtccgcaa 2580

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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

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ccttggcggt catcttgccc tcctcccacc agatcaccat cttgtcgacg caatcgttga 3060

agggaaagtt ctcattggtc cagttgacgc agcaagggcg aattc 3105

<210> SEQ ID NO 22
<211> LENGTH: 3094
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone F1

<400> SEQUENCE: 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

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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

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aacctcttgg agaacctcca gcagcgccct ctagtgtggg atctggtaca atggctgcag 1440

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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

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cgaatgacgg cgtcacgacc atcgctaata accttaccag cacggttcag gtcttctcgg 1860

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aatcggtggg ccgttcctcc ttctactgcc tggaatattt cccctctcaa atgctgagaa 2040

cgggcaacaa ctttgagttc agttacagct tcgaggacgt gcctttccac agcagctacg 2100

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ccaatactat ggccgagcag tcaaagaact ggctgcctgg accctgctat aggcaacagg 2280

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aatatcatct gaatggcaga aactctttga ccaatcctgg cattcccatg gcaaccaaca 2400

aggatgatga ggaccagttc tttcccatca acggggtact ggtttttggc aagacgggag 2460

ctgccaacaa aactacgctg gaaaacgttc tgatgaccag cgaggaggag atcaagacca 2520

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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> SEQ ID NO 23
<211> LENGTH: 3095
<212> TYPE: DNA
<213> ORGANISM: Unknown

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<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone F3

<400> SEQUENCE: 23

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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 gttctttgac agtctctgtt gcctatagca gggtccaggc 840

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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

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aggagcttga accgcagctt cttgggccgg aatccccagt tgttgttgat gagtcgctgc 1380

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ctgtagccga agtagtggtt gtcattggtg gctcctgagc tgctgctgga gatttgcttg 1500

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ttgggtttcg gggctccagg tttcaggtcc caccactcgc gaatgccctc agagaggttg 2220

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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

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ctcattggtc cagttgacgc agcaagggcg aattc 3095

<210> SEQ ID NO 24
<211> LENGTH: 3095
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone F5

<400> SEQUENCE: 24

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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

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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 gttctttgac agtctctgtt gcctatagca gggtccaggc 840

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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

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tcctcgagcc aatctggaag ataaccatcg gcagccatac ctggtttaag ccatttattg 2280

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tgtcaccttg ccaaagtcgt gttccagacg gcgggtgagt tcaaatttga acatccggtc 2820

ctgcaacggc tgctggtgct cgaaggtggt gctgttcccg tcgatcacgg cgcgcatgtt 2880

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ctcattggtc cagttgacgc agcaagggcg aattc 3095

<210> SEQ ID NO 25
<211> LENGTH: 3142
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone H6

<400> SEQUENCE: 25

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cgcgaattcg cctttcgcag agaccaaagt tcaactgaaa cgaattaaac ggtttattga 120

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ttaacaagca attacagatt acgagtcagg tatctggtgc caatggggcg aggctctgaa 180

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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

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atttgcttgt agaggtggtt gttgtatgtg ggcagggccc aggttcgggt gctggtggtg 1620

atgactctgt cgcccagcca ttgggaatcg caatgccaat ttcctgagga attacccact 1680

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gatcccagac cagagggggc 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

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tcgtaggcct tgtcgtgctc gagggccgcg gcgtctgcct cgttgaccgg ctccccttg 2160

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gtaaaaggaa agttctcatt gg 3142

<210> SEQ ID NO 26
<211> LENGTH: 3075
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone H2

<400> SEQUENCE: 26

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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

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atggctgggc gacagagtca tcaccaccag cacccgaacc tgggccctgc ccacatacaa 1560

caaccacctc tacaagcaaa tctccagcca atcaggagcc agcaacgaca accactactt 1620

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cctgggctcg gcgcatcaag gatgcctccc gccgtttcca gcggacgtct tcatggtccc 1920

acagtatgga tacctcaccc tgaacaacgg gagtcaggcg gtaggacgct cttcctttta 1980

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cacttttgaa gacgtgcctt tccacagcag ctacgctcac agccagagtc tggatcggct 2100

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agctaaaaac tggctgcctg gaccttgcta cagacagcag cgtctgtcaa aacaggcaaa 2280

cgacaacaac aacagcaact ttccctggac tgcagctaca aagtatcatc taaatggccg 2340

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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> SEQ ID NO 27
<211> LENGTH: 3128
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 42.8

<400> SEQUENCE: 27

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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

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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

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cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

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cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

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ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

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caaatctcca acgggacatc gggaggaagc accaacgaca acacctactt cggctacagc 1680

acccccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

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gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc 2160

ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220

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aacagcaact ttgcttggac cggtgccacc aagtatcatc tgaatggcag agactctctg 2400

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gttatgctaa ccagtgagga agaaatcaaa accaccaacc cagtggccac agaacagtac 2580

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agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct 2700

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atctgggcca agattcctca cacggacggc aactttcatc cttcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat 2820

cctccaacta ccttcagtca agccaagctg gcgtcgttca tcacgcagta cagcaccgga 2880

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gagggtactt attcagagcc tcgccccatt ggcacccgtt acctcacccg taacctgtaa 3060

ttgcctgtta atcaataaac cggctaattc gtttcagttg aactttggtc tctgcgaagg 3120

gcgaattc 3128

<210> SEQ ID NO 28
<211> LENGTH: 3128
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 42.15

<400> SEQUENCE: 28

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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

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ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

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acccccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

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tacctgactc tgaacaacgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

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gacgtgcctt ttcacagcag ctacgcgcat agccaaagcc tggaccggct gatgaacccc 2160

ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220

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cctccaacta ccttcagtca agccaagctg gcgtcgttca tcacgcagta cagcaccgga 2880

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gagggtactt attcagagcc tcgccccatt ggcacccgtt acctcacccg taacctgtaa 3060

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gcgaattc 3128

<210> SEQ ID NO 29
<211> LENGTH: 3197
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype. clone 42.5b

<400> SEQUENCE: 29

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cccagatcga ccccacccccc 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 gccccccgatg acgcggataa aagcgagccc aagcgggcct 480

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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

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cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

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cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

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ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

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gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacatc gggaggaagc accaacgaca acacctactt cggctacagc 1680

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tacctgactc tgaacaacgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

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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

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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> SEQ ID NO 30
<211> LENGTH: 2501
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 42.1b

<400> SEQUENCE: 30

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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 cttttggggg caacctcggg cgagcagtct tccaggccaa 600

gaagcgggtt ctcgaacctc tcggtctggt tgaggaaggc gctaagacgg ctcctggaaa 660

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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

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tcaggccgtg ggccgttcct ccttctactg cctggagtac tttccttctc aaatgctgag 1440

aacgggcaac aactttgagt tcagctacca gtttgaggac gtgcctttc acagcagcta 1500

tgcgcacagc caaagcctgg accggctgat gaaccccctc atcgaccagt acctgtacta 1560

cctgtctcgg actcagtcca cgggaggtac cgcaggaact cagcagttgc tattttctca 1620

ggccgggcct aataacatgt cggctcaggc caaaaactgg ctacccgggc cctgctaccg 1680

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gcagcaacgc gtctccacga cagtgtcgca aaataacaac agcaactttg cttggaccgg 1740

tgccaccaag tatcatctga atggcagaga ctctctggta aatcccggtg tcgctatggc 1800

aacgcacaag ggcgacgaag agcgattttt 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

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ctacaaatct acaaatgtgg actttgctgt caatactgag ggtacttatt cagagcctcg 2400

ccccattggc acccgttacc tcacccgtaa cctgtaattg cctgttaatc aataaaccgg 2460

ttgattcgtt tcagttgaac tttggtctca agggcgaatt c 2501

<210> SEQ ID NO 31
<211> LENGTH: 3113
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 42.13

<400> SEQUENCE: 31

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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

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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

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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

tttgacttta 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 gccttttcac 2100

agcagctatg cgcacagcca aagcctggac cggctgatga acccccctcat 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 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

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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> SEQ ID NO 32
<211> LENGTH: 3113
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 42.3a

<400> SEQUENCE: 32

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gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

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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

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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

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gaccctcaac caatcggaga acccccgca 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

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gaggtcacgc agaatgaagg caccaagacc atcgccaata accttaccag cacgattcag 1860

gtctttacgg actcggaata ccagctcccg tacgtcctcg gctctgcgca ccagggctgc 1920

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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

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aacctgcaac agcaaaacgc cgctcctatt gtaggggccg tcaacagtca aggagcctta 2640

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cctcacacgg acggcaactt tcatccttcg ccgctgatgg gaggctttgg actgaaacac 2760

ccgcctcctc agatcctgat taagaatata 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> SEQ ID NO 33
<211> LENGTH: 2504
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 42.4

<400> SEQUENCE: 33

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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

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caggccgtgg gccgttcctc cttctactgc ctggagtact ttccttctca aatgctgaga 1440

acgggcaaca actttgagtt cagctaccag tttgaggacg tgcctttca cagcagctac 1500

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gccgggccta ataacatgtc ggctcaggcc aaaaactggc tacccgggcc ctgctaccgg 1680

cagcaacgcg tctccacgac actgtcgcaa aataacaaca gcaactttgc ttggaccggt 1740

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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

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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> SEQ ID NO 34
<211> LENGTH: 3106
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 42.5a

<400> SEQUENCE: 34

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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

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gcgagtggtg ggacttgaaa cctggagccc cgaaacccaa agccaaccag caaaagcagg 960

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gccccattgg cacccgttac ctcacccgta acctgtaatt gcctgttaat caataaaccg 3060

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<210> SEQ ID NO 35
<211> LENGTH: 2489
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 42.10

<400> SEQUENCE: 35

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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

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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

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aacagattcc actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg 1140

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aaggacgacg aggaccagtt ctttcccatc aacggagtgc tggtttttgg caaaacgggg 1860

gctgccaaca agacaacgct ggaaaacgtg ctaatgacca gcgaggagga gatcaaaacc 1920

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aaagaaaaca gcaaacgctg gaatccagag attcagtaca cctcaaatta tgccaagtct 2340

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<210> SEQ ID NO 36
<211> LENGTH: 2495
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 42.3b

<400> SEQUENCE: 36

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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

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gactcggagt accaactgcc gtacgtcctc ggctctgcgc accagggctg cctccctccg 1320

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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

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aaggacgacg aggaccagtt ctttcccatc aacggagtgc tggtttttgg caaaacgggg 1860

gctgccaaca agacaacgct ggaaaacgtg ctaatgacca gcgaggagga gatcaaaacc 1920

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aataatgtgg aatttgctgt caacaacgaa ggggtttata ctgagcctcg ccccattggc 2400

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<210> SEQ ID NO 37
<211> LENGTH: 3098
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 42.11

<400> SEQUENCE: 37

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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

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aactttcacc cgtctcccct gatgggcgga tttggactca aacacccgcc tcctcaaatt 2760

ctcatcaaaa acaccccggt acctgctaat cctccagagg tgtttactcc tgccaagttt 2820

gcctcattta tcacgcagta cagcaccggc caggtcagcg tggagatcga gtgggaactg 2880

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ggcacccgtt acctcacccg taacctgtaa ttacttgtta atcaataaac cggttgattc 3060

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<210> SEQ ID NO 38
<211> LENGTH: 3276
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 42.6a

<400> SEQUENCE: 38

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tgaatctctg gattccagcg tttgctgttt tctttctgca gttcccactc gatctccacg 240

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tctggaggat tagcaggtac cggggtgttt ttgatgagaa tttgaggagg cgggtgtttg 360

agtccaaatc cgtccatcag gggagacggg tgaaagttgc cgtccgtgtg aggaattttg 420

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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

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cagtcacgtg gtgagaagtg gcagtggaat ctgttaaagt caaaataccc ccaggggtg 1440

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atgccctcag agaggttgtc ctcgagccaa tctggaagat aaccatcggc agccatacct 2280

ggtttaagtc atttattgct cagaaacaca gtcatccagg tccacgttga ccagatcgca 2340

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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

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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> SEQ ID NO 39
<211> LENGTH: 3084
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 43.1

<400> SEQUENCE: 39

gaattcgccc tttctacggc tgcatcaact 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 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

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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

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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> SEQ ID NO 40
<211> LENGTH: 2370
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 43.5

<400> SEQUENCE: 40

gaattcgccc tttctacggc tgcgtcaact 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

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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

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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> SEQ ID NO 41
<211> LENGTH: 3123
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 43.12

<400> SEQUENCE: 41

gaattcgccc ttggctgcgt caactggacc aatgagaact ttcccttcaa cgattgcgtc 60

gacaagatgg tgatctggtg ggaggagggc aagatgacgg ccaaggtcgt ggagtccgcc 120

aaggccattc tcggcggcag caaggtgcgc gtggaccaaa agtgcaagtc gtccgcccag 180

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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

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caagaaaggc caccagcccg cgagaaagag actgaacttt gggcagactg gcgactcgga 1380

gtcagtcccc gaccctcaac caatcggaga accaccagca ggccccctctg 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

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tcccggcgtt gccatggcta cccacaagga cgacgaggag cgcttcttcc cgtcaagcgg 2460

agttctaatg tttggcaagc agggggctgg aaaagacaat gtggactaca gcagcgtgat 2520

gctcaccagc gaagaagaaa ttaaaactac taacccagtg gctacagagc agtatggtgt 2580

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ggtggcagac aacctgcagc agaccaacgg agctcccatt gtgggaactg tcaacagcca 2640

gggggcctta 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> SEQ ID NO 42
<211> LENGTH: 3122
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 43.20

<400> SEQUENCE: 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

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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

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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

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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> SEQ ID NO 43
<211> LENGTH: 3117
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 43.21

<400> SEQUENCE: 43

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gacaagatgg tgatctggtg ggaggagggc aagatgacgg ccaaggtcgt ggagtccgcc 120

aaggccattc tcggcggcag caaggtgcgt gtggaccaaa agtgcaagtc ttccgcccag 180

atcgatccca cccccgtgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg 240

aacagcacca ccttcgagca ccagcagccg ttgcaggacc ggatgttcaa atttgaactc 300

acccgccgtc tggagcatga ctttggcaag gtgacgaagc aggaagtcaa agagttcttc 360

-continued

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

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gggtaattcc tcgggaaatt ggcattgcga ttccacatgg ctgggggaca gagtcatcac 1560

caccagcacc cgaacctggg ccctgcccac ctacaacaac cacctctaca agcaaatctc 1620

caacggcacc tcgggaggaa gcaccaacga caacacctat tttggctaca gcacccctg 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

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tttccacagc agctacgcgc acagccagag cctggacagg ctgatgaatc ccctcatcga 2160

ccagtacctg tactacctgg tcagaacgca aacgactgga actggaggga cgcagactct 2220

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accttgctac cggcagcagc gcgtctccac gacaaccaac cagagcaaca acagcaactt 2340

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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 accaggggtt 2640

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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> SEQ ID NO 44
<211> LENGTH: 3121
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 43.23

<400> SEQUENCE: 44

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cgccaaggcc attctcggcg gcagcaaggt gcgtgtggac caaaagtgca agtcttccgc 180

ccagatcgat cccacccccg 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

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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 agcccccтca 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

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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

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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> SEQ ID NO 45
<211> LENGTH: 3122
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 43.25

<400> SEQUENCE: 45

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 caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaaatttg 300

aactcacccg ccgtctggag catgactttg gcaaggtgac gaagcaggaa gtcaaagggt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttccac gtgcgagccc 420

aagcgggcct gcccctcagt cgcggatcca tcgacgtcag accagaaagg gtggagccaa 480

caagagaccc gcccccgatg acgcggatat aagcggaagg agctccggtg gactttgccg 540

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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

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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

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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

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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

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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

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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

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caatacactt ccaactacta caaatctaca aatgtggact ttgctgtcaa cacggagggg 3000

gtttatagcg agcctcgccc cattggcacc cgttacctca cccgcaacct gtaattacat 3060

gttaatcaat aaaccggtta attcgtttca gttgaacttt ggtctctgcg aagggcgaat 3120

tc 3122

<210> SEQ ID NO 46
<211> LENGTH: 3128
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 44.1

<400> SEQUENCE: 46

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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

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cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

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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

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gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tacctgactc tgaacaatgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

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gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc 2160

ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220

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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

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gatggcactt attctgagcc tcgccccatt ggcacccgtt acctcacccg taatctgtaa 3060

ttgctcgtta atcaataaac cggttgattc gtttcagttg aactttggtc tctgcgaagg 3120

gcgaattc 3128

<210> SEQ ID NO 47
<211> LENGTH: 3128
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 44.5

<400> SEQUENCE: 47

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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

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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 ttgggggca 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

acccccctgg 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

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ttgcttgtta atcaataaac cggttgattc gtttcagttg aactttggtc tctgcgaagg 3120

gcgaattc 3128

<210> SEQ ID NO 48
<211> LENGTH: 1933
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 223.10
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1302)..(1302)
<223> OTHER INFORMATION: can be a, c, g or t

<400> SEQUENCE: 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 ggccccctctg 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

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tttccacagc agctacgcgc acagccagag tctggaccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat 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

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gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> SEQ ID NO 49
<211> LENGTH: 1933
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 223.2

<400> SEQUENCE: 49

caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagt gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gttgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca 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

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tttccacagc agctacgcgc acagccagag tctggaccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa 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

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ttactctgag cct 1933

<210> SEQ ID NO 50
<211> LENGTH: 1933
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 223.4

<400> SEQUENCE: 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

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ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg 1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat 1440

gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt 1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc 1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaagt ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gaatgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

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<210> SEQ ID NO 51
<211> LENGTH: 1933
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 223.5

<400> SEQUENCE: 51

caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gccagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca cggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca 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

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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> SEQ ID NO 52
<211> LENGTH: 1933
<212> TYPE: DNA

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<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 223.6

<400> SEQUENCE: 52

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cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aatagcgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca 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

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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

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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> SEQ ID NO 53
<211> LENGTH: 1933
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 223.7

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<400> SEQUENCE: 53

caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccctg 600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggcgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggacc cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

ttctcagatg ctgagaacgg gcaacaactt caccttagc tacaccttcg aggacgtgcc 1020

tttccacagc agctacgcgc acagccagag tctggaccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg 1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat 1440

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aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

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cgttgagatc gagtgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> SEQ ID NO 54
<211> LENGTH: 3123
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone A3.4

<400> SEQUENCE: 54

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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

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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

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tttgacttta acagattcca ctgtcacttc tcaccacgtg actggcagcg actcatcaac 1740

aacaactggg gatttagacc caagaaactc aatttcaagc tcttcaacat ccaagtcaag 1800

gaggtcacgc agaatgatgg aaccacgacc atcgccaata accttaccag cacggtgcag 1860

gtcttcacag actctgagta ccagctgccc tacgtcctcg gttcggctca ccagggctgc 1920

cttccgccgt tcccagcaga cgtcttcatg attcctcagt acggctactt gactctgaac 1980

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atgctgagga cgggaaacaa cttcaccttc agctacactt ttgaagacgt gcctttccac 2100

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agctaccgac agcagcgaat gtctaagacg gctaatgaca acaacaacag tgaatttgct 2340

tggactgcag ccaccaaata ttacctgaat ggaagaaatt ctctggtcaa tcccgggccc 2400

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gaagaagaaa tcagaacaac taatcctgtg gctacagaac aatacggaca ggttgccacc   2580

aaccatcaga gtcaggacac cacagcttcc tatggaagtg tggacagcca gggaatctta   2640

cctggaatgg tgtggcagga ccgcgatgtc tatcttcaag gtcccatttg ggccaaaact   2700

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gaaccccgcc ctattggcac tcgttacctt acccggaact tgtaatttcc tgttaatgaa   3060

taaaccgatt tatgcgtttc agttgaactt tggtctctgc gaagggcgaa ttcgcggccg   3120

cta                                                                3123


<210> SEQ ID NO 55
<211> LENGTH: 3113
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone A3.5

<400> SEQUENCE: 55

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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
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gtcccagacc ctcaaccaat cggagaaccc cccgcagccc cctctggtgt gggatctaat 1440

acaatggctt caggcggtgg ggcaccaatg gcagacaata acgaaggcgc cgacggagtg 1500

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aacaactggg gatttagacc caagaaactc aatttcaagc tcttcaacat ccaagtcaag 1800

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agctaccgac agcagcgaat gtctaagacg gctaatgaca acaacaacag tgaatttgct 2340

tggactgcag ccaccaaata ttacccgaat ggaagaaatt ctctggtcaa tcccgggccc 2400

ccaatggcca gtcacaagga cgatgaggaa aagtatttcc ccatgcacgg aaatctcatc 2460

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gaagaagaaa tcagaacgac taatcctgtg gctacagaac aatacggaca ggttgccacc 2580

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gaaccccgcc ctattggcac tcgttacctt acccggaact tgtaatttcc tgttaatgaa 3060

taaaccgatt tatgcgtttc agttgaactt tggtctctgc gaagggcgaa ttc 3113

<210> SEQ ID NO 56
<211> LENGTH: 3122
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone A3.7

<400> SEQUENCE: 56

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tcaacgattg cgtcgacaag atggtgatct ggtgggagga gggaaagatg accgccaagg 120

tcgtggaatc tgccaaagcc attctgggtg gaagcaaggt tcgtgtggac cagaaatgca 180

ggtcttcggc ccagatcgac ccgactccgg tgattgtcac ctctaacacc aacatgtgcg 240

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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

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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

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caagtcaagg aggtcacgca gaatgatgga accacgacca tcgccaataa ccttaccagc 1860

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aatctcatct ttggaaaaca aggcacagga actaccaatg tggacattga atcagtgctt 2520

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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> SEQ ID NO 57
<211> LENGTH: 3123
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone A3.3

<400> SEQUENCE: 57

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ctgccaaagc cattctgggt ggaggcaagg ttcgtgtgga ccagaaatgc aagtcttcgg 180

cccagatcga cccgactccg gtgattgtca cctctaacac caacatgtgc gccgtgattg 240

acggaaactc gaccaccttc gagcaccagc agccgttgca agaccggatg ttcaaatttg 300

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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

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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

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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

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agctaccgac agcagcgaat gtctaagacg gctaatgaca acaacaacag tgaatttgct 2340

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gaagaagaaa tcagaacaac taatcctgtg gctacagaac aatacggaca ggttgccacc 2580

aaccatcaga gtcagaacac cacagcttcc tatggaagtg tggacagcca gggaatctta 2640

cctggaatgg tgtggcagga ccgcgatgtc tatcttcaag gtcccatttg ggccaaaact 2700

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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> SEQ ID NO 58
<211> LENGTH: 2969
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 42.12

<400> SEQUENCE: 58

gaattcgccc tttctacggc tgcgtcaact 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 agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

-continued

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

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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> SEQ ID NO 59
<211> LENGTH: 3129
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AAV serotype, clone 44.2

<400> SEQUENCE: 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

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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> SEQ ID NO 60
<211> LENGTH: 733
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone C1VP1

<400> SEQUENCE: 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
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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
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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> SEQ ID NO 61
<211> LENGTH: 733
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone C2VP1

<400> SEQUENCE: 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
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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
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        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> SEQ ID NO 62
<211> LENGTH: 733
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone C5VP1[@0002]

<400> SEQUENCE: 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
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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
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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> SEQ ID NO 63
<211> LENGTH: 734
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone AAV4VP1

<400> SEQUENCE: 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
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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
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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> SEQ ID NO 64
<211> LENGTH: 736
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of  AAV serotype, clone AAV1

<400> SEQUENCE: 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
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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> SEQ ID NO 65
<211> LENGTH: 736
<212> TYPE: PRT
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<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone AAV6VP1

<400> SEQUENCE: 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

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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> SEQ ID NO 66
<211> LENGTH: 735
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of  AAV serotype, clone A3.3

<400> SEQUENCE: 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
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            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> SEQ ID NO 67
<211> LENGTH: 735
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of  AAV serotype, clone A3.7

<400> SEQUENCE: 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
```

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```
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
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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> SEQ ID NO 68
<211> LENGTH: 735
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of  AAV serotype, clone A3.4

<400> SEQUENCE: 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
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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
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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> SEQ ID NO 69
<211> LENGTH: 735
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone A3.5

<400> SEQUENCE: 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
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           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
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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> SEQ ID NO 70
<211> LENGTH: 735
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone AAV2

<400> SEQUENCE: 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
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Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser 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
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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> SEQ ID NO 71
<211> LENGTH: 736
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of  AAV serotype, clone AAV3

<400> SEQUENCE: 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
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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
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705                 710                 715                 720

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


<210> SEQ ID NO 72
<211> LENGTH: 737
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of  AAV serotype, clone 3.3bVP1

<400> SEQUENCE: 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
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            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
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<210> SEQ ID NO 73
<211> LENGTH: 644

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<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 223-4

<400> SEQUENCE: 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

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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> SEQ ID NO 74
<211> LENGTH: 644
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 223-5

<400> SEQUENCE: 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
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           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
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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> SEQ ID NO 75
<211> LENGTH: 644
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 223-10
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (434)..(434)
<223> OTHER INFORMATION: can be any amino acid

<400> SEQUENCE: 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
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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
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Tyr Ser Glu Pro

<210> SEQ ID NO 76
<211> LENGTH: 644
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 223-2

<400> SEQUENCE: 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

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        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> SEQ ID NO 77
<211> LENGTH: 644
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 223-7

<400> SEQUENCE: 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
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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
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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> SEQ ID NO 78
<211> LENGTH: 644
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 223-6

<400> SEQUENCE: 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
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    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
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Tyr Ser Glu Pro

<210> SEQ ID NO 79
<211> LENGTH: 738
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 44.1

<400> SEQUENCE: 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

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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> SEQ ID NO 80
<211> LENGTH: 738
<212> TYPE: PRT
<213> ORGANISM: Unknown
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<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 44.5

<400> SEQUENCE: 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

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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> SEQ ID NO 81
<211> LENGTH: 738
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of  AAV serotype, clone 44.2

<400> SEQUENCE: 81

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
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```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

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

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

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

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

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

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

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

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

Gly Lys Lys Gly 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
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        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> SEQ ID NO 82
<211> LENGTH: 738
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 29.3VP1

<400> SEQUENCE: 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
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```
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
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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> SEQ ID NO 83
<211> LENGTH: 738
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 29.5VP1

<400> SEQUENCE: 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
```

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```
           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
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```
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> SEQ ID NO 84
<211> LENGTH: 738
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 42.15

<400> SEQUENCE: 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
```

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```
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
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               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> SEQ ID NO 85
<211> LENGTH: 738
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 42.8

<400> SEQUENCE: 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
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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
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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> SEQ ID NO 86
<211> LENGTH: 733
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 42.13

<400> SEQUENCE: 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
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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> SEQ ID NO 87
<211> LENGTH: 733
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 42.3A

<400> SEQUENCE: 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
```

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```
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
```

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```
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> SEQ ID NO 88
<211> LENGTH: 731
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 42.4

<400> SEQUENCE: 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
```

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```
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> SEQ ID NO 89
<211> LENGTH: 731
<212> TYPE: PRT

-continued

<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 42.5A

<400> SEQUENCE: 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

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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> SEQ ID NO 90
<211> LENGTH: 733
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of  AAV serotype, clone 42.1B

<400> SEQUENCE: 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
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           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
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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> SEQ ID NO 91
<211> LENGTH: 738
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 42.5B

<400> SEQUENCE: 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
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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
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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> SEQ ID NO 92
<211> LENGTH: 738
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 43.1

<400> SEQUENCE: 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
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        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
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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> SEQ ID NO 93
<211> LENGTH: 738
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 43.12

<400> SEQUENCE: 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
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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
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            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> SEQ ID NO 94
<211> LENGTH: 738
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 43.5

<400> SEQUENCE: 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
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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
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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> SEQ ID NO 95
<211> LENGTH: 738
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone AAV8

<400> SEQUENCE: 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
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               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
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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> SEQ ID NO 96
<211> LENGTH: 736
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 43.21

<400> SEQUENCE: 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
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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
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705                 710                 715                 720

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


<210> SEQ ID NO 97
<211> LENGTH: 736
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 43.25

<400> SEQUENCE: 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
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            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> SEQ ID NO 98
<211> LENGTH: 736
<212> TYPE: PRT
<213> ORGANISM: Unknown
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<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 43.23

<400> SEQUENCE: 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

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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> SEQ ID NO 99
<211> LENGTH: 736
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 43.20

<400> SEQUENCE: 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
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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
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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> SEQ ID NO 100
<211> LENGTH: 736
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone AAV9

<400> SEQUENCE: 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
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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
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            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> SEQ ID NO 101
<211> LENGTH: 728
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 24.1

<400> SEQUENCE: 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
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    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
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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> SEQ ID NO 102
<211> LENGTH: 728
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 42.2REAL

<400> SEQUENCE: 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
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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
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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> SEQ ID NO 103
<211> LENGTH: 728
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 7.2VP1

<400> SEQUENCE: 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
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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
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            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> SEQ ID NO 104
<211> LENGTH: 728
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 27.3VP1

<400> SEQUENCE: 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
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    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> SEQ ID NO 105
<211> LENGTH: 728
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 16.3VP1

<400> SEQUENCE: 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

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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> SEQ ID NO 106
<211> LENGTH: 728
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
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<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 42.10

<400> SEQUENCE: 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
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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> SEQ ID NO 107
<211> LENGTH: 728
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 42.3B

<400> SEQUENCE: 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
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```
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
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    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> SEQ ID NO 108
<211> LENGTH: 728
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 42.11

<400> SEQUENCE: 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
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               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
```

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```
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> SEQ ID NO 109
<211> LENGTH: 729
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone F1VP1

<400> SEQUENCE: 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
```

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```
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
```

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```
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> SEQ ID NO 110
<211> LENGTH: 729
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone F5VP1[@0003]

<400> SEQUENCE: 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
```

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```
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
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```
    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> SEQ ID NO 111
<211> LENGTH: 729
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone F3VP1

<400> SEQUENCE: 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
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```
               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
```

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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> SEQ ID NO 112
<211> LENGTH: 735
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 42.6B

<400> SEQUENCE: 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
```

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


<210> SEQ ID NO 113
<211> LENGTH: 685
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone 42.12

<400> SEQUENCE: 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
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```
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> SEQ ID NO 114
<211> LENGTH: 724
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: capsid protein of AAV serotype, clone AAV5CAP

<400> SEQUENCE: 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
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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
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    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> SEQ ID NO 115
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: DraIII restriction enzyme site

<400> SEQUENCE: 115

caccacgtc                                                             9


<210> SEQ ID NO 116
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: AV2cas

<400> SEQUENCE: 116

cgcagagacc aaagttcaac tgaaacga                                       28


<210> SEQ ID NO 117
<211> LENGTH: 255
```

-continued

<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: adeno-associated virus serotype 10

<400> SEQUENCE: 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> SEQ ID NO 118
<211> LENGTH: 258
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: adeno-associated virus serotype 11

<400> SEQUENCE: 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> SEQ ID NO 119
<211> LENGTH: 255
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: adeno-associated virus serotype 12

<400> SEQUENCE: 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> SEQ ID NO 120
<211> LENGTH: 2205
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: adeno-associated virus serotype, clone A3.1vp1

<400> SEQUENCE: 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

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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
```

What is claimed is:

1. A cultured host cell containing a recombinant nucleic acid molecule

encoding an AAV vp1 capsid protein having a sequence comprising amino acids 1 to 738 of SEQ ID NO: 81 (AAVrh.10) or a sequence at least 95% identical to the full length of amino acids 1 to 738 of SEQ ID NO: 81, wherein the recombinant nucleic acid molecule further comprises a heterologous non-AAV sequence.

2. The cultured host cell according to claim **1**, which further comprises a functional rep gene.

3. A cultured host cell containing a recombinant nucleic acid molecule

encoding an AAV vp2 capsid protein having a sequence comprising amino acids 138 to 738 of SEQ ID NO: 81 (AAVrh.10) or a sequence at least 95% identical to the full length of amino acids 138 to 738 of SEQ ID NO: 81, wherein the recombinant nucleic acid molecule further comprises a heterologous non-AAV sequence.

4. The cultured host cell according to claim **3**, which further comprises a functional rep gene.

5. A cultured host cell containing a recombinant nucleic acid molecule

encoding an AAV vp3 capsid protein having a sequence comprising amino acids 204 to 738 of SEQ ID NO: 81 (AAVrh.10) or a sequence at least 95% identical to the full length of amino acids 204 to 738 of SEQ ID NO:

81, wherein the recombinant nucleic acid molecule further comprises a heterologous non-AAV sequence.

6. The cultured host cell according to claim **5**, which further comprises a functional rep gene.

7. A cultured host cell containing a recombinant nucleic acid molecule comprising

(a) nucleotides 845 to 3058 of SEQ ID NO: 59 or a sequence at least 95% identical to nucleotides 845 to 3058 of SEQ ID NO: 59;

(b) nucleotides 1256 to 3058 of SEQ ID NO: 59 or a sequence at least 95% identical to nucleotides 1256 to 3058 of SEQ ID NO: 59; or

(c) nucleotides 1454 to 3058 of SEQ ID NO: 59 or a sequence at least 95% identical to nucleotides 1454 to 3058 of SEQ ID NO: 59,

wherein the recombinant nucleic acid molecule further comprises a heterologous non-AAV sequence.

8. The cultured host cell according to claim **7**, which further comprises a functional rep gene.

9. The cultured host cell according to claim **8**, wherein said nucleotide sequence is at least 95% identical to nucleotides 845 to 3058 of SEQ ID NO: 59.

10. The cultured host cell according to claim **9**, wherein said nucleotide sequence is at least 98% identical to nucleotides 845 to 3058 of SEQ ID NO: **59**.

11. The cultured host cell according to claim **10**, wherein said nucleotide sequence is at least 99% identical to nucleotides 845 to 3058 of SEQ ID NO: 59.

12. The cultured host cell according to claim **8**, wherein said nucleotide sequence is at least 95% identical to nucleotides 1256 to 3058 of SEQ ID NO: 59.

13. The cultured host cell according to claim **12**, wherein said nucleotide sequence is at least 98% identical to nucleotides 1256 to 3058 of SEQ ID NO: 59.

14. The cultured host cell according to claim **13**, wherein said nucleotide sequence is at least 99% identical to nucleotides 1256 to 3058 of SEQ ID NO: 59.

15. The cultured host cell according to claim **8**, wherein said nucleotide sequence is at least 95% identical to nucleotides 1454 to 3058 of SEQ ID NO: 59.

16. The cultured host cell according to claim **15**, wherein said nucleotide sequence is at least 98% identical to nucleotides 1454 to 3058 of SEQ ID NO: 59.

17. The cultured host cell according to claim **16**, wherein said nucleotide sequence is at least 99% identical to nucleotides 1454 to 3058 of SEQ ID NO: 59.

18. The cultured host cell according to claim **2**, wherein the rep gene is from AAV2.

19. The cultured host cell according to claim **4**, wherein the rep gene is from AAV2.

20. The cultured host cell according to claim **6**, wherein the rep gene is from AAV2.

21. The cultured host cell according to claim **8**, wherein the rep gene is from AAV2.

22. The cultured host cell according to claim **1**, wherein the recombinant nucleic acid molecule is a plasmid.

23. The cultured host cell according to claim **3**, wherein the recombinant nucleic acid molecule is a plasmid.

24. The cultured host cell according to claim **5**, wherein the recombinant nucleic acid molecule is a plasmid.

25. The cultured host cell according to claim **5**, wherein the recombinant nucleic acid molecule is a plasmid.

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