

670 680 690 700 710 720
1. AAV2 GTGCTCGTGGAAACCACCGGGGTGAAATCCATGGTCTTGGGACGTTTCC TGAGTCAGATT
2. AAV5_geneb... ACGCTTGTGGAGACCCTCGGCATCTCTTCCATGGTCTTGGCCGCTACGTGAGTCAGATT
3. AAV7_geneb... GTTCTGGTGGAGACCACGGGGTCAAGTCCATGGTGC TAGGCCGCTTCTTGAGTCAGATT
4. AAV8_geneb... GTTCTGGTGGAGACCACGGGGTCAAGTCCATGGTGC TAGGCCGCTTCTTGAGTCAGATT
5. pAAV_RC - ...

730 740 750 760 770 780
1. AAV2 CGCGAAAAAC-TGATTCAGAGCAATTTA-CCGCGGGATCGAG-CCGACTTTGCCAAACTGG
2. AAV5_geneb... CGCGCCAGC-TGGTGAAGTGGTCTTCCAG-GGAATTTGAACCCCA-GATCAACGACTGG
3. AAV7_geneb... CGCGAAGC-TGGTCCAGACCATCTA-CCGCGGGTTCGAG-CCACGCTGCCCAACTGG
4. AAV8_geneb... CGCGAAAAAC-TGGTCCAGACCATCTA-CCGCGGGTTCGAG-CCACGCTGCCCAACTGG
5. pAAV_RC - ...

790 800 810 820 830 840
1. AAV2 TTTCGCGGTAC-AAAGAC-CAGAAATGGCGCCGGAGG-CGGAAACAAGGTGGTGGATGAG
2. AAV5_geneb... GTTCGCATCACCAA-----GGTAAAGAG--GGCGG-AGCCAAATAAGGTGGTGGATTCCT
3. AAV7_geneb... TTTCGCGGTGACCAA-GACGC-GTAATGGCGCCGGCGG-GGGAAACAAGGTGGTGGACGAG
4. AAV8_geneb... TTTCGCGGTGACCAAAGACGCGTAAATGGCGCCGGCGGCGGGAAACAAGGTGGTGGACGAG
5. pAAV_RC - ...

850 860 870 880 890 900
1. AAV2 TGCTACATCCCCAATACCTTTCCTCCCAAACCAGCCGAGCTCAGTGGGCGTGGACT
2. AAV5_geneb... GGGTATATTCCTCCCTACCTGCTGCCGAAGGTTCCAAACCGAGCTTCAGTGGGCGTGGACA
3. AAV7_geneb... TGCTACATCCCCAATACCTTCTGCCCAAGACCAGCCGAGCTGCAGTGGGCGTGGACT
4. AAV8_geneb... TGCTACATCCCCAATACCTTCTGCCCAAGACTTCAGCCGAGCTGCAGTGGGCGTGGACT
5. pAAV_RC - ...

910 920 930 940 950 960
1. AAV2 AATATGGAACAGTATTTAAGCGCTGTGTTGAACTCACGGAGCGTAAACGGTTGGTGGCG
2. AAV5_geneb... AACCTGGAAGAGTATAAATTCGGCCCGCTGAACTTGGAGCGCAAACGGCTCGTCCGG
3. AAV7_geneb... AACATGGAGGAGTATATAAGCGCGTGTGTTGAACTGGCCGAAACGCAAACGGCTCGTGGCG
4. AAV8_geneb... AACATGGAGGAGTATATAAGCGCGTGTGTTGAACTGGCCGAGCGCAAACGGCTCGTGGCG
5. pAAV_RC - ...

970 980 990 1,000 1,010 1,020
1. AAV2 CAGCACTGACGACGTGTTCGAG-A--CGCAGGAGCAGAACAAGAGAATCAGAACTCC
2. AAV5_geneb... CAGTTCTGGAGAGATCTTCGAGCGCTCGCAGGAGGCGGCTTCGACCGT--GAGTTC-
3. AAV7_geneb... CAGCACTGACCCACGTACGACAGA---CGCAGGAGCAGAACAAGGAGAATCTGAACTCC
4. AAV8_geneb... CAGCACTGACCCACGTACGACAGA---CGCAGGAGCAGAACAAGGAGAATCTGAACTCC
5. pAAV_RC - ...

1,030 1,040 1,050 1,060 1,070 1,080
1. AAV2 AATTCTGATGCGCCGGT GATCAGATCAAAAACCTTCAGCCAGGTACATGGAGCTGGTGGG
2. AAV5_geneb... ---TCGGCTGACCCGGT CATCAAAAGCAAGACCTTCAGAAA TACATGGCGCTCGTCAAC
3. AAV7_geneb... AATTCTGACGCGCCCGT GATCAGGTCAAAAACCTTCGCGCGCTACATGGAGCTGGTGGG
4. AAV8_geneb... AATTCTGACGCGCCCGT GATCAGGTCAAAAACCTTCGCGCGCTATATGGAGCTGGTGGG
5. pAAV_RC - ...

1,090 1,100 1,110 1,120 1,130 1,140
1. AAV2 TGGCTCGTGGACAAAGGATACCTCGGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCA
2. AAV5_geneb... TGGCTCGTGGAGCACGGCATCACCTCCGAGAAGCAGTGGATCCAGGAATAACAGGAGAGC
3. AAV7_geneb... TGGCTCGTGGACCAGGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCG
4. AAV8_geneb... TGGCTCGTGGACCAGGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCG
5. pAAV_RC - ...

1,150 1,160 1,170 1,180 1,190 1,200
1. AAV2 TACATCTCCTTCAAATGC GGCTCCAACTCGCGGTCCCAAATCAAGGCAGCTTTGGACAAT
2. AAV5_geneb... TACCTCTCCTTCAACCTCAACGGCAACTCTCGGAGCCAGATCAAGGCCGCGCTCGACAAC
3. AAV7_geneb... TACATCTCCTTCAACGCGCTCCAACTCGCGGTCCAGATCAAGGCCGCGCTGGACAAT
4. AAV8_geneb... TACATCTCCTTCAACGCGCTCCAACTCGCGGTCCAGATCAAGGCCGCGCTGGACAAT
5. pAAV_RC - ...

1,210 1,220 1,230 1,240 1,250 1,260
1. AAV2 GCCGGAAGATATGAGCTTGACTTAAAACCGCCCCCGACTACCTGGTGGG---CAGCAG
2. AAV5_geneb... GCCAACAAATATGAGCTTGACTTAAAAGCGCGTGGACTACCTCGTGGGGAGCTCGT
3. AAV7_geneb... GCCGCAAGATCATGCGCTGACCAAAAACCGCGCCCGACTACCTGGTGGGGCTCTGCTG
4. AAV8_geneb... GCCGCAAGATCATGCGCTGACCAAAAACCGCGCCCGACTACCTGGTGGGGCTCTGCTG
5. pAAV_RC - ...

1,270 1,280 1,290 1,300 1,310 1,320
1. AAV2 CCCGTCGAGGACATTCTCAGCAATTCGGATTTATAAAAATTTTGGAACTAAACGGGTACGAT
2. AAV5_geneb... CCCG---AGGACATTCTAAAAAACAGAACTCTGGCAAATTTTGGAGATGAAATGGCTACGAC
3. AAV7_geneb... CCCG---CGGACATTAAAAACAACCGCATCTACCAGCATCTGGAGCTGAACGGGTACGAT
4. AAV8_geneb... CCCG---CGGACATTACCCAGAACCGCATCTACCAGCATCTGGAGCTGAACGGGTACGAC
5. pAAV_RC - ...

1,330 1,340 1,350 1,360 1,370 1,380
1. AAV2 CC CCAAATA TGC GGT TCCGTCTTTCT GGG ATGGGC CAC GAAAAAGTT CGG C AAG AG GAAC
2. AAV5_geneb... CC GGC TACGC GGA TCC ATC CT CTA CCGGCTGG TGT CAG GCT CTT C AAC AAG AG GAAC
3. AAV7_geneb... CCT GCC TACGC C GGC TCCGTCTTTCT CGGCTGGGC CAGAAAAAGTT CGG G AAG GC CAAC
4. AAV8_geneb... CCT GCC TACGC C GGC TCCGTCTTTCT CGGCTGGGC T CAGAAAAAGTT CGG G AA ACG CAAC
5. pAAV_RC - ...

1,390 1,400 1,410 1,420 1,430 1,440
1. AAV2 ACCATCTGGCTGTTTGG GCC TGC AAC T ACCGG G AAGACCAACAT C GCGGA G GCCAT AGCC
2. AAV5_geneb... ACC GTC TGGCT C T ACGG ACCCGCCAC G ACCGGCAAGACCAACAT C GCGGA G GCCATCGCC
3. AAV7_geneb... ACCATCTGGCTGTTTGG GCC CCGCCAC CACCGCAAGACCAACAT T GCGGA A GCCATCGCC
4. AAV8_geneb... ACCATCTGGCTGTTTGG ACCCGCCAC CACCGCAAGACCAACAT T GCGGA A GCCATCGCC
5. pAAV_RC - ...

1,450 1,460 1,470 1,480 1,490 1,500
1. AAV2 CAC A C TGTGCCCTTC TACGG G T GCGT A AACTGGACCAATGAGAACTTTCCCTTCAA C GAC
2. AAV5_geneb... CAC A C TGTGCCCTTT T TACGGCTGC GT G AACTGGACCAATGA A AACTTTTCCCTTT T AA T GAC
3. AAV7_geneb... CAC G C TGTGCCCTTC TACGGCTGC GT CAACTGGACCAATGAGAACTTTCCCTTCAA C GAT
4. AAV8_geneb... CAC G C TGTGCCCTTC TACGGCTGC GT CAACTGGACCAATGAGAACTTTCCCTTCAA T GAT
5. pAAV_RC - ...

1,510 1,520 1,530 1,540 1,550 1,560
1. AAV2 TG TGTGACAAGATGGTGA TCTGGTGGGAGGAGGG G AAGA TGAC C GC CAAGGT CGTGGAG
2. AAV5_geneb... TG TGT GACAA AATG C T C A T T TGGTGGGAGGAGGG A AAGA TGAC C AA CAAGGT GGT T GAA
3. AAV7_geneb... TG C TGTGACAAGATGGTGA TCTGGTGGGAGGAGGG CAAGA TGAC G GC CAAGGT CGTGGAG
4. AAV8_geneb... TG C TGTGACAAGATGGTGA TCTGGTGGGAGGAGGG CAAGA TGAC G GC CAAGGT CGTGGAG
5. pAAV_RC - ...

1,570 1,580 1,590 1,600 1,610 1,620
1. AAV2 TC GGC CAA AGCCATTCTCGG A GG A AGCAAGGTGCGCGTGGACCA GAA AT GCAAGTC C TC G
2. AAV5_geneb... TCCGCCAAGGCCAT C CT GGG GGG C CA AAGGTGCG GGT C GAT CAGAA AT G T AA ATC CT C T
3. AAV7_geneb... TCCGCCAAGGCCATTCTCGGCGCAGCAAGGTGCGCGTGGACCA AAA GT GCAAGTC G TC C
4. AAV8_geneb... TCCGCCAAGGCCATTCTCGGCGCAGCAAGGTGCGCGTGGACCA AAA GT GCAAGTC G TC C
5. pAAV_RC - ...

1,630 1,640 1,650 1,660 1,670 1,680
1. AAV2 GCCCAGAT A GACCC G AC T CCGTGATCGTCA C C TCCAACA CCAACATGTGC GCCGTGATTT
2. AAV5_geneb... G T T C A A A T G A T T C T A C C C C T G T C A T T G T A A C T T C C A A T A C A A A C A T G T G T G T G G T G
3. AAV7_geneb... GCCCAGATCGACCCACCCCGTGATCGTCA C C TCCAACA CCAACATGTGC GCCGTGATTT
4. AAV8_geneb... GCCCAGATCGACCCACCCCGTGATCGTCA C C TCCAACA CCAACATGTGC GCCGTGATTT
5. pAAV_RC - ...

1,690 1,700 1,710 1,720 1,730 1,740
1. AAV2 GACGGGAAC T C A A C G A C C T T C G A A C A C C A G C A G C C G T T G C A A G A C C G G A T G T T C A A A T T T
2. AAV5_geneb... GA T G G G A A T T C C A C G A C C T T T G A A C A C C A G C A G C C G T G G A G G A C C G C A T G T T C A A A T T T
3. AAV7_geneb... GACGGGAAC A G C A C C A C C T T C G A G C A C C A G C A G C C G T T G C A G G A C C G G A T G T T C A A A T T T
4. AAV8_geneb... GACGGGAAC A G C A C C A C C T T C G A G C A C C A G C A G C C T C T C A G G A C C G G A T G T T T A A G T T C
5. pAAV_RC - ...

1,750 1,760 1,770 1,780 1,790 1,800
1. AAV2 GAACTCACCCGCCGTCTGG A T C A T T G A C T T T G G G A A G G T C A C C A A G C A G G A A G T C A A A G A C
2. AAV5_geneb... GAACTGAC T A A G C G G C T C C C G C A G A T T T T G G C A A G A T T A C T A A G C A G G A A G T C A A G G A C
3. AAV7_geneb... GAACTCACCCGCCGTCTGGAGCACGACTTTGGCAAGGTGAC C A A G C A G G A A G T C A A A G A G
4. AAV8_geneb... GAACTCACCCGCCGTCTGGAGCACGACTTTGGCAAGGTGAC A A A G C A G G A A G T C A A A G A G
5. pAAV_RC - ...

1,810 1,820 1,830 1,840 1,850 1,860
1. AAV2 T T T T T C C G G T G G G C A A A G G --- A T C A C G T G G T T G A G G T G G A G C A T G A A T T C T A C G T C A A A
2. AAV5_geneb... T T T T T T G C T T G G G C A A A G G T C A A T C A G G T G C --- G G T G A C T C A C G A G T T T A A A G T T C C C
3. AAV7_geneb... T T C T T C C G C T G G G C C A G T G --- A T C A C G T G A C C G A G G T G G C G C A T G A T T C T A C G T C A G A
4. AAV8_geneb... T T C T T C C G C T G G G C C A G T G --- A T C A C G T G A C C G A G G T G G C G C A T G A T T T T A C G T C A G A
5. pAAV_RC - ...

1,870 1,880 1,890 1,900 1,910 1,920
1. AAV2 AAGGG -- TGGAGCCA A G A A A A G A C C C G C C C C C A G T G A C G C A G A T A T A A G T G A G C C C A A A C
2. AAV5_geneb... A G G G A A T T G G C G G A A C T A A A G G G G C G --- G A G A A A T C T C T A A A --- C G C C A C T G
3. AAV7_geneb... AAGGG -- C G G A G C C A G C A A A A G A C C C G C C C C G A T G A C G C G G A T A T A A G C G A G C C C A A G C
4. AAV8_geneb... AAGGG -- C G G A G C C A G C A A A A G A C C C G C C C C G A T G A C G C G G A T A A A A G C G A G C C C A A G C
5. pAAV_RC - ...

1,930 1,940 1,950 1,960 1,970 1,980
1. AAV2 G G G T C C G C G A G T C A G T T G C G C A G C C A T C G A C G T C --- A G A C G C G G A A --- G C T T C G A T C A
2. AAV5_geneb... G G T G A C G T C A C - C A A T --- A C T A G C T A T A A A A G T C T G G A G A A G C G G C C A G G C T C T C A T T T
3. AAV7_geneb... G G G C C T G C C C T C A G T C G C G G A T C C A T C G A C G T C --- A G A C G C G G A A G A G C T C C G G T G G
4. AAV8_geneb... G G G C C T G C C C T C A G T C G C G G A T C C A T C G A C G T C --- A G A C G C G G A A G A G C T C C G G T G G
5. pAAV_RC - ...

1,990 2,000 2,010 2,020 2,030 2,040
1. AAV2 ACTACGCAGACAGGTACCAAAACAAATGTTCTCGTCACCGGGGCATGAAATCGATGCTGT
2. AAV5_geneb... GTTCCCGAGACGCCCTCGCACTTCAAGAGTGAATGT-----TGATCCCGCTCTCT
3. AAV7_geneb... ACTTTGCCGACAGGTACCAAAACAAATGTTCTCGTCACCGGGGCATGATTCAGATGCTGT
4. AAV8_geneb... ACTTTGCCGACAGGTACCAAAACAAATGTTCTCGTCACCGGGGCATGCTTCAGATGCTGT
5. pAAV_RC - ...

2,050 2,060 2,070 2,080 2,090 2,100
1. AAV2 TTCCCTGCAGACAATGCGAGAGAAATGAATCAGAATTCAAAATATCTGCTTCACACACGGAC
2. AAV5_geneb... GCGACCGCTCAAATGGAATTCAAAGGAT---GATTGCAA-ATGTGACTATCAATGCTCAA
3. AAV7_geneb... TTCCCTGCAAAACGTGCGAGAGAAATGAATCAGAATTTCAAATTTGCTTCACACACGGGG
4. AAV8_geneb... TTCCCTGCAAAACGTGCGAGAGAAATGAATCAGAATTTCAAATTTGCTTCACACACGGGG
5. pAAV_RC - ...

2,110 2,120 2,130 2,140 2,150 2,160
1. AAV2 AGAAGACTGTTTATAGAGTGCCTTCC---CGTGTGAGAATCTCAACCCCGTTCCTGTCGTCA
2. AAV5_geneb... TTTGACAAACAATTTCTAACAAATGTTGATGAAATGTGAATATTTGAAATCGG-----GGCA-AA
3. AAV7_geneb... TCAGAGACTGTTTATAGAGTGTTCCTCCGCGTGTGAGAATCTCAACCCGGTCT---GTCAGAA
4. AAV8_geneb... TCAGAGACTGCTCAGAGTGTTCCTCCGCGTGTGAGAATCTCAACCCGGTCT---GTCAGAA
5. pAAV_RC - ...

2,170 2,180 2,190 2,200 2,210 2,220
1. AAV2 AAAAGCGTATCAAGAACTGTGCTACATTCATCATATCATGGGAAAGGTGCCAGA---CG
2. AAV5_geneb... AATGGATGATATCTGTCACAAATG---AATCTCACTGTCAAATTTG-----TCAATGGATTTCT
3. AAV7_geneb... AAAAGACGTAATCGAAACTCTGCGGATTCATTCATCTGCTGGGGCGGGGCGCCGAGATTTG
4. AAV8_geneb... AAGAGACGTAATCGAAACTCTGCGGATTCATTCATCTGCTGGGGCGGGGCTCCGAGATTTG
5. pAAV_RC - ...

2,230 2,240 2,250 2,260 2,270 2,280
1. AAV2 CTTGCACTG--CCTGCGATCTGGTCA---AAGTGGATTTGGATGACTGCAATCTTTGAAAC
2. AAV5_geneb... CCCCCTGGGAAAAGGAAACTTGTCAAGATTTGGGATTTTGGACGATCCCAATAAAGAAC
3. AAV7_geneb... CTTGCTCGG--CCTGCGATCTGGTCA---AAGTGGACCTGGATGACTGCTTTTCTGAGC
4. AAV8_geneb... CTTGCTCGG--CCTGCGATCTGGTCA---AAGTGGACCTGGATGACTGCTTTTCTGAGC
5. pAAV_RC - ...

2,290 2,300 2,310 2,320 2,330 2,340
1. AAV2 AATAAAATGATTTAAAATCAGGTAATGGCTGCCGATGGTTATCTTCCAGATTTGGCTCGAGGAC
2. AAV5_geneb... AGTAAATAAAGCGAGT-AGTTCATGCTTTTGGTTGATCACCCTCCAGATTTGGTTGGAAGAA
3. AAV7_geneb... AATAAAATGACTTTAAAATCAGGTAATGGCTGCCGATGGTTATCTTCCAGATTTGGCTCGAGGAC
4. AAV8_geneb... AATAAAATGACTTTAAAATCAGGTAATGGCTGCCGATGGTTATCTTCCAGATTTGGCTCGAGGAC
5. pAAV_RC - ...
ATGGCTGCCGATGGTTATCTTCCAGATTTGGCTCGAGGAC

2,350 2,360 2,370 2,380 2,390 2,400
1. AAV2 ACTCTCTCTGAAGGAATAAAGCAGTGGTGAAGCTCAAACCTGG-CCCAACCACACAAA
2. AAV5_geneb... ---GTGGTGAAGGTCCTTCGCGAGTCTTTGGGCTTGAAGCGGG-CCCAACCACACAAA
3. AAV7_geneb... AACCTCTCTGAAGGATTCGCGAGTGGTGGGACTGAAACCTGGAGCCCGAAACCCAAA
4. AAV8_geneb... AACCTCTCTGAAGGATTCGCGAGTGGTGGGACTGAAACCTGGAGCCCGAAAGCCAAA
5. pAAV_RC - ...
ACTCTCTCTGAAGGAATAAAGCAGTGGTGAAGCTCAAACCTGG-CCCAACCACACAAA

2,410 2,420 2,430 2,440 2,450 2,460
1. AAV2 GCCCGCAGAGCGGCATTAAGGACGACAGCAGGGGTCCTGTGCTTCCTGGGTACAAGTACCT
2. AAV5_geneb... ACCCAATCAGCAGCATCAAGATCAAGCCGGTGGTCTTTGTGCTGCTGTTAATACFACTCT
3. AAV7_geneb... GCCAAC-CAGCAAAAGCAGGACACCGCCGGGGTCTGTGCTTCCTGGCTACAAGTACCT
4. AAV8_geneb... GCCAAC-CAGCAAAAGCAGGACGACGCGGGGGTCTGTGCTTCCTGGCTACAAGTACCT
5. pAAV_RC - ...
GCCCGCAGAGCGGCATTAAGGACGACAGCAGGGGTCCTGTGCTTCCTGGGTACAAGTACCT

2,470 2,480 2,490 2,500 2,510 2,520
1. AAV2 CGGACCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCAGCGGCCCT
2. AAV5_geneb... CGGACCCTGAAACCGGCTTCGATCGAGGAGAGCCGTCAACAGGGCAGACGAGGCTCGCGG
3. AAV7_geneb... CGGACCCTTCAACGGACTCGACAAAGGGGAGAGCCGTCAACCGGCAGACGCAGCGGCCCT
4. AAV8_geneb... CGGACCCTTCAACGGACTCGACAAAGGGGAGAGCCGTCAACCGGCAGACGCAGCGGCCCT
5. pAAV_RC - ...
CGGACCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCAGCGGCCCT

2,530 2,540 2,550 2,560 2,570 2,580
1. AAV2 CGAGCAGCTACAAAGCCTACGACCAGCAGCTCGACAGC-GGAGACAAACCGTACCTCAAG
2. AAV5_geneb... AAGGCAGC-ACAATCTCTGTAACAGCAGCAGCTTGAAGGCGGAGACAAACCCCTACCTCAAG
3. AAV7_geneb... CGAGCAGC-ACAAGGCCCTACGACCAGCAGCTCAA-AGCGGGTGAACAAACCGTACCTCCGG
4. AAV8_geneb... CGAGCAGC-ACAAGGCCCTACGACCAGCAGCTCAA-AGCGGGTGAACAAACCGTACCTCCGG
5. pAAV_RC - ...
CGAGCAGC-ACAAGGCCCTACGACCAGCAGCTCGACAGC-GGAGACAAACCGTACCTCAAG

2,590 2,600 2,610 2,620 2,630 2,640
1. AAV2 TACAACCACGCCGACGCGGAGTTTTCAGGAGCGCTTAAAGAAGATACGTCTTTTGGGGGC
2. AAV5_geneb... TACAACCACGCGGACGCGGAGTTTTCAGGAGAGAGCTCCCGAGCAGACATCTTTGGGGGA
3. AAV7_geneb... TAAACACGCGGACGCGGAGTTTTCAGGAGCGCTTAAAGAAGATACGTCTTTTGGGGGC
4. AAV8_geneb... TAAACACGCGGACGCGGAGTTTTCAGGAGCGCTTAAAGAAGATACGTCTTTTGGGGGC
5. pAAV_RC - ...
TACAACCACGCCGACGCGGAGTTTTCAGGAGCGCTTAAAGAAGATACGTCTTTTGGGGGC

		2,650	2,660	2,670	2,680	2,690	2,700
1. AAV2	AACCTCGGACGAGCAGTCTTCCAGGC	GAA	A	AAGAGGGTTC	T	GAACCTCT	G
2. AAV5_geneb...	AACCTCGGA	AA	G	GCAGTCTT	C	CAGGCCAAGA	A
3. AAV7_geneb...	AACCTCGG	C	G	AGCAGTCTT	C	CAGGCCAAGA	A
4. AAV8_geneb...	AACCTCGG	C	G	AGCAGTCTT	C	CAGGCCAAGA	A
5. pAAV_RC - ...	AACCTCGGACGAGCAGTCTTCCAGGC	GAA	A	AAGAGGGTTC	T	GAACCTCT	G
		2,710	2,720	2,730	2,740	2,750	2,760
1. AAV2	GAGGAA	CC	T	G	TAAGACGGCTCC	G	G
2. AAV5_geneb...	GA	A	G	GGTGCTAAGACGGC	CC	CT	A
3. AAV7_geneb...	GAGGAAGG	C	G	CTAAGACGGCTC	CT	G	A
4. AAV8_geneb...	GAGGAAGG	C	G	CTAAGACGGCTC	CT	G	A
5. pAAV_RC - ...	GAGGAA	CC	T	G	TAAGACGGCTC	G	G
		2,770	2,780	2,790	2,800	2,810	2,820
1. AAV2	A	G	-	CCAGACTCCTCC	T	C	G
2. AAV5_geneb...	A	-	-	AGA	A	G	G
3. AAV7_geneb...	T	C	C	C	C	G	A
4. AAV8_geneb...	T	C	C	C	C	G	A
5. pAAV_RC - ...	A	G	-	CCAGACTCCTCC	T	C	G
		2,830	2,840	2,850	2,860	2,870	2,880
1. AAV2	AATTTTGGTCAGACTGG	A	G	ACGCAG	-	A	C
2. AAV5_geneb...	-	-	-	GTCAGAC	-	G	C
3. AAV7_geneb...	AATTTT	C	G	TCAGACTGG	C	G	A
4. AAV8_geneb...	AATTTTGGTCAGACTGGC	A	G	ACGCAG	-	A	C
5. pAAV_RC - ...	AATTTTGGTCAGACTGG	A	G	ACGCAG	-	A	C
		2,890	2,900	2,910	2,920	2,930	2,940
1. AAV2	A	C	C	A	G	C	-
2. AAV5_geneb...	-	C	C	A	A	C	A
3. AAV7_geneb...	T	C	C	A	G	C	-
4. AAV8_geneb...	T	C	C	A	G	C	-
5. pAAV_RC - ...	A	C	C	A	G	C	-
		2,950	2,960	2,970	2,980	2,990	3,000
1. AAV2	AATGGCAGACAA	T	A	A	A	A	A
2. AAV5_geneb...	A	T	T	G	G	C	A
3. AAV7_geneb...	AATGGCAGACAA	T	A	A	A	A	A
4. AAV8_geneb...	AATGGCAGACAA	T	A	A	A	A	A
5. pAAV_RC - ...	AATGGCAGACAA	T	A	A	A	A	A
		3,010	3,020	3,030	3,040	3,050	3,060
1. AAV2	C	G	A	T	T	C	A
2. AAV5_geneb...	C	G	A	T	T	C	A
3. AAV7_geneb...	C	G	A	T	T	C	A
4. AAV8_geneb...	C	G	A	T	T	C	A
5. pAAV_RC - ...	C	G	A	T	T	C	A
		3,070	3,080	3,090	3,100	3,110	3,120
1. AAV2	C	A	C	T	A	A	A
2. AAV5_geneb...	C	A	C	T	A	A	A
3. AAV7_geneb...	C	A	C	T	A	A	A
4. AAV8_geneb...	C	A	C	T	A	A	A
5. pAAV_RC - ...	C	A	C	T	A	A	A
		3,130	3,140	3,150	3,160	3,170	3,180
1. AAV2	C	G	A	C	A	A	A
2. AAV5_geneb...	C	G	A	C	A	A	A
3. AAV7_geneb...	C	G	A	C	A	A	A
4. AAV8_geneb...	C	G	A	C	A	A	A
5. pAAV_RC - ...	C	G	A	C	A	A	A
		3,190	3,200	3,210	3,220	3,230	3,240
1. AAV2	C	T	G	C	A	C	T
2. AAV5_geneb...	C	A	G	C	A	C	T
3. AAV7_geneb...	C	T	G	C	A	C	T
4. AAV8_geneb...	C	T	G	C	A	C	T
5. pAAV_RC - ...	C	T	G	C	A	C	T
		3,250	3,260	3,270	3,280	3,290	3,300
1. AAV2	C	A	A	G	A	G	A
2. AAV5_geneb...	C	C	G	T	C	C	A
3. AAV7_geneb...	C	A	A	G	A	G	A
4. AAV8_geneb...	C	A	A	G	A	G	A
5. pAAV_RC - ...	C	A	A	G	A	G	A

		3,310	3,320	3,330	3,340	3,350	3,360
1. AAV2		TACGACGACGAT	TGCCAATAACCTT	ACCAGCACGGTT	CAGGTGTTTAC	TGACTCGGAGTA	
2. AAV5_geneb...		CACACACACCAT	CGCCAAACCT	CACTCCACCGT	CAAGTGTTTA	CGGACGACGACATA	
3. AAV7_geneb...		CGTACGACCAT	CGCAATAACCTT	ACCAGCACG	ATTCAGGT	ATCTCCGGACTCGGAATA	
4. AAV8_geneb...		CACCAAGACCAT	CGCCAAACCT	ACCAGCAC	CATCCAGGT	GTTTACGGACTCGGAGTA	
5. pAAV_RC - ...		TACGACGACGAT	TGCCAATAACCTT	ACCAGCACGGTT	CAGGTGTTTAC	TGACTCGGAGTA	
		3,370	3,380	3,390	3,400	3,410	3,420
1. AAV2		CCAGCTCCCGT	TACGTCTCGGCTC	GCGGCA	CAAGGATG	CCCGCGT	TCCCAGCAGA
2. AAV5_geneb...		CCAGCTGCCCT	TACGTCTCGGCTC	AACGGGACC	GAGGGATG	CCCGCGT	TCCCAGCAGA
3. AAV7_geneb...		CCAGCTGCCGT	TACGTCTCGGCTC	GCGCAC	CAGGGTGC	CCCGT	TCCCAGCAGA
4. AAV8_geneb...		CCAGCTGCCGT	TACGTCTCGGCTC	GCGCAC	CAGGGTGC	CCCGT	TCCCAGCAGA
5. pAAV_RC - ...		CCAGCTCCCGT	TACGTCTCGGCTC	GCGGCA	CAAGGATG	CCCGCGT	TCCCAGCAGA
		3,430	3,440	3,450	3,460	3,470	3,480
1. AAV2		CGTCTTCA	TGAGCCACAGTA	TGGATACCT	CACCC	TGAACAACGG	GAGT-CAGG
2. AAV5_geneb...		GGTCTT	TACGCTGCC	GAGTACGG	TACGCGAC	GCTGAAC	CGCGACAACAAGAAAATCC
3. AAV7_geneb...		CGTCTTCA	TGAGCCACAGTA	TGGATACCT	CACCC	TGAACAACGG	GAGT-CAGG
4. AAV8_geneb...		CGTCTTCA	TGAGCCACAGTA	TGGATACCT	CACCC	TGAACAACGG	GAGT-CAGG
5. pAAV_RC - ...		CGTCTTCA	TGAGCCACAGTA	TGGATACCT	CACCC	TGAACAACGG	GAGT-CAGG
		3,490	3,500	3,510	3,520	3,530	3,540
1. AAV2		CAGTAGGACG	CTCTCAATT	TACTGCCT	GGAGTAC	TTTCC	TTCTCAGATGCTGCGTACC
2. AAV5_geneb...		CACCGAGA	GAGCAGC	-TTCTT	CTGCCT	AAGTAC	TTTCCGACCAAGATGCTGAGAACGG
3. AAV7_geneb...		CAGTAGGACG	CTCTCAATT	TACTGCCT	GGAGTAC	TTTCC	TTCTCAGATGCTGAGAACGG
4. AAV8_geneb...		CAGTAGGACG	CTCTCAATT	TACTGCCT	GGAGTAC	TTTCC	TTCTCAGATGCTGAGAACGG
5. pAAV_RC - ...		CAGTAGGACG	CTCTCAATT	TACTGCCT	GGAGTAC	TTTCC	TTCTCAGATGCTGCGTACC
		3,550	3,560	3,570	3,580	3,590	3,600
1. AAV2		GAAACAAC	TTTACCTTC	AGCTACAC	TTT	TGAGGACGT	TCCTTCCACAGCAGCTACGCTC
2. AAV5_geneb...		GCAACAAC	TTT	CAGT	TACCTACA	ACTT	TGAGGACGTGCTCCACCTCCAGCTTCGCTC
3. AAV7_geneb...		GCAACAAC	TTT	CAGT	TCAGCTACA	GCTT	CGAGGACGTGCTTCCACAGCAGCTACGCTC
4. AAV8_geneb...		GCAACAAC	TTT	CAGT	TCAGCTACA	GCTT	CGAGGACGTGCTTCCACAGCAGCTACGCTC
5. pAAV_RC - ...		GAAACAAC	TTTACCTTC	AGCTACAC	TTT	TGAGGACGT	TCCTTCCACAGCAGCTACGCTC
		3,610	3,620	3,630	3,640	3,650	3,660
1. AAV2		ACAGCCAGAG	CTGGACCG	CTCAT	GAAATCC	TCTCAT	CGACCAGTACCTGTATACCTTGA
2. AAV5_geneb...		CCAGCTCAGA	ACC	TGCTCAAG	CTGGCCAA	CCC	GCTGGTGGACCAGTACCTGTACCTGCTTCC
3. AAV7_geneb...		ACAGCCAGAG	CTGGACCG	CTCAT	GAAATCC	TCTCAT	CGACCAGTACCTGTATACCTTGA
4. AAV8_geneb...		ACAGCCAGAG	CTGGACCG	CTCAT	GAAATCC	TCTCAT	CGACCAGTACCTGTATACCTTGA
5. pAAV_RC - ...		ACAGCCAGAG	CTGGACCG	CTCAT	GAAATCC	TCTCAT	CGACCAGTACCTGTATACCTTGA
		3,670	3,680	3,690	3,700	3,710	3,720
1. AAV2		G	CAGAACA	---AACAC	TCCAAGT	GGAACCA	---CACGCAGTCAAGGCTTCAGT
2. AAV5_geneb...		T	GAGCACA	AA	TAACAC	---	TGG---C---GGAGTCCAGT
3. AAV7_geneb...		C	CAGAACA	CA	GAGTAA	CCAGGAGG	CAAGC---TGGAATC
4. AAV8_geneb...		C	TCGGAC	TCA	AACA	---	CAGGAGGACGGAAATACGCAGACTCTGGCTTCAG
5. pAAV_RC - ...		G	CAGAACA	---AACAC	TCCAAGT	GGAACCA	---CACGCAGTCAAGGCTTCAGT
		3,730	3,740	3,750	3,760	3,770	3,780
1. AAV2		T	CAGGCCGG	AGC	GAGTGAC	ATT	CG-GGACCAGTCTAGGAACTGGCTTCC
2. AAV5_geneb...		C	AAGAAC	CTGGCC	-GGAGAT	ACGCC	AACACCTACAAAACTGGTCC
3. AAV7_geneb...		CC	AGGCGGG	-GCC	TTCAC	AT	TGGCCGACCAAGCCAAAGAA
4. AAV8_geneb...		C	AAGT	---	GGCC	TAA	TACAATGGCCAAACAGAACTGGCTGCC
5. pAAV_RC - ...		T	CAGGCCGG	AGC	GAGTGAC	ATT	CG-GGACCAGTCTAGGAACTGGCTTCC
		3,790	3,800	3,810	3,820	3,830	3,840
1. AAV2		ACC	GCCAGCAGCGA	-GTAT	CAAAGACAT	CTGG	CGGA
2. AAV5_geneb...		G	CCGAAC	CCAGGG	CTGG	AACCTGG	GCTCCGGG
3. AAV7_geneb...		T	CCGGCA	CAAGA	-GTCT	CAAAAC	GCTGGATCA
4. AAV8_geneb...		ACC	GCCAGCAGCGA	-GTAT	CAAAGACAT	CTGG	CGGA
5. pAAV_RC - ...		ACC	GCCAGCAGCGA	-GTAT	CAAAGACAT	CTGG	CGGA
		3,850	3,860	3,870	3,880	3,890	3,900
1. AAV2		ACT	GGAGC	TACCAAG	TACCAC	---	CTCAATGGCAGAGACTCT
2. AAV5_geneb...		T	C-GCCAC	GACCAA	-TAGGA	TGGAG	CTC
3. AAV7_geneb...		ACT	GGTGC	CAACAA	ATA	TAC	---
4. AAV8_geneb...		ACT	GGTGC	CAACAA	ATA	TAC	---
5. pAAV_RC - ...		ACT	GGAGC	TACCAAG	TACCAC	---	CTCAATGGCAGAGACTCT
		3,910	3,920	3,930	3,940	3,950	3,960
1. AAV2		---	CATGGCA	---	AGCCACA	AGGACGA	TGG
2. AAV5_geneb...		C	CGAAG	CGGCA	TGACC	AACA	CCCTC
3. AAV7_geneb...		CG	CCATGGCA	---	AC	TACA	AGGACGA
4. AAV8_geneb...		CG	CCATGGCA	---	AC	TACA	AGGACGA
5. pAAV_RC - ...		G	CCATGGCA	---	AGCCACA	AGGACGA	TGG

		3,970	3,980	3,990	4,000	4,010	4,020
1. AAV2		CTCATCTTTGGGAAGCA--AGGCTCAGAGGA--AAACAAAAGTGA--ACATT---GAAAAG					
2. AAV5_geneb...		ATGATCTTTGGAAA--AACGGAGCA--ACCTAACAAAACACT---ACATTG--GAAAAT					
3. AAV7_geneb...		CTGATTTTGGCAAACAATGCTGCC--AGAGACAAATGCGAATACAGCG------AT					
4. AAV8_geneb...		CTCATCTTTGGGAAGCA--AGGCTCAGAGAA--AACAAAAGTGG--ACATT---GAAAAG					
5. pAAV_RC - ...		CTCATCTTTGGGAAGCA--AGGCTCAGAGAA--AACAAAAGTGG--ACATT---GAAAAG					
		4,030	4,040	4,050	4,060	4,070	4,080
1. AAV2		GTCATGATACAGACGAAGAG-GAAATCGAACAACCAATCCCGTGGC-TACGGAGCAGT					
2. AAV5_geneb...		ATGCTCATCACAGCGA-GAGCGAGAGCCAGCCGGTGAACCCCGTGGCGTACAC-ACGTCC					
3. AAV7_geneb...		GTGTAATGACAAAAGAAGAA-GAAATTCGTCCTACAAATCCGTAGC-CACGGAGAAT					
4. AAV8_geneb...		GTCATGCTCACAGCGAAGAA-GAAATCAAACCACTAACCCGTGGC-TACAGGGAAT					
5. pAAV_RC - ...		GTCATGATACAGACGAAGAG-GAAATCAGACAACCAATCCCGTGGC-TACGGAGCAGT					
		4,090	4,100	4,110	4,120	4,130	4,140
1. AAV2		ATGGTTCCTGT-ACTACCAACCTCCAGAGAGGCAACAGACAAAGCAGCT---ACCGCAGAT					
2. AAV5_geneb...		GCGGG-CAGATGGCCACCAACAAACCAGAGCTCCACCA--CTGCCTCCGCGACCGGCACG					
3. AAV7_geneb...		ACGGATAGTCAAGCAGCAAGAA-GAAATTCGTCCTACAAATCCGTAGC-CACGGAGAAT					
4. AAV8_geneb...		ACGGTATCGT-GGCAGATAACTTGC--GCAGCAAACACG-GCTCCCTCAAATGGAACT					
5. pAAV_RC - ...		ATGGTTCCTGT-ACTACCAACCTCCAGAGAGGCAACAGACAAAGCAGCT---ACCGCAGAT					
		4,150	4,160	4,170	4,180	4,190	4,200
1. AAV2		GTCAACACACAAGGCGTCTCTCCAGGCATGGTCTGGCAGGACAGAGAAGTGTACCTTCAG					
2. AAV5_geneb...		TACAACCTCCAGGAAATCGTGCCCGGCACGGTGTGATGGAGAGGGACGTGTACCTCCAA					
3. AAV7_geneb...		GTCAACACCAGGGAGCTTACCTGGCATGGTCTGGCAGAACCGGGACGTGTACCTGCAG					
4. AAV8_geneb...		GTCAACAGCCAGGGGCTTACCTGGCATGGTCTGGCAGAACCGGGACGTGTACCTGCAG					
5. pAAV_RC - ...		GTCAACACACAAGGCGTCTCTCCAGGCATGGTCTGGCAGGACAGAGAAGTGTACCTTCAG					
		4,210	4,220	4,230	4,240	4,250	4,260
1. AAV2		GGGCCATCTGGGCAAAGATTCCACACACGGACGGACAATTTACCCCTCTCCCTCATG					
2. AAV5_geneb...		GGACCCATCTGGGCCAAGATCCCAAGAGCGGGCCACTTTACCCCTCTCCGGCCATG					
3. AAV7_geneb...		GGTCCCATCTGGGCCAAGATTCCACACGGATGGCAACTTTACCCGTCTCTCTTTGATG					
4. AAV8_geneb...		GGTCCCATCTGGGCCAAGATTCCACACGGACGGCAACTTCCACCCGTCTCTCCCTGATG					
5. pAAV_RC - ...		GGGCCATCTGGGCAAAGATTCCACACACGGACGGACAATTTACCCCTCTCCCTCATG					
		4,270	4,280	4,290	4,300	4,310	4,320
1. AAV2		GGTGGATTCCGACTTAAACACCCTCTCCACAGATCTCTCATCAAGAACACCCCGTACCT					
2. AAV5_geneb...		GGCGGATTCCGACTCAAACACCCACCAGCCATGATCTCTCATCAAGAACACGCCGTGCC					
3. AAV7_geneb...		GGCGGCTTTGGACTTAAACACCCTCCAGATCTTGAATCAAGAACACCTCCGTGCC					
4. AAV8_geneb...		GGCGGCTTTGGCTGAAACACCCTCCAGATCTTGAATCAAGAACACGCCGTGTACCT					
5. pAAV_RC - ...		GGTGGATTCCGACTTAAACACCCTCTCCACAGATCTCTCATCAAGAACACCCCGTACCT					
		4,330	4,340	4,350	4,360	4,370	4,380
1. AAV2		GCGAATCTTCGACCACCTTCAATG-CGGCAAAGTTTGTCTCTTCATCACACAGTACCT					
2. AAV5_geneb...		GGAAT--ATC-ACCAGCTTCTGGAGCGTCCCGTCAAGCAGC-TTCATCACCCAGTACAG					
3. AAV7_geneb...		GCTAATCTCCGGAGGTGTCTCTCTCTGCTTCAAGAACACCTCCGTGCC					
4. AAV8_geneb...		GCGATCTCCGACCACCTTCAACCA-GTCAAAGCTGAATCTTTCATCACGCAATACAG					
5. pAAV_RC - ...		GCGAATCTTCGACCACCTTCAATG-CGGCAAAGTTTGTCTCTTCATCACACAGTACCT					
		4,390	4,400	4,410	4,420	4,430	4,440
1. AAV2		CACGGGACACGGTTCAGCGTGGAGATCGAGTGGGAGCTGCAGAAGGAAAAAGCAACCGCT					
2. AAV5_geneb...		CACCGGACA-GGTCACTCGTGGAGATGGAGTGGGAGCTCAAGAAGGAAAAACCAAGAGGT					
3. AAV7_geneb...		CACCGGACA-AGTCAAGCGTGGAAATCGAGTGGGAGCTGCAGAAGGAAAAAGCAAGCGCT					
4. AAV8_geneb...		CACCGGACA-GGTCAAGCGTGGAAATGAGATGGGAGCTGCAGAAGGAAAAAGCAAGCGCT					
5. pAAV_RC - ...		CACGGGACA-GGTTCAGCGTGGAGATCGAGTGGGAGCTGCAGAAGGAAAAAGCAACCGCT					
		4,450	4,460	4,470	4,480	4,490	4,500
1. AAV2		GGAAATCCCGAATTCAGTACACCTTCCAACCTACAACAAGTCTGTTAATCTGTGGACTT-ACC					
2. AAV5_geneb...		GGAAACCCAGAGATCCAGTACACAAACAACCTACAACGA-CCCGAGTTGTGGACTTTGCC					
3. AAV7_geneb...		GGAAACCCGGAGATTTCAGTACACCTTCCAACCTTGAAGAAGCAGACTGGT-GTGGACTTTGCC					
4. AAV8_geneb...		GGAAACCCGAGATCCAGTACACCTTCCAACCTTACAATCTACAAGT-GTGGACTTTGCT					
5. pAAV_RC - ...		GGAAATCCCGAATTCAGTACACCTTCCAACCTACAACAAGTCTGTTAATCTGTGGACTTACC					
		4,510	4,520	4,530	4,540	4,550	4,560
1. AAV2		GTGGATACAAATGGCGTGTATTCAGAGCCTC--GCCCCATGGCACCAAGATACCTGACCT					
2. AAV5_geneb...		CCGGACAGCACCGGGGAATA--CAGAACACAGACCCTATCGGAACCCGATACCTTACCC					
3. AAV7_geneb...		GTGGACAGCCAGGGTGTATTCAGAGCCTC--GCCCCTATGGCACCTGCTTACCTTACCC					
4. AAV8_geneb...		GTGTAATACAGAAAGCGTGTATTCAGAGCCTC--GCCCCATGGCACCCGCTTACCTTACCC					
5. pAAV_RC - ...		GTGGACACAAATGGCGTGTATTCAGAGCCTC--GCCCCATGGCACCAAGATACCTGACCT					
		4,570	4,580	4,590	4,600	4,610	4,620
1. AAV2		GTAATCTGTAAT---TGCCTGT---TA--ATCAATAAACCGTTTAAATCGTTTCAGTTG					
2. AAV5_geneb...		GACCCCTTTAAACCAATTCATGTCCGATACCCTCAAATAAACCGTGT-ATTCTGTCTCAG-TA					
3. AAV7_geneb...		GTAATCTGTAAT---TGCATGT---TA--ATCAATAAACCGTGTGATTCTGTTTCAGTTG					
4. AAV8_geneb...		GTAATCTGTAAT---TGCCTGT---TA--ATCAATAAACCGTGTGATTCTGTTTCAGTTG					
5. pAAV_RC - ...		GTAATCTGTAAT---TGCCTGT---TA--ATCAATAAACCGTTTAAATCGTTTCAGTTG					

