

ENGINEERED ADENO-ASSOCIATED VIRUSES**CROSS-REFERENCE TO RELATED APPLICATIONS**

[0001] This application claims the benefit of priority of Singapore provisional application no. 10202300688R, filed 13 March 2023, the contents of it being hereby incorporated by reference in its entirety for all purposes.

FIELD OF THE INVENTION

[0002] The present invention relates generally to the field of biotechnology. In particular, the present invention relates to engineering and/or attenuating adeno-associated viruses.

BACKGROUND OF THE INVENTION

[0003] Recombinant viral vectors based on adeno-associated virus (AAV) have emerged as an ideal delivery platform for *in vivo* gene transfer and genome editing therapies. AAV vectors are derived from wild-type viruses that naturally infect humans. As a consequence, depending on the AAV vector serotype, up to two-thirds of humans are seropositive to AAV, thereby impacting the use of AAV for gene transfection and transfer. Since AAV capsid structures are very similar with high amino acid sequence homology, the various AAV serotypes can encounter cross-reactivity to antibodies (i.e., naturally occurring AAV serotypes have conserved sequences that are neutralized by the same antibodies).

[0004] Thus, there is an unmet need for adeno-associated viruses that are capable of evading pre-existing anti-AAV antibodies.

SUMMARY

[0005] In one aspect, the present disclosure refers to a composition comprising at least one modified adeno-associated viral (AAV) capsid protein, wherein the composition is resistant to neutralisation or is not neutralised by human neutralising antibodies, wherein the at least one modified adeno-associated viral (AAV) capsid protein is modified at any one or more of residues 24 to 47, 48 to 97, 72 to 121, 120 to 167 and 168 to 217 of an adeno-associated viral (AAV) VP1 capsid protein or an ortholog thereof.

[0006] In another aspect, the present disclosure refers to a nucleic acid sequence encoding the composition described herein, or encoding the one or more modified adeno-associated viral (AAV) capsid proteins described herein.

[0007] In yet another aspect, the present disclosure refers to a vector comprising the nucleic acid sequence disclosed herein.

[0008] In a further aspect, the present disclosure refers to a host cell comprising the vector described herein or the nucleic acid sequence described herein.

[0009] In one aspect, the present disclosure refers to the composition disclosed herein, the nucleic acid disclosed herein, the vector disclosed herein, the host cell disclosed herein, or the adeno-associated virus particle disclosed herein, for use in gene therapy.

[0010] In yet another aspect, the present disclosure refers to a method of identifying an adeno-associated viral (AAV) capsid protein or peptide which is resistant to neutralisation or is not neutralised by human neutralising antibodies, the method comprising (a) contacting the adeno-associated viral capsid protein or peptide with sera known to contain adeno-associated virus neutralising antibodies, thereby allowing the neutralising antibodies to bind to an epitope comprised within the adeno-associated viral capsid protein or peptide; (b) removing the neutralising antibody-bound epitope from the adeno-associated viral capsid protein or peptide; and (c) identifying the adeno-associated viral capsid protein or peptide that did not bind to the neutralising antibodies.

[0011] In a further aspect, the present disclosure refers to a method of preventing an immune response to an engineered adeno-associated virus, the method comprising administering to a subject an engineered adeno-associated virus comprising at least one modified adeno-associated viral (AAV) capsid protein described herein.

BRIEF DESCRIPTION OF THE DRAWINGS

[0012] The invention will be better understood with reference to the detailed description when considered in conjunction with the non-limiting examples and the accompanying drawings, in which:

[0013] **FIG. 1** shows a summary of phage immunoprecipitation sequencing method. FIG. 1A shows an AAV and CRISPR-Cas phage library that were designed with protein sequences from UniProt and NCBI Protein database. The library consists of roughly 10 000 peptides tiles of 49 amino acids with 25 amino acid overlaps. The DNA sequences encoding the peptides tiles were synthesized, cloned, and packaged into T7 phages that display the encoded peptide on the phage surfaces. Next, the phage library was mixed and incubated with patient serum that contains antibodies. The antibodies bound to their target peptide sequences as displayed by the phages, and the complexes were enriched from the sample using protein A/G- coupled beads (IP – immunoprecipitation). After the immunoprecipitation, the genomes of phages bound to antibodies were amplified by polymerase chain reaction (PCR) and sequenced, identifying the peptide sequences bound by the antibodies. The results are represented by a heat map where darker shade represents higher level of antibodies recognizing particular epitope. Assessment of the library representation as an input library (FIG. 1B) and as a cloned library (FIG. 1C), before and after cloning and packaging, are shown. FIG. 1D shows the results of assessment of the library quality by Sanger sequencing of 20 randomly chosen clones.

[0014] **FIG. 2** shows the heatmap results of epitope-mapping of AAV serotypes by human antibodies using PhIP-seq. AAV epitopes recognized by antibodies in pooled serum sample (left) or an individual patient's serum (right) are shown.

[0015] **FIG. 3** shows a column graph showing AAV variants showing increase vector yield. Wild-type AAV-DJ and AAV variants packaging a self-complementary green fluorescent protein (GFP) genome were produced by triple-transfection in HEK293T cells and titrated by quantitative polymerase chain reaction (PCR). Results are shown as mean $\pm$ SD of two independent titrations.

[0016] **FIG. 4** shows fluorescent microscope images of AAV variants showing superior transduction efficiency and neutralisation escape. **FIG. 4A** shows the results of *in vitro* transduction of HEK293 cells with AAV vectors encoding GFP at a multiplicity of infection (MOI) of 20 000. Analysis was performed 48 hours later. **FIG. 4B** shows the results of an *in vitro* neutralisation assay: WT AAV-DJ or AAV-DJ_D213A encoding a green fluorescent protein (GFP) were mixed with a serial dilution of human sera for 1 hour at 37°C. The mixture was then added to the cells and incubated for 48 hours at 37°C.

[0017] **FIG. 5** shows fluorescent microscope images of AAV variants showed escape from pre-existing NAb in human serum. Results of *in vitro* neutralisation assay using WT AAV2 versus AAV2_D213A (**FIG. 5A**), WT AAV9 versus AAV9_D213A (**FIG. 5B**) and WT AAV-DJ versus AAV-DJ_A70R (**FIG. 5C**). AAV vectors at a multiplicity of infection (MOI) of 50 000 (serotypes 2 and 9) or 20 000 (serotype DJ) were mixed with a serial dilution of human sera for 1 hour at 37°C. The mixture was then added to the cells and incubated for 48 hours.

[0018] **FIG. 6** shows a line graph showing results indicating complete resistance to pre-existing neutralising antibodies in human serum with AAV-DJ_D213A and AAV-DJ_A70R_D213A. This figure illustrates the impact of either the D213A or the A70R_D213A amino acid substitutions on the neutralization by pre-existing neutralising antibodies (Nabs) in AAV-DJ. The experiment was performed using an *in vitro* neutralization assay. As a control for 100% transduction efficiency, vectors were mixed only with DMEM (no serum.) The mixture was incubated for 1 hour at 37°C before being added to the cells. After 48 hours of incubation, the green fluorescent protein (GFP) expression was measured. The dotted line at 50 represents neutralising antibody (Nab)-mediated inhibition of AAV transduction by 50%. Solid lines represent relative transduction efficiencies of WT AAV (black), AAV_D213A (Grey, dotted), and AAV-DJ_A70R_D213A (black, dotted) at different dilutions of serum. Error bars represent SD (n = 2 for WT AAV-DJ and AAV-DJ_D213A and n=1 for AAV-DJ_A70R_D213A).

DETAILED DESCRIPTION

[0019] Adeno-associated viruses (AAV) are commercially and clinically effective delivery vectors but are commonly neutralised and rendered ineffective by antibodies in the patients. Thus, the present disclosure describes compositions comprising AAV capsids that are resistant to, or capable of, evading neutralisation by neutralising antibodies that may be present in a host or subject.

[0020] As used herein, the term “AAV” or “adeno-associated virus” refers to a non-pathogenic, small viruses of the *Parvovirus* family which infect humans. The term “AAV” includes, but is not limited to, AAV subtypes, for example, AAV type 1 (AAV-1), AAV type 2 (AAV-2), AAV type 3 (AAV-3), AAV

type 4 (AAV-4), AAV type 5 (AAV-5), AAV type 6 (AAV-6), AAV type 7 (AAV-7), and AAV type 8 (AAV-8). Furthermore, as used herein, the terms “AAV virus”, “AAV viral particle”, or “rAAV vector particle” refer to a viral particle composed of at least one AAV capsid protein (typically by all of the capsid proteins of a wild-type AAV) and an encapsidated nucleotide recombinant AAV vector. If the viral particle comprises a heterologous polynucleotide (i.e. a polynucleotide other than a wild-type AAV genome such as a transgene to be delivered to a mammalian cell), it is typically referred to as a recombinant AAV vector (rAAV vector), a rAAV particle, or a rAAV vector.

[0021] Disclosed herein are compositions comprising AAV capsids resistant to neutralisation by pre-existing human antibodies. In other words, the present specification discloses AAV capsids that are so-called “epitope masked”, and therefore are not bound by neutralising antibodies that may be present in a subject. In one example, the composition is a pharmaceutical composition comprising one or more of the AAV capsid proteins disclosed herein. In another example, the composition comprises one or more of the AAV capsid proteins disclosed herein and pharmaceutically acceptable carriers and/or buffers.

[0022] Without being bound by theory, it is thought that compositions disclosed herein evade antibody neutralisation due to epitope masking. As used herein, the term “epitope masked” refers to an antigenic sequence of a virus, for example, the AAV capsid (i.e., antigen is bound by antibody) disclosed herein which is engineered to remove or minimize the binding of the antibody. The result is evasion of antibody binding (including, but not limited to, that of neutralising antibodies), without compromising or losing the desired function of the AAV (which can be described and/or quantified as a titre (as a measure of infectivity of a virus) and/or transduction efficiency of the AAV). Maintaining desired function of the virus is important because mutation of the antigen while losing function would not be considered “masking”. A loss of function (either infectivity or reduction in virulence or pathogenicity) would instead be understood as viral attenuation.

[0023] Such epitope masking can be performed, for example, by inserting one or more mutations within the relevant sections of the viral genome. The person skilled in the art would be able to insert or generate mutations in the viral genome or sections thereof, or within a specific gene, or replace specific nucleotide residues, for example, by inserting extraneous nucleotides (frame-shift mutations) or by replacement/substitution of specific nucleotides. The same mutations can also be generated on the protein level. A person skilled in the art would be aware of how to perform such amino acid substitution on virus particles.

[0024] As used herein, the term “protein” refers to a whole molecule. In contrast, as used herein, the term “peptide” refers to a sub-segment or part of the whole (protein) molecule.

[0025] As used herein, the term “epitope” refers to an immunogenic peptide sequence within a protein (also referred to in this example as an “antigen”). In other words, an epitope refers to a group of amino acids (peptides or proteins) or other chemical groups exposed on the surface of a molecule (the antigen), which can generate an antigenic response and bind an antibody.

[0026] The antibody antigenic footprint on different adeno-associated virus (AAV) orthologues were identified using phage display, specifically phage-immunoprecipitation sequencing (PhIP-Seq). An antibody epitope common to all tested AAV serotypes was also identified. AAVs engineered for protein residue substitution in this common epitope were shown to be resistant to neutralisation, if not completely resistant to neutralisation by pre-existing antibodies. The use of this modified adeno-associated virus (AAV) will enable more efficacious gene delivery by AAV through evading undesirable antibody immune response. Thus, in one example, there is disclosed a composition comprising at least one modified adeno-associated viral (AAV) capsid protein, wherein the composition is resistant to neutralisation or is not neutralised by human neutralising antibodies.

[0027] Presented herein is also the development of adeno-associated virus (AAV) capsids that are resistant to neutralization by pre-existing antibodies. The present disclosure describes AAVs as part of compositions that are engineered at a B-cell epitope with amino acid sequences that were previously not known to (1) engage the human antibodies and (2) have been shown to evade humoral immunity when engineered. Additionally, the neutralising antibody resistant AAV variants described herein showed an increase *in vitro* transduction efficiency in the presence and in the absence of neutralising antibody (NAbs).

[0028] The present disclosure describes mutations that are performed to obtain mutated or modified adeno-associated virus (AAV) vectors or virus particles. In one example, the mutations are at residues within epitopes residing in the N-terminal regions of the AAV capsid proteins. These residues of the epitopes referred to herein can be, but are not limited to, the following residues: amino acids 24 to 73, amino acids 48 to 93, amino acids 168 to 217, amino acids 48 to 97, amino-acids 72 to 121, amino acids 120 to 167, and combinations thereof. The numbering disclosed herein is provided in reference to the full-length sequence of the AAV VP1 capsid protein.

[0029] A total of five (5) serum samples from Southeast Asian patients and a commercially pooled serum sample (from 526 healthy donors between the ages 18 to 65) were tested in a phage-based immunoprecipitation assay. After identifying enriched peptides immunoprecipitated by the human antibodies, significant antibody binding sites in the N- and C- terminal parts of different AAV serotypes were detected. The C-terminal part of the AAV capsid containing the VP3 region has previously been described as a hotspot for the antibody binding but the data disclosed herein highlights that all human samples were reactive to epitopes from the N-terminal region of AAV capsids (VP1/ VP2 common regions (from 24 to 217 aa) (Figure 2). Without being bound by theory, it is also thought that mutated phage display tiles show decreased binding to human sera (data not shown).

[0030] The N-terminal was therefore chosen as an epitope because it is highly immunogenic based on the phage display data. In addition, much less is known about the N-terminus since it is unstable and the crystal structure of AAV capsid does not capture its structure. Also, the data presented herewith has shown that highly efficient immune evasion is obtained by masking this epitope.

[0031] Thus, in one example, the at least one modified adeno-associated viral (AAV) capsid protein is modified at any one or more of residues 24 to 47, 48 to 97, 72 to 121, 120 to 167 and 168 to 217 of an adeno-associated viral (AAV) VP1 capsid protein or an ortholog thereof. As used herein, the term “ortholog” refers to any of two or more homologous gene sequences found in different species related by linear descent.

[0032] In one example, the at least one modified adeno-associated viral (AAV) capsid protein is modified at any one or more of residues selected from the group consisting of positions 24 to 73 and 48 to 93. In another example, the at least one modified adeno-associated viral (AAV) capsid protein is modified at any one or more of residues selected from the group consisting of residues 24 to 93.

[0033] The AAVs disclosed herein can comprise one or more mutations in order to, for example, epitope mask said virus, resulting in modified adeno-associated viral (AAV) capsid proteins. In one example, the at least one modified adeno-associated viral (AAV) capsid protein comprises at least one, at least two, at least three mutations, or more. In another example, the at least one modified adeno-associated viral (AAV) capsid protein comprises at least one mutation. In yet another example, the at least one modified adeno-associated viral (AAV) capsid protein comprises at least two mutations. In a further example, the at least one modified adeno-associated viral (AAV) capsid protein comprises at least three mutations. In one example, the one or more mutations result in the modified adeno-associated viral (AAV) capsid protein being epitope masked. In other words, the one or more mutations result in the modified adeno-associated viral (AAV) capsid protein being able to evade neutralisation by antibodies already present in a host or a subject.

[0034] The results indicated that the mutations did not affect the genome packaging efficiency. Furthermore, it was observed that few mutations resulted in an increase in yield (Figure 3A and Table 2). Various mutations, as well as multiple mutations in the same variant, are contemplated within the scope of the disclosure as presented herewith. Without being bound by theory, mutations can be included in the claimed variant, so long as the mutation(s) do not impact negatively affect the transduction efficiency of the capsid protein disclosed herein.

[0035] As disclosed above, mutations can be inserted on the gene or protein level. In the present disclosure, the mutation is inserted into the viral genome. In one example, the mutation is selected from the group consisting of a “gca” mutation (alanine), a “cgg” mutation (arginine), and a “tct” mutation (serine). In another example, the mutation is a “gca” mutation (alanine). In another example, the mutation is a “cgg” mutation (arginine). In yet another example, the mutation is a “tct” mutation (serine). In yet another example, the mutation is a “gau” or “gac” mutation (aspartic acid). A person skilled in the art would appreciate that due to codon redundancy, other equivalent mutations may be used other than those described in the present disclosure. In one example, the residues are numbered at positions according to the wild-type sequence. In one example, the wild-type sequence or reference sequence is an adeno-associated viral (AAV) VP1 capsid protein or an ortholog thereof.

[0036] In one example, the at least one mutation is present at any one or more of the residues selected from the group consisting of A70, R168, K169, R170, L171, N172, F173, G174, Q175, T176, G177, D178, A179, D180, S181, V182, P183, D184, P185, Q186, P187, I188, G189, E190, P191A, P192, P195, A193, A194, P195, S196, G197, V198, G199, S200, L201, T202, M203, A204, A205, G206, G207, G208, A209, P210, M211, A212, D213, N214, N215, E216, G217, N215, A70, and combinations thereof.

[0037] In another example, the at least one mutation is selected from the group consisting of A70R, R168A, K169R, R170A, L171A, N172A, F173A, G174A, Q175A, T176A, G177A, D178A, A179R, D180A, S181A, V182A, P183A, D184A, P185A, Q186A, P187A, I188A, G189A, E190A, P191A, P192A, P195D, A193R, A194R, P195A, S196A, G197A, V198A, G199A, S200A, L201A, T202A, M203A, A204R, A205R, G206A, G207A, G208A, A209R, P210A, M211A, A212R, D213A, N214A, N215A, E216A, G217A, N215S, A70R, and combinations thereof.

[0038] In another example, the at least one "gca" mutation (alanine) is present at any one or more of the residues selected from the group consisting of R168, R170, L171, N172, F173, G174, Q175, T176, G177, D178, D180, S181, V182, P183, D184, P185, Q186, P187, I188, G189, E190, P191, P192, P195, S196, G197, V198, G199A, S200, L201, T202, M203, G206, G207, G208, P210, M211, D213, N214, N215, E216, G217, and combinations thereof.

[0039] In another example, the at least one "cgg" mutation (arginine) is present at any one or more of the residues selected from the group consisting of A70, K169, A179, A193, A194, A204, A205, A209, A212, A70, and combinations thereof.

[0040] In another example, the at least one "tct" mutation (serine) is present at N215.

[0041] In another example, the at least one "gau" or "gac" mutation (aspartic acid) is present at P195.

[0042] In one example, the at least one mutation is D213A. In another example, there are two mutations. In another example, there are two mutations, which are D213A and A70R.

Also disclosed herein are modified adeno-associated viral (AAV) capsid protein comprising the one or more mutations disclosed herein, at the residues disclosed herein. This, in one example, there is described at least one modified adeno-associated viral (AAV) capsid protein is selected from the group consisting of AAV-DJ_R168A, AAV-DJ_K169R, AAV-DJ_R170A, AAV-DJ_L171A, AAV-DJ_N172A, AAV-DJ_F173A, AAV-DJ_G174A, AAV-DJ_Q175A, AAV-DJ_T176A, AAV-DJ_G177A, AAV-DJ_D178A, AAV-DJ_A179R, AAV-DJ_D180A, AAV-DJ_S181A, AAV-DJ_V182A, AAV-DJ_P183A, AAV-DJ_D184A, AAV-DJ_P185A, AAV-DJ_Q186A, AAV-DJ_P187A, AAV-DJ_I188A, AAV-DJ_G189A, AAV-DJ_E190A, AAV-DJ_P191A, AAV-DJ_P192A, AAV-DJ_P195D, AAV-DJ_A193R, AAV-DJ_A194R, AAV-DJ_P195A, AAV-DJ_S196A, AAV-DJ_G197A, AAV-DJ_V198A, AAV-DJ_G199A, AAV-DJ_S200A, AAV-DJ_L201A, AAV-DJ_T202A, AAV-DJ_M203A, AAV-DJ_A204R, AAV-DJ_A205R, AAV-DJ_G206A, AAV-DJ_G207A, AAV-DJ_G208A, AAV-DJ_A209R, AAV-DJ_P210A, AAV-DJ_M211A, AAV-DJ_A212R, AAV-DJ_D213A, AAV-DJ_N214A, AAV-DJ_N215A, AAV-DJ_E216A, AAV-DJ_G217A, AAV-DJ_N215S, AAV2_D213A, AAV9_D213A, AAV-DJ_A70R, and

AAV-DJ_A70R_D213A. Non-exhaustive examples of such adeno-associated viral (AAV) capsid proteins can be found in Table 1.

[0043] **Table 1: AAV-DJ variants**

Variant#	Mutation	Variant#	Mutation
Variant#1	AAV-DJ_R168A	Variant#26	AAV-DJ_A193R
Variant#2	AAV-DJ_K169R	Variant#27	AAV-DJ_A194R
Variant#3	AAV-DJ_R170A	Variant#28	AAV-DJ_P195A
Variant#4	AAV-DJ_L171A	Variant#29	AAV-DJ_S196A
Variant#5	AAV-DJ_N172A	Variant#30	AAV-DJ_G197A
Variant#6	AAV-DJ_F173A	Variant#31	AAV-DJ_V198A
Variant#7	AAV-DJ_G174A	Variant#32	AAV-DJ_G199A
Variant#8	AAV-DJ_Q175A	Variant#33	AAV-DJ_S200A
Variant#9	AAV-DJ_T176A	Variant#34	AAV-DJ_L201A
Variant#10	AAV-DJ_G177A	Variant#35	AAV-DJ_T202A
Variant#11	AAV-DJ_D178A	Variant#36	AAV-DJ_M203A
Variant#12	AAV-DJ_A179R	Variant#37	AAV-DJ_A204R
Variant#13	AAV-DJ_D180A	Variant#38	AAV-DJ_A205R
Variant#14	AAV-DJ_S181A	Variant#39	AAV-DJ_G206A
Variant#15	AAV-DJ_V182A	Variant#40	AAV-DJ_G207A
Variant#16	AAV-DJ_P183A	Variant#41	AAV-DJ_G208A
Variant#17	AAV-DJ_D 184A	Variant#42	AAV-DJ_A209R
Variant#18	AAV-DJ_P185A	Variant#43	AAV-DJ_P210A
Variant#19	AAV-DJ_Q186A	Variant#44	AAV-DJ_M211A
Variant#20	AAV-DJ_P187A	Variant#45	AAV-DJ_A212R
Variant#21	AAV-DJ_I188A	Variant#46	AAV-DJ_D213A
Variant#22	AAV-DJ_G189A	Variant#47	AAV-DJ_N214A
Variant#23	AAV-DJ_E190A	Variant#48	AAV-DJ_N215A
Variant#24	AAV-DJ_P191A	Variant#49	AAV-DJ_E216A
Variant#25	AAV-DJ_P192A	Variant#50	AAV-DJ_G217A
Variant #51	AAV-DJ_P195D	Variant #52	AAV-DJ_N215S
Variant #53	AAV2-D213A	Variant #54	AAV9-D213A
Variant #55	AAV-DJ_A70R	Variant #56	AAV-DJ_A70R_D213A

[0044] In one example, the one adeno-associated viral (AAV) capsid protein disclosed herein comprises or is selected from the group consisting of SEQ ID Nos 30 to 57 and 61 to 62, or is encoded by a nucleic acid sequence selected from the group consisting of SEQ ID Nos 1 to 29 and 58 to 60.

[0045] In one example, the at least one adeno-associated viral (AAV) capsid protein does not comprise or consist of a B-cell epitope. In another example, the modified adeno-associated viral (AAV) capsid proteins disclosed herein comprise or are selected from the group consisting of the sequences disclosed herein. See, for example, the sequence listing section of this application.

[0046] The *in vitro* transduction efficiencies of the variants in HEK293, HepG2, and SK-Hep-1 cell lines were tested. The findings indicated that the mutations, with the exception of R170A, did not affect the transduction efficiency of the AAV-DJ variant.

[0047] Few mutants displayed an improvement in transduction efficiency in HEK293T, and SK-Hep1 cells when compared to the wild-type AAV-DJ vector. (Table 2) It is also noted that transduction efficacy may vary in terms of distribution of variants across different tissues and cell populations, as well as in factors like, but not limited to, vector yield, transduction efficiency *in vitro* and biodistribution *in vivo*.

[0048] The ability of the single AAV variants to avoid neutralization by human sera (pooled from 526 healthy donors between the ages 18 to 65) was evaluated using an *in vitro* neutralisation assay. Stringent conditions were used by including undiluted serum (1:1) and dilutions up to 1:316. The exclusion criterion used in ongoing clinical trials for indications requiring systemic administration of AAV is a NAb titre of 1:5.

A number of variants (R168A, T176A, P183A, P187A, P192A, P195A, S196A, G197A, L201A, A205R, N214A, E216A, G217A) showed improved neutralization resistance than WT AAV-DJ (one to two log decrease in NAb titre). In particular, the D213A variant displayed a complete resistance to neutralisation by pre-existing antibodies (titre 1:3.16) (Figure 4B), which with the current exclusion criteria, the patients will be considered as compatible subjects (similar to naïve / no pre-existing antibodies against the AAV). Hence, the compositions and modified AAV capsid proteins disclosed here exhibit evasion of human neutralising antibodies.

[0049] **Table 2: Summary of vector titre yield, *in vitro* transduction efficiency and neutralising antibody (Nab) titre.**

AAV-DJ variant s	Vector titer (GC/μl; n = 3)	Nab titer	Transducti on in HepG2	Transducti on in HEK293	Transducti on in HEK293T (n = 3)	Transducti on in SK1-hep1	Transducti on in SK1-hep1 (n = 3)
(in fold-change to WT)							
WT	3.19E+0 ₉	1:31.6 - 1:10 ₀	1.0	1.0	1	1.0	1
R168A	1.07E+0 ₉	1:10	0.7	1.3	0.98	0.8	0.94
T176A	1.21E+0 ₉	1:10	4.1	3.3	1.1	4.0	
S181A	4.21E+0 ₉	1:31.6	0.5	1.0	1.48	0.4	2.53
V182A	2.09E+0 ₉	1:10	1.8	2.2	0.78	1.5	0.50

AAV-DJ variants	Vector titer (GC/μl; n = 3)	Nab titer	Transduction in HepG2	Transduction in HEK293	Transduction in HEK293T (n = 3)	Transduction in SK1-hep1	Transduction in SK1-hep1 (n = 3)
P183A	2.36E+10	1:10 - 1:31.6	1.4	1.6	0.96	1.2	1.16
D184A	3.09E+09	1:10	2.2	2.5	0.9	1.8	0.69
P185A	1.31E+10	1:31.6	1.7	2.0	1.7	1.3	1.88
Q186A	2.06E+09	1:31.6	1.1	1.7	n.a.	1.0	n.a.
P187A	2.68E+09	1:10 - 1:31.6	0.9	1.3	1.30	0.7	0.70
G189A	3.51E+09	1:10	0.3	0.7	1.9	0.3	1.48
E190A	1.88E+10	1:31.6	0.8	1.0	1.19	0.7	0.54
P191A	1.15E+09	1:31.6	2.0	2.2	n.a.	1.5	n.a.
P192A	1.11E+10	1:10 - 1:31.6	1.2	1.7	1.47	1.2	0.99
A193R	8.06E+08	1:31.6	1.6	1.8	1.21	1.4	1.00
P195A	n.a. (1.49E+08)	1:10	4.3	3.6	n.a.	3.9	n.a.
S196A	2.70E+09	1:10	1.2	1.5	1.53	1.0	1.71
G197A	8.21E+09	1:10	2.6	2.1	0.97	1.6	1.43
V198A	1.25E+09	1:10	1.0	1.9	1.61	1.4	2.18
S200A	1.00E+09	n.a.	1.8	1.9	1.34	1.4	2.21
L201A	1.03E+09	n.a.	4.7	3.8	n.a.	2.3	n.a.
A205R	6.67E+08	1:10	0.9	1.5	1.24	0.9	0.80
G206A	1.96E+10	1:10	1.2	2.0	0.85	1.1	1.32
G208A	5.90E+10	1:31.6	1.2	1.8	1.09	1.4	0.93
D213A	3.51E+09	1:3.16	2.3	2.3	0.96	0.9	0.82

AAV-DJ variants	Vector titer (GC/μl; n = 3)	Nab titer	Transduction in HepG2	Transduction in HEK293	Transduction in HEK293T (n = 3)	Transduction in SK1-hep1	Transduction in SK1-hep1 (n = 3)
N214A	1.93E+09	1:10	1.9	2.1	1.56	1.3	0.83
N215A	1.25E+09	1:10	1.4	2.0	1.51	1.1	2.74
E216A	3.14E+08	1:10	1.4	1.9	0.87	1.5	1.50
G217A	2.84E+09	1:10	2.8	3.1	1.03	2.7	1.30

[0050] Table 3: Non-Alanine substitutions for avoiding neutralising antibody (Nab) recognition.

Variants	NAb Titer
WT-AAV-DJ	1:31.6 - 1:100
AAV-DJ_P195A	1:10
AAV-DJ_P195D	1:10 - 1:31.6
AAV-DJ_N215A	1:10
AAV-DJ_N215S	1:10 - 1:31.6

[0051] Next, it was tested to see whether the D213A substitution enables escape from pre-existing NAbS in human serum across different AAV serotypes. First, AAV2_D213A and AAV9_D213A were produced and the genome titres determined. Similar to previous results obtained with AAV-DJ_D213A, the D213A mutation did not negatively impact bioproduction yield. Notably, the substitution D213A resulted in a reduction in neutralization by pre-existing antibodies, as evidenced by a drop of two logs in Nab titre for AAV2_D213A (titre 1:10 versus 1:316 for WT AAV2) and one log for AAV9_D213A (1:1 versus 1:3.16 for WT AAV9, Table 3).

[0052] Building on the results of epitope-mapping disclosed herein, residues 24-73 and 48-93 were selected for further analysis. Specific residues were identified and selected based on their conservation across a range of AAV serotypes. Following this, AAV-DJ variants were produced and evaluated in their *in vitro* transduction efficiency. A number variants exhibited infectious capabilities. Subsequently, their potential to evade neutralization by pre-existing NAbS in human sera was assessed using an *in vitro* assay. Notably, the AAV-DJ_A70R variant demonstrated resistance to pre-existing NAbS, with a one-log reduction in Nab titre (1:10) compared to wild-type AAV-DJ (Table 3).

[0053] It was sought to determine if combining the A70R and D213A mutations was capable of synergistically enhancing evasion from pre-existing NAbS in human serum. To this end, the double mutant was prodded. It was observed that the A70R_D213A mutation did not impact either the bioproduction yield (Table 3) or the *in vitro* transduction efficiency. The results were similar to those observed for both AAV-

DJ_D213A and AAV-DJ_A70R_D213A, with the Nab titre further dropping to 1:3.16 compared to WT AAV-DJ (1:31.6 - 1:100, Table 4, Figure 6).

[0054] **Table 4: Additional variants for avoiding Nab recognition.**

AAV variant	Genome titre (GC/μl)	Nab titre (1:X)
AAV2_D213A	2.39E+09	10
AAV9_D213A	7.09E+09	1
WT AAV-DJ	1.54E+09	31.6 - 100
AAV-DJ_A70R	2.00E+09	10
AAV-DJ_A70R_D213A	6.50E+09	3.16

[0055] Importantly, maintaining desired function of the virus is important because mutation of the antigen while losing function would not be considered “masking”. Thus, in one example, the at least one mutations present in the modified adeno-associated viral (AAV) capsid protein do not negatively impact the transduction efficiency of modified AAV capsid protein. In other words, the modified adeno-associated viral (AAV) capsid proteins disclosed herein are capable of infection host cells, as well as transfection their payload into said host cell, thereby resulting in expression of said payload by the host cell.

[0056] In another example, the present disclosure describes a nucleic acid sequence encoding the composition disclosed herein, or encoding the one or more modified adeno-associated viral (AAV) capsid proteins as described herein.

[0057] Further disclosed herein is, in one example, a vector comprising one or more nucleic acid sequences disclosed herein. In another example, there is disclosed a vector encoding the one or more modified adeno-associated viral (AAV) capsid proteins disclosed herein.

[0058] Described herein is, for example, a host cell comprising the vector disclosed herein or the nucleic acid sequence disclosed herein. In another example, there is disclosed an adeno-associated virus particle comprising the modified AAV capsid proteins disclosed herein.

[0059] Another use described in the present disclosure is the use of the compositions, vectors, or modified AAV capsid proteins, adeno-associated virus particles disclosed herein in situations where binding to any antibodies present is not desirable. For example, in gene therapy, the vector (for example, a payload-carrying virus particle) needs to reach its intended target (the target cell), among others, in order to be effective. For this reason, vectors that are bound to by antibodies are not considered to be effective in their intended application. Thus, also disclosed herein is the composition, the nucleic acid, the vector, the host cell, or the adeno-associated virus particle disclosed herein, for use in gene therapy. In another example, there is disclosed a method of treating a subject in need thereof, the method of treating a subject comprising administering to the subject a therapeutically effective amount of the composition the nucleic acid, the vector, the host cell, or the adeno-associated virus particle disclosed herein. In yet another example, there is disclose use of the composition, the nucleic acid, the vector, the host cell, or the adeno-associated

virus particle disclosed herein, in the manufacture of a medicament, wherein the medicament is used in or for gene therapy. In a further example, the present disclosure describes use of the composition, the nucleic acid, the vector, the host cell, or the adeno-associated virus particle disclosed herein, in the manufacture of a medicament for gene therapy.

[0060] A further use described herein is when an AAV is to be administered to a subject more than once. Upon first administration, the subject may develop antibodies to the AAV that had been administered, thereby precluding the same subject from receiving further doses or administrations of the same AAV in future. Thus, in one example, the modified AAV capsid proteins disclosed herein do not elicit an immune response in the host. In another example, there is also described a method of preventing an immune response to an engineered adeno-associated virus, the method comprising administering to a subject an engineered adeno-associated virus comprising at least one modified adeno-associated viral (AAV) capsid protein.

[0061] Also disclosed herein is a method of identifying an adeno-associated viral (AAV) capsid protein or peptide which is resistant to neutralisation or is not neutralised by human neutralising antibodies, the method comprising (a) contacting the adeno-associated viral capsid protein or peptide with sera known to contain adeno-associated virus neutralising antibodies, thereby allowing the neutralising antibodies to bind to an epitope comprised within the adeno-associated viral capsid protein or peptide; (b) removing the neutralising antibody-bound epitope from the adeno-associated viral capsid protein or peptide; and (c) identifying the adeno-associated viral capsid protein or peptide that did not bind to the neutralising antibodies. In another example, the adeno-associated viral (AAV) capsid protein or peptide is selected from the group consisting of AAV-DJ, AAV1, AAV2, AAV3, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12 AAV13, or an ortholog thereof.

[0062] The invention illustratively described herein may suitably be practiced in the absence of any element or elements, limitation or limitations, not specifically disclosed herein. Thus, for example, the terms "comprising", "including", "containing", etc. shall be read expansively and without limitation. Additionally, the terms and expressions employed herein have been used as terms of description and not of limitation, and there is no intention in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments and optional features, modification and variation of the inventions embodied therein herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention.

[0063] As used in this application, the singular form "a," "an," and "the" include plural references unless the context clearly dictates otherwise. For example, the term "a genetic marker" includes a plurality of genetic markers to, including mixtures and combinations thereof.

[0064] As used herein, the term "about", in the context of concentrations of components of the formulations, typically means +/- 5% of the stated value, more typically +/- 4% of the stated value, more

typically +/- 3% of the stated value, more typically, +/- 2% of the stated value, even more typically +/- 1% of the stated value, and even more typically +/- 0.5% of the stated value.

[0065] Throughout this disclosure, certain embodiments may be disclosed in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of the disclosed ranges. Accordingly, the description of a range should be considered to have specifically disclosed all the possible sub-ranges as well as individual numerical values within that range. For example, description of a range such as from 1 to 6 should be considered to have specifically disclosed sub-ranges such as from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual numbers within that range, for example, 1, 2, 3, 4, 5, and 6. This applies regardless of the breadth of the range.

[0066] Certain embodiments may also be described broadly and generically herein. Each of the narrower species and sub-generic groupings falling within the generic disclosure also form part of the disclosure. This includes the generic description of the embodiments with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein.

[0067] The invention has been described broadly and generically herein. Each of the narrower species and sub-generic groupings falling within the generic disclosure also form part of the invention. This includes the generic description of the invention with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein.

[0068] Other embodiments are within the following claims and non-limiting examples. In addition, where features or aspects of the invention are described in terms of Markush groups, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group.

EXPERIMENTAL SECTION

Identification of epitopes on AAVs with human sera

[0069] The pre-existing anti-AAV antibodies pose a serious challenge for the efficacy of gene transfer mediated by AAV vectors. While there have been a few studies characterizing the extent of pre-existing immunity in human populations, the identification of the exact epitopes involved has not yet been comprehensively evaluated. To characterize the anti-AAV antibody repertoire in human subjects, a phage display library composed of approximately 10,000 unique tiles across different AAV capsid orthologues was generated (Figure 1). This library also contains tiles from known Cas9, Cas12 and Cas13 proteins. A python script described by Mohan et al. Nature protocols 2018 (PMID: 30190553) was used. It is noted that the phage display tiles referred to herein also consist of segments from the AAV orthologues. The phage display can comprise sequences that differ from the naturally occurring ones, such as single residue or multiple residues substitutions/insertions/deletions. This library has the additional advantage of probing antibody binding to sequence variants.

Design, Production and Characterization of the phage library

[0070] The phage library contained the protein sequences from the most common AAV serotypes (AAV1- AAV13, AAV DJ), together with the most common orthologues of Cas9, Cas12 and Cas13. Each protein was computationally divided into 49-amino acid peptide tiles with a 24-amino acid overlapping window. The amino acid sequences of these tiles were then reverse translated with an *E. coli* codon optimized algorithm called “pepsin” into DNA sequences. This library was provided as a Twist library, with the addition of universal forward, reverse primers, and with EcoRI and HindIII digestion sites inserted to the fragments. The oligo pool was amplified with Q5 Polymerase. The library was then digested with EcoRI and HindIII for 1 hour at 37 °C and ligated into pre-digested T7Select 10-3b Vector Arms (EMD; 16 hours at 16 °C), before being packaged into phages with T7Select® Packaging Extract (EMD). The phage library titre was determined by the plaque assay and the library was further amplified using BLT5403 *E. coli* cultures. The library was then amplified and concentrated by precipitation with 20% PEG8000 and 2M NaCl, before being resuspended in storage buffer (20 mM Tris-HCl, pH 7.5, 100 mM NaCl, 6 mM MgCl₂).

[0071] The library was tested with five (5) different, individual patient sera and a commercially available pooled serum sample that had been collected from 526 patients between the ages of 18 to 65.

[0072] For each sample subjected to the PhIP-seq assay, 10¹¹ pfu of phage library was mixed with sera containing 2 µg of IgG (quantified by ELISA). The samples were incubated for 18 hours at 4°C. As a positive control, 2 µg of commercially available SpCas9 polyclonal antibodies was used. Two technical replicates were performed for each sample. Next, 20µl of protein A and 20µl of protein G Dynabeads were added to each tube and incubated for another 4 hours at 4°C. Beads were washed twice with 170 µl of IP buffer (50 mM Tris-HCl, pH 7.5, 150 mM NaCl, 0.1% NP-40). After removing the wash solution, the beads were directly used for polymerase chain reaction (PCR). For Illumina library preparation, phage DNA was PCR-amplified with Q5 High-Fidelity DNA polymerase (New England Biolabs) in two rounds to produce Illumina libraries containing adaptor sequences and barcodes for multiplexing. The first round of polymerase chain reactions (PCRs) was performed using immunoprecipitated beads as template and with the primers amplifying the tiles.

[0073] In the second polymerase chain reaction (PCR), 2 µL of first reaction was used as template, and unique dual-indexed primers (NEBNext® Multiplex Oligos for Illumina) were used for barcoding. The PCR reactions were purified using SPRI Beads. The quality of the DNA fragments was confirmed on Bioanalyzer and the library was quantified by Qubit. The samples were then pooled in equimolar quantities and submitted for sequencing on a HiSeq with paired-end reads. To determine the significance of enriched peptides from noise that may be introduced by non-specific binding, the sample sets were fit to the Gamma Poisson model in the phip-stat Python package provided by the Laserson Lab (<https://github.com/lasersonlab/hiph-stat>). In brief, after sequencing, the reads were mapped to the original library using Bowtie2. SAM tools were used to count the number of reads for each peptide in the input and for each sample. The gamma Poisson model was fitted to the distribution of the output samples. This mode

was used to generate ($-\log_{10}$) P values for the probability of enrichment of each peptide. For each run, data from mock-IP controls (no antibody) were included with the patient sample data to better account for the abundance and non-specific binding associated with each peptide in the phage library.

[0074] In addition, the generalisable method to mask the other identified epitopes consists of (1) identifying the epitopes via phage display, (2) optionally selecting the strongest / most immune dominant epitopes for masking (as performed in the example described herein), (3) modifying the amino acid sequences of selected epitopes to eliminate the antibody-recognised sequences, (4) validating immune evasion and retention of transduction function.

AAV capsids engineered for immune evasion by epitope-masking

[0075] Based on the epitope-mapping, residues 168 to 217 of the AAV VP1 capsid protein were selected for epitope-masking. These residues had not been previously described to influence the biological properties of AAV vector, nor had these residues been previously known as an antibody epitope of any AAV serotypes. Multiple, evolved AAV variants were generated using alanine screening mutagenesis (Table 1) using the pRep2-AAVCapDJ as a template. The PCR product was then treated with DpnI and T4 polynucleotide kinase at 37 °C for 1 hour before being ligated using T4 DNA ligase and incubated overnight at 16°C. Ligated product was then transformed into chemically competent 5-alpha E. coli. The generated plasmid was Sanger sequenced for sequence verification and the correct clone was amplified and purified using plasmid plus maxi kit. Using this method, the AAV-DJ variants shown in Table 1 were generated.

[0076] **Table 5: Primer sequences for AAV-DJ plasmids cloning.**

Residue	Mutation	Primer name	Primer sequence	SEQ ID NO:
168	R to A	168_SDM_R_A_For	GCAGCCTGCagcaAAAAGATTGA ATTTTGGTCAGACTG	912
		168_SDM_R_A_Rev	TGGCCCGCCTTTCCGGTT (SEQ ID NO: 913)	913
170	R to A	170_SDM_R_A.F or	TGCAAGAAAAGcaTTGAATTTTGG TCAGACTGGAGACGCAG	914
		170_SDM_R_A.Rev	GGCTGCTGGCCCGCCTTT	915
171	L to A	171_SDM_L_A.F or	AAGAAAAAGAgcaAATTTTGGTC AGACTGGAGACGCAGACTCAGT CCCAGACC	916
		171_SDM_L_A.Rev	GCAGGCTGCTGGCCCGCC	917
172	N to A	172_SDM_N_A.For	AAAAAGATTGgcaTTTGGTCAGA CTGGAGACGCAGACTCAG	918
		172_SDM_N_A.Rev	CTTGCAGGCTGCTGGCCC	919
173	F to A	173_SDM_F_A.For	AAGATTGAATgcaGGTCAGACTG GAGACG	920
		173_SDM_F_A.Rev	TTTCTTGCAGGCTGCTGG	921
174	G to A	174_SDM_G_A.for	ATTGAATTTTgcaCAGACTGGAGA CG	922
		174_SDM_G_A.Rev	CTTTTCTTGCAGGCTGC	923

Residue	Mutation	Primer name	Primer sequence	SEQ ID NO:
175	Q to A	175_SDM_Q_A_For	GAATTTTGGTgcaACTGGAGACGCAGAC	924
		175_SDM_Q_A_Rev	AATCTTTTCTTGCAGGC	925
176	T to A	176_SDM_T_A_For	TTTTGGTCAGgcaGGAGACGCAG	926
		176_SDM_T_A_Rev	TTCAATCTTTTCTTGCAGGC	927
177	G to A	177_SDM_G_A_For	TGGTCAGACTgcaGACGCAGACT	928
		177_SDM_G_A_Rev	AAATTCAATCTTTTCTTGCAGGCTG	929
178	D to A	178_SDM_D_A_For	TCAGACTGGAgcaGCAGACTCAG	930
		178_SDM_D_A_Rev	CCAAAATTCAATCTTTTCTTG	931
179	A to R	179_SDM_A_R_For	GACTGGAGACcggGACTCAGTCC	932
		179_SDM_A_R_Rev	TGACCAAAATTCAATCTTTTC	933
180	D to A	180_SDM_D_A_For	TGGAGACGCgcaTCAGTCCCAG	934
		180_SDM_D_A_Rev	GTCTGACCAAAATTCAATCTTTTC	935
181	S to A	181_SDM_S_A_For	AGACGCAGACgcaGTCCCAGACC	936
		181_SDM_S_A_Rev	CCAGTCTGACCAAAATTCAATCTTTTCTTG	937
182	V to A	182_SDM_V_A_For	CGCAGACTCAgcaCCAGACCCTC	938
		182_SDM_V_A_Rev	TCTCCAGTCTGACCAAAATTC	939
183	P to A	183_SDM_P_A_For	AGACTCAGTCgcaGACCCTCAAC	940
		183_SDM_P_A_Rev	GCGTCTCCAGTCTGACCA	941
184	D to A	184_SDM_D_A_For	CTCAGTCCCgcaCCTCAACCAATC	942
		184_SDM_D_A_Rev	TCTGCGTCTCCAGTCTGA	943
185	P to A	185_SDM_P_A_For	AGTCCCAGACgcaCAACCAATCG	944
		185_SDM_P_A_Rev	GAGTCTGCGTCTCCAGTC	945
186	Q to A	186_SDM_Q_A_for	CCCAGACCCTgcaCCAATCGGAG	946
		86_SDM_Q_A_Rev	ACTGAGTCTGCGTCTCCA	947
187	P to A	187_SDM_P_A_For	AGACCCTCAgcaATCGGAGAAC	948
		187_SDM_P_A_Rev	GGGACTGAGTCTGCGTCT	949

Residue	Mutation	Primer name	Primer sequence	SEQ ID NO:
188	I to A	188_SDM_I_A_For	CCCTCAACCAgcaGGAGAACCTCCG	950
		188_SDM_I_A_Rev	TCTGGGACTGAGTCTGCG	951
189	G to A	189_SDM_G_A_For	TCAACCAATCgcaGAACCTCCCG	952
		189_SDM_G_A_Rev	GGGTCTGGGACTGAGTCT	953
190	E to A	190_SDM_E_A_For	ACCAATCGGAgcaCCTCCCGCAG	954
		190_SDM_E_A_Rev	TGAGGGTCTGGGACTGAGTC	955
191	P to A	191_SDM_P_A_For	AATCGGAGAAgcaCCCGCAGCCC	956
		191_SDM_P_A_Rev	GGTTGAGGGTCTGGGACTG	957
192	P to A	192_SDM_P_A_For	CGGAGAACCTgcaGCAGCCCCCT	958
		192_SDM_P_A_Rev	ATTGGTTGAGGGTCTGGGACTG	959
193	A to R	193_SDM_A_R_For	AGAACCTCCCcggGCCCCCTCAG	960
		193_SDM_A_R_Rev	CCGATTGGTTGAGGGTCT	961
194	A to R	194_SDM_A_R_For	ACCTCCCGCAcggCCCTCAGGTG	962
		194_SDM_A_R_Rev	TCTCCGATTGGTTGAGGG	963
195	P to A	195_SDM_P_A_For	TCCCGCAGCCgcaTCAGGTGTGG	964
		195_SDM_P_A_Rev	GGTTCTCCGATTGGTTGAGGGTC	965
196	S to A	196_SDM_S_A_For	CGCAGCCCCCgcaGGTGTGGGAT	966
		196_SDM_S_A_Rev	GGAGGTTCTCCGATTGGTTGAGG GTC	967
197	G to A	197_SDM_G_A_For	AGCCCCCTCAgcaGTGGGATCTC	968
		197_SDM_G_A_Rev	GCGGGAGGTTCTCCGATT	969
198	V to A	198_SDM_V_A_For	CCCCTCAGGTgcaGGATCTCTTAC AATGGC	970
		198_SDM_V_A_Rev	GCTGCGGGAGGTTCTCCG	971
199	G to A	199_SDM_G_A_For	CTCAGGTGTGgcaTCTCTTACAAT GGCTG	972
		199_SDM_G_A_Rev	GGGGCTGCGGGAGGTTCT	973
200	S to A	200_SDM_S_A_For	AGGTGTGGGAgcaCTTACAATGG CTGCAGG	974
		200_SDM_S_A_Rev	GAGGGGGCTGCGGGAGGT	975

Residue	Mutation	Primer name	Primer sequence	SEQ ID NO:
201	L to A	201_SDM_L_A_ For	TGTGGGATCTgcaACAATGGCTGC AGGCGG	976
		201_SDM_L_A_ Rev	CCTGAGGGGGCTGCGGGA	977
202	T to A	202_SDM_T_A_ For	GGGATCTCTTgcaATGGCTGCAGG	978
		202_SDM_T_A_ Rev	ACACCTGAGGGGGCTGCG	979
203	M to A	203_SDM_M_A_ For	ATCTCTTACAgcaGCTGCAGGCGG TGGCG	980
		203_SDM_M_A_ Rev	CCCACACCTGAGGGGGCT	981
204	A to R	204_SDM_A_R_ For	TCTTACAATGcggGCAGGCGGTG GC	982
		204_SDM_A_R_ Rev	GATCCCACACCTGAGGGG	983
205	A to R	205_SDM_A_R_ For	TACAATGGCTcggGGCGGTGGCG	984
		205_SDM_A_R_ Rev	AGAGATCCCACACCTGAG	985
206	G to A	206_SDM_G_A_ For	AATGGCTGCgcaGGTGGCGCAC	986
		206_SDM_G_A_ Rev	GTAAGAGATCCCACACCTG	987
207	G to A	207_SDM_G_A_ For	GGCTGCAGGCgcaGGCGCACCAA	988
		207_SDM_G_A_ Rev	ATTGTAAGAGATCCCACACCTGA GG	989
208	G to A	208_SDM_G_A_ For	TGCAGGCGGTgcaGCACCAATGG	990
		208_SDM_G_A_ Rev	GCCATTGTAAGAGATCCCAC	991
209	A to R	209_SDM_A_R_ For	AGGCGGTGGCcggaCCAATGGCAG	992
		209_SDM_A_R_ Rev	GCAGCCATTGTAAGAGATC	993
210	P to A	210_SDM_P_A_ For	CGGTGGCGCAgcaATGGCAGACA	994
		210_SDM_P_A_ Rev	CCTGCAGCCATTGTAAGAGATCC CAC	995
211	M to A	211_SDM_M_A_ For	TGGCGCACCAgcaGCAGACAATA ACGAG	996
		211_SDM_M_A_ Rev	CCGCCTGCAGCCATTGTA	997
212	A to R	212_SDM_A_R_ For	CGCACCAATGcggGACAATAACG AGGGCGC	998
		212_SDM_A_R_ Rev	CCACCGCCTGCAGCCATT	999
213	D to A	213_SDM_D_A_ For	ACCAATGGCAgcaAATAACGAGG GCGCCGACG	1000
		213_SDM_D_A_ Rev	GCGCCACCGCCTGCAGCC	1001

Residue	Mutation	Primer name	Primer sequence	SEQ ID NO:
214	N to A	214_SDM_N_A_ For	AATGGCAGACgcaAACGAGGGCG CCGACGG	1002
		214_SDM_N_A_ Rev	GGTGCGCCACCGCCTGCA	1003
215	N to A	215_SDM_N_A_ For	GGCAGACAATgcaGAGGGCGCCG ACGG	1004
		215_SDM_N_A_ Rev	ATTGGTGCGCCACCGCCT	1005
216	E to A	216_SDM_E_A_ For	AGACAATAACgcaGGCGCCGACG GAGTG	1006
		216_SDM_E_A_ Rev	GCCATTGGTGCGCCACCG	1007
217	G to A	217_SDM_G_A_ For	CAATAACGAGgcaGCCGACGGAG TGGG	1008
		217_SDM_G_A_ Rev	TCTGCCATTGGTGCGCCA	1009

[0077] The AAV-DJ and the different variants were produced containing a self-complementary GFP genome driven by a ubiquitous Cagl promoter. The genome titre of AAV-DJ variants and the wild-type (WT) AAV-DJ vectors were evaluated using quantitative PCR (qPCR).

AAV vector production

[0078] AAV vectors were produced by triple transfection of HEK293T cells and purified via an iodixanol gradient. Cells were transfected with 20 µg of a helper plasmid, 10 µg of an ITR cargo plasmid, and 10 µg of rep-cap plasmid. 24 hours later, the medium was changed to a fresh culture medium containing 2% foetal bovine serum (FBS). Three days after transfection, cells were collected and resuspended in lysis buffer (Tris HCl pH 7.5, 2 mM MgCl₂, 150 mM NaCl) and lysed in three freeze/thaw cycles. The supernatant was collected and treated with 50 U/ml of benzonase and 1 U/ml of RNase cocktail for 30 minutes at 37 °C to remove unpackaged nucleic acids. After incubation, the lysate was loaded on top of a discontinuous density gradient (15%, 25%, 40%, and 60%) and ultracentrifuged at 54,000 rpm, at 18 °C, for 1.5 hours, on a Type 70 Ti rotor. The 40% fraction was extracted and dialyzed with 1×PBS (pH 7.2) with 0.001% pluronic acid, using Amicon ultra-15 (100 kDa MWCO). The vectors were titrated against an AAV2 RSM vector by quantitative PCR using primers and probe binding within the AAV2 ITR.

In vitro neutralisation assay

[0079] HEK293 expressing adenoviral E4 protein in a doxycycline-inducible manner were seeded in 96-well plate at a density of 2x10⁴ cells/well in 100 µL DMEM containing 10% FBS. The next day, the vectors prepared at a multiplicity of infection (MOI) of 20 000 and were pre-mixed with a serial dilution of human serum and incubated for 1 hour at 37°C. As a positive control, the vector was diluted with DMEM. 10 µL of the mixture was added to the wells and incubated for 48 hours at 37 °C. The total GFP protein was quantified using a GFP quantification kit (Biovision) on a multi-well plate reader (Tecan). The neutralising titre was determined as the highest sample dilution at which at least 50% inhibition occurred.

SEQUENCE LISTING

[0080] The following sequences are disclosed in the present application.

SEQ ID NO:	Name	Sequence
1	AAV-DJ R168A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCACCACAAAGCCCCGAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCAG ACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAGAAGAGGCCTGTAGAGCACTCTCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAgcaAAAAGATTGAATTTTGGTCAGACTGGAGAC GCAGACTCAGTCCCAGACCCTCAACCAATCGGAGAACCtCCC GCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGACAG CGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGAC GGAGTGGGTAATTCTCGGGAATTGGCATTGCGATTCCAC ATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACCT GGGCCCTGCCACCTACAACAACCACCTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGCTACAGCACCCCTGGGGGTATTTGACTTTAACAG ATTCCACTGCCACTTTTCACCACGTGACTGGCAGCGACTCAT CAACAACAAGTGGGGATTCCGGCCCAAGAGACTCAGCTTCA AGCTCTTCAACATCCAGGTCAAGGAGGTACGCGAGAATGAA GGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTCTCGG CTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGGGACGT GTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCCTTCGCAGATGCTGAGAACCGGCAACAACCTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCCACAGCAGTACG CCCACAGCCAGAGCTTGGACCGGTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGACAGCTCTGGGCTTCAGCCAAGGTG GGCCTAATAACAATGGCCAATCAGGCAAAGAAGTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTT TCCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGCGGTTCTTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCTCATGGGTGGATTCCGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACTCTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA

SEQ ID NO:	Name	Sequence
		GCTGCAGAAGGAAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAACCTACTACAAATCTACAAGTGTTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
2	AAV-DJ T176A:	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAAGCTCAAACCTGG CCCACCACCACCAAAGCCCGCAGAGCGGCATAAAGGACGAC AGcaGGGGTCTTTGTGCTTCTTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGGCAG ACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACACGC CGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAGAAGAGGCCTGTAGAGCACTCTCCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGgcaGGAGAC GCAGACTCAGTCCCAGACCCTCAACCAATCGGAGAACCICCC GCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGCAGG CGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGAC GGAGTGGGTAATTCCTCGGGAAATTGGCATTGCGATTCCAC ATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACCT GGGCCCTGCCCACCTACAACAACCACCTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGCTACAGCACCCCTGGGGGTATTTGACTTTAACAG ATTCCACTGCCACTTTTACCACGTGACTGGCAGCGACTCAT CAACAACAACCTGGGGATTCCGGCCCCAAGAGACTCAGCTTCA AGCTCTTCAACATCCAGGTCAAGGAGGTACGCAAGTGA GGACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCGG CTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGCGGACGT GTTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCCTTCGCAGATGCTGAGAACCGGCAACAACATTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATAACAATGGCCAATCAGGCAAGAAGTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAAGTTTTT TCCTCAGAGCGGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGGCGTTCTTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACCTTTTCATCACC

SEQ ID NO:	Name	Sequence
		CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAACAGCAAGCGCTGGAAACCCCGAGATC CAGTACACCTCCAACCTACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCCGTTACCTCACCCGTAATCTGTAA
3	AAV- DJ_S181A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAAGCTCAAACCTGG CCCACCACCACCAAAGCCCGCAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGGAGAGCCGGTCAACGAGGCGAG ACGCCGCGGCCCTCGAGCAGACAAAGCCTACGACCCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAGAAGAGGCCTGTAGAGCACTCTCCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACgcaGTCCCAGACCCTCAACCAATCGGAGAACCtCC CGCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGCAG GCGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGA CGGAGTGGGTAATTCTCGGGAAATTGGCATTGCGATTCCA CATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACC TGGGCCCTGCCACCTACAACAACCACCTCTACAAGCAAAT CTCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCT ACTTCGGCTACAGCACCCCTTGGGGGTATTTTGACTTTAACA GATTCCACTGCCACTTTTACCACGTGACTGGCAGCGACTCA TCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTC AAGCTCTTCAACATCCAGGTCAAGGAGGTCACGCAGAATGA AGGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCC AGGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCG GCTCTGCCACACAGGGGTGCCTGCCTCCGTTCCCGGCGGACG TGTTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTCTACTGCTGGAAT ACTTTCCTTCGCAGATGCTGAGAACCGGCAACAACCTTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATAACAATGGCCAATCAGGCAAAGAAGTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTT TCCTCAGAGCGGGTTCTCATCTTIGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGCGTTCTTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCTCATGGGTGGATTCCGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT

SEQ ID NO:	Name	Sequence
		CCGACCACCTTCAACCAGTCAAAGCTGAACTCTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAAGAAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAATACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
4	AAV- DJ_V182A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAAGCTCAAACCTGG CCCACCACCACCAAAGCCCGCAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCGAG ACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAGAAGAGGCCTGTAGAGCACTCTCCTG TGGAGCCAGACTCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCagcaCCAGACCCTCAACCAATCGGAGAACCICC CGCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGCAG GCGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGA CGGAGTGGGTAATTCTCGGGAATTTGGCATTGCCATTCCA CATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACC TGGGCCCTGCCCACCTACAACAACCACCTCTACAAGCAAAT CTCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCT ACTTCGGCTACAGCACCCCTGGGGGTATTTTGACTTTAACA GATTCCACTGCCACTTTTCAACACGTGACTGGCAGCGACTCA TCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTC AAGCTCTTCAACATCCAGGTCAAGGAGGTACGCAGAATGA AGGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCC AGGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCG GCTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGCGGACG TGTTCAATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCCTTCGCAGATGCTGAGAACCGGCAACAACCTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATAACAATGGCCAATCAGGCAAAGAAGTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAAGTTTTT TCCTCAGAGCGGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGGCGTTCTTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG

SEQ ID NO:	Name	Sequence
		CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACCTCTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAATACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
5	AAV- DJ_P183A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCACCACCAAAGCCCCGAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTCGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCAG ACGCCGCGGCCCTCGAGCACGACAAAAGCCTACGACCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAGAAGAGGCCTGTAGAGCACTCTCCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTcgaGACCCTCAACCAATCGGAGAACCICCC GCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGCAGG CGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGAC GGAGTGGGTAATTCTCGGGAATTGGCATTGCGATTCCAC ATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACCT GGGCCCTGCCCACCTACAACAACCACCTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGCTACAGCACCCCTGGGGGTATTTGACTTTAACAG ATTCCACTGCCACTTTTACCACGTGACTGGCAGCGACTCAT CAACAACAACCTGGGGATTCCGGCCCCAAGAGACTCAGCTTCA AGCTCTTCAACATCCAGGTCAAGGAGGTACGCGAGAATGAA GGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCGG CTCTGCCCAACAGGGCTGCCTGCCTCCGTTCCCGGCGGAGT GTTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCCTTCGCAGATGCTGAGAACCGGCAACAACCTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATAACAATGGCCAATCAGGCAAGAAGTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTT TCCTCAGAGCGGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGGCGTTCTTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAGATTCCACACACGGACGGACATTTTCAC

SEQ ID NO:	Name	Sequence
		CCCTCTCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACTCTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAAACAGCAAGCGCTGGAAACCCCGAGATC CAGTACACCTCCAATACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
6	AAV-DJ_D184A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAAGCTCAAACCTGG CCCACCACCACCAAAGCCCCGAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCAG ACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCTGGAAAGAAGAGGCCTGTAGAGCACTCTCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCagcaCCTCAACCAATCGGAGAACCtCCC GCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGCAGG CGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGAC GGAGTGGGTAATTCCTCGGGAATTGGCATTGCGATTCCAC ATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACCT GGGCCCTGCCCACCTACAACAACCACCTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGCTACAGCACCCCTGGGGGTATTTTGACTTTAACAG ATTCCACTGCCACTTTTACCACGTGACTGGCAGCGACTCAT CAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGTTCA AGCTCTTCAACATCCAGGTCAAGGAGGTCACGCAGAATGAA GGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCGG CTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGCGGACGT GTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCTTTCGAGATGCTGAGAACCGGCAACAACCTTCCAGT TTAATTACACCTTCGAGGACGTGCCTTCCACAGCAGTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCACTCTGGGCTTCAGCCAAGGTG GGCCTAATAAATGGCCAATCAGGCAAAGAAGTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTT TCCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGGCGTTCTTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC

SEQ ID NO:	Name	Sequence
		CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACCTTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAACCTACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
7	AAV- DJ_P185A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCACCACCAAGCCCGCAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCAG ACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAGAAGAGGCCTGTAGAGCACTCTCCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACgcaCAACCAATCGGAGAACCIC CGCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGCAG GCGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGA CGGAGTGGGTAATTCTCGGGAAATTGGCATTGCGATTCCA CATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACC TGGGCCCTGCCCACCTACAACAACCACCTCTACAAGCAAAT CTCCAACAGCACATCTGGAGGATCTTCAAATGACAAACGCCT ACTTCGGCTACAGCACCCCTGGGGGTATTTTGACTTTAACA GATTCCACTGCCACTTTTACCACGTGACTGGCAGCGACTCA TCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTC AAGCTCTTCAACATCCAGGTCAAGGAGGTCACGCAGAATGA AGGCACCAAGACCATCGCCAATAACCTCACCGACCATTC AGGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCG GCTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGCGGACG TGTTTCATGATTCCCAAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCCTTCGCAGATGCTGAGAACCGGCAACAACCTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATAAATGGCCAATCAGGCAAAGAAGTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAAGTTTTT TCCTCAGAGCGGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGGCGTCTCTCC

SEQ ID NO:	Name	Sequence
		AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACCTCTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAAACAGCAAGCGCTGGAAACCCCGAGATC CAGTACACCTCCAATACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
8	AAV- DJ_Q186A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCACCACCAAAGCCCGCAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCGAG ACGCCGCGGCCCTCGAGCAGCACAAGCCTACGACCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACACGC CGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACTGCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCTTGAAAGAAGAGGCCTGTAGAGCACTCTCTTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTgcaCCAATCGGAGAACCiCCC GCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGCAGG CGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGAC GGAGTGGGTAATTCCTCGGGAATTGGCATTGCGATTCCAC ATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACCT GGGCCTTGCCACCTACAACAACCACTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGCTACAGCACCCCTGGGGGTATTTGACTTTAACAG ATTCCACTGCCACTTTTACCACGTGACTGGCAGCGACTCAT CAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCA AGCTTTCAACATCCAGGTCAAGGAGGTCACGCAGATGAA GGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCCTCG CTCTGCCACCAGGGCTGCCTGCCCTCCGTTCCTGGCGGACGT GTTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCTGGAAT ACTTTCTTCGCAGATGCTGAGAACC GGCAACAACCTTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATAACAATGGCCAATCAGGCAAGAAGTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTT TCCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA

SEQ ID NO:	Name	Sequence
		CAAGCAGCTACCGCAGATGTCAACACACAAGGCGTTCTTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACTCTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAATACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
9	AAV- DJ_P187A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCACCACCAAAGCCCGCAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCGAG ACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCCACGC CGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTICTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAGAAGAGGCCTGTAGAGCACTCTCCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTCAagcaATCGGAGAACCtCCC GCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGCAGG CGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGAC GGAGTGGGTAAATTCTCGGGAATTGGCATTGGCATTCCAC ATGGATGGGCGACAGATCATCACCACCAGCACCCGAACCT GGGCCCTGCCCACCTACAACAACCACCTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGGTACAGCACCCCTTGGGGGTATTTTGACTTTAACAG ATTCCACTGCCACTTTTACCACGTGACTGGCAGCGACTCAT CAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCA AGCTCTTCAACATCCAGGTCAAGGAGGTACGCGAGAATGAA GGACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGACTCGGAGTACCAGTGCCGTACGTCTCTCGG CTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGCGGACGT GTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCCTTCGCAGATGCTGAGAACCGGCAACAACCTCCAGT TACTTACACCTTCGAGGACGTGCCTTTCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATAACAATGGCCAATCAGGCAAAGAAGTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTT TCCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC

SEQ ID NO:	Name	Sequence
		AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGCGTTCTTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACCTTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAACCTACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
10	AAV- DJ_G189A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCACCACCAAAGCCCGCAGAGCGGCATAAGGACGAC AGcAGGGGTCTTGTGCTTCTCGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCGAG ACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAGAAGAGGCCTGTAGAGCACTCTCTCG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTCAACCAATCgcaGAACCICCC GCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGCAGG CGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGAC GGAGTGGGTAATTCTCGGGAATTTGGCATTGCGATTCCAC ATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACCT GGGCCCTGCCCACCTACAACAACCACCTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGCTACAGCACCCCTGGGGGTATTTGACTTTAACAG ATTCCACTGCCACTTTTCAACACGTGACTGGCAGCGACTCAT CAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCA AGCTCTTCAACATCCAGGTCAAGGAGGTCACGCAGAATGAA GGACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCGG CTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGCGGACGT GTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCCTTCGCAGATGCTGAGAACCGCAACAACCTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATAACAATGGCCAATCAGGCAAAGAAGTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTT TCCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC

SEQ ID NO:	Name	Sequence
		GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGCGCTTCTTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACTCTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAATACTACAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
11	AAV- DJ_E190A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCACCACCAAAGCCCCGAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCAG ACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGAAAAGAAGAGGCCTGTAGAGCACTCTCCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTCAACCAATCGGAAGcaCC:CCC GCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGCAGG CGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGAC GGAGTGGGTAATTCTCGGGAAATTGGCATTGCGATTCCAC ATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACCT GGGCCCTGCCCACCTACAACAACCACCTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGCTACAGCACCCCTGGGGGTATTTGACTTTAACAG ATTCCACTGCCACTTTTCACCACGTGACTGGCAGCGACTCAT CAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCA AGCTCTTCAACATCCAGGTCAAGGAGGTACGCGAGAATGAA GGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCGG CTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGGGACGT GTTTATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCCTTCGCAGATGCTGAGAACCGGCAACAACCTTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGACAGCTCTGGGCTTCAGCCAAGGTG GGCCTAATAACAATGGCCAATCAGGCAAAGAAGTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTT TCCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGCTCAG

SEQ ID NO:	Name	Sequence
		AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGCGCTTCTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACTCTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAAGAAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAACCTACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
12	AAV- DJ_P191A	ATGGCTGCCGATGGTTATCTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAAGCTCAAACCTGG CCCACCACCACAAAGCCCGCAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCAG ACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAGAAGAGGCCTGTAGAGCACTCTCCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTCAACCAATCGGAGAAgcaCC CGCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGCAG GCGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGA CGGAGTGGGTAATTCTCGGGAATTTGGCATTGCGATTCCA CATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACC TGGGCCCTGCCCACCTACAACAACCACCTCTACAAGCAAAT CTCCAACAGCACATCTGGAGGATCTTCAAATGCAACGCCT ACTTCGGCTACAGCACCCCTGGGGGTATTTTGACTTTAACA GATTCCACTGCCACTTTTACCACGTGACTGGCAGCGACTCA TCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTC AAGCTCTTCAACATCCAGGTCAAGGAGGTACGCAGAAATGA AGGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCC AGGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCG GCTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGCGGACG TGTTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCCTTCGCAGATGCTGAGAACCGGCAACAACCTCCAGT TACTTACACCTTCGAGGACGTGCCTTTCCACAGCAGTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATAACAATGGCCAATCAGGCAAAGAAGTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTT

SEQ ID NO:	Name	Sequence
		TCCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGCGCTTCTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCAC CCTCTCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACTCTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAATACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
13	AAV-DJ_P192A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCACCACCAAAGCCCGCAGAGCGGCATAAGGACGAC AGCaGGGGTCTTGTGCTTCTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCGAG ACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAGAAGAGGCCTGTAGAGCACTCTCCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTCAACCAATCGGAGAACCGg aGCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGCAGG CGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGAC GGAGTGGGTAATTCCTCGGGAATTGGCATTCGATTCCAC ATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACCT GGGCCCTGCCACCTACAACAACCACCTCTACAAGCAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCCGGCTACAGCACCCCTGGGGGTATTTGACTTTAACAG ATTCCACTGCCACTTTTACCACGTGACTGGCAGCGACTCAT CAACAACAATGGGGATTCCGGCCCAAGAGACTCAGCTTCA AGCTCTTCAACATCCAGGTCAAGGAGGTCACGAGAATGAA GGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCGG CTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGCGGACGT GTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCCTTCGCAGATGCTGAGAACCGGCAACAACCTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATAACAATGGCCAATCAGGCAAGAAGTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC

SEQ ID NO:	Name	Sequence
		CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTCCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGCTCAGAGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGACGAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGACAAGCAGCTACCGCAGATGTCAACACACAAGCGCTTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGCCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCCTCATGGGTGGATTCCGGACTTAAACACCCTCCGCCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCTCCGACCACCTTCAACCAGTCAAAGCTGAACTCTTTCATCACCAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGAGCTGCAGAAGGAAAAACAGCAAGCGCTGGAAACCCCGAGATCAGTACACCTCCAACCTACTACAAATCTACAAGTGTGGACTTTGCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATTGGCACCCCGTTACCTCACCCGTAATCTGTAA
14	AAV-DJ_A193R	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGGCCCACCACCACCAAAGCCCGCAGAGCGGCATAAGGACGACAGcaGGGGTCTTGTGCTTCTGGGTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGAGAGCCGGTCAACGAGGCGACGCCCGGCCCTCGAGCACGACAAAAGCCTACGACCCGGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGCGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTTTGGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAGAGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAAGACGGCTCCTGGAAAGAAGAGGCCTGTAGAGCACTCTCCTGTGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAGCAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTCCCAGACCCTCAACCAATCGGAGAACCtCCcgaGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGCAGGCGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGACGGAGTGGGTAATTCCTCGGGAAATTGGCATTGCGATTCCACATGGATGGGCGACAGAGTCATCACCAACGACACCCGAACCTGGGCCCTGCCACCTACAACAACCACCTCTACAAGCAAATCTCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTACTTCGGGTACAGCACCCCTTGGGGGTATTTGACTTTAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGCGACTCATCAACAACAAGTGGGGATTCCGGCCCAAGAGACTCAGTTCAAGCTCTTCAACATCCAGGTCAAGGAGGTCACGCAGAATGAAGGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCCAGGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCGGCTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGCGGACGTGTTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACGGTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAATACTTTCCTTCGCAGATGCTGAGAACCGGCAACAACCTTCCAGTTACTTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACGCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATTGACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGGAGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTGGCCTAATAACAATGGCCAATCAGGCAAAGAAGTGGCTGCCAGGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGCGGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA

SEQ ID NO:	Name	Sequence
		AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTT TCCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGGCGTTCTTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCCTCATGGGTGGATTCCGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACCTTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAACCTACTACAAATCTACAAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
15	AAV- DJ_P195A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCACCACCAAGCCCGCAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTTGCTTCTTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCGAG ACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCCGAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAGAAGAGGCCTGTAGAGCACTCTCCTG TGGAGCCGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTCAACCAATCGGAGAACCICC CGCAGCCgcaTCAGGTGTGGGATCTCTTACAATGGCTGCAGG CGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGAC GGAGTGGGTAATTCTCGGGAATTGGCATTGGCATTTCCAC ATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACCT GGGCCCTGCCCACCTACAACAACCACCTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGCTACAGCACCCCTGGGGGTATTTTGACTTTAACAG ATTCCACTGCCACTTTTCAACACGTGACTGGCAGCGACTCAT CAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCA AGCTCTTCAACATCCAGGTCAAGGAGGTCACGCAGAATGAA GGACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCGG CTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGCGGACGT GTTATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCTTCGCAGATGCTGAGAACCGGCAACAACCTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATACAATGGCCAATCAGGCAAAGAAGTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC

SEQ ID NO:	Name	Sequence
		GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTT TCCTCAGAGCGGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGCGCTTCTTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCTCATGGGTGGATTTCGACTTAAACACCCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACTCGCGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACTCTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAATACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
16	AAV- DJ_S196A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCACCACCAAAGCCCCGAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCAG ACGCCGCGGCCCTCGAGCACGACAAAAGCCTACGACCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAAGAAGAGCGCTGTAGAGCACTCTCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTCAACCAATCGGAGAACCICC CGCAGCCCCCGcaGGTGTGGGATCTCTTACAATGGCTGCAGG CGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGAC GGAGTGGGTAATTCTCGGGAATTGGCATTGCGATTCCAC ATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACCT GGGCCCTGCCACCTACAACAACCACCTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGCTACAGCACCCCTGGGGGTATTTGACTTTAACAG ATTCCACTGCCACTTTTCACCACGTGACTGGCAGCGACTCAT CAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCA AGCTCTTCAACATCCAGGTCAAGGAGGTACGCGAGAATGAA GGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGAAGTACGAGTACCAGCTGCCGTACGTTCTCGG CTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGCGGACGT GTTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCTTCGCAGATGCTGAGAACCGGCAACAACCTTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCCACAGCAGTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCAAGTCTGGGCTTCAGCCAAGGTG GGCCTAATAACAATGGCCAATCAGGCAAAGAAGTGGCTGCCA

SEQ ID NO:	Name	Sequence
		GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTT TCCTCAGAGCGGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGCGCTTCTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACTCTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAATACTACAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
17	AAV- DJ_G197A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCACCACAAAGCCCCGAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCAG ACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAGAAGAGGCCTGTAGAGCACTCTCCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTCAACCAATCGGAGAACCtCC CGCAGCCCCCTCagcaGTGGGATCTCTTACAATGACGAGG CGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGAC GGAGTGGGTAATTCTCGGGAATTGGCATTGCGATTCCAC ATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACCT GGGCCCTGCCCACCTACAACAACCACCTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGCTACAGCACCCCCCTGGGGGTATTTGACTTTAACAG ATTCCACTGCCACTTTTACCACGTGACTGGCAGCGACTCAT CAACAACAACCTGGGGATTCCGGCCCCAAGAGACTCAGCTTCA AGCTCTTCAACATCCAGGTCAAGGAGGTCACGCAGAATGAA GGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCGG CTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGCGGACGT GTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCTTCGAGATGCTGAGAACCGGCAACAACCTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGAGACTCTGGGCTTCAGCCAAGGTG

SEQ ID NO:	Name	Sequence
		GGCCTAATACAATGGCCAATCAGGCCAAAGAACTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAAGTTTTT TCCTCAGAGCGGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGGCGTCTTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTAC CCCTCTCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACTCTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAACCTACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
18	AAV- DJ_V198A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCACCACCAAAGCCCGCAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCAG ACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAGAAGAGGCCTGTAGAGCACTCTCCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTCAACCAATCGGAGAACCC CGCAGCCCCCTCAGGTgcaGGATCTCTTACAATGGCTGCAGG CGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGAC GGAGTGGGTAATTCCTCGGGAAATTGGCATTGCGATTCCAC ATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACCT GGGCCCTGCCACCTACAACAACCACCTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGCTACAGCACCCCCTGGGGGTATTTGACTTTAACAG ATTCCACTGCCACTTTTACCACGTGACTGGCAGCGACTCAT CAACAACAACCTGGGGATTCCGGCCCCAAGAGACTCAGCTTCA AGCTCTTCAACATCCAGGTCAAGGAGGTCACGAGAATGAA GGACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCGG CTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGCGGACGT GTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCCTTCGCAGATGCTGAGAACCGGCAACAACCTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG

SEQ ID NO:	Name	Sequence
		AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATAACAATGGCCAATCAGGCAAAGAACTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAAGTTTTT TCCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGCGCTTCTTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACCTTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAACCTACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
19	AAV- DJ_S200A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCACCACCAAAGCCCGCAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCGAG ACGCCGCGGCCCTCGAGCACGACAAAAGCCTACGACCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACACGCG CGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAAGAAGAGGCCTGTAGAGCACTCTCCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTCAACCAATCGGAGAACCcCC CGCAGCCCCCTCAGGTGTGGGAgcaCTTACAATGGCTGCAGG CGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGAC GGAGTGGGTAATTCTCCTCGGGAATTGGCATTGCGATTCCAC ATGGATGGGCGACAGAGTCATCACCAACAGCACCCGAACCT GGGCCCTGCCACCTACAACAACCACCTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGCTACAGCACCCCTGGGGGTATTTGACTTTAACAG ATTCCACTGCCACTTTTACCACGTGACTGGCAGCGACTCAT CAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCA AGCTCTTCAACATCCAGGTCAAGGAGGTCACGCAAGATGAA GGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGAATCGGAGTACCAGCTGCCGTACGTTCTCGG CTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGGGACGT GTTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCTGGAAAT ACTTTCCTTCGCAGATGCTGAGAACCGGCAACAACCTTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT

SEQ ID NO:	Name	Sequence
		GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATACAATGGCCAATCAGGCAAAGAACTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTT TCCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGCGCTTCTTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACTCTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAACCTACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
20	AAV- DJ_L201A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCACCACCAAAGCCCGCAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCGAG ACGCCGCGGCCCTCGAGCACGACAAGCCTACGACCCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAGAAGAGGCCTGTAGAGCACTCTCCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTCAACCAATCGGAGAACCtCC CGCAGCCCCCTCAGGTGTGGGATCTgcaACAATGGCTGCAGG CGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGAC GGAGTGGGTAATTCTCGGGAATTTGGCATTGCGATTCCAC ATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACCT GGGCCCTGCCCACCTACAACAACCACCTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGCTACAGCACCCCTGGGGGTATTTTGACTTTAACAG ATTCCACTGCCACTTTTCAACACGTGACTGGCAGCGACTCAT CAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCA AGCTCTTCAACATCCAGGTCAAGGAGGTCACGCAGAATGAA GGACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCGG CTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGCGGACGT GTTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCCTTCGCAGATGCTGAGAACCGGCAACAACCTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCACAGCAGCTACG

SEQ ID NO:	Name	Sequence
		CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATAACAATGGCCAATCAGGCAAAGAACTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAAGTTTTT TCCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGCGCTTCTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACCTTTTCATACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAATACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCAT GGCACCCGTTACCTCACCCGTAATCTGTAA
21	AAV- DJ_A205R	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCACCACCAAAGCCCCGAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTCTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCAG ACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAGAAGAGCCCTGTAGAGCACTCTCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTCAACCAATCGGAGAACCICC CGCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTcgaGG CGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGAC GGAGTGGGTAATTCTCGGGAAATTGGCATTTGCGATTCCAC ATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACCT GGGCCCTGCCCACCTACAACAACCACCTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGCTACAGCACCCCTGGGGGTATTTGACTTTAACAG ATTCCACTGCCACTTTTACCACGTGACTGGCAGCGACTCAT CAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCA AGCTCTTCAACATCCAGGTCAAGGAGGTACGCGAGAATGAA GGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCGG CTCTGCCCAACAGGGCTGCCTGCCTCCGTTCCCGGCGGACGT GTTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCCTTCGCAGATGCTGAGAACCGGCAACAACCTCCAGT

SEQ ID NO:	Name	Sequence
		TTACTTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATAACAATGGCCAATCAGGCAAAGAAGTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTT TCCTCAGAGCGGGTTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGCGCTTCTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCTCATGGGTGGATTCCGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACCTTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAAACAGCAAGCGCTGGAAACCCCGAGATC CAGTACACCTCCAATACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
22	AAV- DJ_G206A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCACCACCAAAGCCCCGAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCCTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCAG ACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAGAAGAGGCCTGTAGAGCACTCTCTGT TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTCAACCAATCGGAGAACCtCC CGCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGCagc aGGTGGGCGACCAATGGCAGACAATAACGAGGGCGCCGACG GAGTGGGTAAATTCCTCGGGAATTTGGCATTGCGATTCCACA TGGATGGGCGACAGATCATCACCACCAGCACCCGAACCTG GGCCCTGCCCACCTACAACAACCACCTCTACAAGCAAATCT CCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTAC TTCGGCTACAGCACCCCTGGGGGTATTTTGACTTTAACAGA TTCCACTGCCACTTTTACCACGTGACTGGCAGCGACTCATC AACAACTGGGGATTCCGGCCCAAGAGACTCAGCTTCAA GCTCTTCAACATCCAGGTCAAGGAGGTCACGCAGAAATGAAG GCACCAAGACCATCGCCAATAACCTCACCAGCACCATCCAG GTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCGGC TCTGCCACACAGGGCTGCCTGCCTCCGTTCCCGGCGGACGTG TTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACGGT AGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAATAC

SEQ ID NO:	Name	Sequence
		TTTCCTTCGCAGATGCTGAGAACCGGCAACAACCTCCAGTTT ACTTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACGCC CACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATTGA CCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGGAG GCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTGGG CCTAATACAATGGCCAATCAGGCAAAGAACTGGCTGCCAGG ACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGCGG ATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCAAG TACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCC GGCCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTTTC CTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGCTCAGAG AAAACAAAATGTGGACATTGAAAAGGTCATGATTACAGACGA AGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGCAGT ATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGACAA GCAGCTACCGCAGATGTCAACACACAAGGCGTTCCTCCAGG CATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGCCCA TCTGGGCAAAGATTCCACACACGGACGGACATTTTACCCCT TCTCCCTCATGGGTGGATTTCGGACTTAAACACCCCTCCGCCT CAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCTCC GACCACCTTCAACCAGTCAAAGCTGAACCTTTTCATCACCCA GTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGAGC TGCAGAAGGAAAAACAGCAAGCGCTGGAACCCCGAGATCCA GTACACCTCCAACCTACTACAAATCTACAAAGTGTGGACTTTGC TGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATTG GCACCCGTTACCTCACCCGTAATCTGTAA
23	AAV- DJ_G208A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCACCACCAAAGCCCGCAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCAG ACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAG AGGCTTCTTGAACTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAAGAAGAGGCCTGTAGAGCACTCTCCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTCAACCAATCGGAGAACCcC CGCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGCAG GCGGTgcaGCACCAATGGCAGACAATAACGAGGGCGCCGAC GGAGTGGGTAATTCTCGGGAAATTGGCATTGCGATTCCAC ATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACCT GGGCCCTGCCCACCTACAACAACCACCTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGCTACAGCACCCCTGGGGGTATTTGACTTTAACAG ATTCCACTGCCACTTTTCAACACGTGACTGGCAGCGACTCAT CAACAACAACCTGGGGATTCCGGCCCCAAGAGACTCAGCTTCA AGCTCTTCAACATCCAGGTCAAGGAGGTCACGCAGAATGAA GGACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCGG CTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGCGGACGT GTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG

SEQ ID NO:	Name	Sequence
		GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCCTTCGCAGATGCTGAGAACCGGCAACAACTTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATACAATGGCCAATCAGGCAAAGAAGCTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTT TCCTCAGAGCGGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGCGCTTCTTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACTCTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAACAGCAAGCGCTGGAAACCCCGAGATC CAGTACACCTCCAATACTACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
24	AAV- DJ_D213A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCAACCACAAAGCCCGCAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCAG ACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACACGC CGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAAGAAGAGCCTGTAGAGCACTCTCCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTCAACCAATCGGAGAACCICC CGCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGCAG GCGGTGGCGCACCAATGGCagcaAATAACGAGGGCGCCGAC GGAGTGGGTAAATTCCTCGGGAAATTGGCATTGCGATTCCAC ATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACCT GGGCCCTGCCACCTACAACAACCACCTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGCTACAGCACCCCTGGGGGTATTTGACTTTAACAG ATTCCACTGCCACTTTTACCACGTGACTGGCAGCGACTCAT CAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCA AGCTCTTCAACATCCAGGTCAAGGAGGTCACGAGAATGAA GGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTCTCGG CTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGCGGACGT

SEQ ID NO:	Name	Sequence
		GTTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCTTCGCGAGATGCTGAGAACCGGCAACAACCTTCCAGT TACTTACACCTTCGAGGACGTGCCTTTCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATAACAATGGCCAATCAGGCAAAGAAGTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGG CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAGTTT TCCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGCGTTCTTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACTCTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAACCTACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
25	AAV- DJ_N214A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCACCACCAAAGCCCCGAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCGAG ACGCCGCGGCCCTCGAGCAGACAAAAGCCTACGACCGGAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACACGCG CGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAGAAGAGGCCTGTAGAGCACTCTCCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTCAACCAATCGGAGAACCtCC CGCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGCAG GCGGTGGCGCACCAATGGCAGACgcaAACGAGGGCGCCGAC GGAGTGGGTAAATTCCTCGGGAATTTGGCATTGCGATTCCAC ATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACCT GGGCCCTGCCCACCTACAACAACCACCTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGCTACAGCACCCCTTGGGGGTATTTTGACTTTAACAG ATTCCACTGCCACTTTTCACCACGTGACTGGCAGCGACTCAT CAACAACAAGTGGGGATTCCGGCCCAAGAGACTCAGTTTCA AGCTCTTCAACATCCAGGTCAAGGAGGTCACGCAGAATGAA GGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCCTCGG

SEQ ID NO:	Name	Sequence
		CTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGCGGACGT GTTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCCTTCGCAGATGCTGAGAACCGGCAACAACCTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATACAATGGCCAATCAGGCAAAGAACTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAAGTTTTT TCCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGCGTTCTTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACCTTTTCATACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAACCTACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
26	AAV- DJ_N215A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCACCACCAAAGCCCGCAGAGCGGCATAAGGACGAC AGCaGGGGTCTTGTGCTTCCTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCGAG ACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAAGAAGAGGCCTGTAGAGCACTCTCCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTCAACCAATCGGAGAACCiCC CGCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGCAG GCGGTGGCGCACCAATGGCAGACAATgcaGAGGGCGCCGAC GGAGTGGGTAATTCTCGGGAAATTGGCATTGCGATTCCAC ATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACCT GGGCCCTGCCCACCTACAACAACCACCTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGCTACAGCACCCCCTGGGGGTATTTGACTTTAACAG ATTCCACTGCCACTTTTCAACCACGTGACTGGCAGCGACTCAT CAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCA AGCTCTTCAACATCCAGGTCAAGGAGGTACGCAGAATGAA GGACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA

SEQ ID NO:	Name	Sequence
		GGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCGG CTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGCGGACGT GTTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCTTCGACAGATGCTGAGAACCGGCAACAACCTTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATAACAATGGCCAATCAGGCAAAGAAGTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTCG GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAAGTTTTT TCCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGCGCTTCTTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACTCTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAACCTACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
27	AAV- DJ_E216A	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAGCTCAAACCTGG CCCACCACCACCAAAGCCCCGAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGCAG ACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAGAAGAGGCCTGTAGAGCACTCTCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTCAACCAATCGGAGAACCcCC CGCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGCAG GCGGTGGCGCACCAATGGCAGACAATAACgcaGGCGCCGAC GGAGTGGGTAATTCCTCGGGAAATTGGCATTGGCATTCCAC ATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACCT GGGCCCTGCCACCTACAACAACCACCTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGCTACAGCACCCCTGGGGGTATTTTGACTTTAACAG ATTCCACTGCCACTTTTCACCACGTGACTGGCAGCGACTCAT CAACAACAAGTGGGGATTCCGGCCCAAGAGACTCAGCTTCA AGCTCTTCAACATCCAGGTCAAGGAGGTCACGCAGAATGAA

SEQ ID NO:	Name	Sequence
		GGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCGG CTCTGCCCACCAGGGCTGCCTGCCCTCCGTTCCCGGGGACGT GTTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCTTCGAGATGCTGAGAACCAGCAACAACCTCCAGT TTACTTACACCTTCGAGGACGTGCCCTTCCACAGCAGTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATAACAATGGCCAATCAGGCAAAGAACTGGCTGCCA GGACCTGTTACCGCCAGCAGCGAGTATCAAAGACACTCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTT TCCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGTACCGCAGATGTCAACACACAAGCGCTTCTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTCAGGGGC CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTAC CCCTCTCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACTCTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAAGAAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAACCTACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
28	AAV- DJ_G217A	ATGGCTGCCGATGGTTATCTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGGAAAGCTCAAACCTGG CCCACCACCACAAAGCCCCGAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTGGGTACAAGTACCTCGGACCC TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCAG ACGCCGCGGCCCTCGAGCACGACAAAGCCTACGACCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAGAAGAGGCCTGTAGAGCACTCTCCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTCAACCAATCGGAGAACCtCC CGCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTGCAG GCGGTGGCGCACCAATGGCAGACAATAACGAGgcaGCCGAC GGAGTGGGTAAATTCCTCGGGAAATTGGCATTGCGATTCCAC ATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACCT GGGCCCTGCCCACCTACAACAACCACCTCTACAAGCAAATC TCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTA CTTCGGCTACAGCACCCCTGGGGGTATTTGACTTTAACAG ATTCCACTGCCACTTTTCACCACGTGACTGGCAGCGACTCAT CAACAACAACCTGGGGATTCCGGCCCCAAGAGACTCAGCTTCA

SEQ ID NO:	Name	Sequence
		AGCTCTTCAACATCCAGGTCAAGGAGGTACGCGAGAATGAA GGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCCA GGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCGG CTCTGCCCACCAGGGCTGCCTGCCTCCGTTCCCGGGCGGACGT GTTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCCTTCGCAGATGCTGAGAACCGGCAACAACCTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAACAACAGG AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATAACAATGGCCAATCAGGCAAGAAGTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAAGTTTT TCCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGCGCTTCTTC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAGGATTCCACACACGACGACGACATTTTAC CCCTCTCCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACCTTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAATACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCCATT GGCACCCGTTACCTCACCCGTAATCTGTAA
29	AAV-DJ R168A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPKPAERHKDDS RGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAA KRLNFGQTGDADSVDPQPIGEPPAAPSGVGSLTMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPT YNNHLYKQISNSTSGSSNDNAYFGYSTPWGYDFNRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYLSRTQTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
30	AAV-DJ T176A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPKPAERHKDDS RGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR

SEQ ID NO:	Name	Sequence
		KRLNFGQAGDADSVDPDPQPIGEPPAAPSGVGSLTMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDNRFHCHFS PRDWQRLINNNWGFPRKRLSFKLFNIQVKEVTQNEGKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
31	AAV- DJ_S181A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDS RGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQAGDADSVDPDPQPIGEPPAAPSGVGSLTMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDNRFHCHFS PRDWQRLINNNWGFPRKRLSFKLFNIQVKEVTQNEGKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
32	AAV- DJ_V182A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDS RGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQAGDADSVDPDPQPIGEPPAAPSGVGSLTMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDNRFHCHFS PRDWQRLINNNWGFPRKRLSFKLFNIQVKEVTQNEGKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
33	AAV- DJ_P183A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDS RGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL

SEQ ID NO:	Name	Sequence
		LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVADPQPIGEPPAAPSGVGSLTMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDNRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGTKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRT TNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
34	AAV- DJ_D184A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKAERHKDDS RGLVLPGYKYLGPFGNLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVAPQPIGEPPAAPSGVGSLTMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDNRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGTKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRT TNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
35	AAV- DJ_P185A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKAERHKDDS RGLVLPGYKYLGPFGNLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDAQPIGEPPAAPSGVGSLTMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDNRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGTKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRT TNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
36	AAV- DJ_Q186A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKAERHKDDS RGLVLPGYKYLGPFGNLDKGEPVNEADAAALEHDKAYDRQL

SEQ ID NO:	Name	Sequence
		DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPAPIGEPPAAPSGVGSLTMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITTTSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDNRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
37	AAV-DJ_P187A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDS RGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPQAI GEPPAAPSGVGSLTMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITTTSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDNRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
38	AAV-DJ_G189A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDS RGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPQIAEPPAAPSGVGSLTMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITTTSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDNRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL

SEQ ID NO:	Name	Sequence
39	AAV-DJ_E190A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSD RGLVLPGYKYLGPFGNLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPDPQPIGAPPAAPSGVGSLTMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITTTSTRTWALPT YNNHLYKQISNSTSGSSNDNAYFGYSTPWGYFDFNRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFIQVKEVTQNEGTKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
40	AAV-DJ_P191A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSD RGLVLPGYKYLGPFGNLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPDPQPIGEAPAAAPSGVGSLTMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITTTSTRTWALPT YNNHLYKQISNSTSGSSNDNAYFGYSTPWGYFDFNRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFIQVKEVTQNEGTKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
41	AAV-DJ_P192A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSD RGLVLPGYKYLGPFGNLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPDPQPIGEAPAAAPSGVGSLTMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITTTSTRTWALPT YNNHLYKQISNSTSGSSNDNAYFGYSTPWGYFDFNRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFIQVKEVTQNEGTKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTVPADPPTTFNQSKLNSFITQYSTGQV

SEQ ID NO:	Name	Sequence
		SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
42	AAV- DJ_A193R	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSD RGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPQPIGEPPRAPSGVGS LTMAAGGGAPM ADNNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPTY NNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFNRHFCHFS RDWQRLINNNWGFPRKLSFKLFNIQVKEVTQNEGTKTIANNL TSTIQVFDTSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHSS YAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQGG PNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGATK YHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEKT NVDIEKVMITDEEEIRTTPVATEQYGSVSTNLQRGNRQAATA DVNTQGVLPGMVWQDRDVYLQGPWAKIPHTDGHFHPSPLM GGFGLKHPPPQILIKNTPVPADPPTTFNQSKLNSFITQYSTGQVS VEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYSE PRPIGTRYLTRNL
43	AAV- DJ_P195A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSD RGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPQPIGEPPAAASGVGS LTMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFNRHFCHFS PRDWQRLINNNWGFPRKLSFKLFNIQVKEVTQNEGTKTIANN LTSTIQVFDTSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHSS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTTPVATEQYGSVSTNLQRGNRQAATA ADVNTQGVLPGMVWQDRDVYLQGPWAKIPHTDGHFHPSPLM MGGFGLKHPPPQILIKNTPVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
44	AAV- DJ_S196A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSD RGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPQPIGEPPAAPAGVGS LTMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFNRHFCHFS PRDWQRLINNNWGFPRKLSFKLFNIQVKEVTQNEGTKTIANN LTSTIQVFDTSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHSS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTTPVATEQYGSVSTNLQRGNRQAATA ADVNTQGVLPGMVWQDRDVYLQGPWAKIPHTDGHFHPSPLM

SEQ ID NO:	Name	Sequence
		MGGFGLKHPPPQILIKNTPVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
45	AAV- DJ_G197A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKAERHKDDSD RGLVLPGYKYLGPFGNLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPQPIGEPPAAPSAVGSLTMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDENRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTPVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
46	AAV- DJ_V198A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKAERHKDDSD RGLVLPGYKYLGPFGNLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPQPIGEPPAAPSGAGSLTMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDENRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTPVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
47	AAV- DJ_S200A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKAERHKDDSD RGLVLPGYKYLGPFGNLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPQPIGEPPAAPSGVGALTMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDENRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAAT

SEQ ID NO:	Name	Sequence
		ADVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPL MGGFGLKHPPPQILIKNTPVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
48	AAV- DJ_L201A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKAERHKDDSD RGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPQPIGEPPAAPSGVG SATMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPT YNNHLYKQISNSTSGSSNDNAYFGYSTPWGYFDENRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGTKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTTPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPL MGGFGLKHPPPQILIKNTPVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
49	AAV- DJ_A205R	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKAERHKDDSD RGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPQPIGEPPAAPSGVGSLTMARGGGAPM ADNNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPTY NNHLYKQISNSTSGSSNDNAYFGYSTPWGYFDENRFHCHFS RDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGTKTIANNL TSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHSS YAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQGG PNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGATK YHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEKT NVDIEKVMITDEEEIRTTPVATEQYGSVSTNLQRGNRQAATA DVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLM GGFGLKHPPPQILIKNTPVPADPPTTFNQSKLNSFITQYSTGQVS VEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYSE PRPIGTRYLTRNL
50	AAV- DJ_G206A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKAERHKDDSD RGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPQPIGEPPAAPSGVGSLTMAAAGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPT YNNHLYKQISNSTSGSSNDNAYFGYSTPWGYFDENRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGTKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK

SEQ ID NO:	Name	Sequence
		TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTPVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
51	AAV- DJ_G208A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKAERHKDD RGLVLPGYKYLGPFGNLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPQPIGEPPAAPSGVGS LTMAAGGAAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPT YNNHLYKQISNSTSGSSNDNAYFGYSTPWGYFDNRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGKTIAN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQ GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNP GPAMASHKDDEEKFFPQSGVLIFGKQSEK TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTPVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
52	AAV- DJ_D213A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKAERHKDD RGLVLPGYKYLGPFGNLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPQPIGEPPAAPSGVGS LTMAAGGGAP MAANNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPT YNNHLYKQISNSTSGSSNDNAYFGYSTPWGYFDNRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGKTIAN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQ GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNP GPAMASHKDDEEKFFPQSGVLIFGKQSEK TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTPVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
53	AAV- DJ_N214A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKAERHKDD RGLVLPGYKYLGPFGNLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPQPIGEPPAAPSGVGS LTMAAGGGAP MADANEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPT YNNHLYKQISNSTSGSSNDNAYFGYSTPWGYFDNRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGKTIAN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQ GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT

SEQ ID NO:	Name	Sequence
		KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
54	AAV- DJ_N215A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSD RGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPQPIGEPPAAPSGVGSLTMAAGGGAP MADNAEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDNRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
55	AAV- DJ_E216A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSD RGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPQPIGEPPAAPSGVGSLTMAAGGGAP MADNNAAGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDNRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
56	AAV- DJ_G217A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSD RGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPQPIGEPPAAPSGVGSLTMAAGGGAP MADNNEAADGVGNSSGNWHCDSTWMGDRVITSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDNRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQG

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57	AAV2 D213A	atggctgccgatggttatcttcagattggctcgaggacactctctgaaggaaagacagtggtg gaagctaaaactggcccaccaccacaaagcccgagagcggcataaggacgacagcagggg tcttgtcttctgggtacaagtacctcgaccctcaacggactcgacaaggagagccgggtcaac gaggcagagccggcgccctcgagcagacaaagcctacgaccggcagctcgacagcggaga caaccctgacctcaagtaaccacgccgacggaggttcaggagcgccttaaaagatacgtc ttttgggggcaacctcgagcagcagctctccagcgcaaaaagaggggtcttgaaacctctgggctg gttgaggaaacctttaagacggctccgggaaaaagaggccggtagagcactctctgtggagcc agactcctctcggaaccggaaaggcggccagcagcctgcaagaaaaagattgaatttggtc agactggagacgcagactcagctgaccccgacctctcgagcagccaccagcagcccccct ggtctgggaactaatcagatggctacaggcagtgccgaccaatggcaGCCAataacgagggc gccgacggagtggttaattctcgggaaattggcattgcgattccacatggatggcgacagagtc atcaccaccagcaccgaaacctgggcccgcacctacaacaaccacctctacaacaataatcc agccaatcaggagcctgaacgacaatactactttggctacagcacccttgggggtatttgaact caacagattccactgccactttaccacgtgactggcaagactcatcaacaacaactggggattcc gaccaagagactcaactcaagctttaacattcaagtcagaaggctcagcagaatgacgggtac gacgacgattgccaaataacttaccagcaggttcaggtgttactgactcggagtcaccagctccgt acgtctcggctcgcgcatcaagatgcctcccgccgttccagcagacgtcttcatgtggccac agtatggatacctaccctgaacaacgggagtcaggcagtaggacgctctctatttactgctgga gtactttcctctcagatgctgctaccgggaaacaactttaccttcagctacacttttggagacgttcc ccacagcagctacgctcagccagagctctggacgctcatgaatcctctcatcgaccagctacgt tattacttgagcagaacaacactccaagtgggaaccaccacgcagtcgaaggcttcagtttctcaggc cggagcggagtgacattcgggaccagcttaggaactggctcctggaccctgttacccgccagcagcg agtatcaaaagacatctcgggataacaacaacagtgaaactcgtggactggagctaccaagtaacca cctcaatggcagagactctctggtgaatccgggcccggccatggcagaagccacaaggacgatgaag aaaagtttttctcagagcggggttctcatcttgggaagcaaggctcagagaaaacaatgtggac attgaaaaggtcatgattacagacgaaggagaaatcaggacaaccaatccgtggctacggagca gtatggttctgtatctaccaacctccagagaggcaacagacaagcagctaccgcatgtgcaaacac acaaggcgttcttcaggcatggtctggcaggacagagatgtgtaccttcaggggcccattctgggc aaagattccacacacggacggacattttaccctctccctcatgggtggattcggacttaaacacc ctctccacagattctcatcaagaacacccggtaacctgcgaatccttcgaccacctcagtcggcga aagtttcttctcatcacagactccacgggacaggctcagcgtggagatcagtgaggagctgc agaaggaaaacagcaaacgctggaatcccgaattcagtagactccaactacaacaagctctgttaa tgtggactttactgtggacactaatggcgtgtattcagagcctcgccccattggcaccagatacctga ctctgaatctgtaa
58	AAV6 D213A	atggctgccgatggttatcttcagattggctcgaggacaacctctctgagggcattcgcgagtggtg ggacttgaacctggagccccgaaaccaaagccaaacagcaaaagcagagcagggccggg gtctggtgttcttggctacaagtacctcgacccttcaacggactcgacaagggggagcccgta acggcggcgatgcagcggccctcgagcagcaaaaggcctacgaccagcagctcaaaagcgggtg acaatccgtacctgcgtataaccacgccgacccgagtttcaggagcgtctgcaagaagatacgt cttttgggggcaacctcgggcgagcagctctccaggccaagaagggttctgaaccttttggct ggttgaggaaagtgtaagacggctcctggaaaagaaagtcggtagagcagtcgccacaagag ccagactcctctcgggcatggcaagacagccagcagccgctaaaaagagactcaatttgggt cagactggcgactcagatcagtcagtcctccgacccacaacctctcggaacacctccagcaacccccgc tctgtgggactactacaatggttcagcgggtggcgccaccaatggcaGCCAataacgaagg cgccgacggagtggttaatgcctcaggaaattggcattgcgattccacatggctggcgacagagtc catcaccaccagcaccgaaatgggcttgcacacataacaaccacctctacaagcaaatctcc

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60	AAV-DJ_A70R	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSD RGLVLPGYKYLGPFNGLDKGEPVNEADRAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPDQPIGEPPAAPSGVGSLTMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDNRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGILT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL
61	AAV-DJ_A70R_D21 3A	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSD RGLVLPGYKYLGPFNGLDKGEPVNEADRAALEHDKAYDRQLD SGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL EPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR RLNFGQTGDADSVDPDQPIGEPPAAPSGVGSLTMAAGGGAPM AANNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTY NNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDNRFHCHFS RDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGKTIANNL TSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLT LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS YAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQGG PNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGATK YHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK NVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAATA DVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSP MGGFGLKHPPPQILIKNTVPADPPTTFNQSKLNSFITQYSTGQVS VEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYSE PRPIGTRYLTRNL
62	AAV_DJ_capsid 0-49	ATGGCAGCCGATGGATACCTTCCGGACTGGCTTGAGGACAC ACTGAGCGAAGGTATACGTCACTGGTGGAAATTGAAGCCGG GCCCCGCCGCCGAAGCCGGCTGAGCGTCATAAAGATGAT TCACGCGGGCTGGTTTTACCGGGG
63	AAV_DJ_capsid 24-73	CTGAAACCGGGCCCCGCCGCCGCGGAAACCGGCCGAACGTCA TAAAGATGATAGTCGTGGCCTTGACTGCCGGCTATAAAT ATCTGGGGCCGTTTAATGGTCTGGATAAAGGCCGAACCGGTT AATGAGGCAGATGCTGCAGCGCTT
64	AAV_DJ_capsid 48-97	GGATATAAATACTTAGGACCGTTTAATGGCTTAGACAAAGG CGAGCCGGTAAATGAAGCTGACGCGGCGGCGTTGGAACATG ATAAAGCGTATGATCGCCAGCTTGACAGCGGCGATAACCCG TACTTAAAGTATAATCATGCGGAT

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65	AAV_DJ_capsid 72-121	CTGGAACATGATAAAGCCTATGACCGTCAACTGGACAGTGGAGATAACCCGTATCTGAAATACAATCATGCAGACGCAGAATTCAAGAGCGCCTGAAAGAAGATACGTCATTTGGGGGAAATCTGGGACGTGCTGTGTCCAAGCG
66	AAV_DJ_capsid 96-145	GACGCGGAGTTTCAAGAGCGCCTGAAAGAAGATACAAGTTTCGGAGGAAATCTGGGTCTGTGCGGTATTCCAGGCCAAAAAACGTCTGCTGGAGCCGCTGGGGCTTGTTGAAGAAGCAGCGAAAACAGCGCCGGGCAAAAAACGCCCG
67	AAV_DJ_capsid 120-169	GCTAAAAAACCGCTGCTTGAACCGTTAGGCCTGGTCGAGGAGGCAGCGAAGACTGCACCGGGTAAAAAACGTCCGGTAGAGCATAGTCCGGTGGAACCGGATTCTAGCAGTGGCACGGGCAAGCGGGCCAGCAGCCGGCCCGTAAA
68	AAV_DJ_capsid 144-193	CCGGTGGAACATTACCGGTGGAGCCGGAATCTAGTAGCGGAACCGGCAAAAGCTGGCCAACAACCGGCCCGCAAGCGTTTGAATTTCCGGCCAGACCGGCGATGCGGATAGCGTTCCGGACCCGCAACCGATCGGTGAGCCGCCGGCT
69	AAV_DJ_capsid 168-217	AAACGTCTGAACCTCGGACAGACTGGCGATGCTGATTCTGTACCGGATCCGCAGCCGATTGGCGAACCGCCGGCAGCCCCGTGAGGAGTCGGGTCACTTAATATGGCTGCCGGCGGAGGGGCTCCGATGGCCGATAACAATGAAGGC
70	AAV_DJ_capsid 192-241	GCCGCCCGTCTGGTGTAGGAAGTTTGACAATGGCGGCGGGCGGCGGCGCTCCGATGGCGGATAATAACGAAGGTGCGGATGTGTAGGAAATTCAAGTGTAATTGGCATTGCGATTCTACATGGATGGGCGATCGTGTGATTACA
71	AAV_DJ_capsid 216-265	GGCGCTGATGGTGTGGCAATTCTAGTGGCAATTGGCATTGTGACAGCACTTGGATGGGTGACCGTGTCACTTACCACCTCAACCCGCACTTGGGCCCTGCCGACTTATAATAATCATTTATATAAACAGATTAGTAATAGTACAAGT
72	AAV_DJ_capsid 240-289	ACAACCTCAACACGCACATGGGCACTGCCGACTTACAACAACTATTTATACAAACAAATCTCAAACCTCTACGAGTGGCGGATCTAGCAATGATAACGCGTATTTCCGGTTATAGTACCCCGTGGGGTTACTTTGACTTCAATCGCTTT
73	AAV_DJ_capsid 264-313	AGTGGAGGCTCAAGTAACGATAACGCATATTTCCGGCTATAGTACGCCGTGGGGCTATTTTGATTTTAACCGTTTTTCATTGTTCATTTTCTCCGCGGACTGGCAGCGCTTAATTAACAACAATTGGGGTTCCGCCCGAAACGTTTA
74	AAV_DJ_capsid 288-337	TTCCATTGTCACTTTAGTCCGCGTGACTGGCAGCGTTTAATCAATAATAACTGGGGTTTTTCGTCCGAAGCGTCTGTCAATCAAAATTTTAATATTCAGGTGAAAGAAGTCACGCAGCAATGAAGGCACAAAAACCATTGCCAATAAC
75	AAV_DJ_capsid 312-361	TTGAGTTTCAAACCTTTTAATATCCAGGTTAAAGAAGTCACACAGAATGAAGGTACAAAAACCATTGCAACAACCTGACCTCTACGATCCAGGTCTTTACAGACAGTGAGTATCAGCTGCCGTATGTTTTAGGTTACGCCCATCAG
76	AAV_DJ_capsid 336-385	AACTTAACGAGCACTATTCAGGTATTTACGGATTCTGAATATCAGCTGCCGTATGTGTAGGTTACGCGATCAAGGCTGTTTGGCCCGTTTTCCGGCCGATGTCTTCATGATTCCGCAGTACGGAATACCTGACATTGAATAACGGT
77	AAV_DJ_capsid 360-409	CAGGGCTGCTTGCCGCCGTTTTCCGGCCGATGTTTTATGATCCGCAGTACGGCTATCTTACCTTAAATAATGGTTCTCAAGCAGTTGGGCGCTCATCTTCTATTGCTTGGAATATTTCCCGAGTCAAATGCTTCGTACCGGAAAC

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78	AAV_DJ_capsi d 384-433	GGCTCACAAGCCGTGGGCCGTTCTAGTTTTATTGTCTGGAA TACTTTCCGAGCCAGATGTTACGCACCGGTAATAACTTTCAG TTTACATACACCTTTGAAGATGTCCCGTTTCATTCATCTTATG CCCATAGCCAGTCTCTGGAT
79	AAV_DJ_capsi d 408-457	AATAACTTTCAATTTACGTATACCTTCGAAGATGTACCGTTC CATAGCAGTTATGCGCATTCTCAGTCTTTGGATCGTTTAATG AATCCGTTGATCGACCAATACCTGTATTATCTGTACGCACG CAGACAACGGGGGGAACACTACA
80	AAV_DJ_capsi d 432-481	GACCGCTGATGAACCCGTTGATCGACCAATACCTGTATTAT TTGAGCCGTACACAGACTACCGGCGGGACGACAAATACTCA GACCTTGGGCTTTTACAGGGTGGCCCGAATACGATGGCAA ATCAAGCCAAGAATTGGCTGCCG
81	AAV_DJ_capsi d 456-505	ACAAACACACAGACTTTGGGATTTTCTCAGGGCGGTCCGAA TACTATGGCCAATCAGGCGAAAAATTGGTTGCCGGGTCCGT GTTACCGCCAGCAACGTGTTTCAAAGACATCTCGGATAAC AATAATAGTGAGTATTCTTGGACC
82	AAV_DJ_capsi d 480-529	CCGGGCCCGTGCTACCGTCAGCAGCGTGTGTCTAAAACATC AGCCGATAATAATAATAGCGAATACAGTTGGACCGGAGCCA CCAAATACCATCTTAACGGTCGCGATTCTTTAGTTAACCCGG GCCCGCGATGGCAAGCCATAAG
83	AAV_DJ_capsi d 504-553	ACTGGTGCCACAAAATACCATTGGAATGGGCGTGACAGCTT GGTCAACCCGGGCCCGGCCATGGCTAGTCATAAGGACGATG AAGAAAAATTCTTTCCGCAAAGCGGAGTGTTAATTTTGA AAACAAGGTTTCAGAAAAACTAAT
84	AAV_DJ_capsi d 528-577	AAAGATGATGAAGAAAAGTTTTTCCGCAGAGTGGGGTTCT TATCTTCGGGAAACAGGGAAGCGAAAAAGACAAACGTTGATA TAGAAAAAGTGATGATTACCGACGAAGAAGAGATTCTGACG ACTAACCCGGTGGCAACTGAGCAG
85	AAV_DJ_capsi d 552-601	AATGTAGACATCGAAAAAGTAATGATCACTGATGAAGAGGA AATTCGCACGACCAATCCGGTAGCTACCGAACAATACGGTA GCGTGTCAACTAATCTGCAGCGCGGTAATCGCCAGGCTGCT ACTGCAGATGTGAATACACAGGGA
86	AAV_DJ_capsi d 576-625	CAGTATGGTAGTGTTAGCACAAATCTGCAGCGTGGCAATCG CCAGGCCGCAACGGCAGATGTTAATACTCAGGGCGTGCTGC CGGGTATGGTTTGGCAAGATCGCGACGTGTATTACAGGGT CCGATTTGGGCCAAAATCCCGCAT
87	AAV_DJ_capsi d 600-649	GGAGTTTACCGGGCATGGTGTGGCAAGATCGTGATGTCTA CCTGCAGGGCCCGATATGGGCCAAGATCCCGCATACGGATG GTCATTTCCATCCGAGCCCGCTTATGGGTGGGTTTGGTTTAA AACATCCGCCCGCCGACAGATTTTG
88	AAV_DJ_capsi d 624-673	CATACCGATGGACATTTTCATCCGAGCCCGTTAATGGGTGGT TTTGGTTTGAAGCATCCGCCGCCGACAGATTAATTAATAAAT ACCCCGGTTCCGGCGGACCCGCCGACGACCTTCAATCAGTC AAAACCTGAATAGCTTCATAACG
89	AAV_DJ_capsi d 648-697	CTGATTAAAAACACACCGGTACCGGCAGATCCGCCGACCAC CTTCAACCAATCTAAGCTGAACCTTTTATCACACAGTACTC TACGGGGCAAGTTAGTGTTGAAATTGAGTGGGAGCTTCAAA AAGAAAATTCTAAACGTTGGAAT
90	AAV_DJ_capsi d 672-721	ACCCAGTATAGCACCGGTCAGGTTAGTGTTGGAGATTGAGTG GGAGTTACAAAAAGAGAACTCAAAGCGTTGGAATCCGGAA ATACAATATACATCAAATTATTACAAATCAACCTCAGTCGAT TTTGCTGTAAATACAGAGGGCGTA

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91	AAV1_capsid 0-49	ATGGCAGCAGATGGCTATCTTCCGGATTGGCTTGAAGATAA TCTTAGCGAAGGTATTTCGCGAATGGTGGGATTGAAACCGG GGGCACCGAAACCGAAAGCAAATCAGCAGAAACAGGATGA TGGTCGTGGACTGGTTCTTCCGGGC
92	AAV1_capsid 24-73	CTGAAACCGGGAGCTCCGAAACCGAAAGCCAATCAGCAAA AACAAGATGATGGCCGTGGCCTTGTGCTTCCGGGGTATAAA TATTTAGGCCCGTTTAACGGTTTAGACAAAGGCGAACCGGT CAATGCTGCAGATGCCGCAGCACTG
93	AAV1_capsid 48-97	GGGTATAAATATTTGGGACCGTTTAACGGCCTGGACAAAGG CGAACCGGTGAACCGCGCTGATGCAGCGGCTCTTGAGCATG ATAAAGCGTACGATCAGCAATTAAGGCTGGCGATAATCCG TACTTACGTTACAATCATGCTGAT
94	AAV1_capsid 72-121	CTGGAACATGACAAGGCGTACGACCAACAGCTGAAAGCAG GAGATAATCCGTACCTTCGCTATAATCATGCTGACGCGGAA TTTCAGGAACGTCTGCAGGAGGATACGAGTTTGGGGGCAA TCTGGGTCGCGCGGTGTTTCAGGCT
95	AAV1_capsid 96-145	GATGCAGAGTTTCAAGAGCGTTTACAAGAAGATACCAGCTT TGGCGGTAATCTGGGTCTGCGGTGTTTCAGGCCAAAAAAC GCGTICTGGAACCGCTGGGATTGGTTGAGGAAGGGGCTAAA ACCGCGCCGGGTAAAAAACGTCCG
96	AAV1_capsid 120-169	GCCAAAAAGCGCTACTGGAACCGCTGGGACTTGTGAAGA AGGCGCTAAAACTGCACCGGGTAAAAAGCGCCCGGTGCAAC AAAGTCCGCAGGAACCGGATAGCTCAAGTGGCATTGGTAAG ACTGGTCAGCAGCCGGCCAAGAAA
97	AAV1_capsid 144-193	CCGGTCGAACAATCACCGCAGGAACCGGACTCTTCTTCTGG AATAGGTAAAAACCGGACAGCAGCCGGCAAAGAAACGTCTT AACTTTGGTCAAACAGGGGATAGCGAAAGCGTGCCGGATCC GCAACCGTTGGGCGAACCGCCGGCT
98	AAV1_capsid 168-217	AAACGCCTTAACCTTTGGTCAAACCGGTGACAGCGAAAGCGT GCCGGACCCGCAACCGCTGGGGGAACCGCCGGCAACCCCGG CCGCGGTAGGCCCCGACAACAATGGCTAGTGGCGGTGGTGCT CCGATGGCGGATAATAATGAAGGC
99	AAV1_capsid 192-241	GCTACGCCGGCAGCAGTTGGCCCCGACGACGATGGCATCTGG CGGTGGAGCACCGATGGCCGACAATAACGAAGGGGCGGAT GGAGTTGGCAATGCTTCAGGCAACTGGCATTGTGACTCAAC ATGGTTGGGAGACCGCGTTATCACT
100	AAV1_capsid 216-265	GGAGCGGACGGTGTGGGCAATGCGAGCGGTAATTGGCATTG TGATAGTACATGGCTGGGCGATCGTGTTATCACAACATCTAC ACGCACATGGGCTCTTCCGACATATAACAACCATCTGTACA AACAGATCTCAAGTGCTAGCACT
101	AAV1_capsid 240-289	ACAACGAGTACCCGTACATGGGCGCTGCCGACGTATAACAA TCATCTTTACAAACAGATAAGTAGCGCTTCAACAGGGGCAA GCAACGACAACCATTACTTCGGTTACAGTACGCCGTGGGGT TACTTTGATTTTAACCGTTTTTCAT
102	AAV1_capsid 264-313	ACTGGTGCTTCAAACGACAATCATTATTTTGGCTACTCTACC CCGTGGGGTTACTTTGACTTCAACCGTTTTTCATTGTCATTTA GTCCGCGTGACTGGCAACGTTTGATTAACAACAATTGGGGC TTTCGCCCCGAAACGTTTGAAC
103	AAV1_capsid 288-337	CATTGTCAATTTTACCAGCGTGACTGGCAGCGCCTGATAAAT AACAAATTGGGGTTTCCGTCCGAAACGCCTTAATTTCAAACGTG TTTAATATCCAGGTAAAGGAAGTGACAACCAACGATGGCGT GACTACTATCGCCAATAATTTA

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104	AAV1_capsid 3 12-361	AATTTTAAACTGTTTAAACATTCAAGTGAAGGAAGTCACGAC AAATGACGGGGTCACAACTATCGCAAATAAAGTACGTCTA CGGTTTCAGGTCTTTAGTGATTCTGAATACCAGTTGCCGTACG TTCTTGGTAGCGCTCATCAGGGC
105	AAV1_capsid 3 36-385	TTAACCAGTACTGTACAGGTTTTCAGACTCTGAATACCAA CTTCCGTATGTCCTGGGTAGCGCACATCAGGGGTGCCTGCCG CCGTTTCCGGCCGATGTGTTTCATGATTCCGCAGTACGGATAT CTGACACTTAACAACGGTTCA
106	AAV1_capsid 3 60-409	GGGTGTTTGCCGCCGTTCCCGGCGGACGTGTTTATGATCCCG CAGTATGGATATCTGACTCTTAATAATGGATCTCAGGCCGTG GGTCGTAGCAGCTTTTATTGTCCTGAATATTTCCGTCTCAG ATGCTGCGCACAGGTAATAAC
107	AAV1_capsid 3 84-433	TCTCAGGCGGTTGGCCGTTTCATCATTTTACTGCCTTGAATAC TTTCCGAGTCAAATGCTGCGCACGGGAAACAACCTTACCTTT AGCTACACATTTGAGGAGGTTCCGTTTCATTCTTCATATGCT CATAGCCAGAGTTTGATCGT
108	AAV1_capsid 4 08-457	AATTTTACCTTTAGTTATACTTTTGAAGAAGTGCCGTTTCATT CAAGTTATGCTCATTACAGTCTCTGGATCGTCTGATGAACC CGCTTATCGACCAGTATCTGTATTATTTGAATCGTACTCAGA ATCAGTCAGGCAGTGCGCAG
109	AAV1_capsid 4 32-481	CGTCTGATGAACCCGCTGATTGATCAGTATTTATATTATCTG AACCGTACCCAAAATCAGAGCGGGAGTGCCCAAAATAAGG ACCTTCTGTTTAGTCGTGGTTACCCGGCAGGGATGTCAGTCC AGCCGAAGAATTGGCTGCCGGGG
110	AAV1_capsid 4 56-505	CAAAATAAAGATCTTCTTTTCTCACGCGGAAGCCCGGCCGG TATGTCTGTGCAACCGAAGAAGTGGCTGCCGGGGCCCGTGT ACCGTCAGCAGCGTGTGTCAAAACTAAAACAGATAATAAT AATAGTAATTTACCTGGACAGGA
111	AAV1_capsid 4 80-529	GGTCCGTGTTACCGCCAGCAACGCGTCTCTAAACTAAGAC AGACAACAATAATAGTAACTTTACCTGGACCGGCGCATCAA AATATAACTTAAATGGTCGTGAGAGCATAATAAATCCGGGA ACAGCAATGGCATCACATAAAGAT
112	AAV1_capsid 5 04-553	GGCGCTAGTAAATATAACCTGAATGGTCGCGAGTCAATTAT AAATCCGGGGACCGCGATGGCGTCACATAAGGATGATGAAG ATAAATTTTTTCCGATGTCTGGCGTGATGATTTTCGGAAG AAAGTGCCGGTGCTAGCAATACG
113	AAV1_capsid 5 28-577	GACGACGAAGATAAAATTTTCCCGATGAGCGGAGTGATGAT TTTCGGGAAAGAAAGCGCAGGTGCAAGTAACACTGCACTGG ATAATGTCATGATTACGGACGAAGAAGAAATTAAGCCACA AACCCGGTGGCAACCGAGCGCTTC
114	AAV1_capsid 5 52-601	ACCGCCCTTGACAACGTTATGATTACTGACGAAGAGGAAAT AAAAGCGACCAATCCGGTTGCAACAGAACGTTTTGGGACGG TCGCAGTCAATTTCCAAAGCTCAAGTACAGATCCGCGACC GGAGACGTACATGCAATGGGTGCT
115	AAV1_capsid 5 76-625	TTTGGCACAGTCGCGGTTAATTTCCAGAGCAGCTCAACGGA TCCGGCCACGGGAGATGTACATGCCATGGGGGCATTACCGG GTATGGTCTGGCAAGATCGTGATGTATATCTTCAGGGGCCG ATCTGGGCAAGATCCCGCATACT
116	AAV1_capsid 6 00-649	GCACTGCCGGGCATGGTGTGGCAGGATCGTGATGTCTATTT GCAGGGTCCGATCTGGGCTAAAATACCGCATACTGATGGCC ATTTCCATCCGAGTCCGCTTATGGGCGGTTTCGGCCTTAAAA ATCCGCCGCCGAGATACTGATA

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117	AAV1_capsid 6 24-673	ACCGATGGACATTTTCATCCGAGCCCGCTGATGGGTGGCTTC GGATTGAAAAATCCGCCGCCGCAAATCTTGATCAAAAACAC ACCGGTTCCGGCCAATCCGCCGGCTGAATTTAGCGCTACGA AATTTGCGTCATTACGCAA
118	AAV1_capsid 6 48-697	ATCAAAAATACTCCGGTGCCGGCGAATCCGCCGGCGGAGTT TTCAGCGACTAAATTTGCGAGTTTATAACACAGTATTCAAC GGGACAAGTAAGTGTGAAATAGAGTGGGAACTTCAGAAA GAAAATAGCAAGCGTTGGAATCCG
119	AAV1_capsid 6 72-721	CAGTATAGCACTGGGCAGGTCTCTGTGCGAGATTGAATGGGA ACTTCAGAAAGAAAACTCTAAACGTTGGAATCCGGAGGTAC AATATACATCTAATTATGCTAAATCTGCAAATGTTGATTTTA CAGTCGACAACAATGGGTTGTAT
120	AAV2_capsid 0 -49	ATGGCGGCCGATGGTTACCTGCCGATTGGCTTGAAGATAC GTTAAGCGAAGGTATTGCCAGTGGTGGAACTGAAACCGG GTCCGCCGCCGCCGAAACCGGCTGAGCGCCATAAAGATGAC AGTCGCGGGCTGGTTTGGCCGGGA
121	AAV2_capsid 2 4-73	CTGAAGCCGGGACCGCCGCCGCGGAAACCGGCTGAACGTCA TAAAGATGATAGCCGTGGTCTGGTTCTCCGGGCTATAAATA TTTAGGCCCGTTTAAACGGTCTGGACAAGGGTGAACCGGTCA ATGAGGCTGATGCCGCAGCGCTG
122	AAV2_capsid 4 8-97	GGGTACAAATATCTGGGACCGTTCAACGGTCTGGATAAAGG GGAACCGGTTAACGAAGCCGACGCAGCCGCCCTTGAACATG ATAAAGCGTATGATCGCCAACTGGACTCAGGCGATAATCCG TACCTTAAGTATAATCATGCGGAT
123	AAV2_capsid 7 2-121	TTAGAGCATGACAAAGCGTATGATCGCCAGTTAGACAGCGG TGATAATCCGTATCTGAAATATAATCATGCCGATGCTGAATT TCAGGAACGTCTTAAAGAAGATACGAGCTTCGGAGGTAATC TGGGACGCGCAGTATTCAAGCA
124	AAV2_capsid 9 6-145	GATGCAGAAATTCAGGAGCGTCTTAAGGAGGACACGTCTTT TGGCGGTAACCTTGGTCGCGCCGTATTCCAAGCTAAAAAAC GCGTGCTGGAGCCGTTAGGCCTTGTAGAAGAACCGGTTAAA ACCGCACCGGGCAAAAAGCGTCCG
125	AAV2_capsid 1 20-169	GCGAAAAAACGCGTGCTGGAACCGCTGGGCTTGGTCAAGA GCCGGTGAAGACGGCCCCGGGTAAAAAGCGTCCGGTGGAG CATAGTCCGGTGAACCGGACTCTTCATCTGGAACGGGTAA AGCTGCTCAGCAGCCGGCCCGTAAA
126	AAV2_capsid 1 44-193	CCGGTGAACATTCTCCGGTGGAGCCGGACTCAAGCTCTGG GACCGGAAAAAGCGGGGCAACAGCCGGCTCGCAAACGTTTA AACTTCGGTCAAACCGGCGACGCGGATAGCGTGCCGGATCC GCAGCCGCTTGGCCAGCCGCCGGCT
127	AAV2_capsid 1 68-217	AAACGCCTGAATTTCCGGTCAGACCGGTGATGCTGATTCAGT ACCGGATCCGCAACCGCTGGGTGAGCCGCCGGCAGCGCCGT CTGGCTTAGGTACAAATACCATGGCAACGGGTAGCGGGGCC CCGATGGCGGATAATAATGAAGGC
128	AAV2_capsid 1 92-241	GCAGCCCCGTCAGGATTAGGCACAAATACGATGGCGACAGG TAGTGGTGACCGATGGCCGATAATAATGAAGGTGCGGATG GGGTGGGAAATAGCTCTGGAATTTGGCATTGTGATTCAACT TGGATGGGAGACCGTGTTATTACA
129	AAV2_capsid 2 16-265	GGCGCAGACGAGTAGGCAATAGTTCAGGGAACTGGCATTG CGACAGCACGTGGATGGGAGATCGTGTCATTACCACGTCAA CGCGACCTGGGCGCTGCCGACTTACAATAACCATCTGTAT AAACAAATATCAAGCCAGTCAGGA

SEQ ID NO:	Name	Sequence
130	AAV2_capsid 2 40-289	ACAACGAGCACGCGTACTTGGGCGTTACCGACCTATAATAA CCATTTGTATAAGCAGATTTTCATCTCAGAGCGGAGCTAGCA ACGATAATCATTATTTTGGTTATAGTACACCGTGGGGTTATT TCGATTTTAATCGCTTCCATTGT
131	AAV2_capsid 2 64-313	GGTGCATCAAATGACAATCATTATTTCCGATATAGCACACC GTGGGGTACTTTGATTTTAACCGTTTTCATTGTCAATTTTCT CCGCGCGACTGGCAACGTCTGATCAATAACAATTGGGGATT TCGTCCGAAACGTTTGAATTTT
132	AAV2_capsid 2 88-337	TGTCATTTCTCACCGCGTGATTGGCAACGTTTAATAAACAAT AACTGGGGGTTCCGTCCGAAGCGTCTGAATTTCAAGCTGTTC AATATCCAAGTTAAAGAAGTGACCCAAAACGATGGCACAAC CACAATCGCAAACAATCTGACA
133	AAV2_capsid 3 12-361	TTTAAACTGTTTAATATCCAGGTCAAAGAAGTAACCTAGAA TGATGGCACAACAACCATTTGCTAATAATCTGACCTCTACGGT GCAGGTGTTTACCGATTCTGAATATCAACTTCCGTACGTTCT GGTTCGTGCCCATCAAGGCTGT
134	AAV2_capsid 3 36-385	ACCAGTACTGTCCAGGTGTTTACAGATAGCGAGTACCAATT GCCGTATGTATTGGGTAGTGCCCATCAGGGATGCCTTCCGCC GTTTCCGGCCGATGTAATCATGGTTCGCAATACGGTTATCT GACGTTGAACAACGGTTCTCAA
135	AAV2_capsid 3 60-409	TGTCTGCCGCCGTTTCCGGCGGACGTCTTCATGGTCCGCAG TATGGCTATCTGACGCTGAATAACGGCAGCCAGGCCGTCGG CCGCAGTTCATTTATTGCTTGAATATTTTCCGAGTCAAAAT GCTGCGCACAGGGAATAACTTT
136	AAV2_capsid 3 84-433	CAAGCAGTTGGACGCAGTAGTTTTTACTGTCTGGAATACTTT CCGAGTCAGATGTTACGCACAGGTAACAACCTTTACCTTTTCT TACACGTTTCAAGATGTGCCGTTTCATTCATCATACGCACAT TCACAGAGCCTGGATCGTTTG
137	AAV2_capsid 4 08-457	TTTACTTTTGTATATACATTTGAAGATGTCCCGTTCCATTCTA GTTATGCTCATTCTCAGTCTCTGGATCGTCTGATGAACCCGT TAATCGACCAGTACCTGTACTATTTGAGCCGCACCAACACCC CGAGTGGTACGACCACCCAG
138	AAV2_capsid 4 32-481	CTGATGAATCCGCTGATTGATCAATATTTATATTATCTGAGC CGTACTAACACCCCGAGCGGTACCACTACGCAGTCTCGTCT GCAGTTTAGCCAGGCGGGAGCATCAGATATACGCGATCAGA GTCCGAACTGGCTGCCGGGTCCG
139	AAV2_capsid 4 56-505	CAATCACGTTTGCAGTTTCTCAGGCAGGGGCTTCAGATATA CGCGATCAAAGCCGTAATTGGTTGCCGGGCCCGTGCTATCG TCAGCAGCGTGTGTCAAAAACCAGCGCAGATAATAATAATA GCGAATACTCATGGACCGGCGCT
140	AAV2_capsid 4 80-529	CCGTGCTACCGCCAACAACGTGTGTCAAAAACCAGCGCGGA TAATAATAATAGTGAATATTCATGGACTGGTGCGACCAAAAT ATCATCTGAATGGACGTGATAGTCTGGTCAACCCGGGACCG GCCATGGCTAGCCATAAAGACGAC
141	AAV2_capsid 5 04-553	GCTACAAAATATCATCTGAACGGGCGTGACTCTTTGGTGAA TCCGGGACCGGCCATGGCATCTCATAAAGACGACGAAGAGA AATTCTTTCCGCAAAGCGGCGTGCTGATATTTGGAACACAG GGCTCTGAGAAAAACAATGTGGAC
142	AAV2_capsid 5 28-577	GACGAAGAAAAGTTTTTCCGCAGTCTGGTGTATTGATCTTC GGGAAACAGGGTCTGAAAAAACCAACGTTGATATCGAAAA AGTTATGATCACCGATGAAGAAGAAATTCGTACCACGAATC CGGTTGCAACAGAGCAGTACGGA

SEQ ID NO:	Name	Sequence
143	AAV2_capsid 5 52-601	GATATCGAAAAAGTGATGATAACAGACGAGGAAGAAATTC GCACCACCAACCCGGTAGCCACTGAACAGTACGGTTCAGTG TCTACGAATCTGCAGCGCGGTAACCGTCAGGCCGCAACAGC AGATGTTAATACGCAGGGGGTCTCTG
144	AAV2_capsid 5 76-625	GGCAGCGTTAGCACC AATTTACAGCGCGGTAACCGCCAGGC AGCGACGGCGGATGTAAATACGCAAGGAGTATTGCCGGGTA TGGTATGGCAGGATCGCGATGTTTACCTGCAGGGACCGATT TGGGCGAAAAATTCGCATACAGAT
145	AAV2_capsid 6 00-649	TTGCCGGGCATGGTGTGGCAGGACCGTGATGTATACCTGCA GGGTCCGATTTGGGCGAAGATTCCGCATACCGATGGTCATTT TCATCCGAGTCCGCTGATGGGAGGCTTTGGCTTGAAACATCC GCCGCCGAGATTTTGATTAAT
146	AAV2_capsid 6 24-673	GATGGTCATTTTCATCCGAGCCCGTTAATGGGAGGCTTTGGC CTTAAACATCCGCCGCCGAGATCCTTATAAAAAATACCCC GGTACCGGCAAATCCGAGCACAACTTCTCTGCTGCGAAGT TTGCAAGTTTTATTACCCAATAT
147	AAV2_capsid 6 48-697	AAGAATACGCCGGTACCGGCTAACCCGAGCAGACTTTCTC AGCAGCCA AATTTGCAAGTTTTATCACC AATACTCTACTGG CCAAGTCTCAGTTGAGATTGAATGGGAGCTGCAAAAAGAGA ACTCAAAACGTTGGAACCCGGAA
148	AAV2_capsid 6 72-721	TATAGTACTGGACAGGTGAGTGTAGAAATAGAATGGGAGCT TCAAAAGGAGAATAGCAACGTTGGAACCCGGAAATACAG TATACATCTAATTATAATAAAAGCGTGAATGTTGATTTACCC GTTGACACTAACGGGGTGATAGT
149	AAV3_capsid 0 -49	ATGGCCGCTGACGGCTACTTGCCGGACTGGCTTGAAAGATAA TCTGTGAGAAGGTATTCGTGAATGGTGGGCGCTGAAACCGG GCGTACCGCAACCGAAAGCTAATCAGCAGCATCAGGATAAT CGTCGTGGTCTGTTCTGCCGGGC
150	AAV3_capsid 2 4-73	CTTAAACCGGGTGTAACCGCAACCGAAAGCAAACCAGCAACA TCAAGATAACCGTCGCGGCTTGGTTTTACCGGGATACAAGT ATCTGGGTCCGGGTAATGGTTTGGACAAAGGCGAACCGGTT AATGAAGCTGATGCTGCGGCTCTG
151	AAV3_capsid 4 8-97	GGCTATAAATACCTTGGTCCGGGTAACGGGCTGGACAAGGG AGAGCCGGTAAACGAAGCGGATGCTGCAGCACTGGAGCAT GACAAGGCTTACGATCAGCAGCTGAAGGCCGGTGATAACCC GTACTTGAAATATAATCATGCCGAC
152	AAV3_capsid 7 2-121	CTGGAACATGATAAAGCATAACGACCAACAACCTGAAAGCAG GCGACAACCCGTACCTTAAATACAACCATGCAGATGCGGAG TTTCAGGAACGCTTGCAAGAAGACACATCTTTTGAGGAGAA TCTGGGTCTGTCAGTCTTTCAGGCA
153	AAV3_capsid 9 6-145	GACGCGGAATTTCAAGAACGTCTGCAGGAGGATACTAGCTT TGGCGGGAACCTTAGGTGCGCAGTTTTCCAAGCAAAAAAGC GCATTTTAGAACC GTTGGGTTT AGTTGAAGAAGCTGCAAAA ACCGCCCCGGGTAAAAAAGGTGCG
154	AAV3_capsid 1 20-169	GCGAAGAAGCGTATACTGGAACCGCTGGGGTTAGTGGAAGA AGCAGCAAAGACCGCCCCGGGTAAAAAAGGAGCAGTAGAT CAATCTCCGCAAGAACCGGATTCTCTAGTGGAGTCGGCAA AAGCGGTAAACAGCCGCGCGTAAA
155	AAV3_capsid 1 44-193	GCAGTCGATCAGTCACCGCAAGAGCCGGATTCAAGTTCAGG AGTGGGAAAAAGTGGGAAGCAACCGGCTCGCAACGTTCTG AATTTTGGGCAGACAGGTGATTCTGAAAGTGTCCCGGACCC GCAGCCGTTGGGAGAACCGCCGGCG

SEQ ID NO:	Name	Sequence
156	AAV3_capsid 1 68-217	AAGCGTCTTAACCTTTGGTCAGACCGGTGATAGTGAATCAGT CCCGGACCCGACGCCGCTGGGCGAGCCGCCGGCTGCCCCGA CGAGTCTGGGTTCTAATACAATGGCTTCAGGTGGCGGTGCC CCGATGGCTGATAATAACGAGGGT
157	AAV3_capsid 1 92-241	GCGGCACCGACCTCATTAGGTAGTAATACTATGGCATCAGG GGGTGGTGCCCCGATGGCTGACAACAATGAGGGCGCCGACG GGGTGGAAATAGTTCAGGTAAGTGGCATTGCGACAGCCAG TGGCTGGGAGACCGCGTGATCACT
158	AAV3_capsid 2 16-265	GGCGCCGATGGTGTTGGTAACTCAAGTGGAAACTGGCATTG TGATAGTCAATGGCTTGGGGATCGTGTGATTACTACGAGTA CTCGCACCTGGGCGTTGCCGACCTACAACAATCATTTATATA AGCAGATAAGCAGCCAGAGTGGA
159	AAV3_capsid 2 40-289	ACCACATCTACACGCACATGGGCGCTGCCGACGTACAACAA TCATCTGTATAAACAGATCAGCAGCCAGAGTGGCGCCTCTA ATGACAATCATTATTTTCGGATATTCAACCCCGTGGGGATATT TCGATTTTAATCGCTTCCATTGT
160	AAV3_capsid 2 64-313	GGCGCTAGTAACGATAACCATTACTTTGGTTATTCTACCCCG TGGGGATATTTTCGACTTCAACCGTTTTCATTGTCAATTTAGC CCGCGTGATTGGCAGCGCCTGATCAATAATAATTGGGGGTT TCGTCCGAAAAAGTTGAGCTTC
161	AAV3_capsid 2 88-337	TGCCATTTCAGCCCGCGCGACTGGCAGCGTTTAATAAATAA CAACTGGGGTTTTTCGTCCGAAGAACTGAGTTTCAAGTTATT CAACATTCAGGTGCGTGGTGTTACTCAGAACGACGGGACGA CCACCATAGCAAATAACCTGACC
162	AAV3_capsid 3 12-361	TTTAAACTGTTTAATATCCAGGTGCGCGGCGTGACGCAGAA CGATGGAACCACAACCATTGCAAATAACCTGACCTCTACGG TCCAGGTGTTACCGGATTCTGAGTATCAACTTCCGTACGTTT TAGGATCTGCTCATCAGGGCTGT
163	AAV3_capsid 3 36-385	ACCTCTACGGTACAAGTATTTACAGATTCTGAGTACCAGCTT CCGTATGTGCTTGGCTCAGCGCATCAGGGGTGCGTGCCGCC GTTTCCGGCTGATGTGTTTATGTTGCGCAGTACGGCTACTT AACCTGAACAACGGTAGCCAA
164	AAV3_capsid 3 60-409	TGCTTACCGCCGTTTCCGGCAGACGTTTTTATGGTCCGCAA TATGGCTATCTGACTCTGAATAATGGATCACAGGCAGTCGG ACGCAGTTCATTTTATGCTTGAGTACTTTCCGTCTCAGAT GTTACGCACTGGGAATAACTTC
165	AAV3_capsid 3 84-433	CAAGCGGTTGGGCGCAGCTCTTTCTATTGCCTGGAGTATTTT CCGAGTCAAATGTTGCGTACTGGTAACAACCTCCAGTTCTCT TATACCTTTGAAGATGTTCCGTTTCATTCTTCATACGCCATT CACAGTCTCTGGATCGCTTG
166	AAV3_capsid 4 08-457	TTCCAGTTCTCATATACCTTTGAGGACGTTCCGTTTCATTCAT CATATGCACATTACAATCACTGGACCGCCTGATGAACCCG CTGATCGACCAGTATCTTTACTACCTGAATCGACCCAGGGT ACAACATCAGGAACCACGAAC
167	AAV3_capsid 4 32-481	TTGATGAATCCGCTGATTGATCAGTACTTGTATTATCTGAAT CGTACTCAGGGCAGGACGACGCGGCACAACAACAGAGTCG TTTGCTGTTTAGTCAGGCCGGTCCGCAGTCTATGAGTCTGCA GGCTCGTAATTGGTTGCCGGGT
168	AAV3_capsid 4 56-505	AATCAGTCTCGTCTGCTGTTTACGCCAGGCTGGCCCGCAGAGT ATGTCACTGCAGGCACGCAACTGGTTACCGGGTCCGTGTTAT CGCCAACAACGTCTTTCTAAAACAGCAAATGATAATAATAA CTCAAACCTCCCGTGGACGGCC

SEQ ID NO:	Name	Sequence
169	AAV3_capsid 4 80-529	GGTCCGTGCTATCGCCAACAGCGCTTGAGTAAAACTGCCAA CGACAATAACAATAGTAACCTTCCGTGGACGGCAGCCTCAA AATACCATTTGAACGGACGCGATAGTCTTGATAATCCGGGG CCGGCTATGGCAAGCCATAAGGAT
170	AAV3_capsid 5 04-553	GCAGCAAGTAAGTATCATCTTAATGGGCGTGATAGCCTTGT GAATCCGGGGCCCGGCAATGGCATCACATAAAGATGACGAGG AAAAGTTTTTTCCGATGCATGGCAATTTGATATTCGGAAAAAG AAGGTACAACCGCATCTAACGCG
171	AAV3_capsid 5 28-577	GATGATGAAGAGAAAATTTTTCCGATGCATGGCAATCTTATT TTCGGAAGGAAGGTACGACTGCCTCTAATGCTGAAGTGA CAATGTCATGATTACTGATGAAGAGGAAATCCGTACAACCA ACCCGGTTGCTACGGAGCAGTAC
172	AAV3_capsid 5 52-601	GCTGAACTGGACAATGTCATGATAACCGATGAGGAGGAAAT TCGCACCACGAATCCGGTTGCTACCGAACAGTATGGTACTG TAGCCAACAATCTGCAGAGCTCTAATACTGCGCCGACCACC GGAACCGTTAAACCATCAAGGTGCT
173	AAV3_capsid 5 76-625	TATGGAAGTGTGGCGAACAATTTACAGAGCAGTAACACCGC CCCGACAACAGGGACGGTCAACCATCAAGGGGGCCCTTCCGG GTATGGTCTGGCAGGACCGTGATGICTATTTCAGGGACCG ATCTGGGCGAAAAATTCCGCATACC
174	AAV3_capsid 6 00-649	GCCTTACCGGGCATGGTCTGGCAAGATCGTGATGTATTTA CAGGGGCCGATCTGGGCCAAAATTCCGCATACAGATGGGCA TTTTCATCCGAGCCCGTTGATGGGAGGGTTCGGACTGAAAC ATCCGCCGCCGAGATCATGATT
175	AAV3_capsid 6 24-673	ACGGACGGACATTTTCATCCGAGCCCGCTGATGGGAGGGTT CGGGCTGAAGCATCCGCCGCCGCAAATTATGATCAAGAATA CACCGGTACCGGCTAACCCGCCGACGACCTTAGCCCGGCG AAGTTCGCATCTTTCATCACCCAG
176	AAV3_capsid 6 48-697	ATAAAGAATACTCCGGTACCGGCAAAATCCGCCGACAACGTT TAGTCCGGCGAAGTTCGCGAGTTTTATTACCCAGTACAGCAC GGGCCAGGTGAGCGTTGAAATCGAATGGGAACTGCAGAAA GAAAAATTCAAACCGCTGGAATCCG
177	AAV3_capsid 6 72-721	CAATATAGTACTGGGCAGGTTAGTGTGGAGATAGAATGGGA GCTTCAGAAAGAAAATTCTAAACGCTGGAATCCGGAAATTC AGTACACTTCTAATTACAACAAATCAGTTAATGTGGATTTA CTGTGGATACCAATGGGGTCTAC
178	AAV4_capsid 0 -49	ATGACTGATGGATATTTACCGGATTGGTTAGAAGACAACCT GTCTGAAGGCGTTCGTGAATGGTGGGCATTACAACCGGGCG CTCCGAAACCGAAAGCTAACCAGCAGCATCAAGATAATGCT CGTGGTTTAGTTCTGCCGGGCTAT
179	AAV4_capsid 2 4-73	CAGCCGGGTGCACCGAAACCGAAGGCTAATCAGCAGCATCA GGATAACGCGCGTGGTCTGGTACTTCCGGGATACAAGTATT TAGGACCGGGTAACGGCCTTGACAAAGGCGAACCGGTGAAT GCGGCTGATGCCGCGGCACTGGAA
180	AAV4_capsid 4 8-97	TATAAGTATCTGGGGCCGGGGAACGGTTTGGACAAAGGGGA ACCGGTTAACGCAGCCGATGCTGCTGCGCTTGAACATGACA AAGCATACGATCAACAACCTGAAAGCTGGAGACAATCCGTAT CTTAAATATAATCATGCAGATGCT
181	AAV4_capsid 7 2-121	GAACATGATAAGGCCTATGACCAGCAGCTGAAAGCTGGTGA CAACCCGTACCTTAAATACAATCATGCCGACGACAGAGTTCC AGCAGCGTCTGCAGGGGGACACATTCGGGGGTAACCTT GGTCCGCCGGTCTTCCAGGCTAAG

SEQ ID NO:	Name	Sequence
182	AAV4_capsid 9 6-145	GCCGAGTTCCAACAACGCCTGCAAGGAGACACCTCTTTTGG GGGCAACCTGGGTGCGCGGTATTCCAAGCTAAAAACGCG TGTTAGAACCGCTTGGCTTAGTGGAACAGGCAGGGGAACT GCACCGGGAAGAAACGCCCGCTG
183	AAV4_capsid 1 20-169	AAAAAGCGCGTGCTGGAGCCGCTGGGGTTAGTTGAGCAAGC AGGCGAAACCGCCCCGGGCAAGAAACGTCCGCTGATAGAAT CACCGCAGCAGCCGGACAGCAGTACAGGGATAGGTAAGAA AGGTAAACAGCCGGCTAAAAA
184	AAV4_capsid 1 44-193	CTGATCGAATCACCGCAGCAGCCGGATAGCTCAACCGGGAT TGGAAAAAAGGGCAAACAGCCGGCCAAAAAAACTGGTC TTCGAAGACGAACTGGTGCTGGCGATGGCCCGCCGAGGG TAGCACATCTGGAGCTATGAGTGAT
185	AAV4_capsid 1 68-217	AAACTGGTGTTTCGAGGATGAAACCGGGGAGGTGACGGTCC GCCGGAAGGCTCAACGAGCGGAGCGATGTCTGATGATAGTG AAATGCGCGCTGCGGCAGGCGGAGCAGCAGTAGAAGGCGG ACAGGGGGCTGATGGTGTGGGTAAT
186	AAV4_capsid 1 92-241	GATGATTGAGAAATGCGCGCTGCGGCCGGGGGAGCTGT TGAGGGTGGCCAGGGTGCCGATGGCGTTGGGAATGCAAGTG GTGATTGGCATTGCGACTCAACTTGGTCAGAGGGTCATGTC ACGACTACAAGCACACGTAATTGG
187	AAV4_capsid 2 16-265	AATGCTTCTGGGGATTGGCATTGTGACTCAACGTGGAGTGA GGGCCATGTACAGACCACGAGTACCCGTACCTGGGTGCTTC CGACCTACAACAACCATCTGTACAAACGTCTGGGCGAGAGC CTGCAATCTAACACTTATAATGGT
188	AAV4_capsid 2 40-289	TGGGTACTGCCGACTTATAACAACCATTTATATAAACGTCTG GGCGAAAGTCTGCAGAGTAACACGTATAACGGTTTTAGCAC ACCGTGGGGTTATTTGATTTCATCGTTTTTCATTGCCATTT TCTCCGCGTGACTGGCAGCGT
189	AAV4_capsid 2 64-313	GGCTTTAGTACCCCGTGGGGTATTTTGACTTTAATCGTTTC CATTGCCATTTTAGTCCGCGCGACTGGCAGCGCTTAATAAAT AACAACCTGGGGATGCGCCGAAGGCTATGCGCGTGAAGAT CTTCAATATTCAGGTTAAAGAA
190	AAV4_capsid 2 88-337	CGCTTAATCAATAATAATTGGGGTATGCGTCCGAAGGCAAT GCGTGTTAAATTTTTAATATTCAGGTCAAAGAAGTGACAA CAAGCAATGGTGAAACTACAGTAGCGAATAATTTAACCTCT ACAGTCCAGATTTTTGCCGATTCT
191	AAV4_capsid 3 12-361	GAGGTAACCTACATCTAATGGAGAGACAACAGTTGCAAATAA CTTGACCAGCACCGTCCAAATTTTGCTGATTCTTATGA GTTGCCGTACGTGATGGATGCGGGACAAGAAGGGAGTCTGC CGCCGTTCCCGAACGATGTGTTT
192	AAV4_capsid 3 36-385	AGTTCATACGAACTTCCGTATGTTATGGATGCCGGTCAAGA GGGAAGTCTGCCGCGTTTCCGAATGACGTGTTTCATGGTACC GCAATATGGTTATTGCGGGCTGGTAACCGGTAACACAAGTC AGCAACAGACCGACCGTAACGCC
193	AAV4_capsid 3 60-409	TTTATGGTTCCGCACTACGGTTATTGTGGGCTGGTCACCGGT AATACTTCACAGCAACAGACTGACCGTAACGCATTTTACTGT TTAGAATATTTTCCGAGTCAGATGCTGCGTACAGGGAACAA CTTTGAAATAACATATAGTTTT
194	AAV4_capsid 3 84-433	GCTTTCTACTGTCTGGAATATTTTCCGAGTCAGATGCTTCGT ACAGGGAATAACTTCGAAATTACATATTTTCGAAAAAGT GCCGTTTCATTCTATGTACGCTCATAGTCAGTCTTTAGACCG CTTAATGAATCCGCTGATCGAC

SEQ ID NO:	Name	Sequence
195	AAV4_capsid 4 08-457	TTTGAAGAGGTGCCGTTTCATTCTATGTATGCCCATTCACAG AGCCTTGATCGTCTGATGAATCCGCTGATTGATCAATATCTG TGGGGGCTGCAATCTACTACTACTGGTACCACGCTGAATGC AGGTACGGCAACCACCAATTTT
196	AAV4_capsid 4 32-481	GACCAGTACCTGTGGGGTCTGCAGTCAACCACCACCGGAAC CACTCTGAATGCCGGGCACTGCGACTACGAATTTTACAAAAC TTCGTCCGACCAACTTTAGTAATTTTAAGAAAACTGGCTGC CGGGGCCGAGTATTAACAGCAG
197	AAV4_capsid 4 56-505	TTTACGAAATTACGTCCGACCAATTTCTCAAATTTCAAAAAA AACTGGTTGCCGGGACCGTCAATTAACAGCAGGGCTTCAG CAAGACTGCTAACCAAACTACAAAATTCCGGCGACCGGAT CTGATAGTCTGATCAAGTATGAA
198	AAV4_capsid 4 80-529	CAGGGATTTAGCAAAACCGCTAATCAAAATTATAAGATCCC GGCGACAGGGTCAGACTCTTTGATTAAGTACGAGACGCATA GCACCTTAGATGGCCGTTGGAGCGCTCTTACCCCGGGTCCGC CGATGGCAACCGCCGGTCCGGCA
199	AAV4_capsid 5 04-553	GAAACCCATAGTACATTGGATGGGCGTTGGTCTGCACTTAC GCCGGGCCCCCGGATGGCGACCGCGGGGCCCGCGATAGCA AGTTTTCAAACAGCCAGCTGATTTTIGCTGGCCCGAAACAG AATGGTAACACTGCTACCGTTCCG
200	AAV4_capsid 5 28-577	GCAGACAGTAAATCTCAAACAGCCAATTAATCTTTGCCGG CCCGAAAACAGAATGGAAATACAGCAACCGTACCGGGAACTC TGATCTTCACGAGTGAAGAGGAGTTGGCCGCGACCAATGCG ACAGACACGGATATGTGGGGAAAC
201	AAV4_capsid 5 52-601	CCGGGCACGCTGATCTTTACCAGCGAGGAAGAAGTGGCAGC CACGAACGCCACGGATACGGACATGTGGGGCAATCTGCCGG GGGGTGATCAGAGCAACTCAAATCTTCCGACCGTAGATCGT TTAACGGCTTTGGGCGCAGTTCCG
202	AAV4_capsid 5 76-625	AATCTGCCGGGAGGTGACCAGTCAAATAGCAATCTGCCGAC CGTAGATCGTCTTACAGCCCTGGGTGCTGTTCCGGGTATGGT GTGGCAGAATCGCGATATATATTATCAGGGACCGATTGGG CAAAAATTCCGCATACCGATGGA
203	AAV4_capsid 6 00-649	CCGGGTATGGTATGGCAAAACCGTGATATCTATTACCAGGG GCCGATTTGGGCTAAGATACCGCATACCGATGGACATTCC ATCCGAGCCCGTTAATAGGTGGTTTGGTTTGAAACATCCGC CGCCGCAGATTTTTATTAAAAAT
204	AAV4_capsid 6 24-673	GGTCATTTCCATCCGTCACCGCTTATTGGGGGGTTCCGGTTTA AAACATCCGCCCGCCGAGATTTTTATCAAGAACTCCCGT GCCGGCAAAACCGGCCACGACGTTTTCTAGCACTCCGGTCA ACTCTTTTATTACCCAATATTCA
205	AAV4_capsid 6 48-697	AATACGCCGGTACCGGCAAAATCCGGCCACAACCTTTTCTAG CACACCGGTAAATTCAATTTATCACCCAGTATAGCACCGGCC AGGTATCTGTGCAGATTGACTGGGAAATTCAGAAAGAACGT TCAAAACGCTGGAACCCGGAGGTT
206	AAV4_capsid 6 72-721	AGTACCGGCCAGGTATCTGTTCAAATTGACTGGGAGATTCA GAAAGAACGCTCAAAACGCTGGAATCCGGAGGTTTCAGTTTA CGTCAAACTATGGACAGCAAAATCTTTATTATGGGCCCCG GATGCTGCCGGCAAAATATACCGAG
207	AAV5_capsid 0 -49	ATGAGTTTTGTGGATCATCCGCCGATTTGGCTTGAAGAAGT AGGAGAGGGTCTGCGTGAATTTTGGGTCTGGAGGCGGGCC CGCCGAAACCGAAACCGAATCAGCAGCATCAGGATCAGGCC CGTGGGTAGTCCTTCCGGGATAT

SEQ ID NO:	Name	Sequence
208	AAV5_capsid 2 4-73	GAAGCGGGGCCGCCGAAGCCGAAACCGAACCAACAACATC AGGACCAGGCACGCGGATTAGTTTTGCCGGGCTATAATTAC CTGGGGCCGGGCAACGGGTTGGATCGTGGAGAACCGGTGAA TCGTGCAGATGAAGTGGCACGCGAG
209	AAV5_capsid 4 8-97	TATAATTATTTAGGGCCGGGTAAACGGTCTGGATCGCGGAGA GCCGGTCAATCGCGCAGACGAGGTGGCTCGCGAGCATGACA TATCATATAATGAACAGCTGGAAGCCGGGGACAACCCGTAT CTGAAGTATAATCATGCCGATGCA
210	AAV5_capsid 7 2-121	GAACATGATATCTCATATAACGAACAACCTGAAGCTGGAGA TAACCCGTATTTGAAATATAACCATGCTGACGCCGAATTTCA AGAGAACTTGCGGATGACACTTCATTCCGTGGAACTTAG GTAAGGCGGTTTTCCAGGCTAAG
211	AAV5_capsid 9 6-145	GCAGAGTTCCAGGAAAAAAGTGGCGGATGATACAAGTTTTGG CGGCAATTTGGGGAAGGCGGTGTTTCAGGCGAAAAAACGCG TATTGGAACCGTTTGGCCTGGTTGAAGAAGGTGCTAAAACG GCCCCGACGGGCAAAACGCATTGAC
212	AAV5_capsid 1 20-169	AAAAAACGCGTGCTTGAACCGTTTGGCCTTGTGGAGGAAGG GGCTAAGACTGCCCGACCGGTAACGTATAGACGATCATT TTCCGAAACGCAAAAAAGCACGTACCGAGGAAGACAGTAA ACCGTCAACGAGTTTCAGACGCCGAG
213	AAV5_capsid 1 44-193	GATGATCATTTCCCGAAGCGTAAAAAAGCACGTACAGAGGA AGACAGCAAACCGAGCACGTCAAGCGACGCTGAGGCGGGG CCGAGTGGTAGCCAGCAATTACAGATACCGGCCAGCCGGC AAGCTCTCTGGGGGCTGATACTATG
214	AAV5_capsid 1 68-217	GAGGCCGGACCGTCTGGAAGCCAACAGCTTCAGATTCCGGC CCAGCCGGCGTCAAGTCTGGGTGCCGACACCATGAGTGCTG GTGGTGGAGGTCCGCTTGGTGATAACAACCAAGGCGCCGAT GGCGTGGGCAACGCATCAGGTGAT
215	AAV5_capsid 1 92-241	ATGAGTGCCGGTGGTGGCGGCCCGCTGGGCGACAATAATCA GGGTGCTGACGGAGTGGGTAATGCATCAGGGGATTGGCATT GCGATAGCACTTGGATGGGAGACCGTGTGGTTACAAAATCT ACACGTACATGGGTGCTGCCGAGC
216	AAV5_capsid 2 16-265	GACTGGCATTGTGATTCAACTTGGATGGGTGATCGTGTGTA ACCAAGAGCACGCGCACTTGGGTCTTACCGAGCTATAATAA TCATCAATATCGTGAAATAAAATCAGGATCTGTGGATGGGA GCAATGCGAACGCCTATTTTGGT
217	AAV5_capsid 2 40-289	AGTTATAATAACCATCAATACCGCGAGATTAAGAGCGGCAG TGTTGATGGAAGTAACGCCAACGCCTATTTTGGATATAGCA CGCCGTGGGGGTATTTTGACTTTAACCGTTTCCATTACATT GGTCACCGCGTGACTGGCAGCGT
218	AAV5_capsid 2 64-313	GGCTATTCAACTCCGTGGGGCTATTTTGACTTCAACCGTTT CATAGCCATTGGTCACCGCGTGACTGGCAGCGCCTGATCAA CAACTATTGGGGTTTCCGTCCGCGTTCTCTGCGTGTGAAAAT TTTCAATATTCAGGTTAAAGAA
219	AAV5_capsid 2 88-337	CGCCTGATCAACAATTATTGGGGGTTCCGTCCGCGTAGTTTG CGCGTCAAAATTTTAAATATTCAGGTAAAAGAAATTACGGT GCAGGACAGTACCACCACCATGCCAATAATCTGACCAGCA CAGTGCAGGTTTTTACGGACGAT
220	AAV5_capsid 3 12-361	GAAGTTACCGTTCAAGATAGTACCACTACTATAGCCAATAA CTTGACCAGTACAGTCCAGGTGTTACAGATGACGATTATC AACTGCCGTATGTAGTTGGGAATGGTACGGAAGGATGCCTG CCGGCCTTTCGCCCGCAGGTGTTT

SEQ ID NO:	Name	Sequence
221	AAV5_capsid 3 36-385	GATGATTATCAGCTGCCGTATGTCGTGGGAAACGGTACCGA AGGTTGTCTTCCGGCGTTCCCGCCGCAAGTATTCACACTGCC GCAATATGGGTACGCTACGCTGAACCGTGATAATACAGAGA ATCCGACAGAGCGTTCTAGTTTC
222	AAV5_capsid 3 60-409	TTTACCCTTCCGCAGTATGGATATGCCACATTAAATCGTGAC AACACCGAGAACCCGACCGAGCGTAGCAGTTTTTTCTGCTT GGAGTACTTTCCGTCTAAGATGTTACGCACTGGCAACAATTT CGAGTTTACATACAACCTTCGAA
223	AAV5_capsid 3 84-433	TTCTTTTGTCTGGAATATTTTCCGTCTAAGATGCTGCGCACT GGAAATAATTTTCAATTTACCTACAACCTTTGAAGAGGTCCC GTTTCATAGCTCTTTCGCCCCGAGTCAAAACCTGTTCAAGCT GGCTAACCCGTTAGTCGATCAG
224	AAV5_capsid 4 08-457	GAAGAGGTACCGTTTCATAGTTCTTTCGCACCGAGCCAGAA TTTATTTAAACTTGCAAAACCGCTGGTAGATCAATATCTGTA TCGCTTTGTGTCAACCAACAATACGGGGGGCGTGCAATTCA ATAAGAACCTGGCAGGTGCGTAT
225	AAV5_capsid 4 32-481	CAGTATCTTTACCGTTTTGTGTCTACCAACAATACCGGAGGC GTACAATTTAATAAAAAATCTGGCAGGTGCTACGCAAACAC CTACAAAAACTGGTTTCCGGGGCCGATGGGGCGCACACAAG GTTGGAATTTGGGAAGTGGGGTG
226	AAV5_capsid 4 56-505	TATGCGAATACTTACAAAAATTGGTTTCCGGGTCCGATGGGT CGTACGCAAGGCTGGAATCTGGGTAGCGGTGTGAATCGCGC CTCTGTGTCAGCATTTGCGACTACAAACCGTATGGAATTAGA AGGTGCCAGTTATCAGGTGCCG
227	AAV5_capsid 4 80-529	GTAACCGTGCGAGTGTCTCTGCCTTTGCAACTACAAACCGC ATGGAGCTTGAAAGGTGCATCATATCAGGTGCCGCCGACGCC GAATGGCATGACAAATAATCTGCAAGGCTCAAACACCTATG CACTGGAAAAATACCATGATTTTC
228	AAV5_capsid 5 04-553	CCGCCGCAACCGAATGGCATGACTAATAATTTACAAGGGTC AAATACCTATGCGCTGGAAAAATACAATGATATTTAACAGCC AGCCGGCTAATCCGGGCACAACCGCGACTTATCTGGAAGGT AACATGTTAATTACCAGCGAAAGC
229	AAV5_capsid 5 28-577	TTCAATAGTCAGCCGGCGAACC CGGGCACCACGGCAACCTA CTTAGAAGGTAACATGCTGATAACAAGTGAATCAGAAACGC AACCGGTCAATCGCGTTGCTTATAACGTTGGCGGTCAAATG GCCACCAATAATCAGTCTAGCACT
230	AAV5_capsid 5 52-601	AGTGAGACCCAACCGGTCAATCGCGTAGCATATAATGTGGG TGGACAGATGGCGACCAATAACCAAGTCTTCTACGACAGCCC CGGCTACTGGCAGTATAACCTGCAGGAAATCGTTCCGGGC TCAGTCTGGATGGAACGCGACGTT
231	AAV5_capsid 5 76-625	ACCACAGCGCCGGCCACCGGCACGTATAATTTACAAGAAAT AGTACCGGGTTCAGTGTGGATGGAACGCGATGTATATCTGC AGGGGCCGATATGGGCCAAAAATACCGGAAACCGGTGCCCAT TTTCATCCGAGCCCGGAATGGGA
232	AAV5_capsid 6 00-649	GTTTATCTGCAGGGACCGATCTGGGCTAAGATCCCGGAAAC TGGGGCCCCATTTTCATCCGAGTCCGGCCATGGGAGGGTTCCG GCCTGAAACATCCGCCGCCGATGATGCTTATTAAGAATACT CCGGTGCCGGGCAACATCACCTCA
233	AAV5_capsid 6 24-673	GGTGGCTTTGGTCTGAAACATCCGCCGCCGATGATGCTGAT AAAAAACACGCCGGTACCGGGTAATATCACATCTTTCAGCG ACGTACCGGTGAGTAGCTTTATAACCCAATATAGTACGGGG CAAGTTACCGTAGAAATGGAATGG

SEQ ID NO:	Name	Sequence
234	AAV5_capsid 6 48-697	AGTTTCTCTGATGTCCCGGTATCATCATTTTATTACCCAGTAC AGTACGGGCCAGGTTACCGTCGAAATGGAATGGGAATTAAA AAAGGAAAATTCTAAACGTTGGAATCCGGAATACAATATA CGAATAATTATAACGATCCGCAA
235	AAV5_capsid 6 72-721	TGGGAAC TGAAAAAGGAAAAC TCAAAACGCTGGAACCCGG AGATTCAATATACAAACAATTATAATGATCCGCAATTTCGTA GATTCGCGCCGACTCTACTGGAGAATACCGCACCACTCG TCCGATTGGTACACGTTATCTGACT
236	AAV6_capsid 0 -49	ATGGCAGCCGATGGCTATCTGCCGGATTGGCTGGAGGATAA TTTGTCTGAAGGTATTCTGTGAATGGTGGGATTTGAAACCGG GTGCGCCGAAACCGAAGGCCAACCCAGCAAAAACAGGACGA TGGTCGCGGACTGGTACTGCCGGGG
237	AAV6_capsid 2 4-73	CTGAAACCGGGTGCTCCGAAGCCGAAAGCGAATCAGCAGA AACAAGATGATGGCCGTGGGTGGTGTGCGGGGTACAAA TATCTTGGTCCGTTCAATGGTTTGGATAAAGGTGAACCGGTT AATGCCGCGGACGCGGCCGCTTA
238	AAV6_capsid 4 8-97	GGTTACAAATATTTGGGTCCGTTTAAATGGGTGGATAAAGG GGAACCGGTCAATGCGGCCGATGCAGCAGCTCTGGAACATG ATAAAGCATATGATCAGCAACTGAAAGCCGGTGATAATCCG TACTTACGTTACAATCATGCCGAC
239	AAV6_capsid 7 2-121	TTAGAACATGACAAGGCTTACGATCAGCAGCTGAAAGCGGG CGATAATCCGTACCTGCGTTATAACCATGCGGATGCTGAATT TCAAGAGCGCTTACAGGAAGATAACCAGCTTTGGCGGGAATT TAGGACGCGCAGTATTTCAGCT
240	AAV6_capsid 9 6-145	GATGCGGAATTTTCAGGAACGTCTGCAGGAAGATACGTCTTT TGGGGGTAACTTGGGCGTGCGGTGTTCCAAGCTAAAAAAC GCGTTCTTGAACCGTTTGGTCTGGTCTGAAGAAGGAGCCAAA ACGGCTCCGGGTAAAAAACGTCCG
241	AAV6_capsid 1 20-169	GCAAAAAAACCGGTTTTTGAACCGTTTTGGCTTGGTTGAGGA AGGCGCGAAAAACGGCCCCGGGGAAAAAACGTCGGGTAGAG CAAAGTCCGCAGGAGCCGACTCAAGTAGCGGCATCGGAA AAACGGGTCAACAGCCGGCAAAAAAG
242	AAV6_capsid 1 44-193	CCGGTGGAGCAGTCAACCGCAAGAACCGGATTCTTCTAGTGG CATTGGGAAAACGGGTGACGAGCCGGCCAAAAAACGCTTAA ACTTTGGCCAAACCGGCGACAGTGAATCTGTTCCGGACCCG CAGCCGCTGGGTGAACCGCCGGCG
243	AAV6_capsid 1 68-217	AAACGCTTGAATTTTGGTTCAGACAGGGGATTGAGAACTCTGT GCCGGATCCGCAGCCGCTTGGCGAGCCGCGCGACCCCGG CCGCAGTAGGGCCGACCACAATGGCTAGCGGCGGCGGTGCA CCGATGGCTGATAACAACGAGGGC
244	AAV6_capsid 1 92-241	GCAACCCCGGCCGCTGTGGGTCCGACGACTATGGCAAGTGG TGGTGGCGCTCCGATGGCGGACAATAACGAAGGTGCGGATG GTGTGGGGAACGCCAGCGGAAATTGGCATTGTGATTCTACC TGGTTGGGAGATCGCGTGATTACC
245	AAV6_capsid 2 16-265	GGAGCGGATGGGGTTGGAACGCGTCAGGTAATTGGCATTG CGATTCAACGTGGCTGGGCGACCGTGTAATCACCACGTCAA CGCGTACCTGGGCGTTGCCGACCTACAATAATCATCTGTATA AACAGATATCTAGCGCCAGTACC
246	AAV6_capsid 2 40-289	ACCACATCAACACGCACGTGGGCGTTGCCGACCTACAATAA TCATCTTTATAAACAGATTAGCAGCGCTAGCACGGGTGCGA GCAATGATAACCATTATTTTGGTTACAGCACCCCGTGGGGCT ATTTTGATTTAATCGCTTCCAT

SEQ ID NO:	Name	Sequence
247	AAV6_capsid 2 64-313	ACGGGCGCATCAAACGACAACCATTATTTTGGCTATAGCAC ACCGTGGGGCTATTTTGATTTC AACCGCTTCCATTGTCATTT AGTCCGCGTGACTGGCAACGCCTGATTAACAATAATTGGGG GTTTCGTCCGAAACGCCTGAAC
248	AAV6_capsid 2 88-337	CATTGTCATTTTAGCCCGGIGATTGGCAGCGTCTTATAAAC AACAATTGGGGGTTTCGCCCCGAAACGCTGTAATTTTAACT GTTTAATATCCAGGTAAAAGAAGTCACAACCAATGACGGAG TGACCACTATTGCTAATAATCTG
249	AAV6_capsid 3 12-361	AACTTTAAATTATTTAATATACAGGTGAAGGAGGTTACCAC CAATGATGGTGTCACTAATTTGCTAACAATTTAACCTCAAC CGTACAAGTTTTTTCAGACAGTGAGTACCAATTGCCGTACGT GCTGGGGTCTGCACATCAAGGA
250	AAV6_capsid 3 36-385	CTTACGAGCACCGTGCAGGTTTTTAGCGATTCTGAATATCAA TTGCCGTATGTTTTAGGCTCAGCACATCAAGGATGTTTACCG CCGTTTCCGGCTGACGTATTCATGATCCCGCAGTACGGGTAT CTGACCTTAAATAACGGGAGT
251	AAV6_capsid 3 60-409	GGTTGCCTGCCGCCGTTTCCGGCAGACGTGTTTATGATCCCG CAGTACGGCTATCTGACACTGAACAATGGAAGTCAAGCTGT CGGACGTAGCTCATTTTATTGCCTGGAATATTCCCGAGTCA GATGTTACGCACAGGCAATAAT
252	AAV6_capsid 3 84-433	AGTCAGGCAGTAGGTTCGCAGCAGCTTCTACTGCCTGGAATA TTTTCCGAGTCAGATGTTACGTACTGGGAACAATTTACATT TAGCTACACTTTTCGAGGATGTACCGTTTCATAGCTCATATGC CCATTACAGAGTTTAGACCGC
253	AAV6_capsid 4 08-457	AATTTACGTTTTTCATACACTTTTGAAGATGTACCGTTCCAT AGCTCATATGCTCATAGTCAGAGCTTAGACCGTCTGATGAA CCCGCTGATCGACCAGTATCTTTATTACTTAAATCGTACTCA AAATCAATCAGGGTCAGCGCAG
254	AAV6_capsid 4 32-481	CGCTTAATGAATCCGCTGATCGACCAGTATCTTTATTATCTG AACCGCACCCAGAACCAATCTGGTTCTGCACAAAATAAAGA TTTACTGTTTAGCCGTGGTAGTCCGGCCGGCATGTCTGTGCA GCCGAAGAAATGGCTGCCGGGC
255	AAV6_capsid 4 56-505	CAGAACAAAGACCTGTTGTTCTCTCGTGGATCACCGGCCGG GATGAGTGTACAGCCGAAAAATTGGCTGCCGGGGCCCGTGT ATCGTCAGCAGCGTGTGAGTAAACTAAAACCGATAACAAT AACTCTAACTTCACCTGGACAGGC
256	AAV6_capsid 4 80-529	GGTCCGTGCTATCGCCAGCAGCGTGTGTCTAAAACTAAAAAC TGATAACAACAACAGTAATTTTACCTGGACCGGGGCCCTCAA AATACAACCTGAACGGTCGCGAGAGTATCATTAACCCGGGT ACGGCGATGGCCTCACATAAAGAC
257	AAV6_capsid 5 04-553	GGCGCGTCAAAAATACAATTTAAATGGCCGCGAATCAATTAT AAACCCGGGCACAGCCATGGCCAGCCATAAGGACGATAAG GATAAATTTTTTCCGATGAGTGGGGTCATGATCTTCGGAAG GAATCAGCCGGCGCATCTAATACA
258	AAV6_capsid 5 28-577	GATGACAAAGATAAATTTTTTCCGATGTCTGGGGTGATGAT ATTCGGGAAAGAATCAGCGGGTGCATCTAATACAGCTCTGG ATAATGTTATGATTACTGATGAAGAAGAAATCAAAGCAACC AATCCGGTAGCAACAGAGCGTTTT
259	AAV6_capsid 5 52-601	ACCGCCCTGGATAACGTAATGATTACAGACGAAGAAGAAAT AAAAGCCACCAACCCGGTGGCAACCGAGCGCTTTGGAACAG TCGCCGTTAATCTGCAGAGTAGTTCTACGGATCCGGCCACCG GAGACGTGCATGTGATGGGCGCG

SEQ ID NO:	Name	Sequence
260	AAV6_capsid 5 76-625	TTTGGTACAGTGGCAGTTAACCTTCAGAGCAGCAGCACAGA CCCGGCTACCGGAGATGTGCATGTCATGGGGGCCCTGCCGG GTATGGTGTGGCAGGATCGCGATGTCTACTTACAAGGGCCG ATTTGGGCGAAAATCCCGCATACG
261	AAV6_capsid 6 00-649	GCCCTGCCGGGGATGGTATGGCAAGACCGTGACGTATATT GCAAGGCCCGATATGGGCAAAAATTCGCGATACCGACGGTC ATTTCCATCCGTCACCGTTAATGGGAGGTTTCGGCTTGAAGC ATCCGCCGCCGCAAATCTTGATT
262	AAV6_capsid 6 24-673	ACCGATGGACATTTTCATCCGTCACCGTTGATGGGGGGGTTT GGGTTGAAACATCCGCCGCCGAGATCCTTATAAAAAATAC CCCGGTACCGGCGAACCCGCCGGCTGAATTTTCAGCGACAA AATTTGCCAGCTTTATAACGCAG
263	AAV6_capsid 6 48-697	ATAAAAAATACCCCGGTACCGGCGAACCCGCCGGCCGAGTT TAGTGCCACCAAGTTCGCATCATTTATTACACAGTATAGTAC CGGTCAGGTGAGTGTGAGATAGAATGGGAATTGCAGAAGG AAAACAGTAAACGCTGGAATCCG
264	AAV6_capsid 6 72-721	CAGTACTCTACTGGCCAGGTATCAGTGGAAATTGAGTGGGA ACTGCAGAAGGAAAATTCAAAACGCTGGAACCCGGAAGTCC AGTATACTTCTAATTACGCAAAAAGTGCTAATGTAGACTTCA CCGTAGACAATAATGGCTTGAT
265	AAV7_capsidY P_077178.1 0- 49	ATGGCAGCCGACGGTTATCTGCCGGATTGGTTAGAAGATAA TTTGAGCGAAGGTATCCGTGAATGGTGGGATCTGAAGCCGG GGGCACCGAAACCGAAGGCTAACCCAGCAGAAACAGGACAA CGGGCGCGGCTTGGTACTGCCGGGA
266	AAV7_capsidY P_077178.1 24- 73	TTGAAACCGGGTGCCCCGAAGCCGAAGGCGAACCCAGCAGA AACAGGATAACGGTCGCGGGCTGGTGTACCGGGCTATAAG TATCTTGGGCCGTTCAACGGTTTGATAAAAGGTGAACCGGT CAATGCAGCAGACGCCGCTGCGTTG
267	AAV7_capsidY P_077178.1 48- 97	GGATATAAGTACTTAGGTCCGTTTAAATGGCTTAGACAAGGG TGAGCCGGTTAATGCAGCCGATGCGGCCGACTGGAACATG ATAAAGCGTATGATCAACAGTTGAAAGCTGGGGACAATCCG TACCTGCGCTACAATCATGCGGAT
268	AAV7_capsidY P_077178.1 72- 121	CTGGAACATGATAAGGCATATGACCAGCAATTAAGCCGG AGATAATCCGTACCTGCGTTATAACCATGCTGATGCCGAGTT CCAAGAACGTTTGCAGGAGGATACTTCATTTGGGGGCAACC TGGGCCGTGCGGTTTTCCAAGCT
269	AAV7_capsidY P_077178.1 96- 145	GATGCTGAATTTACAGGAACGTTTACAGGAAGACACTAGCTT CGGAGGCAATCTGGGCCGCGCCGTATTCCAGGCAAAAAAGC GTGTTCTTGAGCCGCTGGGCTTAGTAGAAGAAGGCGCCAAA ACTGCGCCGGCAAAGAAACGCCCG
270	AAV7_capsidY P_077178.1 120- 169	GCGAAAAAACGTTATTAGAGCCGCTGGGCTGGTGGAGGA GGGAGCAAAGACCGCGCCGCCAAAAAACGTCCGGTAGAA CCGAGCCCGCAGCGCAGCCCGGACTCTAGTACGGGAATTGG TAAGAAGGGTCAGCAACCGGCGCGC
271	AAV7_capsidY P_077178.1 144- 193	CCGGTTGAGCCGTCTCCGCAGCGTTCACCGGACAGTAGCAC TGGCATTGGGAAAAAAGGTCAGCAGCCGGCACGTAAAGCGCT TAAACTTTGGTCAAACCGGCGACTCAGAAAGTGTCCCGGAT CCGCAACCGCTTGGCGAACCGCCG
272	AAV7_capsidY P_077178.1 168- 217	CGCAAACGTCTTAACCTCGGACAGACTGGCGATAGCGAGAG TGTTCCGGATCCGCAGCCGCTTGGCGAACCGCCGCGCAGCGC CGAGTTCTGTGGGTAGCGGAACGGTGGCTGCAGGGGGTGA GCCCCGATGGCGGACAATAACGAA

SEQ ID NO:	Name	Sequence
273	AAV7_capsidY P_077178.1 192-241	CCGGCGGCCCCGTCTTCAGTAGGTAGTGGCACTGTTGCAGC AGGCGGAGGTGCGCCGATGGCGGATAATAATGAAGGTGCA GACGGCGTTGGTAACGCCTCAGGGAAGTGGCATTGTGATAG CACCTGGTTGGGCGACCGCGTCATA
274	AAV7_capsidY P_077178.1 216-265	GAAGGTGCAGATGGCGTGGGTAATGCGAGCGGGAAGTGGC ATTGCGATTCTACTTGGCTTGGTGATCGCGTGATCACGACCT CAACGCGCACTTGGGCCCTGCCGACATATAACAACCATCTG TACAAGCAGATTAGTAGCGAAACA
275	AAV7_capsidY P_077178.1 240-289	ATAACGACGTCAACTCGTACTTGGGCGTTACCGACATATAA TAATCATTTGTACAAACAGATCAGCTCAGAAACAGCCGGCT CAACCAATGATAACACGTATTTCCGGTATTCTACTCCGTGGG GGTATTTTCGATTTCACCGCTTT
276	AAV7_capsidY P_077178.1 264-313	ACAGCTGGAAGCACTAATGACAATACATATTTTGGTTATAG CACACCGTGGGGGTATTTTCGATTTCAATCGTTTTCATTGCCA TTTTAGCCCGCGTGATTGGCAACGTCTGATTAACAACAATTG GGGCTTCCGTCCGAAAAAACTT
277	AAV7_capsidY P_077178.1 288-337	TTCCATTGTCTTTCTCTCCGCGTGATTGGCAACGTCTTATTA ATAACAAGTGGGGATTTTCGTCCGAAGAAATTGCGTTTCAAA CTGTTTAACATTCAAGTCAAAGAAGTCACTAAGTCAACGACGG CGTCACCACCATTGCAAACAAT
278	AAV7_capsidY P_077178.1 312-361	CTGCGTTTCAAGTTGTTAATATTCAGGTCAAAGAGGTTACG ACGAATGATGGGGTGACTACGATTGCGAATAACCTTACCAG CACAATCCAAGTTTTTTCAGATAGCGAATATCAACTGCCGTA TGTTCTGGGAAGTGCGCATCAG
279	AAV7_capsidY P_077178.1 336-385	AACTTGACTAGCACCATCCAAGTGTTCACTGACTCTGAATAC CAGTTGCCGTATGTTCTGGGTTCTGCGCATCAGGGTTGTCTT CCGCCGTTTCCGGCGGATGTGTTATGATCCCGCAGTACGGA TATCTTACGCTGAATAATGGG
280	AAV7_capsidY P_077178.1 360-409	CAGGGATGCCTGCCGCCGTTTCCGGCTGATGTATTTATGATT CCGCAGTATGGGTATCTGACGTTAAATAATGGTTCTCAGAGT GTCGGTCGTAGTTCTTTCTATTGTTTGAATACTTTCCGAGTC AGATGCTGCGCACGGGAAAC
281	AAV7_capsidY P_077178.1 384-433	GGATCTCAGTCAGTAGGTGCTAGTTCTTTTACTGCCTGGAG TACTTCCCGAGCCAGATGTTGCGCACCGGTAACAACCTTTGA GTTTTATATAGCTTTGAAGATGTTCCGTTTCATAGTTCTTAT GCCCATAGCCAAAGTCTGGAT
282	AAV7_capsidY P_077178.1 408-457	AACAATTTTGAGTTTTCTTATTCTTTTGAAGATGTTCCGTTTC ATTCATCTTACGCCCATTCACAGAGCTTAGATCGTCTGATGA ATCCGCTGATCGACCACTTGTATTACCTTGCTCGTACAC AGAGCAATCCGGGGGGTACA
283	AAV7_capsidY P_077178.1 432-481	GATCGTTTGATGAATCCGCTGATCGACCACTACCTGTATTAC TTGGCCCGTACCCAGTCTAATCCGGGTGGTACTGCTGGCAAC CGCGAACTGCAATTTTATCAGGGCGGCCCGAGTACGATGGC CGAACAGGCCAAAAAACTGGCTT
284	AAV7_capsidY P_077178.1 456-505	ACAGCTGGCAATCGCGAGTTACAATTCTATCAGGGCGGCC GTCTACGATGGCCGAACAGGCCAAAAAATTGGTTACCGGGCC CGTGTTTTCTGTCAGCAGCGCGTCAGTAAACGCTGGATCAG AACAACAATAGCAACTTCGCTTGG
285	AAV7_capsidY P_077178.1 480-529	CTGCCGGGTCCGTGCTTTCCGCAACAGCGTGTTGTCAAAGAC ATTAGATCAGAAACAACAATTCTAATTTTGCCTGGACTGGAG CCACTAAATATCATTTGAATGGACGCAACTCACTGGTGAAT CCGGGAGTAGCTATGGCGACTCAT

SEQ ID NO:	Name	Sequence
286	AAV7_capsidY P_077178.1 504-553	TGGACCGGCGCCACGAAATATCATCTTAATGGTCGTAATAG TCTGGTTAATCCGGGAGTGGCCATGGCCACTCATAAAGACG ATGAAGATCGTTTTTCCCGTCATCTGGAGTACTTATCTTTG GAAAACTGGGGCAACCAACAAA
287	AAV7_capsidY P_077178.1 528-577	CATAAGGACGATGAGGATCGCTTTTTTCCGAGCAGCGGTGT ACTGATTTTTGGTAAAACTGGCGCTACCAATAAAACACAC TTGAGAATGTTTTAATGACAAATGAGGAAGAGATCCGTCCG ACCAATCCGGTAGCAACGGAAGAA
288	AAV7_capsidY P_077178.1 552-601	AAAACGACGCTTGAAAACGTTTTAATGACGAACGAAGAAGA AATTCGTCCGACGAATCCGGTAGCAACCGAAGAATATGGGA TTGTGTCTCTAATCTGCAAGCAGCTAATACAGCCGCGCAG ACACAGGTCGTCAATAATCAGGGG
289	AAV7_capsidY P_077178.1 576-625	GAGTATGGTATTGTGAGCAGTAATCTTCAGGCTGCTAACAC AGCTGCACAAACCCAAGTGGTGAACAATCAGGGCGCGCTGC CGGGCATGGTGTGGCAGAATCGTGATGTCTACCTCAGGGT CCGATCTGGGCTAAGATTCCGCAT
290	AAV7_capsidY P_077178.1 600-649	GGTGCCTGCCGGGTATGGTGTGGCAGAACCGTGATGTGTA TCTGCAAGGACCGATTGTTGGGCTAAGATCCCGCATACGGATG GTAACCTTCATCCGAGTCCGCTTATGGGTGGATTGGCCTTA AACATCCGCCGCCGAGATCCTG
291	AAV7_capsidY P_077178.1 624-673	CATACGGACGGAAACTTTCATCCGAGCCCGCTGATGGGTGG CTTTGGTTTTAAAGCATCCGCCGCCGCAAACTCTTAATTA TACGCCGGTGCCGGCGAACC CGCGGAGGTGTTTACTCCGG CGAAGTTCGCTTCATTATCACG
292	AAV7_capsidY P_077178.1 648-697	TTGATTAAAAATACGCCGGTTCGGGCCAACCCGCCGGAAGT GTTTACCCCGGCTAAATTCGCGTCATTTATCACACAATACTC AACTGGCCAAGTGAGCGTTGAAATAGAGTGGGAATTACAAA AGGAAAATTCAAAACGCTGGAAC
293	AAV7_capsidY P_077178.1 672-721	ACTCAGTATAGTACCGGCCAAGTAAGTGTGAAATCGAATG GGAACTGCAGAAAGGAAAACAGCAAACGCTGGAAATCCGGAA ATTGAGTATACTTCAAACCTTGAAAAACAGACGGGTGTGGA CTTTGCAGTTGACTCACAAGGTGTA
294	AAV8_capsid 0-49	ATGGCAGCAGACGGTTATCTGCCGGACTGGCTTGAAGACAA CTTGTCAGAAAGGCATCCGTGAATGGTGGGCTTTGAAGCCGG GCGCCCCGAAACCGAAAGCCAACCAACAGAAACAGGATGA CGGCCGTGGATTGGTCTGCCGGGG
295	AAV8_capsid 24-73	CTGAAACCGGGAGCGCCGAAACCGAAGGCAAATCAGCAGA AACAGGATGACGGTCCGCGGACTGGTGCTGCCGGGATATAAA TATCTGGGTCCGTTTAATGGTCTGGACAAAGGTGAGCCGGTT AATGCAGCAGATGCCGCTGCTTTG
296	AAV8_capsid 48-97	GGCTACAAGTATCTTGGCCCGTTAATGGACTGGACAAAGG CGAACCGGTAAATGCTGCGGACGCCGCCGATTAGAGCATG ACAAGGCATATGATCAGCAGCTGCAAGCAGGCGACAATCCG TACCTGCGCTACAACCATGCAGAC
297	AAV8_capsid 72-121	CTGGAACATGATAAGGCGTATGATCAGCAACTGCAGGCGGG TGATAATCCGTATCTGCGTTACAATCATGCCGACGCTGAGTT TCAGGAACGCCTTCAGGAAGATACGTCAATTCGGCGGGAATT TGGGCCGCGCCGTGTTTCAAGCT
298	AAV8_capsid 96-145	GATGCGGAATTTAGGAACGCCTGCAGGAAGATACCAGTTT TGTTGGTAATCTTGGACGTGCTGTATTCCAGGCTAAAAAAC GTGTTTTAGAACCGCTTGGTCTGTAGAGAAGGTGCGAAG ACGGCGCCGGGCAAAAAACGTCCG

SEQ ID NO:	Name	Sequence
299	AAV8_capsid 1 20-169	GCTAAGAAACGCGTCTTGGAGCCGCTGGGTCTGGTCGAGGA AGGTGCGAAAAACGGCCCCGGGGAAAAAGCGCCCGTTGAG CCGAGCCCGCAACGTTACCCGATTCTACAGGTATCGG CAAGAAGGGTCAGCAACCGGCGCGT
300	AAV8_capsid 1 44-193	CCGGTGGAAACCGAGTCCCGCAGCGTTCCTCCGGACTCTAGTAC AGGAATTGGAAAAAAGGACAACAGCCGGCCCGTAAGCGC TTGAACTTTGGACAAAACGGGAGACAGTGAATCAGTGCCGGA CCCGCAGCCGCTGGGGGAACCGCCG
301	AAV8_capsid 1 68-217	CGCAAACGCTTAAACTTTGGCCAGACTGGTGATTACAGAGAG CGTCCCGGATCCCGCAGCCGCTGGGCGAGCCGCCGGCGGCTC CGAGTGGTGTGGGCCGAACACGATGGCGGCTGGGGGTGGG GCCCCGATGGCAGATAACAATGAG
302	AAV8_capsid 1 92-241	CCGGCAGCTCCGTCAGGTGTAGGCCCGAATACAATGGCCGC GGGCGGTGGGGCCCCGATGGCCGACAATAATGAAGGTGCCG ATGGTGTAGGGTCAAGCTCAGGTAATTGGCATTGTGATTCTA CATGGCTGGGTGATCGTGTGATT
303	AAV8_capsid 2 16-265	GAGGGTGCCGATGGTGTAGGCTCTTCATCAGGTAATTGGCA TTGCGACAGTACATGGTTGGGAGATCGTGTAAATAACCACAA GTACCCGCACTTGGGCTCTGCCGACATAACAACCATCTGT ATAAGCAGATTTCAAACGGCACG
304	AAV8_capsid 2 40-289	ATTACAACAAGTACCCGTAATTGGGCTTTGCCGACTTACAAC AATCATTTGTATAAACAGATTAGTAACGGGACATCTGGTGG GGCGACGAACGACAATACTTACTTTGGCTACAGCACACCGT GGGGTTATTTTGACTTTAATCGC
305	AAV8_capsid 2 64-313	ACAAGTGCGGCGCTACTAACGACAATACGTATTTCCGATA TAGTACACCGTGGGGATATTTTGATTTTAACCGCTTCCATTG CCATTTTAGCCCGCGCGACTGGCAACGCCTGATTAATAACA ACTGGGGTTTCGCCCCGAAGCGT
306	AAV8_capsid 2 88-337	CGCTTCCATTGTCATTTTCTCCGCGCGACTGGCAGCGCTTA ATCAATAATAATTGGGGCTTCCGCCGAAACGCCTGAGTTTC AACTGTTTAATATCCAGGTCAAAGAAGTGACTCAAAACGA AGGTACTAAAACCATTGCAAAT
307	AAV8_capsid 3 12-361	CGCCTGTCTTTTAACTGTTTAACATCCAGGTTAAAGAGGTA ACACAGAACGAAGGTACCAAACTATTGCAAACAATCTGAC TTCAACTATTCAAGTTTACCCGACTCAGAATATCAGCTTCC GTACGTACTGGGGAGTGCCCAT
308	AAV8_capsid 3 36-385	AATAACTTAACGTCTACGATACAAGTCTTCACTGATTCTGAA TATCAATTGCCGTACGTACTGGGCAGCGCGCATCAGGGTTG TCTGCCGCCGTTCCCGGCAGATGTTTTATGATTCCGCAGTA CGGCTATTTAACCTTGAATAAT
309	AAV8_capsid 3 60-409	CATCAAGGTTGTCTTCCGCCGTTTCCGGCGGATGTCTTTATG ATCCCGCAGTATGGTTACCTGACGCTTAATAACGGAAGTCA AGCAGTGGGTTCGACGAGTTTCTACTGCCTGGAATACTTCC GTCACAAATGTTACGCACCGGT
310	AAV8_capsid 3 84-433	AACGGTTCTCAAGCTGTTGGCCGTTCTAGCTTTTATTGTCTG GAATATTTCCGAGTCAGATGCTGCGTACGGGGAACAACTT TCAGTTTACATACACATTCGAAGACGTCCCCGTTCATAGTTC ATATGCCCATTTCTCAATCTCTT
311	AAV8_capsid 4 08-457	GGTAACAATTTTCAGTTCACGTACACGTTTGAAGACGTTCCG TTTCATTCTCTTATGCCATTCTCAGAGTCTGGACCGCCTG ATGAATCCGTTGATTGACCAGTATTTATACTACCTGAGCCGT ACTCAGACAACGGGGGGCACA

SEQ ID NO:	Name	Sequence
312	AAV8_capsid 4 32-481	CTGGATCGTCTTATGAACCCGCTGATCGACCAATACCTTTAC TACCTGTCTCGCACACAACTACGGGCGGGACGGCTAACAC TCAGACTCTGGGCTTTTCACAGGGCGGCCCCGAACACTATGG CGAATCAGGCAAAAAATTGGCTG
313	AAV8_capsid 4 56-505	ACCGCAAACTCAGACATTGGGTTTCAGCCAGGGCGGTCC GAACACTATGGCAAATCAGGCGAAAAATTGGCTGCCGGGTG CGTGCTACCGTCAACAGCGTGTGAGCACGACAACGGGGCAG AATAATAACAGTAATTTCGCATGG
314	AAV8_capsid 4 80-529	TTGCCGGGTCCGTGCTATCGTCAGCAACGCGTGTCTACAACG ACCGGACAGAACAAATAATAGTAATTTTCGCATGGACCGCAGG TACGAAATATCATTTAAATGGACGCAACTCTTTAGCCAATCC GGGCATTGCAATGGCAACGCAT
315	AAV8_capsid 5 04-553	TGGACCGCAGGCACAAAATATCATCTGAATGGGCGTAAGTC TCTGGCAAACCCGGGAATCGCTATGGCTACGCATAAAGATG ATGAGGAACGTTTTTTTCCGTCAAATGGCATTCTGATATTTG GCAACAGAACGCCGCTCGTGAT
316	AAV8_capsid 5 28-577	CATAAGGACGATGAGGAGCGTTTCTTTCCGTCAAATGGGAT TCTGATTTTTGGCAAGCAAAATGCAGCCCGTGATAATGCTG ATTATAGCGACGTAATGCTGACCAGCGAAGAAGAGATTAAA ACTACTAACCCGGTCGCGACAGAA
317	AAV8_capsid 5 52-601	GATAATGCAGATTATAGTGACGTAATGCTTACCTCAGAAGA GGAGATAAAGACAATAATCCGGTAGCAACCGAAGAATAC GGCATTGTTGCAGATAATCTGCAACAACAAAATACAGCTCC GCAGATTGGTACGGTAAATAGCCAG
318	AAV8_capsid 5 76-625	GAAGAATATGGAATCGTCGCCGACAACCTTACAACAGCAAAA TACTGCCCGCAAATTGGAACGGTGAACAGTCAGGGGGCCC TGCCGGGTATGGTCTGGCAAAATCGCGATGTGTACCTTCAA GGTCCGATTTGGGCTAAAATTCCG
319	AAV8_capsid 6 00-649	CAGGGAGCTCTGCCGGGTATGGTCTGGCAAAATCGTGACGT GTATCTGCAGGGACCGATTGTTGGGCTAAAATACCGCATACAG ATGGCAATTTTCATCCGTCTCCGCTGATGGGTGGATTGGCT TGAAACATCCGCCGCCGAGATA
320	AAV8_capsid 6 24-673	CCGCATACTGATGGCAACTTTCATCCGAGTCCGTTGATGGGT GGCTTCGGCTTAAACATCCGCCGCCGCAAATCCTGATTAA AAATACCCCGGTGCCGGCGGATCCGCCGACCACGTTTAATC AGAGCAAACTGAACAGCTTTATA
321	AAV8_capsid 6 48-697	ATTCTGATTAATAAATACTCCGGTGCCGGCAGACCCGCCGAC TACATTCAACCAAAGCAAAGTGAATAGTTTATTACACAAT ACTCAACAGGACAGGTCTCAGTAGAAATCGAATGGGAGTTA CAGAAGGAAAATTCTAAACGTTGG
322	AAV8_capsid 6 72-721	ATTACACAGTATTCTACGGGTCAAGTTAGTGTGAGATTGAG TGGGAGCTGCAAAAAGAAAATAGCAAACGTTGGAATCCGG AAATACAGTACACCAGCAATTATTATAAAAGCACGAGTGTT GATTTTGCTGTGAACACTGAGGGC
323	AAV9_capsid 0 -49	ATGGCGGCGGATGGGTATCTGCCGGATTGGCTGGAGGATAA TCTGAGTGAGGGAATCCGCGAATGGTGGGCCCTTAAGCCGG GTGCGCCGACGCCGAAAGCAAACAGCAGCATCAAGATAAT GCGCGCGGCCTTGTACTGCCGGGG
324	AAV9_capsid 2 4-73	CTGAAACCGGGAGCCCCGAGCCGAAAGCCAACCAACAAC ATCAAGATAACGCACGTGGACTGGTTCTTCCGGGTACAAA TACTTGGGGCCGGCAATGGCTTGGACAAGGGAGAACCGGT TAATGCCGCCGATGCTGCAGCATTG

SEQ ID NO:	Name	Sequence
325	AAV9_capsid 4 8-97	GGTTACAAGTACCTGGGCCCCGGGTAACGGGTTAGATAAGGG TGAGCCGGTTAATGCCGCGGATGCCGCCGCCCTTGGAACATG ACAAGGCTTATGATCAGCAGCTGAAGGCAGGTGATAATCCG TATCTTAAATATAATCATGCCGAT
326	AAV9_capsid 7 2-121	TTAGAACATGATAAGGCTTATGATCAGCAGTTAAAAGCAGG AGATAATCCGTATCTTAAATATAACCATGCTGATGCCGAATT TCAGGAGCGTCTGAAAAGAGGACACCAGCTTCGGCGGTAACC TGGGGCGCGCTGTCTTTCAGGCG
327	AAV9_capsid 9 6-145	GATGCTGAATTTTCAGGAGCGTTTTAAAGGAAGATACATCATT TGGCGGGAACCTGGGACGCGCAGTTTTTCAGGCTAAGAAGC GTTTGCTGGAACCGTTGGGTCTGGTTCGAAGAAGCAGCGAAA ACGGCTCCGGGGAAGAAGCGCCCCG
328	AAV9_capsid 1 20-169	GCCAAAAAACGTCCTTCTGGAACCGCTGGGTCTGGTAGAAGA AGCAGCGAAGACTGCTCCGGGAAAAGAAACGCCCCGTGGAG CAAAGTCCGCAAGAACCGGACTCAAGCGCTGGGATAGGGA AGTCTGGTGCAGCCCGGCAAGAAG
329	AAV9_capsid 1 44-193	CCGGTTCGAACAATCACCGCAGGAACCGGACTCATCAGCGGG GATCGGAAAAAGTGGCGCCAGCCGGCTAAAAAACGTCTGA ATTTTGGGCAGACCGGCGATACTGAATCAGTTCCGGACCCG CAGCCGATTGGCGAACCGCCGGCG
330	AAV9_capsid 1 68-217	AAACGCCTGAACCTTTGGCCAAACGGGGGACACTGAAAGCGT GCCGGATCCGCAGCCGATTGGCGAGCCGCCGGCAGCTCCGT CAGGCGTTGGAAGTCTGACAATGGCGTCAGGTGGCGGCGCT CCGGTTGCAGATAACAACGAAGGC
331	AAV9_capsid 1 92-241	GCGGCTCCGTCTGGAGTCGGATCTTTAACTATGGCATCTGGC GGTGGAGCTCCGGTCGCCGATAACAACGAAGGAGCCGACG GTGTGGGCAGCTCTTCTGGGAACCTGGCATTGTGACTCTCAAT GGCTGGGTGATCGTGTTATCACT
332	AAV9_capsid 2 16-265	GGCGCTGATGGCGTAGGTTCTTCAAGTGGGAATTGGCATTG TGATTCTCAATGGCTGGGTGATCGCGTTATCACTACAAGTAC ACGTACATGGGCGCTGCCGACATATAACAATCATTTATACA AACAGATTAGCAACTCTACATCT
333	AAV9_capsid 2 40-289	ACAACAAGCACGCGTACATGGGCGCTGCCGACCTATAACAA TCATCTTTATAAACAGATAAGCAATTCAACTAGCGGGGGAA GCAGCAACGATAACGCGTATTTTGATATAGTACGCCGTGG GGTTACTTTCGATTTCAATCGCTTT
334	AAV9_capsid 2 64-313	TCAGGCGGTAGCAGTAATGACAACGCGTATTTTGGTTATAG CACCCCGTGGGGTTATTTTGATTTCACCCGCTTTCATTGCCA TTTCAGCCCGCGTGACTGGCAGCGCTTGATAAATAATAATTG GGGCTTCCGTCCGAAGCGCCTG
335	AAV9_capsid 2 88-337	TTTCATTGTCATTTCTCACCGCGCGACTGGCAACGCCTTATA AACAATAACTGGGGCTTTCGTCCGAAACGTCTTAACCTTAAA CTTTTCAATATACAAGTCAAAGAGGTTACCGATAATAATGG CGTTAAAAACAATCGCAACAAC
336	AAV9_capsid 3 12-361	CTTAATTTTAAATTATTCAACATCCAGGTCAAAGAGGTCACC GACAATAATGGAGTAAAAACCATAGCAACAATCTGACAA GTACTGTGCAGGTTTTTACGGATAGCGATTATCAGTTACCGT ATGTGTTGGGCAGCGCTCATGAA
337	AAV9_capsid 3 36-385	AACCTTACGAGCACCGTACAAGTGTTTACTGATAGTGATTAT CAGCTGCCGTACGTATTAGGAAGTGCCCATGAAGGGTGTTT GCCGCCGTTCGCCGGGACGTGTTTATGATCCCGCAGTATGG ATATCTTACGTTGAATGATGGA

SEQ ID NO:	Name	Sequence
338	AAV9_capsid 3 60-409	GAAGGTTGTCTGCCGCCGTTTCCGGCAGACGTCTTTATGATT CCGCAGTACGGATACCTTACCTTGAACGATGGTTCTCAGGC GGTTGGTCGCTCAAGTTTTTACTGTCTGGAATATTTCCCGAG TCAGATGCTGCGTACCGGAAAT
339	AAV9_capsid 3 84-433	GGGAGCCAGGCGGTGGGACGTTTCATCATTCTACTGCCIGGA ATATTTTCCGAGTCAGATGTTACGTACCGGGAATAACTTTCA GTTCTCATATGAATTTGAGAATGTCCGTTCCATTCTTCTTAC GCGCATCTCAGAGCCTGGAC
340	AAV9_capsid 4 08-457	AATAACTTCCAGTTTATGTTATGAATTTGAAAACGTGCCGTTT CATTCAAGCTACGCGCATAGCCAGAGTTTATGATCGTCTGAT GAATCCGCTGATCGATCAGTATCTGTACTACCTGAGCAAAA CCATTAATGGCTCTGGCCAGAAC
341	AAV9_capsid 4 32-481	GATCGCTTAATGAACCCGCTTATTGATCAATACTTATATTAT CTTTCAAAAACGATCAATGGAAGTGGTCAGAACCAACAGAC CCTGAAATTTTCAGTTGCGGGTCCGTCTAATATGGCTGTCCA GGGGCGCAACTACATTCCGGGT
342	AAV9_capsid 4 56-505	AATCAGCAGACGTTGAAATTTTCAGTTGCCGGACCGTCTAAT ATGGCCGTTTCAGGGACGCAATTACATTCCGGGTCCGTCTTAT CGTCAACAGCGCGTGAGTACAACGGTGACACAAAATAATAA TTCAGAGTTTGCATGGCCGGGT
343	AAV9_capsid 4 80-529	GGTCCGAGCTATCGCCAGCAACGTGTGAGCACGACCGTTAC GCAGAATAATAACAGTGAATTTGCCTGGCCGGGTGCTTCTA GCTGGGCATTAAATGGGCGTAATAGTCTGATGAATCCGGGA CCGGCAATGGCTAGCCATAAAGAA
344	AAV9_capsid 5 04-553	GGGGCATCTTCTTGGGCTTTAAACGGTCGCAACAGCTTAATG AACCCGGGCCCGGCTATGGCGTCACATAAGGAAGGCGAAG ACCGTTTTTTCCCGTTGAGCGGGTCTTTGATTTTCGGCAAGC AGGGTACAGGCCGTGACAACGTT
345	AAV9_capsid 5 28-577	GAAGGGGAAGACCGTTTCTTTCCGCTGAGCGGGAGCTTGAT TTTCGGGAAGCAGGGACAGGACGCGATAATGTTGACGCCG ACAAGGTTATGATAACAAATGAAGAAGAGATAAAAAACAAC CAATCCGGTTGCCACCGAAAGTTAT
346	AAV9_capsid 5 52-601	GTTGATGCTGACAAGGTGATGATTACAAACGAGGAGGAGAT TAAACCACTAATCCGGTCGCCACCGAAAGTTACGGTCAGG TTGCAACAAACCATCAGTCAGCACAGGCGCAGGCCCAAACG GGCTGGGTTTCAGAATCAGGGTATT
347	AAV9_capsid 5 76-625	TACGGTCAAGTTGCAACAAACCATCAGTCAGCACAGGCCCA GGCGCAAACCTGGATGGGTACAAAACCAAGGTATCTTACCGG GGATGGTCTGGCAAGACCGCGATGTGTATCTGCAAGGCCCG ATTGGGCGAAAATTCCGCATACC
348	AAV9_capsid 6 00-649	ATTTTACCGGGAATGGTTTGGCAGGATCGCGATGTATATTTA CAAGGGCCGATCTGGGCCAAGATCCCGCATACTGATGGA CTTCCATCCGTCTCCGCTGATGGGTGGATTTGGGATGAAACA TCCGCCGCCGAGATCCTGATC
349	AAV9_capsid 6 24-673	ACCGATGGGAACTTTCATCCGTCTCCGTTAATGGGAGGGTTC GGAATGAAACATCCGCCGCCGCAAATTCTGATCAAAAATAC CCCGGTGCCGGCGACCCGCCGACCGCCTTTAATAAAGATA AATTAACCTCATTTATCACCCAG
350	AAV9_capsid 6 48-697	ATTAAAAATACACCGGTCCCGGCCGACCCGCCGACGGCATT TAACAAGGATAAGTTAAATTCTTTTATAACACAGTACAGCA CGGGCCAGGTACGCGTGAAATTGAGTGGAATTACAAAAG GAAAACCTCTAAACGCTGGAATCCG

SEQ ID NO:	Name	Sequence
351	AAV9_capsid 672-721	CAGTATTCTACTGGTCAGGTTTCAGTTGAGATTGAATGGGAGCTGCAAAAAGAAAACAGCAAACGCTGGAACCCGGAAATACAGTATACAAGTAATTATTACAAATCTAACAAACGTCGAATTTGCCGTGAATACCGAAGGTGTCTAC
352	AAV10_capsid 0-49	ATGGCTGCAGATGGGTACTTGCCGGATTGGTTAGAGGATAACCTGAGTGAAGGGATCCGCGAATGGTGGGATCTGAAACCGGGGGCGCCGAAACCGAAAGCGAATCAACAAAAACAGGACGATGGTCTGGATTGGTCTTACCGGGA
353	AAV10_capsid 24-73	CTGAAGCCGGGTGCGCCGAAGCCGAAGGCAAAATCAGCAGAGCAGGACGACGCTGGCCTGGTTCTGCCGGGTACAAAGTATCTGGGTCCGTTCAACGGACTGGATAAGGGTGAACCGGTGAACGCGCAGACGACGAGCTCTT
354	AAV10_capsid 48-97	GGTTACAAATATTTAGGTCCGTTCAACGGTCTGGATAAAGGCCGAACCGGTAAACGCGCGGATGCAGCAGCTCTTGAACATGACAAAGCATATGATCAACAACCTGAAGGCTGGTGATAATCCGTACTTACGTTATAATCATGCCGAT
355	AAV10_capsid 72-121	TTGGAACATGATAAGGCTTACGACCAGCAATTGAAAGCAGGAGATAACCCGTACCTGCGTTATAACCATGCCGATGCAGAGTTCCAAGAACGCTTGCAGGAAGACACGTCATTCGGTGGGAATCTTGGGCGTGCCGTGTTCCAAGCC
356	AAV10_capsid 96-145	GATGCTGAGTTTCAGGAACGTCCTCAGGAAGATACCAGTTTGGTGGAATCTGGGTGCGCTGTTTTCCAGGCCAAGAAACGCGTGTTGGAACCGCTGGGATTGGTAGAAGAGGCGGCAAAAACGGCGCCGGGCAAAAAGCGTCCG
357	AAV10_capsid 120-169	GCCAAAAAACGTGTGCTGGAACCGCTGGGCTTAGTTGAAGAGGCTGCGAAGACCGCCCCGGGCAAAAACGTCGGTGGAAACCGTCTCCGACGCTCTCCGACTCTTCTACCGGCATTGGCAAGAAGGGCCAGCAGCCGGCAAAA
358	AAV10_capsid 144-193	CCGGTAGAACCGTCACCGCAGCGTTCTCCGGATAGTAGTACGGGGATCGGTAAAAAGGGGCAAGCAGCCGGCAAAAAGCGCTTAATTTCCGTCAAACCTGGTGAAAGCGAATCTGTGCCGATCCGCAGCCGATAGGGGAACCGCCG
359	AAV10_capsid 168-217	AAAAAACGTTTAAACTTTGGTCAGACAGGAGAAAGTGAGAGTGTCGCCGACCCGACGCGATTGGAGAGCCCGCGCAGGACCGAGTGGATTAGGTAGCGGGACTATGGCGCAGGAGGTGGTGCACCGATGGCGGACAATAACGAG
360	AAV10_capsid 192-241	CCGGCGGGACCGTCAGGATTGGGAAGCGGTACTATGGCGGCGGGCGGTGGTGCCCCGATGGCGGATAATAACGAAGGCGCGGACGGAGTGGGTAGTAGCTCTGGTAATTGGCATTGTGATAGCACTTGGCTTGGTGACCGTGTGATT
361	AAV10_capsid 216-265	GAAGGCGCAGATGGCGTTGGCTCTAGTTCAGGGAATTGGCA TTGTGACTCAACATGGCTGGGTGATCGTGTAATTACGACTAGTACCCGCACCTGGGCACTGCCGACTTATAATAATCATTTATA TAAACAGATTAGCAACGGAAACC
362	AAV10_capsid 240-289	ATAACTACGTCAAACCTCGTACCTGGGCGCTTCCGACGTACAATAATCATCTGTACAAACAAATTAGCAACGGGACATCTGGAGGAGTACTAATGATAACACGTATTTTGGCTACAGTACGCCGTGGGGCTATTTTGATTTTAACCGT
363	AAV10_capsid 264-313	ACCTCAGGCGGTAGCACGAATGATAATACTTACTTTGGATACCTCAACTCCGTGGGGTTACTTTGATTTCAATCGTTTTTCATTGCATTTTCAGCCCGCTGACTGGCAGCGTTTGATAAATAACAA TTGGGGTTTTCTGCCGAAGCGT

SEQ ID NO:	Name	Sequence
364	AAV10_capsid 288-337	CGCTTTCATTGTCATTTTCAGTCCGCGTGAAGTGGCAGCGTTTA ATCAACAATAATTGGGGATTCCGTCCGAAGCGTCTGTCTTTC AACTGTTCAACATTCAGGTGAAAGAAGTCACCCAAAATGA AGGTACCAAAACCATCGCTAAT
365	AAV10_capsid 312-361	CGTCTGTCAATTTAAGTTGTTTAATATCCAGGTAAAAGAAGTA ACGCAAAACGAGGGGACTAAAACGATTGCAATAATCTGAC CTCTACCATTCAAGTGTTCACCGATAGCGAATATCAACTGCC GTATGTGCTTGGAAGCGCACAT
366	AAV10_capsid 336-385	AACAACCTTGACCTCTACCATTTCAGGTTTTTCACAGATTTCAGAA TACCAATTACCGTACGTCCTGGGCAGCGCTCATCAAGGCTG CTTGCCGCGGTTTTCCGGCGGATGTGTTTCATGATACCGCAATA TGGCTATCTTACGCTGAATAAT
367	AAV10_capsid 360-409	CATCAGGGGTGTCTTCCGCGGTTTCCGGCAGATGTATTTATG ATTCCGCAATACGGTTATCTGACATTAACAACGGATCACA GGCCGTGCGTCGCAGCTCTTTCTACTGTCTTGAATACTTCCC GTACACAGATGTTGCGCACCGGG
368	AAV10_capsid 384-433	AACGGTAGTCAGGCGGTGGGTCGTAGCTCATTTTTATTGCTTG GAATATTTCCGTCTCAAATGTTACGTACAGGGAATAACTTT GAATTTTCATATACCTTCGAAGATGTTCGTTTTCAITCATCTT ACGCACATAGCCAGTCATTA
369	AAV10_capsid 408-457	GGTAATAACTTTGAATTTAGCTATACGTTTGAGGATGTACCG TTTCATAGCTCTTATGCACATAGCCAAAGCCTGGACCGCCTG ATGAACCCGTTGATTGATCAGTATCTTTATTATCTTTCTCGC ACACAGTCTACTGGAGGCACG
370	AAV10_capsid 432-481	TTAGACCGTCTTATGAACCCGCTTATCGATCAGTACCTGTAC TATCTGAGTCGTACGCAGAGCACAGGGGGAACCTCAGGGCAC ACAACAGTTATTGTTTAGTCAGGCAGGCCCGGCCAATATGT CTGCGCAAGCCAAGAATTGGTTA
371	AAV10_capsid 456-505	ACCCAGGGCACGCAGCAGCTTTTATTCTCACAGGCCGTCC GGCAAAACATGAGCGCGCAGGCCAAGAATTGGCTGCCGGGTG CGTGCTACCGTCAACAACGCGTCTCTACGACCTTGAGCCAG AATAACAATAGCAACTTTGCTTGG
372	AAV10_capsid 480-529	CTTCCGGGACCGTGTTATCGTCAACAGCGTGTCTCTACAAC TTATCTCAGAATAATAATAGCAATTTTCGATGGACCGGAGC TACAAAGTATCATCTGAACGGACGTGATTCACTGGTTAATCC GGGTGTGCGGATGGCAACCCAT
373	AAV10_capsid 504-553	TGGACCGGCGCGACAAAGTACCATCTGAACGGCCGTGATAG CCTGCTGAATCCGGGTGTTGCAATGGCGACGCATAAAGATG ATGAGGAGCGTTTTTTTCCGTCTTCAGGGGTATTGATGTTTCG GAAAACAGGGCGCTGGTCTGTAT
374	AAV10_capsid 528-577	CATAAGGATGATGAAGAGCGTTTCTTCCCGAGCAGCGGGGT TTTGATGTTCCGTAACAGGGGGCTGGCCGCGATAATGTGG ATTATAGCAGCGTCATGCTGACGAGCGAAGAAGAGATCAAG ACAACCAACCCGGTCCGCGACTGAA
375	AAV10_capsid 552-601	GACAACGTCGATTATAGTAGCGTTATGCTGACATCTGAGGA AGAGATCAAACTACTAATCCGGTGGCCACAGAGCAATATG GTGTCGTTGCGGACAATCTGCAACAGGCGAACACCGGCCCCG ATTGTAGGTAACGTCAATTCTCAG
376	AAV10_capsid 576-625	GAACAGTATGGTGTAGTAGCCGATAATTTGCAACAGGCGAA TACCGGACCGATCGTCGGGAATGTGAATAGCCAAGGCGCAC TGCCGGGGATGGTCTGGCAGAATCGCGACGTTTACCTGCAG GGTCCGATCTGGGCGAAGATCCCCG

SEQ ID NO:	Name	Sequence
377	AAV10_capsid 600-649	CAAGGTGCCCTTCCGGGCATGGTCTGGCAGAATCGTGACGT ATATTTGCAGGGTCCGATCTGGGCGAAGATACCGCATACTG ACGGGAATTTTCATCCGTCTCCGTGATGGGTGGCTTCGGCT TAAACATCCGCCGCCGAGATA
378	AAV10_capsid 624-673	CCGCATACAGACGGTAATTTCCATCCGTCTCCGCTTATGGGT GGATTTGGTTTGAAACATCCGCCGCCGAGATTTTGATTAAA AATACCCCGGTGCCGGCCGATCCGCCGACCACATTAGCCA AGCAAACTGGCCTCTTTTATA
379	AAV10_capsid 648-697	ATTCTGATTAATAAATACGCCGGTTCGGCGGACCCGCCGAC GACATTTAGCCAAGCTAACTTGCCAGCTTTATAACACAGT ATAGCACCGGACAGGTAAAGTGTAGAAATTGAATGGGAGCTG CAGAAAGAAAAATAGCAAACGCTGG
380	AAV10_capsid 672-721	ATTACGCAGTACAGCACTGGACAGGTGTCAGTGGAATAGA ATGGGAACTGCAGAAAGAAAACAGCAAACGCTGGAACCCG GAAATCCAGTACACCAGCACTACTACAAAAGTACCAATGT GGATTTTGCACTGAATACAGAAGGA
381	AAV11_capsid 0-49	ATGGCGGCGGATGGCTACTTGCCGGATTGGCTGGAAGATAA CTTAAGTGAGGGCATTCTGAATGGTGGGACGTGAAACCGG GTGCACCGAAACCGAAGGCAAACAGCAAAAACAGGATGA CGGCCGCGGGTTGGTATTACCGGGG
382	AAV11_capsid 24-73	CTGAAACCGGGAGCTCCGAAACCGAAAGCTAATCAACAGA AACAGGATGATGGTCGCGGTTTAGTCCTGCCGGGTATATAA TACCTGGGCCCCTTTAACGGCCTGGATAAAGGTGAACCGGT GAATGCTGCTGATGCCGCTGCTCTG
383	AAV11_capsid 48-97	GGTTATAAATATTTAGGACCGTTTAATGGTTTAGATAAGGGT GAACCGTTAATGCCGCAGATGCAGCCGCGCTTGAACATGA TAAAGCGTATGACCAACAATTAAGCGGGAGATAAACCGT ATTACGTTATAATCATGCTGAT
384	AAV11_capsid 72-121	CTTGAACATGATAAGGCCTATGACCAGCAGCTTAAAGCAGG AGATAATCCGTACCTGCGTTATAATCATGCCGACGCCGAATT TCAGGAGCGCTTGCAGGAAGATACGTCTTTTGGGGGCAACC TTGGACGTGCAGTTTTTCAGGCT
385	AAV11_capsid 96-145	GACGCGGAATTTTCAGGAGCGTTTACAGGAAGATACCAGCTT CGGGGGTAATCTTGGTCGCGCTGTTTTTCAGGCTAAGAAAC GTGTGCTGGAGCCGTTGGGATTGGTCGAAGAGGGTGCGAAG ACAGCGCCGGGAAAGAAACGTCCG
386	AAV11_capsid 120-169	GCGAAAAAACGTGTTCTGGAGCCGCTGGGACTTGTTGAAGA GGGTGCGAAAACCGCCCCGGGAAAAAAGCGCCCGTTAGAG AGTCCGCAAGAACCGGATTCATCATCTGGTATCGGGAAAAA AGGAAAAACAGCCGGCGCGCAAACGT
387	AAV11_capsid 144-193	CCGCTTGAAAGCCCGCAAGAGCCGGATTCTAGTAGCGGAAT TGGGAAGAAAGGCAAACAGCCGGCCCGCAAACGTTTAAATT TCGAGGAAGATACTGGTGCAGGCGACGGACCGCCGGAAGG AAGCGATACCTCAGCCATGTCATCA
388	AAV11_capsid 168-217	CGTCTGAATTTTCAGGAGGATACTGGCGCGGGTGATGGGCC GCCGGAGGGCAGCGACACCTCAGCAATGAGCAGCGACATC GAAATGCGCGCGGCTCCGGGAGGTAACCCGTAGATGCGGG GCAGGGGTCAGACGGTGTGGGGAAT
389	AAV11_capsid 192-241	TCTGATATAGAAATGCGTGCCGCCCGGGTGGAATGCGGT CGATGCGGGACAGGGGAGCGATGGCGTGGGCAACGCGAGC GGTGATTGGCATTGCGATAGTACATGGTCAGAAGGGAAGGT CACAACAACGTCTACGCGCACATGG

SEQ ID NO:	Name	Sequence
390	AAV11_capsid 216-265	AATGCTTCAGGTGATTGGCATTGTGATTCAACCTGGTCTGAA GGCAAGGTAACCTACAACCTCTACACGTACGTGGGTTTTGCC GACCTATAATAACCATCTTTACTTACGCTTGGGGACAACCAG TAGCTCTAATACCTATAATGGC
391	AAV11_capsid 240-289	TGGGTTCGCGGACGTACAATAATCATCTTTACCTGCGTCTG GGTACCACATCTAGTTCTAATACGTATAATGGGTTGAGCAGC CCGTGGGGATATTTTGACTTTAATCGTTTCCATTGTCATTCT CACCGCGCGATTGGCAGCGT
392	AAV11_capsid 264-313	GGCTTCAGCAGCGCGTGGGGCTATTTTCGATTTCAACCGCTTC CATTGTCAATTCAGCCCGCGTGATTGGCAGCGCCTTATCAAT AACAACTGGGGCCTGCGCCGAAAGCCATGCGTGTGAAAAT TTTTAACATCCAAGTAAAGGAA
393	AAV11_capsid 288-337	CGTCTGATAAACAATAACTGGGGATTGCGTCCGAAAGCAAT GCGCGTTAAGATCTTTAATATACAAGTTAAAGAAGTTACGA CCAGTAATGGAGAAACGACGGTTGCAAAACAACCTTACGAGC ACGGTCCAGATCTTTGCCGACAGC
394	AAV11_capsid 312-361	GAAGTGACAACGTCTAATGGCGAGACAACCGTTGCAAACAA CCTGACCAGCACAGTTCAAATCTTCGCGGACTCTAGTTATGA ATTGCCGTATGTAATGGACGCAGGGCAGGAAGGAAGTTTAC CGCCGTTCCCGAATGACGTGTTT
395	AAV11_capsid 336-385	AGCAGCTACGAACCTGCCGTATGTGATGGATGCCGGACAGGA AGGTTCAATACCGCCGTTCCCGAATGACGTGTTTATGGTCCC GCAGTATGGTTACTGCGGTATTGTGACGGGCGAAAAATCAAA ACCAAACCGATCGCAATGCGTTC
396	AAV11_capsid 360-409	TTTATGGTTCGCGAGTATGGCTATTGTGGTATTGTAACCGGT GAAAATCAAAATCAGACAGATCGCAATGCGTTTTATTGTCT GGAGTATTTCCCGTCTCAGATGCTGCGCACCGGTAACAATTT TGAAATGGCATATAACTTCGAG
397	AAV11_capsid 384-433	TTTTATTGTTTAGAGTATTTCCCGAGCCAGATGCTGCGTACA GGTAATAATTTTGAGATGGCTTACAATTTGAAAAAGTTCCG TTCCATAGTATGTATGCGCATTCTCAGAGCCTGGACCGCCTT ATGAATCCGTTATTGGATCAA
398	AAV11_capsid 408-457	GAGAAAGGTACCGTTCCATAGCATGTATGCTCATAGCCAGAG CCTTGACCGCCTTATGAATCCGTTGTTAGACCAGTATCTTTG GCATCTGCAGTCAACGACGAGCGGCGAGACCTTAAATCAGG GGAACGCCGCCACAACGTTCCGGC
399	AAV11_capsid 432-481	CAGTATTTGTGGCATTTACAGAGCACAAACGAGCGGAGAGAC TTTGAATCAAGGCAACGCGGCGACGACGTTTGGGAAAATAC GTTCTGGCGATTTTGCTTTTTATCGCAAAAACCTGGTTACCGG GTCCGTGCGTTAAACAACAACGT
400	AAV11_capsid 456-505	GGAAAGATCCGCTCTGGCGATTTTCGCATTTATCGCAAAAAT TGGCTGCCGGGTCCGTGTGTAAAACAGCAACGCTTCAGCAA AACCGCAAGCCAGAACTATAAAATACCGGCCTCTGGTGGCA ATGCTCTGCTGAAATATGACACG
401	AAV11_capsid 480-529	CGTTTTTCAAAAACCTGCGAGCCAGAATTATAAAATTCCGGCT AGTGGCGGAAACGCCCTTCTGAAGTATGACACACATTATAC ATTGAACAACCGCTGGAGCAATATTGCTCCGGGACCGCCGA TGGCCACTGCCGGTCCGAGTGAT
402	AAV11_capsid 504-553	ACGCATTATACGCTTAATAACCGTTGGTCAAAATATTGCACCG GGTCCGCCGATGGCTACAGCGGGTCCGAGCGATGGGGATT TAGCAATGCACAGTTAATTTCCCGGGTCCGAGTGTACCCGG TAATACCACTACGAGCGCGAAC

SEQ ID NO:	Name	Sequence
403	AAV11_capsid 528-577	GATGGGGACTTTTCAAACGCGCAGCTGATCTTCCGGGGGCC GAGCGTTACTGGAAATACCACTACGTCAGCAAACAACCTGC TGTTTACCAGCGAAGAAGAAATCGCCGCTACCAATCCGCGC GATACCGACATGTTCCGGTCAGATC
404	AAV11_capsid 552-601	AATAATTTATTATTCACGTCAGAGGAAGAGATTGCTGCTAC GAACCCGCGCGATACGGACATGTTCCGGTCAGATCGCAGATA ATAACCAAAAACGCCACGACTGCCCGATTACAGGAAATGTG ACTGCGATGGGTGTGTTACCGGGT
405	AAV11_capsid 576-625	ATTGCCGACAACAATCAGAACGCGACGACTGCCCGGATCAC CGGAAACGTGACCGCCATGGGGGTGCTTCCGGGCATGGTTT GGCAGAACCGTGATATTTATTATCAAGGCCGATCTGGGCA AAAATTCGCGATGCCGATGGTCAT
406	AAV11_capsid 600-649	GGCATGGTGTGGCAGAACCGTGACATTTATTATCAGGGTCC GATCTGGGCCAAAATCCCGCATGCAGATGGTCATTTCCATCC GTCACCGCTGATCGGGGGCTTCGGATTAAAGCATCCGCCGC CGCAGATATTTATTAATAAATACA
407	AAV11_capsid 624-673	CATTTTCATCCGAGCCCGCTGATTGGCGGGTTCGGGGCTTAAA CATCCGCCGCCGCGAGATTTTATCAAGAATACCCCGGTCCCG GCGAATCCGGCCACCACCTTCACGGCAGCGCGTGTGATAG TTTTATTACACAGTACTTACT
408	AAV11_capsid 648-697	ACACCGGTGCCGGCAAATCCGGCAACAACGTTTACTGCAGC GCGCGTTGATTCTTTTATTACACAATATTCTACTGGTCAGGT TGCGGTGCAGATTGAATGGGAAATCGAGAAGGAGCGCTCAA AACGTTGGAATCCGGAAGTCCAA
409	AAV11_capsid 672-721	ACGGGTCAGGTCGCAGTCCAGATCGAATGGGAAATTGAGAA GGAACGTAGCAAACGTTGGAATCCGGAAGTCCAGTTTACGA GCAACTACGGAAACCAATCTTCAATGCTGTGGGCGCCGGAC ACCACCGGGAATATACCGAGCCG
410	AAV12_capsid 0-49	ATGGCCGCCGATGGATATCTGCCGGATTGGCTTGAAAGATAA TCTTAGTGAAGGGATACGTGAGTGGTGGGCATTGAAGCCGG GCGCCCCGCAACCGAAAGCAAACCAGCAGCATCAGGATAA CGGACGCGGCTTGGTCCTTCCGGGT
411	AAV12_capsid 24-73	CTGAAACCGGGCGCACCGCAGCCGAAAGCGAATCAGCAAC ATCAAGATAACGGCCGTGGCCTTGTCTTCCGGGATACAAA TATCTGGGTCCGTTTAAATGGCTGGACAAGGGTGAGCCGGT AAATGAAGCTGATGCAGCAGCGTTA
412	AAV12_capsid 48-97	GGATATAAATACCTGGGCCCCGTTCAACGGTTTAGATAAGGG TGAACCGGTGAATGAAGCAGATGCAGCAGCGTTAGAACATG ATAAAGCCTATGACAAACAGCTGGAGCAGGGTGACAATCCG TACCTGAAATATAATCATGCGGAC
413	AAV12_capsid 72-121	CTGGAGCATGACAAGGCATATGATAAACAACCTGGAACAAG GCGACAATCCGTATCTTAAGTACAACCATGCCGATGCAGAA TTTCAACAGCGCTTAGCAACCGATACTTCATTTGGTGGAAT CTTGGCCGCGCAGTATTTACAGGCC
414	AAV12_capsid 96-145	GACGCAGAATTTTACGACGCGCTTGGCAACCGATACATCTTTT GGAGGTAACCTGGGCCGTGCGGTTTTTCAGGCAAAGAAACG TATCCTGGAGCCGCTTGGCCTGGTTGAGGAGGGCGTTAAAA CAGCCCCGGGGAAGGCGCCCG
415	AAV12_capsid 120-169	GCCAAAAACGTATATTAGAGCCGCTGGGGCTGGTTGAGGA GGGGGTTAAACTGCACCGGGCAAGAAACGCCCGTTGGAG AAAACGCCGAACCGCCCGACAAACCCGGACAGCGGGGAAAG CACCGGCTAAAAAAAACAAAAAGAT

SEQ ID NO:	Name	Sequence
416	AAV12_capsid 144-193	CCGCTTGAGAAGACCCCGAATCGTCCGACCAATCCGGATAG TGGGAAAAGCTCCGGCTAAAAAAAAGCAGAAAGATGGAGAG CCGGCCGATAGTGCTCGTCGCACATTAGACTTTGAAGATAG CGGCGCGGGCGATGGACCGCCGGAA
417	AAV12_capsid 168-217	GATGGCGAGCCGGCGGACTCTGCTCGCCGTACCCCTGGATTIT GAAGATAGCGGAGCTGGGGACGGGCCCGCGGAAGGAAGCA GCAGCGGAGAAAATGTCACATGATGCAGAAAATGCGCGCAGC ACCGGGGGGGAATGCAGTCGAGGCC
418	AAV12_capsid 192-241	GAAGGTTCTAGCTCTGGGGAAATGAGCCATGATGCGGAGAT GCGTGCCGCACCGGGTGGCAATGCCGTGAGGCTGGTCAGG GTGCTGATGGGGTGGGCAACGCGTCTGGCGACTGGCATTGT GACAGTACTTGGAGCGAAGGTCGC
419	AAV12_capsid 216-265	GCGGGACAAGGGGCGAGATGGTGTGGGCAACGCCTCTGGGG ATTGGCATTGTGATAGTACTTGGAGTGAGGGACGTGTCACG ACAACGAGCACCCGTACTTGGGTGTTACCGACCTATAATAA TCATCTGTATCTGCGCATAGGCACT
420	AAV12_capsid 240-289	CGCGTAACAACAACAAGTACTCGCACATGGGTATTGCCGAC TTATAACAATCATCTTTACCTGCGTATAGGCACGACCGCCAA TAGTAACACATACAATGGTTTTTCTACACCGTGGGGCTACTT CGACTTTAATCGCTTCCATTGT
421	AAV12_capsid 264-313	ACTACTGCCAATAGCAATACTTATAATGGCTTCAGCACTCCG TGGGGATATTTTGACTTTAACCGTTTCCATTGCCATTTTAGTC CGCGCGACTGGCAACGTCTGATTAACAACAACGGGGCCTG CGTCCGAAGTCTATGCGTGTG
422	AAV12_capsid 288-337	TGCCATTTTTCTCCGCGCGACTGGCAGCGCCTTATTAATAAT AACTGGGGCCTGCGCCCGAAAAGTATGCGCGTAAAAATTTT CAATATACAGGTCAAAGAAGTTACTACTTCTAACGGTGAAA CTACGGTCGCTAACAATTTAACT
423	AAV12_capsid 312-361	GTCAAAATCTTTAACATTCAGGTGAAAGAGGTAAACGACCAG CAATGGAGAAAACAACGGTCGCCAACAATCTGACAAGCACA GTACAAATTTTTGCCGACTCTACTTATGAGCTTCCGTATGTC ATGGATGCTGGCCAGGAGGGAAAGT
424	AAV12_capsid 336-385	ACCTTACC GTTCAAATTTTGCTGATAGCACCTACGAAC TT CCGTATGTTATGGACGCGGGACAGGAGGGTAGTTTTCCGCC GTTCCGAACGACGTCCTTATGGTCCCGCAATACGGCTACTG TGGTGTAGTGACCGGTAAAAAC
425	AAV12_capsid 360-409	TCCTTCCCGCCGTTTCCGAATGACGTGTTTCATGGTACCGCAA TACGGCTACTGTGGTGTGGTCACAGGGAAAAACCAAACCA GACGGATCGTAATGCATTCTATTGCTTGAATACTTCCCGTC TCAGATGTTACGCACCGGAAAT
426	AAV12_capsid 384-433	AATCAGAATCAGACAGACCGCAATGCATTCTATTGTTTGGGA ATATTTTCCGAGCCAGATGCTGCGTACAGGTAATAATTTCGA AGTGTCTTATCAGTTCGAGAAGGTTCCGTTTCATTCAATGTA TGCGCATAGCCAATCACTTGAT
427	AAV12_capsid 408-457	AACAAC TTTGAAGTTTCATATCAGTTTGAAAAGGTCCCGTTT CATTCAATGTACGCACATTCACAGTCATTGGACCGCATGATG AACCCGCTGTTGGATCAGTATTTATGGCATTACAGAGTACT ACAAC TGGTAACAGTCTGAAT
428	AAV12_capsid 432-481	GATCGCATGATGAATCCGTTACTTGATCAATATCTGTGGCAT CTGCAGTCAACTACTACTGGAAATCTCTGAACCAAGGTAC AGCGACCACTACTTATGGGAAGATCACAAACGGGCGACTTTG CTTATTATCGTAAAAACTGGTTA

SEQ ID NO:	Name	Sequence
429	AAV12_capsid 456-505	AACCAGGGGACGGCTACTACAACGTATGGAAAAATTACGAC TGGTGACTTCGCATATTATCGTAAAAATTGGCTGCCGGGTGC CTGTATAAAACAGCAGAAATTCTCTAAGAATGCAAACCAGA ATTACAAGATCCCCGGCTAGCGGT
430	AAV12_capsid 480-529	CTGCCGGGCGCATGCATTAAACAACAGAAATTTCAAAGAA TGCTAATCAAAATTATAAAATTCGGGCTTCTGGGGGAGACG CATTATTGAAATATGATACGCATACTACGCTGAATGGTCGTT GGICTAACATGGCGCCGGGCCCCG
431	AAV12_capsid 504-553	GGGGGCGATGCCCTGTAAAGTATGATACTCATACCACACT GAACGGCCGTTGGAGTAATATGGCACCGGGTCCGCCGATGG CTACAGCAGGAGCCGGCGATTCTGACTTTTCTAACTCTCAGC TTATTTTCGCTGGGCCGAATCCG
432	AAV12_capsid 528-577	CCGCCGATGGCAACCGCAGGGGCGGGTGATTCAGACTTTTC AAACAGTCAGTTAATTTTCGCCGGACCGAATCCGAGCGGAA ATACTACGACGTCAAGTAATAACCTTTTATTTACCTCAGAGG AAGAGATTGCCACTACCAATCCG
433	AAV12_capsid 552-601	CCGTCAGGTAACACCACAACGTCTAGCAATAACCTGTTATTT ACATCAGAAGAAGAAATAGCCACGACAAATCCGCGTGACA CGGACATGTTTGGCCAAATTGCTGACAATAATCAAAATGCG ACCACCGCTCCGCATATAGCTAAC
434	AAV12_capsid 576-625	CCGCGCGACACAGATATGTTCCGGTCAAATTGCTGATAATAA CCAGAATGCCACTACAGCGCCGCATATAGCAAATCTGGACG CGATGGGTATAGTTCCGGGAATGGTATGGCAGAACCGCGAT ATTTACTATCAAGGGCCGATATGG
435	AAV12_capsid 600-649	AATTTAGACGCGATGGGTATTGTACCGGGTATGGTTTGGCA AAATCGTGACATATATTACCAGGGACCGATATGGGCCAAGG TACCGCATACTGATGGACATTTTCATCCGAGCCCCGTTAATGG GAGGGTTCGGCCTGAAACATCCG
436	AAV12_capsid 624-673	TGGGCTAAAGTACCGCATACTGACGGTCATTTTCATCCGAGT CCGCTGATGGGTGGTTTCGGTCTGAAACATCCGCCGCCGCA AATCTTCATCAAAAACACACCGGTGCCGGCGAACCCGAATA CTACGTTCAGTGCCGCACGCATC
437	AAV12_capsid 648-697	CCGCCGCCGCAAAATTTTATTAAAAATACACCGGTACCGGC CAATCCGAACACCACATTTAGTGCCGCGGTATCAATAGCTT TCTGACGCAGTATAGCACCGGACAAGTCGCTGTGCAGATTG ATTGGGAAATCCAGAAGGAACAT
438	AAV12_capsid 672-721	ATAAACAGTTTCTTGACCCAATATTCAACAGGCCAGGTGGC GGTTCAGATAGACTGGGAGATTAGAAAGAGCATAGCAAAC GTTGGAATCCGGAGGTTCAAGTTCACGTCTAATTATGGAACCC AAAATAGCATGTTATGGGCTCCG
439	AAV13_capsid 0-49	ATGACCGACGGGTATCTGCCGGAAGTGGTTGGAAGATAACTT GTCTGAAGGTGTGCGCGAATGGTGGGCTCTGCAACCGGGCG CACCGAAACCGAAAGCTAATCAGCAGCATCAGGACAACGC ACGTGGCTTAGTTTTACCGGGATAT
440	AAV13_capsid 24-73	CAGCCGGGAGCGCCGAAACCGAAAGCCAACCAGCAACATC AAGATAACGCACGTGGTCTTGTTACCGGGGTATAAGTAT CTTGGCCCGGGAACGGTCTGGACAAAGGTGAACCGGTAA CGCTGCCGATGCCCGGGCATTAGAA
441	AAV13_capsid 48-97	TATAAATATCTGGGCCCGGGCAATGGTCTTGATAAAGGGA GCCGGTTAATGCAGCTGACGCAGCCGCTCTGGAGCATGATA AAGCCTATGATCAGCAACTGAAAGCCGGGGATAACCCGTAC CTGAAGTACAATCATGCTGATGCG

SEQ ID NO:	Name	Sequence
442	AAV13_capsid 72-121	GAACATGATAAGGCGTATGATCAGCAATTAAGCGGGTGA TAATCCGTATCTTAAATATAATCATGCCGATGCAGAGTTTCA AGAACGTTTGCAGGAAGATACGAGTTTCGGCGGAAATCTTG GTCGTGCCGTTTTTCAGGCAAAA
443	AAV13_capsid 96-145	GCCGAATTTTCAGGAGCGTCTGCAGGAAGATACATCATTGG CGGTAACCTAGGTTCGCGCAGTTTTCCAGGCAAAAAACGTA TTCTGGAACCGCTTGGCTTGGTTGAAGAAGCGGCCAAAAACA GCTCCGGGTAAAAAACGTCGGGTG
444	AAV13_capsid 120-169	AAAAAGCGTATTTTGGAAACCGCTGGGCTTAGTAGAAGAAGC GGCGAAAACCGCCCCGGGGAAAAAGCGCCCGGTGGAAACAA AGTCCGGCTGAGCCGATTCTTCAAGTGGTATTGGCAAGAG CGGTCAGCAGCCCGCCCCGCAACGC
445	AAV13_capsid 144-193	GTTGAACAGAGCCCCGGCAGAACCGGACAGTTCTTCTGGGAT TGGTAAATCTGGTCAGCAGCCGGCACGCAACGCCTGAATT TCGGTCAGACGGGTGACACCGAAAGCGTGCCGGATCCGCAG CCGCTTGGTCAACCGCCGGCGGCT
446	AAV13_capsid 168-217	CGTCTGAACCTTCGGGCAGACGGGCGACACTGAAAGTGTGCC GGATCCGCAGCCGCTTGGGCAGCCGGCAGCACCAGCG GGGTTGGCTCAACAACAATGGCAAGCGGTGGTGGTGCACCG ATGGCGGACAATAATGAAGGCGCT
447	AAV13_capsid 192-241	GCTCCGAGCGGTGTTGGGAGCACAACTATGGCGTCTGGCGG CGGCGCCCCGATGGCTGACAACAATGAGGGTGCCGATGGAG TCGGGAACCTCTTCAGGCAACTGGCATTGTGATTCTCAGTGGC TTGGTGACCGTGTAATCACCCT
448	AAV13_capsid 216-265	GCGGATGGCGTTGGCAATAGTTCAGGCAACTGGCATTGTGA TTCTCAGTGGCTGGGTGATCGCGTAATTACCACCAGCACAC GCACATGGGCCCCTGCCGACTTATAACAACCATTATATAAG CAAATATCTAGCCAAAGCGGCGCT
449	AAV13_capsid 240-289	ACTAGTACGCGTACCTGGGCTTTACCGACTTATAATAACCAT TTGTATAAACAGATCAGTTCACAATCAGGAGCTACGAATGA TAATCATTATTTTGGGTATTCTACACCGTGGGGTTATTTGA TTTTAATCGTTTTTCATTGTCAT
450	AAV13_capsid 264-313	GCAACTAATGATAACCATTATTTCCGGCTATAGTACTCCGTGG GGATACTTTGATTTTAATCGTTTCCATTGCCATTTTTCACCGC GCGATTGGCAACGCCTGATTAACAACAATTGGGGTTTCCGT CCGAAACGTCTGAATTTTAAA
451	AAV13_capsid 288-337	CATTTTAGCCCGCGTGATTGGCAGCGTTTAATAAACAACAAT TGGGGTTTTCGCCCGAAGCGCCTGAACTTCAAAGTGTTAAT ATACAGGTCAAAGAAGTAACACAGAATGATGGAACAACAA CCATTGCAACAACCTTACTAGC
452	AAV13_capsid 312-361	AAGTTATTTAATATCCAAGTGAAAGAAGTTACGCAGAACGA TGGCACGACTACAATCGCCAACAATCTGACTTCAACAGTGC AGGTATTCACGGATTCTGAATATCAACTGCCGTATGTGCTGG GATCTGCCCATCAGGGTTGTCTG
453	AAV13_capsid 336-385	TCTACCGTACAAGTTTTTACTGATTGAGAATATCAACTGCCG TACGTTTTAGGCTCAGCTCATCAAGTTGTCTTCCGCCGTTT CCGGCAGATGTTTTTATGGTGCCGCAATATGGATATCTGACG TTGAATAACGGCAGTCAGGCA
454	AAV13_capsid 360-409	TTACCGCCGTTTCCGGCAGATGTTTTATGGTCCCGCAGTAC GGTTATCTTACTCTGAATAACGGCAGTCAAGCTGTTGGACGC AGCAGCTTTTATTGTCTGGAATACTTCCCGAGCCAAATGTTA CCACAGGAAATAATTTTCAG

SEQ ID NO:	Name	Sequence
455	AAV13_capsid 384-433	GCTGTTGGCCGTAGCAGCTTCTATTGTTTGGGAATATTTTCCG AGTCAGATGCTGCGCACCGGCAACAACCTCCAGTTTAGCTA TACCTTCGAAGATGTGCCGTTTCATAGCAGCTACGCTCATAG TCAGTCATTGGATCGCTTAATG
456	AAV13_capsid 408-457	CAGTTTTCATATACGTTTGAAGACGTGCCGTTCCATTCTTCT TATGCCCATAGCCAGTCACTGGATCGTTTAATGAACCCGCTG ATTGATCAATATTTTATACTATTTAAATCGTACCCAGACCGCC TCAGGGACACAGCAGAGTCGC
457	AAV13_capsid 432-481	ATGAACCCGTTAATTGATCAGTACCTGTACTATCTGAACCGC ACTCAAACGGCATCTGGCACTCAGCAAAGTCGCCTGCTGTT CAGTCAGGCGGGTCCGACGAGCATGAGCTTACAGGCCAAAA ACTGGTTGCCGGGACCGTGTAT
458	AAV13_capsid 456-505	CGTCTGCTTTTATGCCAGGCTGGACCGACCTCTATGAGCTTG CAAGCTAAAAATTGGCTGCCGGGCGCGTGCTATCGTCAGCA GCGTCTGTCAAAGCAGGCGAATGATAATAATAATTCAAAC TCCCGTGGACAGGAGCCACTAAG
459	AAV13_capsid 480-529	TACCGCCAACAGCGTCTTAGCAAACAAGCTAACGACAATAA TAATTCAAATTTTCCGTGGACAGGCGCGACAAAATACCATTT AAATGGTCGCGACAGCTTAGTGAACCCGGGTCCGGCGATGG CAAGCCATAAAGATGATAAAGAA
460	AAV13_capsid 504-553	AAATACCATCTGAACGGACGTGATTCAATTAGTGAATCCGGG CCCGGCTATGGCATCACATAAGGATGATAAAGAGAAATTTT TCCCGATGCATGGAACGCTGATTTTGGAAAAAGAGGGTACT AACGCCAATAATGCCGATTTAGAA
461	AAV13_capsid 528-577	GAGAAATTTTTTCCGATGCATGGGACTCTTATATTTGGGAAG GAAGGCACCAATGCTAACAATGCCGACTTAGAAAACGTTAT GATTACCGACGAAGAGGAGATCCGCACCACCAATCCGGTTG CTACCGAGCAGTATGGCACCGTC
462	AAV13_capsid 552-601	GAGAATGTCATGATTACGGATGAAGAAGAAATCCGTACGAC TAATCCGGTGGCGACCGAGCAGTACGGAACAGTGTCTAACA ATCTTCAGAACTCAAACGCCGGTCCGACCACTGGAACCGTG AACCATCAAGGCGCACTGCCGGGC
463	AAV13_capsid 576-625	GTTAGCAATAATTTGCAAAATTCTAACGCGGGTCCGACCAC GGGCACTGTCAATCATCAGGGTGCTCTGCCGGGCATGGTGT GGCAGGACCGCGATGTGTATTTACAGGGTCCGATCTGGGCG AAAATACCGCATACTGATGGTCAT
464	AAV13_capsid 600-649	GGAATGGTTTGGCAAGATCGTGACGTGTACTTGCAGGGACC GATATGGGCAAAAATTCCGCATACAGATGGTCATTCCATC CGTCACCGCTGATGGGAGGTTTTGGCTTAAACATCCGCCG CCGCAATAATGATTAATAATACA
465	AAV13_capsid 624-673	CATTTTCATCCGTCTCCGTTGATGGGAGGCTTCGGCCTGAAA CATCCGCCGCCGCAAATTATGATTAAAAATACGCCGGTTCC GGCCAACCCGCCGACCAACTTCAGTGCTGCAAAATTCGCAA GTTTTATTACACAGTATAGCACT
466	AAV13_capsid 648-697	ACACCGGTTCCGGCAAACCCGCCGACGAATTTTAGTGCAGC AAAAATCGCCAGCTTTATAACCCAGTATTCACGGGACAGG TCAGCGTGGAAATCGAGTGGGAACTGCAGAAGGAAAAACAG CAAGCGCTGGAACCCGGAGATCCAG
467	AAV13_capsid 672-721	ACGGGACAGGTCAGCGTGGAAATAGAATGGGAGTTACAAA AAGAAAACCTCTAAACGTTGGAATCCGGAAATACAGTATACC AGCAATTATAATAAATCAGTCAATGTTGATTTTACTGTGGAT ACCAATGGGGTGTATAGCGAACCG

SEQ ID NO:	Name	Sequence
468	AAV13_Rep 0-49	ATGCCGGGGTCTATGAGATTGTATTGAAAGTGCCGAGTGA TCTGGATGAGCATTTACCGGGTATTTCAGATAGTTTTGTCAA TTGGGTGGCTGAGAAAGAATGGGAATTGCCGCCGATTACAG ACATGGACCTTAATCTGATTGAA
469	AAV13_Rep 24-73	AGTTTCGTCAATTGGGTGGCAGAAAAAGAATGGGAATTGCC GCCGATAGCGATATGGATTTAAATCTTATTGAACAAGCAC CGTTGACAGTTGCCGAAAAACTGCAGCGTGAATTTCTGGTC GAGTGGCGTCGCGTGAGCAAGGCA
470	AAV13_Rep 48-97	GAACAGGCTCCGCTTACCGTAGCAGAAAAGCTGCAACGTGA GTTCTTGTGTAATGGCGTCGTGTTTCAAAGGCACCGGAAGC CTTGTTTTTCGTGCAGTTTGAAAAAGGAGACTCTTATTTTCA TTTACATATATTAGTCGAAACC
471	AAV13_Rep 72-121	GCCCCGGAAGCTCTTTTTTTTGTTCAGTTTGAGAAAGGAGAT AGTTATTTTCATCTTCATATCCTGGTGGAAACCGTTGGTGT AAAAGTATGGTAGTTGGCCGCTATGTAAGTCAAATCAAAGA GAAATTAGTAACACGCATATAT
472	AAV13_Rep 96-145	ACTGTGGGTGTGAAATCTATGGTGGTAGGTCGCTACGTAAG CCAGATTAAGGAGAAATTAGTTACGCGCATTTATCGCGGAG TTGAGCCGCAGCTGCCGAAC TGGTTCGCAGTTACGAAAACC CGTAACGGTGCAGGCGGTGTAAC
473	AAV13_Rep 120-169	TATCGTGGAGTCGAACCGCAACTGCCGAATTGGTTTGCAGT AACAAAACTCGTAATGGCGCAGGGGGTGGTAACAAAAGTA GTGGATGATTGTTACATTCCGAATTATTTGTTACCGAAGACG CAACCGGAGCTGCAATGGGCCTGG
474	AAV13_Rep 144-193	AATAAAGTGTTGATGATTGTTATATTCCGAATTATTTACTG CCGAAGACTCAGCCGGAATTACAGTGGGCATGGACTAATAT GGATCAGTATCTGAGCGCTTGCCCTGAATTTAGCTGAACGTA AGCGCCTGGTAGCCCAGCATTTG
475	AAV13_Rep 168-217	TGGACCAATATGGACCAGTACTTGTGAGCATGTCTGAACTTG GCGGAACGTAAACGTCTGGTAGCACAGCATCTGACGCATGT GTCACAGACACAGGAGCAGAATAAGGAGAATCAGAATCCG AACAGCGATGCCCCGGTGATTGCG
476	AAV13_Rep 192-241	TTGACTCATGTATCTCAAACGCAGGAACAGAATAAAGAGAA TCAGAATCCGAATAGCGATGCCCCGGTTATACGTTCAAAGA CGTCTGCCCCGTATATGGAGCTTGTCGGTTGGTTGGTTGATC GCGGCATTACGAGCGAAAAACAG
477	AAV13_Rep 216-265	CGTTCTAAAACCAGCGCCCGTTACATGGAATTAGTAGGGTG GCTGGTTGATCGTGGAATTACATCAGAAAAACAATGGATT AAGAGGATCAGGCTAGCTATATCAGCTTCAATGCGGCCAGC AATAGCCGCTCACAAATTAAGCT
478	AAV13_Rep 240-289	CAGTGGATCCAGGAAGACCAGGCCTCATACATCAGTTTAA CGCAGCTAGCAACAGTCGTAGCCAGATCAAGGCTGCGCTGG ATAATGCCAGCAAATTCATGTCTTGACCAAGACCGCGCCG GACTACTTAGTGGGAAACAATCCG
479	AAV13_Rep 264-313	GCTGCCCTTGATAATGCCAGCAAATTTATGTCATTAACAAAA ACAGCTCCGGATTATCTTGTGGGCAATAATCCGCCGGAAGA TATAACATCTAATCGTATTTACAAAATTCTGGAGATGAATGG TTACGATCCGCAATACGCCGCA
480	AAV13_Rep 288-337	CCGCCGGAAGATATAACCAGTAATCGCATCTACAAAATCTT AGAAATGAATGGCTATGATCCGCAGTATGCCGCAAGCGTGT TCCTGGGTGGGCACAGAAAAAGTTTGGCAAGCGTAACACC ATCTGGTTATTTGGCCCGCGACC

SEQ ID NO:	Name	Sequence
481	AAV13_Rep 31 2-361	GCGAGCGTCTTTCTTGGTTGGGCGCAGAAAAAGTTTGGGAA ACGCAACACAATTTGGTTGTTTGGCCCGCAACCACCGGTA AGACCAACATCGCGGAAGCCATTGCACATGCGGTGCCGTTT TACGGATGCGTGAATTGGACTAAT
482	AAV13_Rep 33 6-385	ACTACCGGCAAGACAAACATTGCGGAAGCAATTGCTCATGC CGTGCCGTTCTATGGGTGCGTGAACCTGGACGAACGAGAAT TTCCGTTCAACGATTGCGTTGATAAAAATGGTCATATGGTGGG AAGAAGGTAAAAATGACTGCGAAA
483	AAV13_Rep 36 0-409	AACGAAAACTTCCCGTTTAACGATTGTGTAGATAAAAATGGT CATCTGGTGGGAGGAAGGAAAGATGACGGCCAAAGTAGTT GAATCTGCGAAAGCTATACTGGGTGGCAGCAAAGTCCGTGT CGACCAGAAATGCAAAAGCAGCGCC
484	AAV13_Rep 38 4-433	AAAGTGGTGGAAAGCGCAAAAGCGATCCTGGGAGGGAGCA AAGTACGCGTCGATCAGAAATGCAAGAGCTCAGCTCAGATT GATCCGACCCCGGTTATAGTTACTAGCAATACCAATATGTGT GCCGTAATTGATGGCAATAGTACG
485	AAV13_Rep 40 8-457	GCTCAGATCGATCCGACCCCGGTTATTGTTACATCAAATACC AATATGTGCGCCGTAATCGATGGTAATTCAACAACCTTCGA GCATCAGCAGCCGTTACAAGATCGTAIGTTAAGTTTGAAC GACAAAACGCCCTTGAGCATGAT
486	AAV13_Rep 43 2-481	ACTACATTCGAACATCAGCAACCGCTGCAGGATCGTATGTTT AAATTTGAGCTGACCAAACGTCTTGAACATGATTTTGGGAA AGTCACAAAACAAGAAAGTCAAAAGATTTTTTCGCTGGGCGT CTGATCATGTACGGAAGTCTCA
487	AAV13_Rep 45 6-505	GATTTCCGTAAGTTACAAAACAGGAAGTCAAGGATTTCTT CCGTTGGGCCAGTGACCATGTAAGTGAAGTCAGTCATGAAT TTTACGTTTCGAAGGGTGGAGCTCGTAAGCGCCCGGCTCCG AACGACGCAGATATCAGCGAACCG
488	AAV13_Rep 48 0-529	AGCCATGAATTTTACGTGCGTAAGGGAGGGGCCGTAACG CCCGGCGCCGAACGATGCCGATATTAGTGAACCGAAGCGCG CATGCCCAGCGTTGCACAACCGAGTACCAGTGATGCTGAA GCACCGGTGCGATTATGCCGATCGT
489	AAV13_Rep 50 4-553	CCGAAACGTGCATGTCCGAGTGTGCGCGAGCCGTCAACGTC AGATGCGGAAGCACCGGTGGATTATGCCGATCGTTATCAGA ACAAGTGCAGTCGTCAITGGGTATGAATCTGATGCTGTTTC CGTGTCGTCAAGTGGAGCGCATG
490	AAV13_Rep 52 8-577	CGCTACCAGAATAAATGTAGCCGTCATGTTGGCATGAACCT GATGTTATTTCCGTGTCGTCAAGTGCAGAACGATGAACCAGA ATGTTGATATTTGTTTACCCATGGAGTCATGGATTGCGCTG AATGCTTTCCGGTCTCTGAAAGT
491	AAV13_Rep 55 2-601	ATGAATCAGAATGTGATATTTGCTTCACTCATGGTGTATG GATTGTGCAGAGTGCTTTCCGGTTTCTGAGTCACAGCCGTA TCAGTGGTGCAGCAAGCGCACATATCAAAAACCTTTGCCCGAT TCATCATATTATGGGCCGTGCC
492	AAV12_Rep 0- 49	ATGCCGGGTTTCTACGAAGTTGTTATCAAGGTGCCGTCAGAT CTGGATGAACATTTACCGGGCATAAGTGATAGTTTGTCAAC TGGGTGGCTGAAAAAGAGTGGGAAGTCCCGCCGACTCAGA TATGGATCAAAACCTGATCGAG
493	AAV12_Rep 24 -73	TCATTTGTGAAGTGGGTGGCCGAAAAAGAGTGGGAGCTGCC GCCGATTCTGATATGGACCAGAACCTGATTGAACAAGCGC CGTTAACTGTAGCGGAAAAGTTACAGCGTGAATTTCTGGTG GAATGGCGTCGCGTGAGCAAGTTT

SEQ ID NO:	Name	Sequence
494	AAV12_Rep 48-97	GAACAAGCCCCGCTTACCGTGGCGGAAAAATTGCAGCGTGA ATTTCTGGTCGAGTGGCGTCGTGTTAGTAAGTTCTTGGAAGC CAAGTTTTTCGTCCAATTCGAGAAAGGCGATAGTACTTTCA TCTGCATATTTTAATAGAAATC
495	AAV12_Rep 72-121	TTTTTAGAAGCAAAATTCCTCGTACAGTTTGAAAAAGGGGA TTCTTACTTTTCATCTTCATATCCTGATCGAGATAACCGGTGT GAAAAGCATGGTGGTGGGACGTTATGTCAGTCAGATTCCGC ACAAGTTAATTCACGCATCTAT
496	AAV12_Rep 96-145	ATCACCGGGGTAAATCAATGGTAGTTGGCCGCTATGTCTCT CAGATCCGCGATAAACTTATTCAGCGTATTATCGTGGGGTA GAGCCGCAACTGCCGAATTGGTTTGGCGTCACCAAAACACG CAATGGTGCAGGCGGTGGTAAT
497	AAV12_Rep 120-169	TATCGTGGGTAGAAACCGCAGCTGCCGAAGTGGTTGCGGTT ACCAAAACCCGTAATGGAGCAGGAGGTGGTAACAAAGTTGT TGACGAATGTTATATACCGAATTATCTGTTACCGAAGGTGCA GCCGAGTTGCAGTGGGCGTGG
498	AAV12_Rep 144-193	AATAAGGTGGTCGACGAGTGTATATTCGGAATTATTTATTG CCGAAAGTTCAGCCGGAAGTGCAGTGGGCGTGACAAATAT GGAAGAGTATATAAGTGCATGTCTGAATTTGGCAGAACGTA AACGTTTGGTTGCGCAACATCTG
499	AAV12_Rep 168-217	TGGACTAATATGGAAGAATACATCTCTGCCTGTTGAATTTG GCAGAACGTAAACGTCTGGTCGCCCAACATCTGACTCATGT GAGCCAAACGCAAGAGGGGGATAAAGAAAACCTTAACCCG AATAGTGACGCACCGGTAATTCGT
500	AAV12_Rep 192-241	TTAACGCATGTCTCTCAGACACAGGAAGGAGATAAAGAGAA TTTGAATCCGAATAGTGATGCACCGGTAATCCGCAGCAAGA CAAGCGCCCGTTATATGGAATTGGTTGGATGGCTGGTAGAT AAAGGAATAACAAGCGAAAAACAA
501	AAV12_Rep 216-265	CGCAGTAAACATCTGCGCGTTATATGGAAGTGGTTGGGTG GTTGGTGGATAAGGGCATCACGAGCGAGAAACAGTGGATT AAGAAGACCAAGCGTCATATATCTCATTTAATGCCGCTAGC AACAGTCGCTCTCAAATTAAGCC
502	AAV12_Rep 240-289	CAGTGGATTTCAGGAAGATCAGGCATCATATATCAGTTTAA CGCCGCGAGCAATTCTCGTAGCCAGATCAAAGCGGCTTTAG ATAATGCATCAAAAATCATGAGCTTAACCAAGACGGCACCG GATTATCTGATTGGTCAGCAGCCG
503	AAV12_Rep 264-313	GCGGCCCTGGATAATGCATCTAAAATAATGTCTCTGACCAA GACAGCGCCGACTATCTGATTGGACAGCAGCCGTTGGTG ATATTACGACCAACCGTATATATAAAATTCTTGAGCTGAAC GGCTACGATCCGCAATATGCAGCG
504	AAV12_Rep 288-337	CCGGTAGGCGATATAACAATAATCGTATTTATAAAATTCTT GAGCTTAATGGTTATGACCCGAGTATGCGGCTTCAGTTTTT CTTGGCTGGGCTCAGAAAAAGTTTGGTAAACGCAACACGAT CTGGCTTTTCGGCCCCGGCTACT
505	AAV12_Rep 312-361	GCTAGTGTATTTCTGGGGTGGGCCCAGAAAGAAATTCGGCAA ACGTAATACGATTGGCTGTTCCGGCCCGGCGACGACTGGTA AAACAAACATCGCAGAAAGCAATTGCGCATGCTGTCCGTTT TACGGGTGCGTAAACTGGACAAAT
506	AAV12_Rep 336-385	ACAACCGGGAAAAACCAACATAGCAGAAAGCCATTGCCCATGC CGTACCGTTTTATGGTTGTGTTAACTGGACCAACGAAAACTT CCCGTTTAATGATTGTGTGGATAAAATGGTTATTTGGTGGGA AGAAGGTAAAAATGACTGCAAG

SEQ ID NO:	Name	Sequence
507	AAV12_Rep 36 0-409	AACGAAAACCTCCCGTTCAATGATTGCGTTGATAAAATGGTT ATCTGGTGGGAAGAAGGTAAAATGACCGCCAAAGTGGTTGA GAGTGCAAAAGCAATTCTTGGCGGGTCTAAAGTCCGCGTGG ATCAAAAGTGCAAAGCCTCTGCG
508	AAV12_Rep 38 4-433	AAGGTGTAGAAAAGTGCGAAGGCGATCTTAGGCGGGAGCA AAGTACGTGTGGATCAGAAATGTAAGGCGAGCGCGCAGATT GATCCGACTCCGTTATTGTAACCTCAAACACTAATATGTGT GCTGTGATTGATGGCAACTCTACG
509	AAV12_Rep 40 8-457	GCCCAGATCGATCCGACGCCGGTGATCGTAACGAGTAACAC CAATATGTGCGCCGTTATAGATGGGAACAGTACCACCTTCG AGCATCAGCAACCGCTGCAAGACCGTATGTTTAAATTTGAG TTAACACGTGCGCTGGACCATGAT
510	AAV12_Rep 43 2-481	ACCACATTTGAGCATCAACAGCCGCTGCAAGACCGCATGTT TAAATTTGAGTTGACTCGCCGTCTGGATCATGATTTCTGGGAA AGTGACAAAGCAGGAAGTTAAAGATTTTTTTCGTTGGGCGG CCGATCATGTGACCGATGTGGCG
511	AAV12_Rep 45 6-505	GATTTCTGGGAAAGTGACTAAGCAAGAAGTGAAGGATTTCTT CCGTTGGGCGCGAGATCATGTTACCGACGTGGCAGATGAAT TTTATGTGACGAAGGGCGGAGCGAAAAAGCGCCCGCACCG AGCGATGAGGACATAAGTGAACCG
512	AAV12_Rep 48 0-529	GCTCATGAGTTTTACGTCACAAAGGGTGGGGCGAAAAACG CCCGGCTCCGTCTGACGAAGACATTAGCGAACCGAAACGCC CGCGCGTTAGCTTCGCGCAGCCGGAGACCAGTGACGCGGAA GCGCCGGGTGACTTTGCGGATCGT
513	AAV12_Rep 50 4-553	CCGAAACGTCCGCGTGTGAGCTTTGCACAGCCGGAAACGAG CGACGCGGAAGCCCCGGGCGATTTTCGAGATCGTTATCAAA ACAAATGTAGCCGTATGCCGGGATGCTGCAGATGCTGTTT CCGTGTAAAACGTGTGAACGCATG
514	AAV12_Rep 52 8-577	CGTTATCAAAATAAATGTTCTCGTCATGCTGGAATGTTGCAG ATGCTGTTCCCGTGTAAAACCTGCGAACGTATGAACCAGAA CTCTAATGTTTGCTTTACACATGGGCAAAAAGACTGTGGCG AATGTTTCCCGGGGAGCGAAAGT
515	AAV12_Rep 55 2-601	ATGAACCAAAATTCAAACGTATGCTTCACGCATGGTCAAAA GGATTGTGGTGAATGCTTTCGGGGAGCGAAAGCCAACCGG TCAGCGTTGTTTCGCAAAACTTATCAGAAATTATGTATCCTGC ATCAGCTGCGCGGCGCCCCGGAA
516	AAV11_Rep 0- 49	ATGCCGGGGTTTTATGAAATTGTTATTAAAGTGCCGTCTGAC CTGGATGAGCATCTGCCGGGTATTAGTGATTCAATTTGTGAAC TGGGTGCGGAAAAAGAATGGGAACCTCCGCCGATTTCAGA TATGGACCGTAACCTTGATCGAA
517	AAV11_Rep 24 -73	TCTTTTGTTAACTGGGTTGCGGAAAAAGAATGGGAACTGCC GCCGGATTACAGACATGGACCGTAACCTAATCGAGCAAGCTC CGTTAACGGTTCGAGAAAAAGTTGCAACGTGATTTTTTGGTTC ATTGGCGTCTGTTTCTAAAGCT
518	AAV11_Rep 48 -97	GAACAGGCTCCGTTAACCGTAGCTGAGAACTTCAGCGTGA TTTTCTGGTCCATTGGCGTCGCGTAAGCAAGGCACCGGAAG CCCTTTTTTTCGTGCAGTTCGAGAAGGGGAATCATACTTTC ATCTGCATGTACTTGTGAAACA
519	AAV11_Rep 72 -121	GCACCGGAAGCGCTGTTTTTTCGTGCAATTTGAAAAAGCGCA ATCTTATTTTCATCTTCATGTGCTGGTTGAAACCACGGGTGT TAAATCAATGGTGTGGTTCGCTTTCGTAGCCAGATTTCGTGA TCGTTTAGTGCAGACAATTTAT

SEQ ID NO:	Name	Sequence
520	AAV11_Rep 96-145	ACAACTGGCGTTAAATCAATGGTACTGGGACGTTTCTGAG CCAAATTCGCGATCGCCTTGTCAGACAATCTATCGCGGAGT TGAACCGACGCTGCCGAAGTGGTTTGCTGTGACAAAACTC GTAATGGCGCTGGCGGCGGTAAT
521	AAV11_Rep 120-169	TATCGCGGAGTTGAGCCGACACTGCCGAATTGGTTIGCGGTT ACAAAAACCCGCAATGGCGCAGGGGGTGGCAATAAAGTTGT TGACGAATGTTATATTCCGAATTATCTGTTACCGAAAACTCA ACCGGAATTGCAGTGGGCATGG
522	AAV11_Rep 144-193	AATAAAGTAGTCGACGAATGCTATATTCCGAAGTATTTACTG CCGAAAACTCAACCGGAATTACAATGGGCCTGGACAAATAT GGAAGAATATATTTCTGCATGTTTAACTTGGCAGAACGTA AGCGTTTGGTCGCACAGCATCTG
523	AAV11_Rep 168-217	TGGACCAACATGGAAGAATACATTAGTGCTTGCTGAACTT GGCCGAGCGTAAACGTTTAGTTGCGCAACATCTGACTCATG TCTCTCAAACACAGGAACAGAACAAGAGAATTTAAATCCG AACAGTGACGCACCGGTAATCCGT
524	AAV11_Rep 192-241	CTGACTCATGTATCTCAAACACAGGAGCAGAATAAGGAAAA TCTTAACCCGAATAGCGATGCGCCGGTAATACGCAGTAAGA CCTCAGCTCGCTACATGGAAGTGGTTGGCTGGTTGGTTGACC GTGGAATCACCTCAGAAAAACAG
525	AAV11_Rep 216-265	CGCTCAAAAACCTCAGCGCGTTATATGGAATTAGTCGGTTG GCTGGTCGATCGCGGCATTACATCAGAAAAACAGTGGATT AAGAGGACCAGGCATCTTATATATCATTTAATGCAGCAAGC AACAGCCGCTCACAAATCAAGGCG
526	AAV11_Rep 240-289	CAGTGGATCCAGGAAGATCAAGCCTCATACTAGCTTTAA CGCTGCATCTAACAGCCGTAGTCAAATCAAGGCCGCCCTTG ATAATGCGGGCAAAATTATGGCGTTGACAAAATCTGCACCG GATTATTTAGTCGGCCCGTCTCTT
527	AAV11_Rep 264-313	GCGGCCCTGGACAATGCTGGGAAAATTATGGCACTGACTAA AAGCGCTCCGGACTATCTTGTTGGGTCCGTCACTTCCGGCCGA CATTAAAGCAAACCGCATTTACCGTATATTGGAATTAAATG GCTATGATCCGGCATATGCTGGT
528	AAV11_Rep 288-337	CTGCCGGCGGATATTAAAGCTAACCGTATTTATCGTATCCTG GAGTTAAATGGGTATGATCCGGCTTATGCAGGTTCAGTATTC CTTGTTGGGCCAGAAAAAGTTTGGCAAACGCAATACCAT CTGGCTGTTCCGGCCCGCAACC
529	AAV11_Rep 312-361	GGAAGCGTGTTCTTAGGGTGGGCCCAGAAAAAGTTTGAAAA ACGTAACACCATTTGGTTATTGGTCCGGCGACGACCGGTA AAACTAATATCGCAGAGGCAATTGCGCATGCTGTACCGTTC TATGGTTGTGTGAATTGGACTAAT
530	AAV11_Rep 336-385	ACGACTGGTAAAACCAACATTGCCGAAGCCATTGCACATGC GGTGCCGTTCTATGGTTGCGTGAAGTGGACCAACGAGAACT TTCCGTTCAACGATTGTGTTGATAAAATGGTAATATGGTGGG AAGAAGGCAAAATGACTGCAAAA
531	AAV11_Rep 360-409	AACGAGAACTTTCCGTTCAATGATTGCGTTGACAAGATGGTT ATTTGGTGGGAAGAAGGTAAAATGACAGCCAAAGTAGTCGA AAGTGCAAAAAGCGATTTTAGGCGGCAGCAAAGTACGTGTCTG ATCAGAAATGCAAGTCAAGTGCT
532	AAV11_Rep 384-433	AAGGTGGTGGAAAGCGCAAGGCTATTCTGGGGGGTAGCAA AGTTCGCGTCGATCAAAAATGCAAGAGCAGCGCCCAAATTG ATCCGACGCCGGTGATTGTTACGAGTAACACTAACATGTGT GCGGTTATCGATGGCAATAGCACC

SEQ ID NO:	Name	Sequence
533	AAV11_Rep 40 8-457	GCGCAAATCGATCCGACGCCGGTGATTGTTACAAGCAATAC CAATATGTGTGCGGTAATCGATGGGAACAGCACGACCTTCG AGCATCAGCAGCCGCTGCAGGATCGTATGTTCAAATTTGAG CTGACCCGTCGTCTGGAACATGAC
534	AAV11_Rep 43 2-481	ACTACGTTTGAGCATCAACAACCGCTTCAAGATCGCATGTTT AAATTTGAACTGACTCGTCGCTTGGAGCATGATTTTGGCAAG GTAACATAAGCAGGAAGTCAAGGAGTTTTTTCGTTGGGCCCA AGATCATGTGACCGAGGTGGCA
535	AAV11_Rep 45 6-505	GATTTTCGGAAGGTAACCAAGCAGGAGGTGAAAAGAGTTCTT TCGTTGGGCTCAAGACCATGTAACCGAAGTAGCGCATGAAT TTTATGTTTCGAAGGGGGGCGCCACTAAACGCCCGGCGCCG TCAGATGCTGATATAAGTGAACCG
536	AAV11_Rep 48 0-529	GCTCATGAGTTTTATGTGCGCAAAGGAGGGGCGACGAAACG CCCGGCGCCGTCTGATGCTGATATTAGCGAACCGAAACGCG CCTGTCCGAGCGTCCCGGAACCGTCTACAAGTGACGCGGAA GCTCCGGTGGATTTTGCAGATCGT
537	AAV11_Rep 50 4-553	CCGAAACGCGCGTGTCCGTCAGTTCGGAACCGAGTACTTC TGATGCAGAAGCCCCGGTGGATTTTTCGCGATCGTTACCAGA ATAAATGCTCACGCCATGCGGGCATGTTGCAGATGTTATTCC CGTGCAAAACGTGCGAACGCATG
538	AAV11_Rep 52 8-577	CGTTACCAGAATAAATGCTCTCGTCATGCCGGTATGTTACAA ATGTTATTTCCGTGTAACCTGCGAACGCATGAACCAGAA CTTCAACGTTTGCTTTACCCATGGTGTGCGCGACTGTAGTGA ATGTTTTCCGGGCGCAAGTGAA
539	AAV11_Rep 55 2-601	ATGAATCAGAATTTTAACGTATGTTTTACCCATGGTGTTCGT GATTGCAGTGAGTGTTCGCGGTGCTTCTGAGTCACAACCG GTTGTGCGTAAAAAACTTATCAGAAGTTATGCGCGATTCAT TCATTTATTAGTTCGTGCGCCG
540	AAV10_Rep 0- 49	ATGCCGGGATTTTATGAGATTGTAATAAAAGTCCCGAGCGA CTTAGATGAGCATCTGCCGGGTATCTCAGATTCTTTTGTGAA CTGGGTCGCCGAAAAGGAATGGGAATTGCCGCCGATTACAG ACATGGATCGCAATCTGATCGAA
541	AAV10_Rep 24 -73	AGTTTTGTAAATTGGGTGCTGAAAAAGAGTGGGAGTTACC GCCGATTACAGATGGATCGCAATCTGATTGAACAGGCGC CGCTGACTGTGGCGGAGAAGTTGCAGCGGATTTCCTGGTT CATTGGCGTCGCGTTTCAAAGGCA
542	AAV10_Rep 48 -97	GAACAGGCACCGCTGACCGTGGCTGAAAAATTGCAACGCGA TTTTTTGGTGCATTGGCGTCGCGTGTCAAAGGCCCGGAAGC ATTATTCTTCGTACAGTTTGAAAAAGGCGAGTCTTATTTTCA TTTGCATGTATTGGTAGAAACC
543	AAV10_Rep 72 -121	GCCCCGGAGGCTTTGTTTTTCGTGCAATTTGAAAAAGGTGAG TCATATTTTCATTTACATGTTCTGGTCGAAACAACTGGTGTT AAATCTATGGTTCTGGGTCGCTTCCTGAGTCAGATTCTGTGAT CGTTTAGTTCAGACTATTAC
544	AAV10_Rep 96 -145	ACCACAGGAGTTAAGAGTATGGTTCTGGGACGTTTCCTGAG TCAGATTGCGGACCGCTTAGTCCAGACCATATATCGTGGGGT TGAACCGACCTTGCCGAATTGGTTTGCGGTGACAAAAACTC GTAATGGAGCAGGCGGTGGCAAT
545	AAV10_Rep 12 0-169	TACCGCGGTGTGCAACCGACACTGCCGAATTGGTTCGCAGT AACTAAGACGCGTAATGGGGCGGGAGGGGGTAACAAAGTG GTAGATGAGTGTTACATCCCGAATTACCTTCTTCCGAAGACA CAACCGGAGTTACAGTGGGCGTGG

SEQ ID NO:	Name	Sequence
546	AAV10_Rep 14 4-193	AACAAAGTCGTAGATGAATGTTATATCCCGAATTATTTGTTA CCGAAAACCCAACCGGAATTACAATGGGCGTGGACGAACAT GGAGGAATACATTAGCGCGTGTCTGAACCTTGCAGAACGTA AACGTCTTGTGGCACAGCATCTT
547	AAV10_Rep 16 8-217	TGGACTAACATGGAAGAATACATAAGCGCGTGTAAACCT GGCTGAGCGTAAACGTTTGGTAGCTCAGCATTTGACGCATG TTAGCCAGACCCAGGAGCAGAATAAGGAGAACCTGAATCCG AACAGTGACGCGCCGGTGATCCGT
548	AAV10_Rep 19 2-241	CTGACGCATGTATCTCAGACGCAGGAACAGAATAAAGAGAA CTTGAATCCGAACCTCTGACGCTCCGGTAATCCGCAGTAAAA CTTCAGCCCGCTATATGGAACCTGGTCGGTTGGTTAGTAGACC GTGGGATTACTTCAGAAAAGCAA
549	AAV10_Rep 21 6-265	CGTTCTAAAACGTCTGCACGTTACATGGAACCTGGTTGGATG GCTTGTGGACCGTGGCATTACTAGCGAAAAGCAGTGGATTTC AGGAAGATCAAGCGTCATACATCAGCTTCAACGCCGCTAGT AATTCTCGTAGCCAAATTAAAGCT
550	AAV10_Rep 24 0-289	CAGTGGATTTCAGGAAGACCAGGCGTCTTATATTTTCATTCAAT GCTGCATCAAATTCTCGTTCACAGATTAAAGCTGCTCTGGAT AATGCAGGTAAGATTATGGCACTTACCAAAGCGCCCCGGA TTACTTGGTAGGCCCGAGCCTT
551	AAV10_Rep 26 4-313	GCGGCGCTGGATAATGCAGGCAAGATCATGGCCTTAACGAA AAGTGCCCCGGACTATCTTGTTCGGCCCGTCTTTACCGGCAGA TATCAAAGCTAATCGCATTTATCGCATCTGGAACCTGAATGG TTACGACCCGGCGTACGCTGGG
552	AAV10_Rep 28 8-337	CTTCCGGCAGATATTAAGCTAATCGCATTTACCGCATCCTG GAATTAACCGTTACGATCCGGCCTATGCCGGCTCTGTGTTT CTGGGTTGGGCTCAAAAAAAGTTTGGCAAACGTAACACAAT CTGGCTGTTTGGGCCGGCTACC
553	AAV10_Rep 31 2-361	GGCAGTGTGTTTCTGGGCTGGGCACAAAAAAAGTTCGGCAA GCGTAACACCATATGGTTGTTTCGGTCCGGCGACCAACCGCA AACTAACATTGCGGAGGCCATTGCTCATGCTGTTCCGTTCT ATGGTTGCGTAAATTGGACCAAT
554	AAV10_Rep 33 6-385	ACCACTGGGAAAAACAAACATCGCTGAAGCGATCGCGCATGC AGTGCCGTTTACGGTTGCGTGAATTGGACGAATGAGAACT TTCCGTTTAATGACTGCGTTGATAAAATGGTCATCTGGTGGG AGGAGGGTAAAATGACGGCTAAA
555	AAV10_Rep 36 0-409	AATGAAAACCTCCCGTTTAACTGACTGCGTGGACAAAATGGT TATTTGGTGGGAGGAAGGGAAAAATGACCGCCAAAGTCGTAG AGAGCGCGAAAGCTATCCTGGGTGGTAGCAAAGTGCAGCTG GATCAGAAATGCAAAAGCTCTGCG
556	AAV10_Rep 38 4-433	AAGGTTGTGAGAGCGCGAAGGCCATTTGGGTGGCTCAAA AGTACGCGTCGATCAGAAATGTAAGAGTAGTGCCCAAATCG ATCCGACACCGGTTATTGTTACGTCAAATACGAATATGTGTG CTGTGATCGACGGTAATAGTACC
557	AAV10_Rep 40 8-457	GCACAAATCGATCCGACGCCGTTATCGTCACGTCTAACAC CAATATGTGCGCAGTAATAGATGGGAACTCAACCACATTCTG AACATCAGCAGCCGTTGCAGGATCGTATGTTTAAATTTCGAA CTTACTCGTCGCTTAGAGCATGAT
558	AAV10_Rep 43 2-481	ACGACCTTTGAACATCAACAGCCGCTGCAGGATCGTATGTTT AAGTTCGAATTGACCCGCCGCTGGAGCATGATTTTGGTAA GGTAACCAAACAGGAGGTTAAAGAATTTTTTCGTTGGGCCC AGGACCATGTTACCGAAGTTACA

SEQ ID NO:	Name	Sequence
559	AAV10_Rep 45 6-505	GATTTCTGGGAAGGTTACGAAACAGGAAGTCAAAGAATTTTT CCGCTGGGCCCAGGATCATGTTACCGAAGTTACTCATGAGTT CTATGTTTCGCAAAGGTGGAGCAACAAAGCGTCCGGCCCCGT CAGATGCAGACATTAGTGAGCCG
560	AAV10_Rep 48 0-529	ACGCATGAATTTTACGTACGCAAAGGAGGTGCTACAAAACG TCCGGCCCCGAGCGACGCGGACATATCAGAGCCGAAACGCG CTTGCCCGTCTGTGGCGGAACCGAGTACGAGCGATGCAGAA GCACCGGTCTGATTTTCGCGGATCGT
561	AAV10_Rep 50 4-553	CCGAAGCGTGCTTGTCCGAGCGTGGCCGAGCCGAGCACATC AGATGCAGAAAGCTCCGGTTGATTTTTCGGATCGCTATCAAA ACAAATGTTTACGTATGCTGGTATGTTACAGATGTTATTTT CGTGTAACCTGTGAACGCATG
562	AAV10_Rep 52 8-577	CGCTATCAGAATAAATGCAGCCGTCATGCGGGCATGCTGCA AATGCTTTTTCCGTGCAAAACCTGTGAACGCATGAATCAGA ATTTTAATGTATGTTTACACATGGTGTACGTGATTGCAGTG AATGCTTCCCGGGCGCTAGCGAG
563	AAV10_Rep 55 2-601	ATGAACCAAACTTTAATGTGTGTTTTACACATGGCGTTCGT GACTGTTTCAAGATGTTTTCCGGGTGCAAGCGAGTCACAACC GGTTGTTTCGTAAGAAAACCTATCAAAAGCTGTGCGCAATCC ATCATTTACTGGGTCTGTCGCGCC
564	AAV8_Rep 0- 49	ATGCCGGGGTTTTACGAAATTGTGATTAAGGTACCGAGCGA CCTGGATGAGCATCTGCCGGGAATTTCTGATTCATTCTGTTAA TTGGGTGCGCGAAAAAGAATGGGAGCTTCCGCCGGATAGCG ATATGGATCGTAACCTGATTGAA
565	AAV8_Rep 24- 73	AGTTTTGTAAATTGGGTAGCAGAAAAGGAATGGGAGCTGCC GCCGATTCTGATATGGATCGCAACCTGATCGAGCAAGCAC CGCTGACAGTTGCCGAGAAGCTGCAGCGTGACTTCTTGGTC CAATGGCGTCTGTGTTTCTAAAGCA
566	AAV8_Rep 48- 97	GAGCAAGCACCGCTGACGGTTCGAGAAAAAATTACAGCGCG ATTTTCTGGTACAATGGCGCGCGTATCAAAAGCCCCGGAA GCCCTTTTCTTTGTCCAGTTTGAGAAGGGGGAATCATATTT CATTTGCATGTGCTGGTAGAGACG
567	AAV8_Rep 72- 121	GCTCCGGAAGCTCTGTTCTTTGTCCAGTTTGAAAAAGGCGAG TCTTATTTTCATCTTCATGTCCTGGTTCGAAACCACTGGCGTT AAATCTATGTTTCTGGGACGTTTCTGTCTCAGATACGCGAA AAATTAGGTCCGGATCATTTA
568	AAV8_Rep 96- 145	ACGACGGGAGTGAATCTATGGTGCTGGGCCGTTTCTTAAG CCAGATTCGCGAAAAAGTTGGGCCCGGACCATCTGCCGGCGG GAAGCAGTCCGACCCTGCCGAATTGTTTGCAGTAACCAAA GATGCGGTGATGGCACCGGCGGGA
569	AAV8_Rep 120 -169	CTGCCGGCAGGATCTAGCCCGACATTACCGAATTGGTTCGCT GTTACCAAAGACGCGGTGATGGCCCCGGCAGGAGGCAATAA AGTAGTCGATGAATGCTATATCCCGAATTATTTATTGCCGAA GACTCAACCGGAACTGCAGTGG
570	AAV8_Rep 144 -193	GGGGGAAACAAAGTAGTCGATGAATGTTACATACCGAATTA TTTACTGCCGAAGACTCAGCCGGAGTTGCAGTGGGCGTGGA CCAATATGGAAGAGTATATAAGCGCGTGCCTGAACCTTGCG GAGCGCAAACGTTTAGTTGCGCAA
571	AAV8_Rep 168 -217	TGGGCGTGGACGAACATGGAAGAGTATATCAGTGCTTGTCT GAATCTTGCTGAACGTAAACGTCTGGTTGCTCAGCATCTTAC ACATGTATCACAAACACAGGAACAGAACAAAGGAAAACTTA AATCCGAATAGCGACGCTCCGGTT

SEQ ID NO:	Name	Sequence
572	AAV8_Rep 192-241	CAACATCTGACTCATGTCTCTCAGACCCAAGAACAGAATAA GGAAAATTTGAATCCGAATAGCGATGCGCCGGTTATTCGTT CAAAAACATCTGCCCCTACATGGAATTAGTAGGCTGGTTA GTTGACCGTGGCATTACATCAGAG
573	AAV8_Rep 216-265	GTTATCCGTTCAAAGACCTCAGCTCGTTATATGGAAGTGGTC GGCTGGCTGGTTGATCGTGGTATAACAAGTAAAAACAATG GATCCAGGAGGATCAGGCCTCATACATTTCATTCAATGCGG CTAGCAACTCACGCAGTCAGATT
574	AAV8_Rep 240-289	GAAAAACAATGGATACAAGAGGATCAGGCAAGTTATATTTTC TTTTAACGCGGCCAGCAATTCACGCTCTCAAATTAAGCTGC TCTGGATAATGCAGGTAAAATCATGGCACTGACAAAGAGCG CGCCGGATTATCTTGTGCGCCCCG
575	AAV8_Rep 264-313	ATTAAGGCCGCGTTAGATAACGCGGGCAAGATAATGGCGCT GACAAAGTCTGCACCGGATTATTTGGTTGGTCCGTCCTGCC GGCGGACATAACGCAGAAATCGTATTTACCGCATTTTGGCATT GAATGGGTATGATCCGGCTTAT
576	AAV8_Rep 288-337	CCGTCTTTACCGGCGGATATCACTCAAAACCGTATTTATCGC ATTTTGGCGTTGAACGGGTATGACCCGGCCTATGCTGGCAGT GTCTTTTGGGGTGGGCACAAAAAAGTTTGGTAAGCGTAA TACCATATGGTTGTTCCGTCCG
577	AAV8_Rep 312-361	TATGCGGGGTCTGTATTTCTTGGTTGGGCTCAGAAAAAGTTT GGGAAGCGCAATACTATATGGCTTTTCGGTCCGGCAACGAC TGGAAAGACGAATATCGCAGAAGCAATCGCCCATGCTGTTT CGTCTATGGCTGCGTAAATTGG
578	AAV8_Rep 336-385	CCGGCAACGACCGGGAAAAACCAACATTGCCGAGGCAATTGC ACATGCTGTTCCGTTTATGGATGTGTTAATTGGACAAATGA GAATTTCCCGTTCAATGATTGCGTGGACAAGATGGTCATTTG GTGGGAAGAGGGAAAGATGACG
579	AAV8_Rep 360-409	TGGACCAACGAAAAATTTCCCGTTTAAATGACTGCGTGGATAA AATGGTTATCTGGTGGGAAGAAGGTAAAATGACGGCAAAA GTAGTGGAGTCAGCCAAAGCAATTTTAGGTGGTTCAAAGGT GCGTGTAGATCAAAAATGTAAAAGT
580	AAV8_Rep 384-433	ACCGCGAAAAGTGGTAGAAAAGCGCGAAGGCTATCTTGGGAG GCAGCAAGGTTCCGCTAGATCAAAAATGCAAGTCTAGTGCC CAGATTGATCCGACTCCGGTGATTGTGACCAGCAATACTAA TATGTGCGCAGTCATTGATGGTAAT
581	AAV8_Rep 408-457	TCAAGTGCTCAAATTGATCCGACTCCGGTAATTGTACCTCA AATACAAATATGTGCGCGGTCATAGATGGTAATAGTACAAC TTTTGAACATCAGCAGCCGCTGCAAGATCGTATGTTAAATT CGAACTGACCCGTCGTTTGGAG
582	AAV8_Rep 432-481	AATAGTACCACCTTTTGAACATCAACAACCGTTGCAGGATCG TATGTTCAAATTTGAGCTGACCCGCCGCTCTGGAGCATGATTT TGGTAAAGTAACAAAACAAGAAGTAAAGGAGTTCTTTCGTT GGCCTCTGATCATGTAAGTAA
583	AAV8_Rep 456-505	GAGCATGATTTTGGCAAAGTAACCAACAGGAAGTAAAGG AATTTTCCGTTGGGCATCTGATCATGTAACAGAGGTAGCGC ATGAGTTCTATGTTTCGTAAAGGAGGCGCATCTAAACGTCCG GCGCCGATGATGCGGACAAAAGT
584	AAV8_Rep 480-529	GAAAGTGGCGCATGAATTTTATGTCCGTAAAGGCGGCGCCTC TAAACGCCCCGCCCCGGATGACGCGGATAAAAGTGAACCGA AGCGCGCTGTCCGAGCGTAGCGGATCCGTCTACTTCTGATG CAGAGGGAGCTCCGGTTGATTTT

SEQ ID NO:	Name	Sequence
585	AAV8_Rep 504-553	TCTGAACCGAAGCGCGCCTGTCCGTCTGTGGCCGATCCGAG TACATCAGACGCAGAGGGTGCCCCGGTTGATTTTGCCGACC GTTATCAGAATAAATGTAGCCGCCATGCCGGCATGTTACAG ATGCTTTTCCCGTGTAAACATGT
586	AAV8_Rep 528-577	TTTGCTGATCGCTATCAGAACAAAGTGTAGTCGTCATGCAGGT ATGTTACAGATGTTATTTCCGTGCAAGACCTGCGAGCGCATG AACCAGAAATTTAACATTTGTTTCACCCATGGAGTGCGTGAT TGCAGTGAGTGTTTCCGGGC
587	AAV8_Rep 552-601	TGCGAGCGTATGAATCAGAATTTCAATATCTGCTTCACCCAT GGCGTCCGTGATTGCAGTGAATGTTCCCGGGTGATCTGAA AGCCAGCCGGTCGTACGCAAACGCACGTATCGCAAACGTGTG CGCTATACATCATCTGCTTGGC
588	AAV8_Rep 576-625	GGCGTGTCAGAAAGTCAACCGGTGGTCCGCAAGCGTACCTA TCGTAAACTGTGCGCGATCCATCATCTGCTGGGACGTGCTCC GGAGATTGCCTGCTCTGCCTGTGATCTGGTTAATGTCGATCT GGATGACTGTGTCTCAGAGCAG
589	AAV7_Rep 0-49	ATGCCGGGTTTCTACGAAATAGTGATTAAAGTCCCGAGCGA TCTGGATGAGCATCTGCCGGGAATCTCTGACAGCTTCGTTAA TTGGGTGGCCGAGAAGGAATGGGAGCTGCCGCCGATTACAG ATATGGATCTGAACCTGATCGAG
590	AAV7_Rep 24-73	TCTTTTGTGAATTGGGTGCGAGAAAAGGAGTGGGAAC TGCC GCCGATAGCGATATGGATTTAAACCTTATTGAACAAAGCTC CGCTGACTGTGGCCGAAAAACTTCAACGTGATTTTCTGGTG AGTGCGCCCGCTGAGCAAAGCG
591	AAV7_Rep 48-97	GAGCAGGCACCGCTGACCGTTGCGGAAAAACTTCAGCGCGA TTTCTTGGTCCAGTGGCGTCGCGTTAGCAAAGCACCGGAGG CCCTTTTTTTCGTGCAATTTGAGAAAGGTGAGAGTTATTTCC ATTACATGTACTGGTGGAGACG
592	AAV7_Rep 72-121	GTCCTCGGAAGCTCTTTTTTTTGTTCAGTTTGAAAAAGGGGAA TCATATTTCCATTACATGTGTTAGTGGAACAACCGGGGTA AAATCTATGGTTCTGGGCCGCTTTCTGTCTCAGATACGCGAA AACTGGTTCAGACTATTTAT
593	AAV7_Rep 96-145	ACCACCGGCGTTAAATCTATGGTTTTAGGACGTTTCCTGTCA CAAATTCGTGAGAAGTTGGTGCAAACCATCTATCGTGGTGT AGAGCCGACTCTGCCGAAC TGTTTCGCAGTGACTAAAACCC GCAATGCTGCGGGAGGCGGAAAC
594	AAV7_Rep 120-169	TACCGTGGCGTGGAACCGACATTACCGAATTGGTTTGCGGTT ACTAAGACCCGCAACGGAGCTGGGGGTGGGAACAAAGTCG TTGACGAATGTTATATTCGGAACATCTGCTGCCGAAAACCC AACCGGAAC TGCA GTGGCATGG
595	AAV7_Rep 144-193	AATAAAGTTGTGGATGAATGTTATATTCCGAACTATTTACTG CCGAAAACTCAGCCGGAAC TGCAATGGGCCTGGACAAATAT GGAGGAATATATCTCAGCTTGCTTGAACTTGCGGAGCGCA AGCGCTTAGTGGCCAGCATTTA
596	AAV7_Rep 168-217	TGGACGAATATGGAAGAGTACATATCTGCATGCTTAAACCT GGCAGAACGTAAACGCTTGGTGGCGCAGCATCTTACGCATG TTTCTCAGACGCAGGAACAAAATAAAGAAAATCTTAATCCG AACTCTGATGCTCCGTTATCCGT
597	AAV7_Rep 192-241	CTGACTCATGTGTCACAAACCCAGGAGCAAAACAAAGAAAA CCTGAATCCGAATAGTGATGCACCGGTGATACGCTCAAAAA CATCTGCCGTTATATGGAAC TGTTGGCTGGTTAGTCGACC GTGGAATAACCTCAGAAAAACAA

SEQ ID NO:	Name	Sequence
598	AAV7_Rep 216-265	CGCAGTAAACTAGCGCCCGCTATATGGAAGTGGTGGGTTG GTTAGTTGATCGCGGCATCACGAGCGAAAAGCAGTGGATCC AAGAAGATCAGGCGTCATACATTAGCTTCAATGCGGCGAGT AACAGTCGCAGTCAAATCAAAGCG
599	AAV7_Rep 240-289	CAGTGGATTCAAGAAGACCAGGCCAGCTATATATCTTTTAA CGCTGCCTCAAATAGTCGTTCTCAAATCAAGGCAGCCTTGG ATAATGCAGGCAAAAATCATGGCACTGACTAAAAGCGCCCCG GACTATTTAGTTGGACCGTCTCTG
600	AAV7_Rep 264-313	GCTGCTCTGGACAACGCTGGTAAAATCATGGCCTTGACGAA GTCAGCGCCGGATTACTTGGTCGGCCCGCTTTACCGGCTGA CATTAAGACAAATCGCATCTACCGTATACTGGAATTGAATG GTTATGATCCGGCCTACGCGGGC
601	AAV7_Rep 288-337	TTACCGGCTGACATCAAAACAAATCGTATCTATCGTATTTTG GAACTGAACGGATATGATCCGGCCTACGCCGGCAGCGTTTT CCTGGGTTGGGCGCAAAAGAAGTTTGGTAAACGTAACACCA TTTGGCTGTTCCGCCCGGCAACG
602	AAV7_Rep 312-361	GGCTCAGTATTCTTGGGCTGGGCCAGAAAAAATTTGGGAA GCGCAACACAATTTGGCTGTTTGGACCGGTACGACCGGCA AGACGAACATTGCCGAGGCTATTGCCCATGCGGTGCCGTTTT ATGGGTGTGTCAATTGGACCAAT
603	AAV7_Rep 336-385	ACTACTGGCAAGACAAATATTGCAGAAGCTATTGCCCATGC CGTACCGTTTTACGGTTGCGTTAACTGGACCAATGAGAATTT CCCGTTTAATGATTGTGTGGATAAAATGGTTATTTGGTGGGA AGAAGGGAAAATGACTGCGAAA
604	AAV7_Rep 360-409	AATGAGAACTTTCCGTTCAATGATTGCGTGGATAAGATGGT AATCTGGTGGGAAGAGGGCAAGATGACGGCTAAAGTCGTTG AAAGTGCTAAAGCCATTCTGGGTGGAAGCAAAGTGCCTGTG GACCAGAAAGTGTAAGTAGCGCC
605	AAV7_Rep 384-433	AAGGTAGTCGAAAGCGCCAAAGCAATATTAGGTGGCAGCA AGTCCGCGTGGATCAGAAATGTAAGTCTTCTGCGCAGATT GATCCGACACCGGTGATTGTGACTAGTAATACAAATATGTG CGCCGTGATTGATGGAAACTCAACG
606	AAV7_Rep 408-457	GCGCAGATCGATCCGACTCCGGTGATTGTTACGAGCAATAC AAACATGTGCGCTGTAATAGATGGCAACTCTACCACATTTG AGCATCAACAGCCGTTACAGGACCGTATGTTTAAAGTTTGAA CTGACTCGTCCGCTTGAGCATGAT
607	AAV7_Rep 432-481	ACGACATTTCGAGCATCAGCAGCCGTTACAAGACCGTATGTT TAAATTTCGAACTGACACGTCGCCTGGAACATGACTTTGGGA AAGTGACTAAACAGGAAGTGAAGGAGTTCTTTTCGTTGGGCT TCTGATCATGTAACCGAAGTAGCT
608	AAV7_Rep 456-505	GATTTTGGTAAAGTGACGAAACAAGAGGTTAAAGAATTTTT CCGTTGGGCTTCAGACCATGTAAGTGAAGTGGCGCATGAAT TTTACGTACGCAAGGGTGGGGCGTCAAAGCGCCCGGCTCCG GACGATGCGGATATATCAGAACCG
609	AAV7_Rep 480-529	GCTCATGAGTTTTATGTGCGCAAAGGCGGAGCATCAAAACG CCCGGCGCCGGATGACGCGGATATATCAGAGCCGAAGCGCG CGTGTCCGTCTGTAGCGGATCCGTCAACGTCTGATGCCGAG GGAGCCCCGGTCGATTTTCGCGGAT
610	AAV7_Rep 504-553	CCGAAACGCGCTTGTCCGAGCGTAGCGGATCCGTCAACCTC TGATGCCGAAGGTGCGCCGGTTGATTTTGCAGATCGCTACC AGAACAAATGCTCACGTCATGCAGGCATGATTAGATGCTG TTTCCGTGTAAAACCTGCGAACGT

SEQ ID NO:	Name	Sequence
611	AAV7_Rep 528-577	GATCGCTATCAGAATAAATGTTCTCGTCATGCCGGGATGAT ACAGATGTTGTTCCCGTGCAAAACCTGCGAACGTATGAATC AAAAC TTCAATATTTGCTTTACTCATGGAGTACGTGATTGTT TGGAGTGCTTTCCGGGTGTCTCA
612	AAV7_Rep 552-601	CGCATGAACCAGAATTTCAATATCTGCTTTACTCATGGGGTA CGTGATTGTCTTGAATGCTTTCCGGGGGTAAGTGAGTCTCAA CCGGTCGTTTCGTAAAAAACATACCGTAAATTGTGTGCAAT CCATCATTTGTTAGGTCGTGCC
613	AAV6_Rep 0-49	ATGCCGGGTTTTTATGAAATCGTAATCAAAGTTCCGAGCGAT CTGGATGAACATCTGCCGGGAATCTCTGATAGCTTTGTTAAC TGGGTAGCTGAAAAAGAATGGGAAC TTCCGCCGATAGTGA TATGGACTTAAACTTAATTGAA
614	AAV6_Rep 24-73	TCTTTTGTGAATTGGGTAGCTGAAAAAGAATGGGAAC TGCC GCCGGATTCTGACATGGATCTTAACCTGATTGAACAAGCGC CGTTGACCGTTGCAGAGAAGTTACAGCGCGATTTTGTGTGC AGTGCGCTCGTGTCAGCAAAGCG
615	AAV6_Rep 48-97	GAACAGGCGCCGCTGACGGTGGCCGAAAAATTGCAGCGTGA CTTCTGGTTCAATGGCGCCGCTCTCAAAGGCCCGGAAG CACTGTTTTTTGTACAATTTGAGAAAGGCGAATCTTATTTTC ATTTGCATATTCTGGTGGAACA
616	AAV6_Rep 72-121	GCACCGGAGGCGTTATCTTTGTGCAGTTTGAAAAAGGCGA GTCTTATTTTCATCTTCATATTCTGGTTGAAACACGGGGGT TAAGAGTATGGTACTTGGACGCTTCTGTACAGATACGTG ATAAATTGGTCCAAACCATCTAT
617	AAV6_Rep 96-145	ACTACAGGGGTTAAATCAATGGTATTAGGACGTTTTTTAAGC CAGATCCGCGATAAATTAGTACAAACAATATACCGTGAAT AGAACCGACGCTTCCGAATTGGTTTGCTGTAACCAAAACAC GTAATGGCGCTGGTGGCGGGAAT
618	AAV6_Rep 120-169	TATCGCGGCATCGAGCCGACCCTGCCGAATTGGTTTCGAGTT ACCAAAACACGCAACGGCGCTGGCGGTGGTAATAAGGTTGT TGATGAGTGCTATATCCCGAATTACTTATTGCCGAAGACTCA ACCGGAATTACAGTGGGCCTGG
619	AAV6_Rep 144-193	AATAAAGTTGTTGATGAATGCTATATACCGAATTATCTGCTG CCGAAAACCCAGCCGGAAC TTCAAGTGGGCGTGGACCAATAT GGAGGAATATATTTACGCGTGTTTAAATTGGCTGAACGTA AACGTTTAGTTGCACATGATTTG
620	AAV6_Rep 168-217	TGGACCAACATGGAAGAGTATATTTACGCGTGTTTAACTT GGCGGAACGCAACGCCTGGTCGCGCATGACTTGACTCATG TGTCACAGACTCAAGAACAGAATAAAGAAAACCTGAACCCG AACAGTGATGCACCGGTTATTCGT
621	AAV6_Rep 192-241	CTGACCCATGTTTACAGACTCAAGAACAGAATAAAGAAAA TCTTAATCCGAACAGCGATGCGCCGGTAATTTCGACGAAAA CCAGTGCTCGTTATATGGAGCTGGTAGGCTGGCTGGTAGAT CGTGGTATCACGAGCGAAAAAGCAG
622	AAV6_Rep 216-265	CGTTCTAAAACTAGTGCGCGCTACATGGAGCTTTAGGGTG GCTGGTGGATCGCGGTATCACTTCTGAAAAGCAGTGGATTCT AGGAGGATCAGGCGTCTTATATTTCTTTCAACGCTGCGTCAA ACAGTCGCTCACAATTAAGCA
623	AAV6_Rep 240-289	CAATGGATCCAAGAAGATCAGGCATCATATATCAGTTTAA TGCGGCATCAAACAGCCGAGTCAGATAAAGGCAGCCCTGG ATAATGCGGGGAAAAATCATGGCCCTGACAAAAAGTGCTCCG GATTACCTGGTTGGACCGGCACCG

SEQ ID NO:	Name	Sequence
624	AAV6_Rep 264-313	GCAGCGCTGGATAATGCAGGCAAGATTATGGCCTTGACTAA GAGCGCCCCGGATTATTTAGTAGGGCCGGCACCGCCGGCTG ATATAAAGACCAACCGCATTTACCGCATTTTAGAATTGAAT GGTTATGACCCGGCGTATGCCCGT
625	AAV6_Rep 288-337	CCGCCGGCAGACATTAACAAACAAATCGCATTTATCGTATACT GGAACCTTAATGGGTATGATCCGGCATATGCCGGGCAGTGTAT TTTTAGGTTGGGCACAAAAACGCTTTGAAAAGCGTAATACA ATCTGGTTATTCGGTCCGGCGACC
626	AAV6_Rep 312-361	GGCAGTGTATTCTGGGGTGGGCGCAGAAACGTTTTGGTAA ACGCAATACCATTTGGCTGTTCCGACCGGCAACGACCGGAA AAACAAATATAGCTGAGGCTATCGCCCATGCTGTCCCGTTTT ACGGCTGCGTGAATTGGACAAAT
627	AAV6_Rep 336-385	ACCACAGGTAAAAACAAACATCGCCGAAGCCATTGCCATGC CGTACCGTTTTATGGGTGCGTAAACTGGACAAATGAAAATT TTCCGTTTAATGATTGTGTGGATAAAATGGTGATTGGTGGG AAGAAGGAAAAATGACTGCTAAA
628	AAV6_Rep 360-409	AATGAAAATTTCCGTTCAACGATTGTGTGCGATAAAATGGTC ATTTGGTGGGAGGAAGGTAAATGACTGCCAAAGTAGTGGA ATCAGCTAAGGCAATCCTTGGAGGTAGTAAAGTGCGTGTGG ATCAGAAGTGTAAGAGCAGTGCA
629	AAV6_Rep 384-433	AAGGTGTCGAAAAGCGCTAAGGCCATTTTAGGTGGTAGCAA AGTTCGCGTCGATCAAAAATGCAAGAGCTCTGCCCAAATCG ACCCGACTCCGGTTATAGTGACTAGCAATACGAACATGTGC GCTGTGATTGATGGTAATAGTACC
630	AAV6_Rep 408-457	GCTCAGATTGATCCGACGCCGTTATTGTAAACATCAAAATAC GAATATGTGCGCAGTTATCGATGGCAATTCAACAACTTTGA ACATCAACAGCCGCTGCAGGACCGTATGTTCAAGTTTGAAT TGACTCGTCGCCTGGAGCATGAT
631	AAV6_Rep 432-481	ACCACTTTTGAACATCAACAACCGTTGCAGGACCGTATGTTT AAATTCGAGTTAACCCGCCGTCTGGAACATGATTTTCGGCAA GGTTACGAAACAAGAGGTTAAAGAGTTTTTTCGCTGGGCGC AGGATCATGTTACAGAGGTAGCC
632	AAV6_Rep 456-505	GATTTTGGGAAAGTAACTAAACAGGAAGTTAAAGAGTTTTT CCGTTGGGCCCAGGATCATGTCAGTGAAGTGGCGCATGAGT TCTACGTACGTAAAGGGGGCGCTAATAAGCGTCCGGCACCG GATGACGCCGACAAATCAGAACCG
633	AAV6_Rep 480-529	GCCCATGAATTTTATGTGCGTAAGGGTGGAGCGAATAAACG CCCGCGCCCGGATGATGCCGATAAAAGTGAACCGAAACGTG CGTGCCCGAGCGTGGCTGATCCGTCTACATCAGACGCCGAA GGAGCCCCGTTGATTTTGCTGAT
634	AAV6_Rep 504-553	CCGAAACGTGCATGTCCGAGTGTGCGGATCCGAGTACCTC AGATGCTGAGGGCGCTCCGGTAGACTTTGCTGACCGCTACC AAAATAAGTGCAGTCGTCATGCGGGTATGTTACAGATGTTG TTCCGTTGAAGACGTGTGAACGT
635	AAV6_Rep 528-577	GATCGTTATCAGAACAAATGTAGCCGCCATGCCGGTATGCT GCAGATGCTGTTCCCGTGTAAGACCTGTGAGCGCATGAATC AGAATTTCAACATTTGCTTCACCCATGGGACGCGTGACTGTA GTGAGTGTTTTCCGGGAGTCTCT
636	AAV6_Rep 552-601	CGTATGAATCAGAACTTTAACATCTGTTTTACACATGGTACC CGCGACTGTAGTGAATGTTTCCCGGGAGTCTCAGAAAGCCA ACCGGTGGTCCGTAAACGTAACCTACCGTAAACTGTGTGCTAT TCATCATCTTCTGGGACGTGCC

SEQ ID NO:	Name	Sequence
637	AAV5_Rep 0-49	ATGGCCACGTTTTACGAAGTGATAGTGC GCGTTCGTTTCGAT GTCGAGGAGCATCTGCCGGGGATTAGCGATTCAATTCGTCGA TTGGGTCACAGGACAGATTTGGGAATTACCGCCGGAGTCTG ATCTTAATCTTACCTTGGTAGAA
638	AAV5_Rep 24-73	AGTTTTGTGATTTGGGTTACCGGTCAGATCTGGGAATTGCCG CCGGAAAGCGACCTTAATCTGACACTGGTGGAAACAGCCGCA GTTAACGGTAGCGGATCGCATCCGCCGCGTCTTCTGTACGA ATGGAACAAATTTTCAAACAA
639	AAV5_Rep 48-97	GAGCAACCGCAGCTGACCGTTGCCGACCGCATACGTCGTGT GTTTCTTTATGAATGGAATAAGTTCAGCAAGCAAGAATCAA AATTTTTGTCCAATTTGAGAAAGGCTCTGAATACTTTCATT TACATACGTTAGTCGAGACAAGT
640	AAV5_Rep 72-121	CAAGAGAGCAAATTTTTCGTTCAATTTGAAAAGGGTAGCGA ATATTTCCATCTGCATACACTGGTCGAAACAAGTGGAAATTC ATCTATGGTGTGGGGCCGCTACGTTAGCCAAATTCGTGCGCA ACTGGTGAAGGTTGTGTTTCAA
641	AAV5_Rep 96-145	AGTGGTATTAGTTCATGGTTCTTGGGCGTTATGTAAGCCAA ATCCGCGCGCAATTAGTAAAAGTTGTCTTTCAGGGAATTGA GCCGCAGATAAACGATTGGGTTGCAATTACAAAGGTTAAGA AGGGTGGGGCAAATAAAGTCGTC
642	AAV5_Rep 120-169	CAAGGAATCGAACCGCAGATTAATGATTGGGTGGCGATAAC CAAAGTTAAAAAGGGGGCGCTAATAAGGTCGTTGATTCTG GCTACATACCGCGTATTTACTCCGAAAGTTCAGCCGGAA CTGCAGTGGGCTGGACCAATCTG
643	AAV5_Rep 144-193	GTGGATAGCGGGTATATTCCGGCTTACCTGCTGCCGAAAAGT ACAGCCGGAGCTGCAATGGGCGTGGACGAACCTTGATGAAT ACAACTGGCGGCACTGAATTTGGAAGAACGTAAGCGCCTT GTAGCACAGTTTCTGGCGGAGAGT
644	AAV5_Rep 168-217	CTTGATGAATATAAACTGGCTGCACTTAATCTGGAAGAACG TAAGCGTCTGGTTGCACAATTTTAGCGGAATCAAGCCAGC GTTCTCAGGAAGCCGCTTCTCAGCGTGAGTTCTCAGCAGATC CGGTAATTAAGTCTAAAACCTCT
645	AAV5_Rep 192-241	TCTAGTCAGCGTTCACAGGAGGCAGCAAGTCAGCGTGAATT TAGTGCCGATCCGTTATAAAAAGTAAACTAGCCAGAAGT ACATGGCACTGGTAAACTGGCTGGTGGAACATGGCATTACT TCTGAGAAGCAGTGGATTACAGGAG
646	AAV5_Rep 216-265	TCACAGAAATATATGGCTCTGGTGAATTGGCTTGTAGAACA TGGTATAACTTCTGAGAAACAGTGGATACAGGAAAACCAGG AAAGTTATTTGAGTTTAATTCTACAGGTAATTCACGCAGTC AGATTAAGGCAGCCCTGGACAAC
647	AAV5_Rep 240-289	GAAAATCAGGAATCATATCTGAGCTTTAACTCAACTGGCAA TTCACGTTACAAATTAAGCTGCACTGGATAACCGGACGA AAATAATGTCTTTGACTAAAAGCGCTGTGGATTATCTGGTCG GCTCTTCACTGCCGAGGATATC
648	AAV5_Rep 264-313	AATGCCACCAAAATTATGAGCCTGACTAAATCAGCGGTGGA CTACCTGGTTGGAAGTTCAGTGCCGGAAGATATTCAAAAA ATCGTATTTGGCAAATATTCGAGATGAATGGATATGATCCG GCGTACGCCGTTCAATTTTATAC
649	AAV5_Rep 288-337	ATATCAAAGAACCGTATCTGGCAGATTTTGAAATGAATGG TTATGATCCGGCTTATGCGGGTAGCATTTTATATGGTTGGTG CCAGCGCAGTTTAATAAACGTAATACCGTCTGGCTGTACG GACCGGCAACAACGGTAAGACT

SEQ ID NO:	Name	Sequence
650	AAV5_Rep 312-361	TACGGATGGTGTCTAGCGTTTCATTCAACAAACGCAACACCGTGTGGTTATACGGCCCGGCAACCACCGGCAAGACTAACATTGCGGAAGCAATAGCGCATACCGTGCCGTTTTATGGTTGCGTA AACTGGACGAACGAGAACTTCCG
651	AAV5_Rep 336-385	ACGAATATCGCTGAGGCGATTGCGCATACGGTCCCGTTTACGGCTGTGTGAATTGGACGAACGAGAACTTCCCGTTTAATGATTGCGTCGATAAAAATGCTGATCTGGTGGGAAGAGGGCAAGATGACAAAACAAAGTGGTTGAGAGC
652	AAV5_Rep 360-409	CCGTTTAACGATTGCGTAGATAAGATGCTGATATGGTGGGAAGAAGGAAAAATGACTAACAAAGTCGTGTAATCTGCGAAGGCGATCCTGGGGGGGAGCAAAGTTCGTGTAGATCAAAAATGCCAAATCTTCTGTCCAAATAGATTCT
653	AAV5_Rep 384-433	AGCGCCAAGGCGATTTTGGGCGGATCTAAAGTTCGCGTAGATCAGAAAATGCAAGTCTTCTGTTTCAGATTGATTCTACTCCGGTGATAGTTACTAGTAACACCAATATGTGTGTGGTTCGTCGACGTAACTCTACCACGTTTCAACAT
654	AAV5_Rep 408-457	TCTACTCCGGTTATTGTACGAGTAATACCAATATGTGTGTCTGTGGTAGACGGAAATAGCACAACTTCAACATCAGCAACCGCTGGAAGATCGTATGTTCAAATTCGAACCTACTAAACGCTTACCGCCGGACTTTGGCAAAATC
655	AAV5_Rep 432-481	CATCAACAGCCGCTGGAAGATCGCATGTTTAAAGTTCGAGCTGACAAAACGCTTACCGCCGGACTTTGGAAAAATTACTAAGCAGGAAGTGAAAGATTTTTTGCCTGGGCGAAAGTGAATCAGGTGCCGGTGACCCATGAGTTTAAAG
656	AAV5_Rep 456-505	ATTACGAAGCAAGAGGTGAAAAGATTTTTTGTCTGGGCAAAAGTGAATCAGGTGCCGGTCACACATGAATTTAAAGTGCCGCGCGAGTTAGCAGGCACTAAAGGTGCGGAGAAAAGCCTGAAACGTCCGCTGGGCGATGTTACAAAT
657	AAV5_Rep 480-529	AAGGTACCGCGTGAACCTGGCGGGTACTAAGGGTGCAGAAAATCATTGAAGCGCCCGCTGGGTGACGTACCAATACTAGCTATAAAAGCCTGGAGAAACGCGCCCGTCTGAGCTTCGTCCCGGAAACCCGCGCTCTTCAGACGTG
658	AAV5_Rep 504-553	AATACATCTTATAAGTCTCTGGAAAAGCGTGCGCGTTTATCTTTTGTGCCGGAACTCCGCGTTCTTCAGATGTAAGTGTGGATCCGGCTCCGCTGCGCCCGCTTAATTGGAATAGCCGCTATGATTGTAAATGCGACTATCATGCT
659	AAV5_Rep 528-577	GTGACTGTCTGATCCGGCTCCGCTTCGTCCGCTGAATTGGAACTCACGCTACGATTGTAAGTGTGACTACCATGCGCAGTTCGATAATATTAGCAACAAATGTGACGAATGCGAATATCTTAATCGCGTAAGAACGGATGTATTTGT
660	AAV5_Rep 552-601	GCTCAATTTGACAACATCAGCAATAAATGTGATGAATGTGAGTACCTGAACCGTGGCAAAAATGGGTGTATTTGTCATAACGTAACCCATTGCCAAATCTGTCATGGGATCCCGCCGTGGGAAAAAGAAAACCTGTCTGACTTCGGC
661	AAV4_Rep 0-49	ATGCCGGGTTTCTACGAGATCGTTCTGAAGGTACCGTCAGACCTGGATGAACATCTGCCGGGTATAAGTGATAGCTTCGTAACTGGGTTGCAGAGAAAAGAGTGGGAGCTGCCGCCGGATAGCGACATGGATTTAAATCTTATAGAA
662	AAV4_Rep 24-73	AGTTTTGTCTCATGGGTTGCTGAGAAAAGATGGGAACTGCCGCCGATTCTGACATGGATCTTAACCTTATAGAACAGGCACCGTTGACGGTCGCGGAAAAACTGCAACGTGAATTTCTGTGAGTGGCGCCCGCTGAGCAAAGCG

SEQ ID NO:	Name	Sequence
663	AAV4_Rep 48-97	GAACAAGCGCCGCTGACGGTCGCGGAAAAAGCTGCAACGCG AATTTTTGGTAGAATGGCGTCGTGTCTCAAAAAGCACCGGAA GCCCTGTTCTTTGTTTCAGTTTGAAAAAGGCGACTCATATTTT CATTTGCATATTTTGGTTGAAACT
664	AAV4_Rep 72-121	GCACCGGAAGCGCTGTTCTTTGTCCAATTCGAGAAAAGGCGA TTCTTATTTTCATCTGCATATTCTGGTGGAACGGTGGGCGT GAAGAGCATGGTCGTTGGACGTTACGTGTCTCAAATTAAG AGAAGCTGGTGACACGTATATAT
665	AAV4_Rep 96-145	ACAGTGGGGGTTAAATCTATGGTAGTTGGGCGCTATGTGTCT CAGATTAAAGGAGAACTGGTTACCCGCATTTATCGTGGTGT CGAACCGCAGCTGCCGAATTGGTTCGCCGTCACGAAAACAC GTAATGGGGCTGGGGGAGGAAAT
666	AAV4_Rep 120-169	TATCGCGGTGTCGAACCGCAACTGCCGAATTGGTTTGCAGTT ACGAAAACCCGTAATGGTGCCGGCGGGGCAACAAAGTGG TGGACGATTGCTATATTCCGAATTATCTGCTGCCGAAAACCTC AGCCGGAACCTTCAGTGGGCATGG
667	AAV4_Rep 144-193	AATAAGGTTGTGCGACGATTGCTACATACCGAACTATTTATTA CCGAAAACGCAGCCGGAAGTGCAGTGGGCATGGACAAACA TGGACCAGTATATAAGCGCGTGTTTAAATCTGGCTGAACGT AAACGTCTGGTTGCACAGCATTTA
668	AAV4_Rep 168-217	TGGACGAACATGGATCAGTACATCAGTGCTTGTCTGAACCT GGCAGAACGTAAACGTCTGGTTGCTCAACATCTGACACATG TTTCTCAGACGCAGGAACAGAATAAAGAGAATCAAATCCG AACTCTGATGCGCCGGTGATTCTG
669	AAV4_Rep 192-241	CTTACACATGTGTACAGACACAAGAACAGAACAAAGAGA ACCAGAACCCGAATAGTGACGCGCCGGTTATACGTTCTAAA ACAAGCGCGCGTTATATGGAATTGGTTGGTTGGCTTGTGAC CGCGGCATTACCAGTGAAAAACAG
670	AAV4_Rep 216-265	CGCAGTAAACTAGCGCGCGCTACATGGAAGTGGTTGGATG GTTAGTTGATCGTGGCATCACGTCAGAGAAACAGTGGATTCT AGGAGGATCAGGCAAGCTATATTTCTTTCAATGCGGCATCT AACTCTCGCTCACAGATCAAAGCG
671	AAV4_Rep 240-289	CAATGGATTCAAGAGGACCAGGCCTCTTACATAAGTTTAA TGCAGCGTCTAATAGTCGCTCTCAGATTAAAGCGGCGCTGG ATAATGCCTCTAAGATTATGTCTCTGACAAAGACCGCCCCG GATTACTTGGTTCGGTCAAAACCCG
672	AAV4_Rep 264-313	GCGGCTCTGGATAACGCAAGTAAATCATGAGTCTGACGAA AACGGCACCGGATTACCTGGTCGGTCAGAATCCGCCGGAAG ATATAAGTTCAAACCGCATTTATCGCATTTTAGAAATGAACG GCTATGATCCGCAGTATGCAGCC
673	AAV4_Rep 288-337	CCGCCGGAAGACATTTCTAGCAACCGCATTTATCGTATTTTA GAAATGAACGGATATGATCCGCAATATGCTGCCTCAGTGTT TCTTGGTTGGGCGCAGAAGAAATTTGGAAAGCGTAATACCA TTTGGCTGTTTGGCCCGGCGACC
674	AAV4_Rep 312-361	GCGAGCGTGTTTTTGGGTTGGGCCCAGAAAGAAATTTGGCAA ACGCAATACCATTGGTTATTGGGCCGGCCACTACAGGTA AAACAAATATCGCGGAGGCGATCGCGCATGCAGTCCCGTTC TATGGGTGCGTAAATTGGACAAAC
675	AAV4_Rep 336-385	ACGACCGGGAAAACTAACATCGCAGAAGCCATCGCACATGC GGTTCCGTTTTACGGTTGCGTTAATTGGACGAATGAAAATTT CCCGTTTAACGACTGCGTTGACAAAATGGTAATTTGGTGGG AAGAGGGCAAAATGACGGCCAAA

SEQ ID NO:	Name	Sequence
676	AAV4_Rep 360-409	AACGAAAATTTCCCGTTTAACGATTGCGTAGATAAAATGGT AATTTGGTGGGAAGAGGGTAAGATGACGGCAAAAGTGGTA GAATCAGCGAAGGCGATTCTGGGCGGTTCAAAGGTGCGTGT AGATCAGAAATGTAAGTCAAGCGCA
677	AAV4_Rep 384-433	AAAGTGGTTGAGTCAGCAAAAAGCCATTCTGGGGGGCAGTAA GGTCCGCGTTGACCAAAAGTGTAAGTCTAGTGCGCAGATTG ATCCGACCCCGGTTATAGTAACATCAAATACTAACATGTGT GCCGTTATCGATGGTAACTCAACG
678	AAV4_Rep 408-457	GCGCAGATAGATCCGACACCGGTAATCGTTACATCTAATAC CAACATGTGCGCAGTGATAGACGGGAACAGTACAACGTTCCG AACATCAACAACCGTTACAGGATCGTATGTTCAAATTTGAA CTGACAAAGCGTTTGGAAACATGAT
679	AAV4_Rep 432-481	ACTACCTTTGAACATCAGCAGCCGCTTCAGGATCGCATGTTT AAATTCGAGCTGACGAAGCGTCTTGAACATGATTTTGGCAA AGTCACAAAACAGGAGGTGAAAGATTCTTTTCGTTGGGCGA GTGACCATGTTACAGAGGTCAT
680	AAV4_Rep 456-505	GACTTCGGAAAGGTGACTAAACAAGAAGTTAAAGATTTTTT CCGCTGGGCCAGTGATCATGTCACTGAAGTAACTCATGAAT TTTATGTACGCAAGGGTGGGGCTCGCAAACGCCCGGCTCCG AATGATGCCGACATCAGCGAGCCG
681	AAV4_Rep 480-529	ACGCATGAGTTCTACGTGCGCAAAGGTGGCGCACGTAAACG CCCGGCACCGAATGATGCGGATATTTCTGAACCGAAACGTG CATGCCCGTCAGTGGCTCAACCGAGCACTTCAGACGCCGAA GCACCGGTAGACTACGCTGATCGT
682	AAV4_Rep 504-553	CCGAAACGTGCGTGTCCGTCAGTGGCCAGCCGAGCACCTC AGATGCAGAAGCTCCGGTCGACTATGCAGACCGCTACCAGA ACAAGTGCACTCGCCATGTGGGGATGAACTTAATGTTGTTTC CGTGTCGTCACTGTGAACGTATG
683	AAV4_Rep 528-577	CGTTATCAAAATAAATGTAGTCGTATGTAGGAATGAACTT AATGCTGTTCCCGTGCCGCCAATGTGAACGCATGAACCAGA ATGTAGACATATGCTTCACGCATGGGGTAATGGATTGTGCA GAATGTTTTCCGGTCTCTGAAAGC
684	AAV4_Rep 552-601	ATGAATCAGAACGTGGATATCTGTTTTACTCATGGAGTAATG GATTGCGCAGAATGTTTTCCGGTTAGCGAGAGCCAGCCGGT TTCTGTGGTGCGCAAACGTACCTATCAGAAACTGTGTCCGAT CCATCATATTATGGGTCTGTCG
685	AAV3_Rep 0-49	ATGCCGGGATTTTATGAAATTGTGCTTAAAGTGCCGTCAGAT CTGGATGAGCGCCTTCCGGGAATCAGTAACAGTTTCGTAAA TTGGGTGGCCGAAAAAGAATGGGATGTTCCGCCGATTACG ATATGGATCCGAATCTGATTGAA
686	AAV3_Rep 24-73	AGCTTTGTGAACCTGGGTTGCAGAAAAAGAATGGGATGTGCC GCCGACTCTGACATGGACCCGAATTTAATAGAACAAGCTC CGCTTACCGTGGCCGAAAAGTTACAACGCGAGTTCTTAGTC GAATGGCGCCGTGTAAGCAAAGCA
687	AAV3_Rep 48-97	GAGCAAGCGCCGCTTACCGTCGCCGAAAAATTGCAGCGTGA GTTTTTGGTTGAGTGGCGCCGTGTGAGTAAAGCGCCGGAAG CGCTGTTCTTCGTTCAGTTTGAGAAAGGTGAAACCTATTTCC ATCTGCATGTCCTTATAGAAACG
688	AAV3_Rep 72-121	GCTCCGGAAGCGTTGTTTTTGTGTCAGTTTGAGAAAGGCGA GACATACTTTTCATCTGCATGTTTTAATAGAGACGATTGGTGT TAAATCAATGGTCTGTGGGCGTTATGTTAGTCAGATCAAAG AAAACTGGTAACGCGTATATAT

SEQ ID NO:	Name	Sequence
689	AAV3_Rep 96-145	ACTATTGGTGTAAAAAGTATGGTTGTGGGGCGCTATGTATCA CAAATCAAAGAAAAATTAGTTACACGTATATATCGTGGTGT TGAACCGCAGTTGCCGAATTGGTTCGCTGTGACCAAAACGC GCAATGGCGCAGGCGGAGGCAAT
690	AAV3_Rep 120-169	TATCGTGGTGTCTGAACCGCAACTGCCGAATTGGTTCGCGGT GACTAAAACCTCGTAACGGCGCAGGTGGAGGAAATAAGGTG GTCGATGACTGCTACATTCCGAACTACCTGCTGCCGAAGACT CAACCGGAACCTCAATGGGCGTGG
691	AAV3_Rep 144-193	AATAAAGTTGTGGATGATTGTTATATCCGAACTACCTTCTG CCGAAAACGCAACCGGAACTGCAATGGGCATGGACTAACAT GGACCAGTATTTGAGTGCATGCCTGAACCTAGCTGAGCGCA AACGCCTGGTCGCCCAACATCTG
692	AAV3_Rep 168-217	TGGACAAATATGGACCACTACCTGTCTGCCTGCTTAAACCTT GCAGAGCGCAAAACGTCCTGGTGGCCAGCATTTGACTCATGT AAGTCAGACTCAGGAACAGAACAAAGAAAAATCAGAATCCG AACAGTGACGCGCCGGTCATTCGT
693	AAV3_Rep 192-241	CTGACGCATGTTAGTCAGACTCAGGAACAAAATAAAGAGAA TCAGAACCCGAACCTCAGACGCCCGGTTATACGCTCAAAAA CCAGTGCTCGTTATATGGAACCTGTGGTGGCTGGTTGATC GCGGTATCACCTCAGAGAAACAA
694	AAV3_Rep 216-265	CGCAGCAAAACCTCTGCTCGTTATATGGAACCTGTGGTGG CTTGTAGACCGTGGTATAACCAGTGAAAAGCAGTGGATTCA GGAAGACCAGGCTTCATACATATCATTCAACGCGACCTCAA ATAGCCGTAGCCAGATAAAAAGCT
695	AAV3_Rep 240-289	CAGTGGATCCAGGAAGATCAGGCCTCTTACATTAGTTTCAA CGCGGCGAGTAACAGTCGCTCACAGATTAAGGCAGCCCTGG ACAATGCAAGTAAATCATGAGTTTAACAAAAACGGCTCCG GATTATTTAGTTGGTTCTAACCCG
696	AAV3_Rep 264-313	GCAGCCCTGGATAATGCCAGCAAGATAATGTCTCTGACAAA AACGGCGCCGGATTACTTAGTCGGAAGTAATCCGCCGGAAG ATATTACAAAAAATCGTATTTACCAAATCCTTGAGTTAAATG GTTACGATCCGCAATATGCCGCA
697	AAV3_Rep 288-337	CCGCCGGAAGACATTACCAAGAATCGTATATACCAGATTCT GGAGTTGAACGGATACGATCCGCAATATGCAGCCAGCGTAT TCTGGGGTGGGCCAGAAAAAATTTGGCAAACGCAATACA ATTTGGCTGTTCCGGTCCGGCTACG
698	AAV3_Rep 312-361	GCGTCTGTCTTCTGGGCTGGGCGCAGAAAAAATTTGGAAA ACGTAATACGATTGGCTGTTTGGACCGGCGACCACAGGCA AAACGAATATTGCCGAAGCTATTGCGCATGCAGTCCCGTTCT ATGGATGTGTGAATTGGACAAAT
699	AAV3_Rep 336-385	ACAACAGGGGAAGACGAACATTGCAGAAAGCTATAGCTCATGC AGTACCGTTCTACGGGTGCGTCAATTGGACCAACGAAAAC TCCCGTTCAATGACTGTGTGGATAAAATGGTGATCTGGTGG GAGGAGGGTAAAAATGACGGCTAAA
700	AAV3_Rep 360-409	AATGAGAATTTCCGTTTAAACGATTGTGTTGATAAGATGGTG ATATGGTGGGAAGAAGGAAAAATGACAGCGAAAAGTGGTAG AGAGCGCCAAAAGCAATTTTGGGCGGAAGTAAAGTTCGCGTG GATCAGAAATGCAAAATCTTCAGCG
701	AAV3_Rep 384-433	AAAGTTGTGGAAAAGTGCAAAAGCCATACTGGGCGGATCAAA GGTTTCGCGTTGATCAGAAATGCAAAAGCTCTGCTCAGATTG AGCCGACCCCGTAATCGTTACATCAAATACGAATATGTGC GCTGTTATTGATGGCAATAGCACA

SEQ ID NO:	Name	Sequence
702	AAV3_Rep 408-457	GCGCAGATCGAACCGACACCGGTTATTGTGACCTCTAACAC AAATATGTGCGCTGTCATTGACGGAAATTCAACCACCTTTGA ACATCAGCAACCGTTGCAGGATCGTATGTTGAATTTGAACT GACACGTCGCCTGGATCATGAT
703	AAV3_Rep 432-481	ACTACGTTTGAACATCAACAGCCGCTGCAGGATCGCATGTTT GAATTTGAGTTAACGCGTCGCCTGGACCATGACTTCGGAAA GGTGACGAAGCAGGAAGTTAAAGACTTCTTTCGTTGGGCTA GTGACCATGTACGGATGTGGCA
704	AAV3_Rep 456-505	GACTTTGGGAAGGTTACGAAACAGGAGGTTAAAGATTTTTT TCGCTGGGCTAGTGATCATGTGACAGATGTGGCCCATGAAT TTTATGTTTCGTAAAGGCGGTGCTAAGAAGCGCCCGGCCAGT AATGACGCCGATGTTAGTGAACCG
705	AAV3_Rep 480-529	GCCCATGAGTTTTATGTTTCGTAAAGGAGGCGCAAAAAACG CCCGGCCAGCAATGATGCTGATGTCTCAGAACCGAAACGTG AATGCACGAGTTTAGCACAACCGACCACTAGTGATGCAGAA GCACCGGCAGATTATGCAGATCGC
706	AAV3_Rep 504-553	CCGAAGCGTGAATGCACGAGTTTAGCGCAGCCGACTACCTC TGACGCCGAAGCACCGGCCGATTATGCAGATCGCTACCAGA ATAAATGCTCTCGTCATGTCGGCATGAATCTGATGTTATTTT CGTGCAAAACTTGCGAACGTATG
707	AAV3_Rep 528-577	CGCTACCAAAACAAATGCTCTCGCCATGTTGGAATGAATCT GATGCTTTTCCCGTGCAAAACGTGTGAGCGTATGAACCAAA TAAGCAATGTGTGTTTACACATGGTCAACGTGATTGCGGG GAATGTTTCCCGGGTATGTCTGAA
708	AAV3_Rep 552-601	ATGAATCAAATTAGTAACGTGTGCTTTACGCATGGCCAGCG CGACTGCGGCGAATGTTTCCCGGGCATGTCAGAGTCACAAC CGGTTTCAGTTGTGAAGAAAAAACGTATCAGAAGTTATGT CCGATCCATCATATTTGCGGCCGT
709	AAV2_Rep 0-49	ATGCCGGGTTTTTATGAAATTGTAATCAAAGTACCGAGCGA TTTAGACGAACATCTGCCGGGAATTTCTGACAGTTTCGTGAA TTGGGTTGCAGAAAAGGAGTGGGAATTGCCGCCGATAGCG ATATGGATCTGAATTTAATCGAG
710	AAV2_Rep 24-73	TCTTTTGTGAACCTGGGTAGCCGAGAAAGAATGGGAGTTACC GCCGGACAGTGACATGGATTTAACTTAATCGAACAGGCAC CGCTGACAGTTGCGGAGAAAAGTGCAGCGCATTTTCTGACA GAATGGCGCCGCGTTTCAAAGCG
711	AAV2_Rep 48-97	GAGCAAGCGCCGTTGACGGTAGCGGAAAAGCTGCAGCGTG ACTTCTTAACGGAATGGCGTCGCGTTTCAAAGCACC GGAA GCGCTGTTCTTCGTACAGTTCGAGAAAAGGAGAAAGTTATTC CATATGCATGTGTTAGTAGAGACC
712	AAV2_Rep 72-121	GCGCCGGAAGCGCTGTTTTTTGTACAATTTGAAAAAGGCGA ATCATACTTCCATATGCATGTGCTGGTTGAAACGACCGGCGT CAAATCTATGGTTCTGGGGCGCTTCTGTCTCAGATCCGCGA AAAATTGATACAACGCATTTAT
713	AAV2_Rep 96-145	ACTACCGGCGTTAAGTCTATGGTTCTGGGCCGCTTTTTATCT CAAATCCGCGAAAACTGATTCAACGCATTTACCGTGGAAT CGAACCGACTCTGCCGAAGTGGTTCGCGGTGACAAAGACTC GCAACGCGCGGGAGGCGGGAAT
714	AAV2_Rep 120-169	TATCGCGGGATAGAACCGACTCTGCCGAAGTGGTTCGCGGT AACCAAGACACGTAATGGAGCTGGTGGCGGAAATAAAGTG GTGGATGAATGTTATATACCGAATTATCTTTTCCGAAAACC CAGCCGGAGTTGCAGTGGGCCTGG

SEQ ID NO:	Name	Sequence
715	AAV2_Rep 144-193	AACAAAGTGGTAGATGAATGCTACATTCCGAATTATCTGTT ACCGAAGACCCAACCGGAGTTACAATGGGCGTGGACCAATA TGGAACAGTACCTTAGCGCATGTTTAAATCTTACCGAACGTA AACGTTTGGTTGCTCAGCATCTG
716	AAV2_Rep 168-217	TGGACGAACATGGAACAGTATTTATCAGCGTGTCTGAATCT GACAGAGCGCAAACGTTTGGTGGCGCAACATCTGACTCATG TTTCTCAGACTCAAGAACAGAATAAGGAGAATCAGAACCCG AATAGCGATGCCCCGGTCATTTCG
717	AAV2_Rep 192-241	TTGACACATGTTAGCCAAACTCAGGAGCAAAATAAAGAGAA TCAAAACCCGAATAGTGACGCCCGGTGATCCGTTCAAAAA CGTCTGCACGCTATATGGAGCTTGTGGGATGGCTGGTTGAC AAAGGCATAACGTCTGAAAAACAG
718	AAV2_Rep 216-265	CGCAGCAAAACTAGCGCCCGTTATATGGAAGTGGTGGTTG GCTTGTGGATAAAGGGATCACGTCTGAGAAGCAATGGATCC AGGAAGACCAAGCATCATATATTTCTTTAACGCGGCTAGT AATTCACGCTCTCAAATAAAGCG
719	AAV2_Rep 240-289	CAGTGGATTCAAGAGGATCAGGCGAGCTATATTAGCTTTAA TGCAGCTTCAAATAGCCGTAGCCAAATCAAGGCGGCTCTTG ACAATGCGGGAAAAATAATGAGTCTTACCAAACCGCGCCG GACTATTTAGTGGGCCAGCAGCCG
720	AAV2_Rep 264-313	GCGGCCTTAGACAATGCCGGAATAATCATGTCTTTGACCAA AACTGCGCCGATTATTTAGTGGGTGAGCAACCGGTGGAAG ATATTAGCAGTAATCGCATCTATAAAATCCTGGAGTTGAAT GGTTATGATCCGCAATATGCTGCA
721	AAV2_Rep 288-337	CCGGTGGAGGATATTTCAAGCAATCGCATCTATAAGATTCT GGAGCTGAACGGTTACGACCCGCAATATGCCGCCAGTGTCT TTCTGGGTTGGGCAACGAAAAAGTTTGGGAAGCGCAATACG ATCTGGCTTTTTGGTCCGGCTACC
722	AAV2_Rep 312-361	GCGTCTGTCTTTTTAGGTTGGGCTACGAAAAAGTTTGGTAAA CGTAATACAATCTGGCTTTTTGGCCCGGCCACTACAGGTA ACAAACATAGCAGAGGCGATTGCGCATACAGTTCCGTTTTA TGGTTGTGTTAATTGGACAAAT
723	AAV2_Rep 336-385	ACCACCGGGAAGACCAACATTGCGGAAGCCATCGCCCATAC AGTTCCGTTCTATGGGTGTGTAAGTGGACAAACGAAAAAT TCCCGTTCAATGATTGCGTCGATAAGATGGTTATCTGGTGGG AAGAAGGCAAAATGACGGCGAAA
724	AAV2_Rep 360-409	AACGAAAACTTCCCGTTTAAACGACTGTGTGGATAAAATGGT CATCTGGTGGGAAGAAGGTAAATGACAGCAAAAGGTGGTC GAAAGCGCCAAAGCAATTCTTGGGGGTCTAAGGTCCGTGT CGATCAGAAATGTAAATCAAGTGCC
725	AAV2_Rep 384-433	AAAGTTGTGGAAAGCGCTAAAGCCATCCTGGGTGGCTCAA AGTGCCTGTTGACCAGAAGTGCAAAAGTTCTGCACAAATAG ATCCGACTCCGGTCATAGTAACCAGTAACACTAACATGTGT GCCGTTATAGACGGAAATAGTACC
726	AAV2_Rep 408-457	GCGCAATCGACCCGACACCGGTGATTGTTACCAGCAATAC CAACATGTGTGAGTCATAGACGGCAACTCAACCACATTG AACATCAACAGCCGCTGCAGGATCGTATGTTTAAAGTTGAG TTAACGCGTCTGTCGATCATGAC
727	AAV2_Rep 432-481	ACTACCTTCGAACATCAGCAGCCGCTGCAGGATCGTATGTTT AAATTTGAACTGACGCGCCGTCTTGATCATGACTTCGGGAA AGTTACCAACAGGAAGTAAAGGATTTTTTCGTGGGCCA AAGATCATGTAGTAGAAGTGGA

SEQ ID NO:	Name	Sequence
728	AAV2_Rep 456-505	GATTTTGGTAAGGTGACAAAACAAGAAGTGAAAGATTCTT CCGCTGGGCTAAAGATCATGTCTGGAGGTAGAGCATGAAT TTTATGTTAAAAAAGGTGGAGCTAAAAAGCGCCCGCCCCG TCAGACGCAGATATTTCTGAGCCG
729	AAV2_Rep 480-529	GAGCATGAATTTTATGTTAAGAAAGGGGTGCTAAAAAACG TCCGGCCCCGTGATGCCGATATTTCTGAACCGAAGCGCG TTCGCGAAAAGCGTGGCACAAACCGTCAACATCAGATGCCGAG GCGTCTATTAATTATGCGGACCGC
730	AAV2_Rep 504-553	CCGAAACGCGTCCGCGAGAGCGTCGCTCAGCCGAGCACGTC TGACGCCGAAGCATCTATTAACATATGCAGATCGCTATCAAA ATAAATGTAGCCGTATGTCTGGTATGAACCTGATGCTTTTCC CGTGCCGCCAATGCGAACGCATG
731	AAV2_Rep 528-577	CGTTACCAAAATAAATGCTCTCGCCATGTCGGATGAACCT GATGTTATTTCCCGTGGCGTCAGTGCGAACGCATGAATCAGA ACAGCAACATATGCTTCACACATGGGCAGAAAGATTGTTTA GAATGTTTCCCGGTGAGTGAGAGT
732	AAV2_Rep 552-601	ATGAATCAAAATTCAAATATATGTTTTACCCATGGACAAAA AGACTGCTTGGAGTGTTTCCCGGTGAGCGAGTCTCAGCCGG TGTCTGTTGTAAAAAAGCCTATCAAAAACTTTGTTACATTC ATCATATAATGGGCAAGGTGCCG
733	AAV1_Rep 0-49	ATGCCGGGCTTTTACGAAATTGTCTATAAAGTGCCGAGCGA CTTGGACGAGCATCTGCCGGGGATCAGCGATTCAATTTGTTT ATGGGTTGCCGAAAAAGAGTGGAATTACCGCCGGATTGAG ACATGGATCTGAATCTGATCGAA
734	AAV1_Rep 24-73	AGCTTTGTGTCATGGGTGGCTGAAAAGGAATGGGAGCTGCC GCCGATAGCGACATGGATCTGAATTTAATTGAACAAGCGC CGCTTACAGTTGCCGAAAAACTGCAGCGTGACTTTCTGGTCC AATGGCGCCGCTGTCTAAAGCG
735	AAV1_Rep 48-97	GAACAAGCCCCGTTGACCGTTGCAGAAAAACTGCAGCGTGA TTTCTGGTCCAGTGGCGCCGTGTGAGCAAAAGCTCCGGAGG CACTTTTTTTCGTGCAATTTGAAAAAGGAGAGAGTTACTTTC ATCTGCATATACTGGTTGAAACC
736	AAV1_Rep 72-121	GCGCCGGAAGCACTTTTCTTTGTACAATTTGAGAAGGGCGA GTCATATTTCCATTACATATTCTGGTTGAGACAACCGGTGT GAAAAGCATGGTATTAGGCCGCTTTTAAAGCCAAATCCGTG ATAAACTGGTCCAAACCATTAT
737	AAV1_Rep 96-145	ACGACGGGTGTAAAGTCTATGGTTTTAGGACGCTTTCTGTCA CAGATACGTGACAAACTGCTTCAGACGATATACCGTGGCAT CGAGCCGACGCTTCCGAACCTGGTTTTGCGGTTACCAAAACCC GTAATGGTGCGGGTGGCGGCAAT
738	AAV1_Rep 120-169	TATCGTGGTATCGAGCCGACTCTCCGAATTGGTTTGCAGTA ACTAAAACCCGTAAACGGTGCGGGAGGGGGCAACAAAGTTGT CGATGAATGCTATATTCCGAACACTTGCTGCCGAAAACAC AACCGGAGCTTCAATGGGCGTGG
739	AAV1_Rep 144-193	AACAAAGTCGTAGATGAATGTTATATCCCGAACTATCTTCTT CCGAAAACCCAGCCGGAGTTACAGTGGGCCTGGACGAACAT GGAAGAAATATATTAGCGCCTGCCTGAACTTGGCAGAGCGTA AACGTCTGGTGGCCAGCATTTG
740	AAV1_Rep 168-217	TGGACCAACATGGAGGAATATATCTCTGCGTGTCTTAACCTG GCAGAACGTAAACGCCTGGTGGCACAGCATTTGACCCATGT ATCTCAAACACAAGAACAGAATAAAGAAAAATCTGAACCCG AACAGTGACGCACCGGTAATCCGC

SEQ ID NO:	Name	Sequence
741	AAV1_Rep 192-241	CTGACACATGTAAGTCAGACTCAGGAGCAGAATAAAGAAA ATTTAAATCCGAACAGCGATGCTCCGGTAATACGTTCAAAA ACATCTGCCCCGTTACATGGAACTGGTCGGATGGCTGGTGA TCGCGGCATAACCTCAGAAAAACAA
742	AAV1_Rep 216-265	CGCAGCAAAACAAGCGCGCGCTATATGGAAC TGGTTGGATG GCTGTTGATCGCGGCATCACTTCAGAGAAGCAGTGGATCC AAGAAGACCAGGCGTCTTATATTCTTTAATGCCGCCAGCA ACAGCCGTAGTCAGATTAAAGCT
743	AAV1_Rep 240-289	CAGTGGATTTCAGGAAGATCAGGCCTCTTATATCAGTTTAAAT GCCGCAAGCAACTCTCGTTCACAGATTAAAGCGGCTCTGGA TAATGCCGGCAAAATTATGGCGCTGACAAAATCTGCCCCGG ACTATCTGGTGGGACCGGCGCCG
744	AAV1_Rep 264-313	GCCGCACTGGATAATGCAGGCAAGATCATGGCTTTAACAAA AAGCGCCCCGATTATCTGGTAGGCCCGGCTCCGCCGCGCCG ACATTAAACCAATCGCATTTATCGCATTTTGGAGCTGAACG GTTATGAACCGGCGTACGCTGGC
745	AAV1_Rep 288-337	CCGCCGGCGGATATTAAGACTAATCGCATTTACCGCATACTT GAGCTGAATGGTTATGAACCGGCCTACGCCGGATCTGTGTTT CTGGGCTGGGCACAAAAACGTTTTGGCAAGCGCAATACTAT TTGGCTTTTTGGACCGGCAACT
746	AAV1_Rep 312-361	GGAAGCGTTTCTCGGGTTGGGCTCAAAAGCGTTTGGTAA ACGCAATACAATTTGGTTATTTGGCCCGGCAACTACTGGAA AAACCAACATCGCAGAGGCAATCGCGCATGCCGTTCCGTTT TATGGGTGCGTGAATTGGACGAAC
747	AAV1_Rep 336-385	ACTACTGGTAAAACAAATATTGCTGAAGCGATTGCTCATGC CGTACCGTTTTATGGGTGCGTGAAC TGGACGAATGAGAATT TTCCGTTTAAACGATTGCGTTGACAAGATGGTTATCTGGTGGG AAGAAGGTAAAATGACAGCAAAA
748	AAV1_Rep 360-409	AATGAGAATTTCCCGTTTAAATGATTGTGTGACAAAATGGTT ATTTGGTGGGAGGAGGAAAGATGACCGCAAGGTCGTTGA AAGTGCCAAAGCGATCTTAGGCGGTAGCAAAGTCCGTGTGG ATCAAAAATGCAAATCTTCAGCC
749	AAV1_Rep 384-433	AAAGTTGTGGAAGCGCTAAAGCGATCTTAGGCGGTTCTAA AGTGCGTGTGGACCAGAAATGTAAAAGTTCAGCCCAGATTG ACCCGACACCGGTTATCGTGACAAGCAACACTAATATGTGT GCACTGATTGACGGTAATTCAACG
750	AAV1_Rep 408-457	GCCCAGATAGATCCGACGCGGTCATTGTTACCTCTAATACC AATATGTGCGCTGTCATAGATGGCAATAGCACGACGTTTGA ACATCAGCAACCGTTACAAGACCGCATGTTTAAATTCGAGT TGACACGCCGCTTAGAGCATGAC
751	AAV1_Rep 432-481	ACGACTTTTGAACATCAACAACCGTTGCAAGATCGCATGTTT AAGTTTGAGCTTACGCGTCGTCTTGAACATGATTTTGGCAAA GTCACGAAACAGGAAGTTAAAGAATTTTTTCGCTGGGCGCA GGACCATGTCACCGAAGTCGCG
752	AAV1_Rep 456-505	GATTTTGGTAAAGTCACCAAACAAGAGGTCAAAGAATTTT TCGCTGGGCACAGGATCATGTGACAGAAGTTGCCCATGAGT TTTATGTCCGCAAGGGGGGGGCAATAAACGCCCGGCACCG GATGATGCTGATAAGTCAGAACCG
753	AAV1_Rep 480-529	GCACATGAATTTTATGTACGTAAGGGAGGTGCAACAAACG TCCGGCACCGGATGACGCAGATAAAAGTGAGCCGAAACGTG CTTGCCCGAGTGTGGCTGATCCGAGCACCAGTGATGCCGAG GGGACCGGTTGATTTTGCTGAT

SEQ ID NO:	Name	Sequence
754	AAV1_Rep 504-553	CCGAAACGCGCATGTCCGTCTGTCGCGGATCCGTCAACCAGCGATGCGGAAGGAGCGCCGGTAGATTTTGCTGATCGTTACCAGAATAAATGCAGTCGTCATGCAGGGATGCTTCAGATGTTGTTCCGTGTAAACTTGTGAACGC
755	AAV1_Rep 528-577	GATCGCTATCAGAATAAATGTAGTCGTCATGCAGGAATGCTGCAAAATGTTATTTCCGTGCAAAACGTGTGAACGCATGAATCAGAATTTTAACATTTGCTTCACCCATGGTACCCGTGACTGCTCTGAATGTTTTCCGGGCGTTTCT
756	AAV1_Rep 552-601	CGTATGAACCAAAATTTCAATATTTGCTTTACTCATGGCACTCGCGATTGCTCAGAATGTTTCCCGGGAGTAGCGAATCTCAGCCGGTGGTCCGCAACGCACATACCGTAAATTATGTGCTATCCATCATCTGCTTGGCCGTGCT
757	AAV2_AAP 0-49	ATGGAGACTCAAACGCAGTATTTAACACCGAGTCTGAGTGA CTCACATCAACAACCGCCGTTGGTTTGGGAACTGATTGCTTG GTTGACAGGCGGTAGCACATCAGTGGCAGACAATAACCCGTG CACCGACGGAATGGGTAATTCCG
758	AAV2_AAP 24-73	TTGATACGTTGGCTGCAAGCAGTTGCACATCAATGGCAGACCATCACAGTGCCCCGACAGAATGGGTTATTCGCGCGAGATTGGTATCGCCATTCCGCATGGGTGGGCTACGGAAAAGCAGCCGCCGGCTCCGGAGCCGGGTCCG
759	AAV2_AAP 48-97	CCGCGTGAGATTGGTATCGCCATACCGCATGGGTGGGCAACGGAATCTTCACCGCCGGCGCCGGAACCGGGTCCGTGCCCGCGACCACCACCACTAGTACCAACAAATTCGGGTAACCAAGAACCGCGTACGACCATCAACACC
760	AAV2_AAP 72-121	CCGTGCCCCGCCGACTACGACCACCTCAACCAACAAATTTCCGGCAAATCAGGAACCGCGTACCACTATTACTACTTTGGCAA CTGCCCCGCTGGGCGGCATTCTGACAAGTACAGACAGCACGGCAACGTTTCATCATGTGACGGGT
761	AAV2_AAP 96-145	ACCTTGGAACCCGCCGTTGGGTGGGATCCTGACTAGCAC TGATAGTACGGCTACGTTCCATCATGTGACTGGCAAGGACAGCAGCACGACAACCGGTGATAGTGACCCGCGCGATAGCACGAGTAGTAGTTTGACCTTTAAAAGT
762	AAV2_AAP 120-169	GGCAAAGATAGTTCAACGACTACAGGAGATTCAGACCCGCGTGACAGTACATCAAGTAGCTTAACATTCAAATCAAAGCGTTCTCGTCGTATGACAGTCCGTCGTCGCTGCCGATTACACTGCCGGCACGCTTTCGTTGCCCTTCTG
763	AAV2_AAP 144-193	TCAAAACGTAGCCGCCGTATGACCGTACGCCGTCGTTTGCCGATAACTTTGCCGGCTCGTTTTCGCTGTCTGCTGACACGTTCTACAAGTAGCCGTACTAGCAGTGCGCGCCGTATAAAGGATGCCTCACGCCGCTCTCAGCAGACC
764	AAP 0-49	ATGGAGACCCAGACTCCGTATTTAACCCCGTCTGTCTGACTCTCATCAGCAGCCGCCGTTAGTATGGGAGTTGATTGCTGGTTGCAGGCCGTGCGACATCAGTGGCAGACTATTACACGTGCCCGACTGAATGGGTTATCCCG
765	AAP 24-73	TTAATCCGTTGGCTTCAGGCGGTGGCCCATCAGTGGCAGACATAACGCGTGCTCCGACGGAATGGGTGATTCCGCGTGAAA TTGGGATCGCGATCCCGCATGGATGGGCTACCGAGTCAAGTCCGCCGGCGCCGGCTCCGGGTCTG
766	AAP 48-97	CCGCGCGAAATTGGTATTGCAATCCCGCATGGATGGGCCACCGAGTCAAGCCCGCCGGCCCCGGCGCCGGGGCTGTGTCCGCGACCACCACGATTTGCACGAGCCGTTTCCCGGCAATCAAGAGCATCGCACCACCACGACCACT

SEQ ID NO:	Name	Sequence
767	AAP 72-121	CTGTGTCCGCCGACCACAACAATATGCACCAGCCGTTTCCCG GCTAACCAGGAACATCGCACAAACGACAACACTACTCTTGCAAC TGCTCCGTTAGGTGGTATTCTGACTAGTACCGACAGCACAGC TACTTTCCATCATGTACCGGT
768	AAP 96-145	ACGCTGGCCACCGCACCGCTGGGCGGGATCCTGACTAGCAC CGACTCAACTGCTACATTCCATCATGTAACGGGCAAAGATT CTAGCACTACAACCGGTGATTCTGATCCGAAGGATAGCACC AGTTCTTGCCTTACTTTCAAGTCT
769	AAP 120-169	GGTAAAGATAGTAGTACAACCACTGGTGATTGATCCGAA AGACAGTACTAGCAGCTGTTTGACATTTAAAAGCCGTCGTTT ACGCCGCATGACCGTACGCCGCCGCTGCCGATAAATCTGTC CGGCGCGCTTCCGCTGCCTTTTA
770	AAP 144-193	AGTCGTGCTCACGCCGCATGACCGTGCGTCGCCGCTTACCG ATTACCTTACCGGCCCGTTTCCGTTGTCTGCTTACCCGCAGC ACGAGCAGTCGTACCTCAAGCGCCCGCCGTATTAAAGATGC TAGCCGCCGTTTTC AACGCACC
771	AAV2_Xprotei n 0-49	ATGGTACTTTATCTGCCGACGTCACGTGAAGCCACAGACAA ACAACCTCCGCAGATGTCTACCCATAAAGCATTTTTTCAGGC GTGGTCTGGGCGTACTGAAATGTGTACCTTTCGCGGTCCGAG TGGCCAGCGTTTCCATACACGT
772	AAV2_Xprotei n 24-73	TTTTTCAAGCATGGAGTGGTCTGTAACCGAAATGTGCACATTC CGTGGTCCGAGCGGTCAACGTTTTTCATACCCGTACGGATATA TTTACTCCGTTACCGTCTTGGGTGGATTCTGATCTGAATACA CTGCTTCATCGCTTAGCTCA
773	AAV2_Xprotei n 48-97	CGCACCGACATCTTACACCCGCTGCCGTCTTGGGTGGATAGC GATTTAAACACTTTACTGCATCGCTTCAGTAGTCGTACGCCG CGTTATTTACGCATCCTGCGCCCGCCGTCAGTACGCCAAAGC CTGTTACCGAGTAGCCATTCA
774	AAV2_Xprotei n 72-121	TCTCGTACACCGCGCTATTTACGCATTCTTCGTCCGCCGAGT GTTTCGTCACTGCTGCGGAGCTCTATTCAACTCCGCGT GATCGCTCTGCCTGGCGTTCATCAGGTTCTTGTGCGCCGTA AACTGCGAATGCTGGTATTCCG
775	AAV2_Xprotei n 96-145	TCTACTCCGCGTGATCGCAGCGCCTGGCGTAGCTCAGGTAG CTGTCGTCTGTAACCGCAAACGCTGGTATTCCGAAATTCTC AACCTTCCGACCACAACCTCTTACTTATGTGGACATTACT TTGGACGCTGATGGCATGCATT
776	AVIAN_AAV_ capsid 0-49	ATGAGCTTAATCTCTGATGCCATTCCGGATTGGTTAGAACGC CTGGTTTCGTAAAGGTGTTAATGCGGCCGCGGATTTTACCAT TTAGAATCAGGTCCGCCGCCGCGAAAGCGAATCAGCAAAC TCAGGAAAGTCCGGAAGGAT
777	AVIAN_AAV_ capsid 24-73	GATTTCTACCATTTAGAATCTGGCCCCGCCGGCACCGAAGGC GAACCAGCAAAACACAGGAAAGCCCGGAAAAAGATGATAGC CGCGTTTATGTGTTCCCGGGCTACAAGTACCTGGGCCCGTTC AATGGGCTGGATAAAGGGGAACCG
778	AVIAN_AAV_ capsid 48-97	GATGATTACGTGGTCTGGTTTTTCCGGGCTATAAGTATTTA GGACCGTTCAACGGTTTGGACAAGGGCGAACCGTTAACGA AGCGGATGCGGCAGCGCTGGAACATGATAAGGCCTATGATC TGGAAGTGAAGACGGTCATAAT
779	AVIAN_AAV_ capsid 72-121	CCGGTGAACGAAGCGGATGCCGCCGATTAGAACATGATAA AGCATATGATTTAGAAGTGAAGATGGACATAATCCGTATT TCGAGTATAATGAAGCCGATCGCCGCTTTCAGGAGCGTCTG AAAGACGACACCTCATTCGGTGGC

SEQ ID NO:	Name	Sequence
780	AVIAN_AAV_capsid 96-145	AATCCGTACTTTGAATATAACGAAGCGGACCGTCGTTTCAA GAACGTCTTAAGGACGACACTAGCTTTGGCGGTAACCTTGG CAAGGCTATCTTTCAAGCGAAGAAGCGTGTACTGGAACCGT TTGGCCTGATCGAACAACCGGAT
781	AVIAN_AAV_capsid 120-169	GGTAACTTAGGTAAGGCCATTTTCAGGCCAAAAAACGTGT GCTGGAACCGTTTGGCCTTATCGAACAGCCGGATAATACTG CTGGTACGGGTGAAAAACGCCCGGAACGTGTCTGATGATTTT TTTCCGAAGAAGAAAAAGGCAAAA
782	AVIAN_AAV_capsid 144-193	GACAATACGGCGGGCACTGGTGAAAAACGTCCGGAACGTGT GGATGACTTCTTCCCGAAGAAAAAGAAAGCAAAGACCGAA CAGGGCAAAACCCCGGCGCAAAACCGGTGAGGACCCGGGAG AGGGTACGTCTATCTAATGCAGGTTCT
783	AVIAN_AAV_capsid 168-217	AAAACAGAGCAAGGTAAAACCCCGGCCAGACGGGGGAAG ACCCGGGGGAGGGGACCTCTAGCAACGCCGGAAGCTCTGCG CCGTCTATCTGTGGGCTCAAGCGTAATGGCCGAGGGAGGAGG TGGCCCGGTGGGGGATGCGGGTCAA
784	AVIAN_AAV_capsid 192-241	AGTTCAGCACCGAGTAGCGTAGGCAGCAGTGTCTATGGCAGA GGGAGGGGGTGGCCCGTTCGGCGATGCAGGCCAGGGGGCG GATGGTGTGGTAACTCAAGTGGTAACTGGCATTTGCGATTTC ACAGTGGCTGGATAACGGTGTAGTA
785	AVIAN_AAV_capsid 216-265	CAGGGCGCCGACGGTGTGGAACTCATCTGGCAATTGGCA TTGCGATTCTCAGTGGTTGGACAAATGGCGTTGTTACGCGTAC CACTCGCACCTGGGTTTTACCGAGCTATAATAACCATCTGTA TAAACGTATTCAAGGCCCGGGC
7863	AVIAN_AAV_capsid 240-289	GTCACGCGCACACGCGTACCTGGGTACTGCCGTCTTATAAT AATCATCTGTACAAACGCATCCAAGGCCCGGGAGGTACAGA TAACAATAATAAATATTTTGGCTTTTCAACGCCGTGGGGGTA TTTCGATTACAACCGCTTTCAT
787	AVIAN_AAV_capsid 264-313	GGTGGGACAGATAATAACAACAAGTACTTTGGTTTTAGCAC GCCGTGGGGCTATTTTGATTATAATCGCTTCCATTGTCTTT CAGCCCGCGTGATTGGCAGCGCCTGATTAATAACAATTGGG GCATACGTCCGAAGGCTATGCGC
788	AVIAN_AAV_capsid 288-337	CATTGTCTTTTTAGCCCGCGTGATTGGCAGCGTCTGATCAAT AACAACTGGGGGATTCGTCCGAAGGCCATGCGTTTCCGCTT ATTCAATATCCAAGTTAAGGAAGTTACCGTTCAAGATAGTA ATACCACGATCGCAAATAAATTG
789	AVIAN_AAV_capsid 312-361	CGCTTTCGCTTGTTAATATACAGGTTAAAGAAGTGACTGTA CAGGATTCAAACACTACCATCGCGAACAACCTTACAAGTAC GGTCCAGGTCTTTGCCGATAAAGACTACCAGCTGCCGTATGT GTTAGGGAGCGCAACCGAGGGG
790	AVIAN_AAV_capsid 336-385	TTGACTTCAACCGTGCAAGTATTTGCAGATAAAGGATTATCAG TTGCCGTATGTGCTGGGCTCAGCAACGGAAGGTACCTTTCCG CCGTTCCCGGCCGACATCTATACCATTCCGCAGTACGGTTAC TGTACGCTTAACTATAACAAT
791	AVIAN_AAV_capsid 360-409	GGCACCTTTCCGCCGTTCCCGGCTGACATTTATACTATCCCG CAGTATGGTTACTGCACGCTGAATTATAATAATGAAGCCGT AGATCGTAGTGCGTTCTATTGCTTAGACTACTTCCCGTCAGA CATGTTACGCACGGGAAATAAT
792	AVIAN_AAV_capsid 384-433	AATGAAGCCGTGGACCGCAGTGCATTCTATTGTCTTGACTAT TTTCCGTCTGATATGCTGCGTACTGGCAATAATTTTGAATTT ACGTATACGTTTGAGGATGTCCCGTTTCATAGTATGTTTGCT CATAATCAGACACTGGACCGT

SEQ ID NO:	Name	Sequence
793	AVIAN_AAV_capsid 408-457	AATTTTCGAGTTTACGTACACCTTTGAGGATGTGCCGTTTCAT TCTATGTTTCGCGCATAATCAGACGTTAGATCGTTTAATGAAT CCGCTGGTTGATCAGTATTTATGGGCGTTTCTTCAGTCAGC CAGCCGAGCTCAGGTCAGCGT
794	AVIAN_AAV_capsid 432-481	CGCTTAATGAACCCGCTGGTGGACCAGTATTTGIGGGCTTTT TCTAGCGTTAGCCAGCCGAGTTCTGGACAGCGCCGCTGAA TTATTCTCGTGGTACCAAAAAATAATATGGCCGTTCAATATAA AAACTGGCTGCCGGGGCCGTTT
795	AVIAN_AAV_capsid 456-505	CGTCGTTTGAACCTACTCACGCGGCACAAAGAACAATATGGC AGTTCAATATAAAAAATTGGTTACCGGGCCCGTTTTCGCGA TCAACAGATTTATACAGGCGCCTCTAATATTACACAGAACA ACGTGTTTAACGTTTGGGATAAA
796	AVIAN_AAV_capsid 480-529	TTTTTTCGCGATCAGCAGATTTATACAGGCGCATCTAATATT ACACAGAACAACGTATTTAATGTATGGGACAAGGGAAAGCA GTGGGTCATAGATAATCGCACAACTTGATGCAGCCGGGCC CGGCGCGCGCAACCACTTTTCA
797	AVIAN_AAV_capsid 504-553	AAAGGTAAACAATGGGTCATAGATAATCGCACCAACCTGAT GCAGCCGGGGCCGGCTGCGGCTACCACATTACGCGGTGAGC CGGATCGCCAGGCTATGCAAAATACCCTGGCCTTTCTCGTA CCGTCTACGACCAAACTACATCT
798	AVIAN_AAV_capsid 528-577	AGCGGCGAACCGGATCGCCAGGCAATGCAGAACACCCTGGC CTTTTCACGTACTGTTTATGATCAGACTACCAGTACCGCAGA TCGTAACCAACTGTTAATAACGAACGAAGATGAGATCCGCC CGACAAATAGTGTCGGTATAGAT
799	AVIAN_AAV_capsid 552-601	TCAACGGCGGATCGCAACCAGCTGTTGATTACCAATGAAGA TGAGATTTCGTCCGACAAATAGCGTGGGGATCGACGTATGGG GTGTCTGTTCCGAATAATCAGCAGAGTAATGTTAGCCCGGGA AATCGTACAGGGGTAAACAATCAG
800	AVIAN_AAV_capsid 576-625	GATGTTTGGGGCGTTTGTCCGAATAATCAACAGAGCAACGT CTCTCCGGGGAACCGCACTGGCGTGAATAATCAAGGTGCTT TACCGGGCATGGTTTGGCAGAACCGTGACATTTATCTGCAG GGTCCGATATGGGCAAAAGTACCG
801	AVIAN_AAV_capsid 600-649	CAAGGGGCTCTTCCGGGTATGGTATGGCAAAATCGCGACAT TTATTTGCAGGGCCCGATTGGGCGAAAGTCCCGGATACAG ATAATCATTTTCATCCGTCTCCGCTGATCGGTGGGTTTGGTT GTAAACATCCGCCCGCGCAATT
802	AVIAN_AAV_capsid 624-673	CCGGATACAGACAATCATTTCCATCCGTCTCCGTTAATTGGT GGGTTCGGCTGTAAGCATCCGCCGCCGAGATATTATCAA GAATACCCCGGTTCCGGCGAATCCGCCGGAACATTCCAAA CTGCTAAAGTAGCTTCATTTATT
803	AVIAN_AAV_capsid 648-697	ATATTCATCAAAAATACGCCGGTACCGGCAATCCGCCGGA GACTTTTCAAACGGCGAAGGTTGCCTCTTTTATTAATCAGTA TTCAACTGGCCAGTGCACCGTGGAATTTTGGGAACTGA AAAAGGAGACTAGTAAGCGCTGG
804	AVIAN_AAV_capsid 672-721	ATTAATCAGTATAGCACGGGGCAATGCACAGTGGAATTTT CTGGGAATTAAGAAAGAAACGTCTAAACGCTGGAATCCGG AAATCCAGTTACCTCTAACTTTGGTAATGCTGCCGATATTC AATTCAGTGTAAGTGACACGGGA
805	Bovine_cap 0-49	ATGAGTTTGTGGATCATCCGCCGGATTGGCTGGAATCTATC GGTGACGGGTTCCGCGAGTTTTAGGTCTTGAAGCCGGGCC GCCGAAGCCGAAAGCGAATCAACAGAAACAAGATAATGCC CGCGGATTGGTTTTGCCGGGGTAT

SEQ ID NO:	Name	Sequence
806	Bovine_cap 24-73	GAAGCAGGTCCGCCGAAACCGAAAGCGAATCAGCAGAAAC AGGATAATGCGCGTGGGCTGGTATTACCGGGTTACAAGTAT CTTGGACCGGGCAACGGGCTGGATAAGGGCGACCCGGTTAA CTTTGCAGACGAGGTAGCCCGCGAA
807	Bovine_cap 48-97	TATAAATATCTGGGACCGGGAAATGGCCTGGATAAAGGAGA CCCGGTAAACTTCGCTGACGAGGTGGCTCGTGAGCATGATT TAAGCTATCAAAAACAATTAGAGGCGGGGGATAACCCGTAT TTAAATATAATCATGCCGACGCA
808	Bovine_cap 72-121	GAACATGATCTGTCTTATCAGAAACAACCTGGAGGCCGCGCA TAACCCGTACCTGAAATATAATCATGCGGATGCCGAATTC AGGAAAACTGGCCAGTGATACCAGCTTTGGGGGAACCTG GGGAAAGCAGTGTTCAGGCGAAA
809	Bovine_cap 96-145	GCTGAATTTCAAGAAAAATTGGCATCTGATACGAGTTTGG CGGAAATCTGGGAAAGGCGGTTTTTCAGGCTAAAAACGTA TCTTGGAGCCGCTGGGATTGGTGAAACCCCGGATAAAACG GCCCCGGCCGCAAAAAAACGTCCG
810	Bovine_cap 120-169	AAAAAACGTATATTGGAACCGTTAGGACTGGTTGAGACGCC GGATAAACAGCTCCGGCTGCAAAAAACGTCCGTTGGAGC AGAGCCCGCAGGAACCGGACTCATCTTCAGGTGTAGGTAAA AAGGGTAAACAGCCGGCTCGTAAA
811	Bovine_cap 144-193	CCGTTAGAGCAAAGTCCGCAAGAGCCGGACTCTAGCTCTGG CGTTGGTAAAAAGGGCAAGCAGCCGGCTCGCAACGTTTGA ATTTTGATGATGAGCCGGGGCAGGTGATGGTCCGCCGCCG GAAGGGCCGTCATCAGGTGCGATG
812	Bovine_cap 168-217	AAACGTCTGAATTTGACGATGAGCCGGGCGCGGGTGATGG TCCGCCGCCGGAAGGACCGTCATCTGGCGCCATGAGTACCG AAACAGAAATGCGTGCCGCTGCCGGTGGAATGGGGGGGAT GCAGGTCAGGGCGCCGAGGGCGTG
813	Bovine_cap 192-241	ATGTCAACTGAAACGGAAATGCGTGCCCGGGCTGGAGGGAA CGGCGCGGATGCTGGTCAGGGTGCCGAGGGTGTTGGGAATG CAAGTGCGGATTGGCATTGTGATAGTACCTGGTCAGAGAGT CATGTAACAACCACATCTACCCGT
814	Bovine_cap 216-265	GTAGGGAATGCAAGTGGCGATTGGCATTGTGATTCTACGTG GAGCGAAAGTCATGTGACAACCACTTCTACTCGACCTGGG TGCTGCCGACATATAACAATCATCTGTACTTACGCTGGGCA GTAGCAATGCGTCTGATACGTTT
815	Bovine_cap 240-289	CGTACCTGGGTGTTGCCGACATATAACAATCATCTGTATCTT CGTCTGGGGAGCTCAAATGCTAGCGATACCTTAATGGTTTT AGCACGCCGTGGGGTTATTTGACTTTAATCGCTTTCATTGC CATTTTTCTCCGCGCGATTGG
816	Bovine_cap 264-313	TTTAATGGCTTTTCTACTCCGTGGGGCTATTTGACTTTAATC GTTTTCATTGCCATTTAGCCCCGCGCGATTGGCAGCGTTTGA TAAATAACCATTGGGGGCTTCGCCGAAAAGCATGCAAGTC CGCATCTTTAATATCCAGGTA
817	Bovine_cap 288-337	TGGCAGCGCCTGATTAATAATCATTGGGGTTTGCGCCGAA ATCTATGCAGGTGCGCATCTTCAATATCCAAGTAAAGGAAG TTACCACCTCTAACGGTGAAACCACAGTTAGTAATAACCTG ACCAGCACTGTACAGATCTTTGCT
818	Bovine_cap 312-361	GTGAAGGAAGTTACCACAAGCAACGGCGAGACTACCGTCTC TAATAACTTAACATCTACAGTTCAGATCTTTGCGGATAGCAC CTATGAACCTCCGTACGTGATGGATGCCCGACAGGAAGGAT CTTTACCGCCGTTTCCGAATGAC

SEQ ID NO:	Name	Sequence
819	Bovine_cap 336-385	GCCGATTCTACTTATGAATTGCCGTATGTTATGGATGCCGGT CAGGAAGGATCATTGCCGCCGTTCCCGAATGATGTTTTCATG GTCCCGCAGTATGGTTATTGTGGTTTAGTCACGGGTGGTTCT TCTCAGAACCAGACCGATCGC
820	Bovine_cap 360-409	GACGTTTTTATGGTTCCGCAGTACGGCTATTGTGGTCTGGTC ACAGGTGGGTCAACACAGAATCAGACCGATCGCAATGCATT TTATTGTCTTGAATACTTCCGAGCCAAATGTTACGTACCGG GAACAAC TTCGAGATGGTATAT
821	Bovine_cap 384-433	CGCAATGCCTTCTATTGCTTAGAATATTTTCCGAGTCAGATG TTACGTACTGGTAATAATTCGAGATGGTTTATAAATTCGAA AATGTCCCGTTTCATTCTATGTATGCACATTCACAGTCACTG GATCGTCTTAGAATCCGTTG
822	Bovine_cap 408-457	TACAAATTCGAGAACGTGCCGTTTCATTCAATGTATGCCCAT AGCCAGTCTTTGGACCGCTTAATGAATCCGTTACTTGATCAA TATTTGTGGGAGTTGCAATCAACAACGAGCGGGGGGACACT GAATCAGGGTAACTCAGCAACT
823	Bovine_cap 432-481	TTGCTGGATCAGTACTTGTGGGAGCTGCAGTCTACTACGTCA GGCGGTACATTAAATCAGGGAACTCAGCGACGAACTTCGC CAAGCTGACTAAAACCAATTTCAGTGGTTATCGTAAAAACT GGTTACCGGGCCCGATGATGAAA
824	Bovine_cap 456-505	ACAAACTTCGCTAAACTTACTAAAACAAATTTAGCGGCTAT CGTAAGAACTGGTTGCCGGGTCCGATGATGAAACAGCAGCG CTTTTCAAAAACCGCCAGTCAAAATTACAAGATACCGCAGG GCCGCAACAATAGTCTGTTACAT
825	Bovine_cap 480-529	AAACAGCAGCGTTTTTCTAAAACAGCGTCTCAGAATTACAA AATCCCGCAGGGTCGCAACAATTCTCTGCTGCATTATGAAA CTCGTACGACGCTGGATGGTTCGCTGGAGCAACTTCGCACCG GGAACAGCAATGGCAACTGCGGCC
826	Bovine_cap 504-553	CATTACGAAACACGCACGACGCTGGATGGTCTGTTGGTCTAA CTTTGCCCGGGTACAGCCATGGCCACCGCAGCCAACGACG CGACCGACTTCAGTCAAGCGCAGCTTATTTTCGCGGGTCCGA ATATCACTGGGAACACAACCTACC
827	Bovine_cap 528-577	GCTAACGACGCCACCGATTTTAGCCAGGCACAGTTAATCTTC GCTGGCCCGAATATTACCGGTAACACGACCACTGATGCAAA TAATTTGATGTTTACTTCAGAAGATGAGTTACGTGCCACAAA CCCGCGGACACCGACTTATTT
828	Bovine_cap 552-601	ACAGATGCAAAATAACTTAATGTTACGAGCGAGGATGAACT GCGTGCTACTAACCCGCGTGACACAGATCTGTTCCGGTCATCT TGCTACCAACCAGCAGAACGCTACCACCGTCCCGACGGTTG ACGATGTAGATGGAGTCGGCGTT
829	Bovine_cap 576-625	TTTGGCCATTTGGCCACTAATCAGCAAAATGCCACCACGGT ACCGACGGTTGATGATGTTGATGGCGTAGGCGTGTACCCGG GGATGGTTTGGCAAGATCGTGACATTTATTACCAAGGTCCG ATCTGGGCCAAGATCCCGCATACC
830	Bovine_cap 600-649	GTTTATCCGGGAATGGTGTGGCAAGATCGTGATATTTATTAT CAGGGGCCGATCTGGGCCAAAATCCCGCATACGGATGGACA TTTTTCATCCGTCTCCGCTGATCGGCGGATTTGGACTGAAATC ACCGCCGCCGACAGATATTTATC
831	Bovine_cap 624-673	ACCGATGGGCGATTTTCATCCGTCACCGTTGATTGGCGGTTTT GGCTTGAAAAGTCCGCCGCCGACAGATTTTATAAAGAATAC TCCGGTTCGGGCTAACCCGGCGACCACCTTCTACCGGCTCG CATTAATAGCTTCATTACACAG

SEQ ID NO:	Name	Sequence
832	Bovine_cap 648-697	ATTAAAAACACGCCGGTGCCGGCTAACCCGGCCACCACCTT TAGTCCGGCACGTATTAACAGCTTTATTACACAGTACTCAAC AGGACAGGTTGCAGTTAAGATTGAATGGGAGATTACAGAAAG AACGTTCAAAACGTTGGAATCCG
833	Bovine_cap 672-721	CAGTATTCTACCGGCCAGGTTGCAGTCAAGATCGAATGGGA AATTCAGAAAGAACGCTCTAAACGCTGGAACCCGGAGGTCC AATTCACCAGTAATTACGGCGCTCAGGACAGCCTGCTGTGG GCCCCGGACAACGCCGGCGCTTAT
834	Bovine_Rep 0-49	ATGGCGACCTTTTATGAAGTAATTGTTCTGTTGCCGTTTCGAT GTCTGAAGAACATCTTCCGGGCATTTCTGACAAATTCGTTGAC TGGGTTACAGGCCAAATTTGGGAACCTCCGCCGGAAGCGA CTTGAATCTGACCCTTATTGAA
835	Bovine_Rep 24-73	AATTTTCGTTGATTGGGTACCGGCCAAATCTGGGAACCTGCC GCCGGAATCAGATCTGAATTTGACGCTTATAGAACAACCCGC AGCTTACGGTCGCAGACCGCATTCGTCGCGTGTCTCTTTATG AATGGAATAAATTTCTAAACAG
836	Bovine_Rep 48-97	GAGCAGCCGCAACTTACAGTGGCTGATCGCATTCGTCGTGT GTTTTTATATGAATGGAATAAATTTTCAAAACAAGAAAGCA AATTTTTCGTGCAGTTTCGAAAAAGGCAGCGAGTACTTCCATT TACATACACTGGTCGAGACCAGC
837	Bovine_Rep 72-121	CAAGAAAGCAAGTTTGTTCAGTTTCGAAAAGGTTAGCGA ATATTTTCATTTGCATACGTTGGTCGAGACGAGCGGAATCTC ATCTATGGTTCTGGGTCGTTATGTTAGCCAGATTCTGTGCACA ACTTGTAAGTTGTTTTTCAA
838	Bovine_Rep 96-145	TCTGGTATTAGCAGCATGGTCCTTGGCCGTTACGTTTCACAA ATACGCGCACAATTAGTAAAAGTTGTTTCCAGAATATAGA ACCGCGTATCAATGATTGGGTTGCTATTACTAAAGTCAAGA AGGGAGGCGCAAATAAGGTAGTG
839	Bovine_Rep 120-169	CAAAACATCGAACCGCGCATAAATGATTGGGTTGCCATTAC AAAGGTGAAAAAGGTGGTGCTAACAAAGTTGTCTGATAGTG GGTATATTCCGGCGTATTTATTGCCGAAAGTTCAACCGGAGC TGCAATGGGCATGGACAAACCTT
840	Bovine_Rep 144-193	GTGGATTCTGGTTACATCCCGGCGTATCTGTTGCCGAAGGTA CAACCGGAGCTGCAATGGGCTTGGACCAACCTGGAAGAATA CAAACCTGGCCGCCCTTGAACCTGGAGGAACGCAAACGTCCTGG TGGCACAATTCCAGCTTGAAAGC
841	Bovine_Rep 168-217	CTGGAAGAATATAAACTGGCGGCGCTGAATCTTGAAGAGCG TAAGCGTCTTGTTGCACAGTTCAGCTGGAATCAAGCCAGC GTTACAGGAAGCCTCTAGCCAGCGCGATGTCTCTGCTGAC CCGGTTATTAAGTAAAACATCA
842	Bovine_Rep 192-241	TCAAGCCAGCGCAGTCAGGAAGCCTCATCACAACGCGATGT CAGTGCCGATCCGGTTATCAAGAGTAAAACAAGTCAGAAGT ATATGGCTCTGGTATCTTGGCTTGTGAGCATGGAATTACCA GTGAAAAACAGTGGATCCAGGAA
843	Bovine_Rep 216-265	TCACAAAAATATATGGCACTTGTGAGCTGGCTGGTGGAACA TGGCATCACCTCTGAAAAGCAATGGATTACAGGAGAACCAAG AGTCATATTTGTCTTTAACTCAACCGGCAATAGTCGTAGTC AGATCAAAGCAGCTTTGGATAAC
844	Bovine_Rep 240-289	GAGAACAGGAGAGCTACCTGAGCTTCAATAGTACAGGAAA TAGCCGTTCTCAAATTAAGGCCGCTCTGGATAATGCATCAA AAATAATGAGCTTAACGAAATCAGCTAGCGATTATCTGGTT GGTCAGACCGTACCGGAAGACATC

SEQ ID NO:	Name	Sequence
845	Bovine_Rep 264-313	AATGCGTCTAAAATTATGAGCTTGACCAAGAGCGCATCAGATTATCTTGTCGGGCAGACTGTCCCGGAGGACATAAGCGAAAACCGCATCTGGCAGATTTTCGATTAAATGGGTATGATCCGGCCTATGCAGGTTTCAGTCTTATAC
846	Bovine_Rep 288-337	ATCAGTGAGAATCGCATCTGGCAAATTTTIGACTTGAATGGTATGACCCGGCATACGCCGGTTCTGTCTGTATGGTTGGTGTACTCGCGCGTTTGGCAAGCGCAATACCGTATGGCTTTATGGTCCGGCCACGACGGGTAAACG
847	Bovine_Rep 312-361	TATGGCTGGTGTACGCGCGCTTTTGGCAAGCGTAATACGGTGTGGTTATATGGTCCGGCAACCACAGGCAAAACGAATATTGCGGAAGCAATATCACATACTGTCCCGTTTTACGGGTGTGTCAATTGGACCAACGAAAAATTTCCG
848	Bovine_Rep 336-385	ACTAACATTGCCGAGGCGATTTCTCATACAGTTCCGTTTTATGGGTGTGTGAATTGGACCAACGAGAACTTCCCGTTCAACGATTGCGTAGAAAAGATGTTGATCTGGTGGGAGGAGGGTAAGATGACAAGTAAGTTGTGCAACCG
849	Bovine_Rep 360-409	CCGTTTAACGACTGTGTGCAAAAAGATGCTGATTTGGTGGGAGGAGGTAAAAATGACTAGTAAAGTGGTTCGAGCCGGCAAAA GCCATCCTTGGTGGATCACGCGTACGCGTGGACCAAAAATGCAAATCATCAGTCCAAGTGGATTCT
850	Bovine_Rep 384-433	CCGGCTAAAGCAATCTTAGGTGGTAGCCGCGTTCGTGTTGATCAGAAATGCAAATCTAGCGTACAAGTTGATAGTACTCCGGTGATAATTACCAGTAATACAAACATGTGCGTCGTTGTTGATGTAACTCAACCACCTTTGAGCAT
851	Bovine_Rep 408-457	AGCACGCCGGTAATTATTACCTCTAATACCAACATGTGCGTGTAGTAGATGGGAACAGCACTACCTTTGAACATCAGCAGCCGCTGGAGGACCGCATGTTCCGTTTTGAGCTTATGCGTCGCCTGCCGCCGATTTTGGCAAAATA
852	Bovine_Rep 432-481	CATCAGCAGCCGCTGGAGGATCGTATGTTCCGCTTTGAGCTGATGCGCCGCTGCCGCCGATTTTGGTAAGATTACTAAACAAGAGGTGAAAGATTTCTTCGCTTGGGCTAAAGTCAATCAGTTCCGGTAACACATGAATTTATG
853	Bovine_Rep 456-505	ATTACAAAAACAGGAAGTAAAGACTTTTCGCCTGGGCGAAAGTCAACCAGGTACCGGTGACCCATGAGTTCATGGTGCCGA AAAAAGTCGCTGGTACTGAGCGTGCTGAGACCTCACGCAAA CGCCCGCTGGATGATGTGACGAAC
854	Bovine_Rep 480-529	ATGGTCCCGAAAAAAGGTGGCCGGTACGGAGCGCGCTGAAACGTCTCGTAAACGCCCGTTAGACGACGTCACAAATACTAATTATAAAAGCCCGGAAAAACGTGCGCGCCTGTCTGTCTACCGGAAACCCCGCTAGCTCTGACGTG
855	Bovine_Rep 504-553	AATACAAATTATAAAAGTCCGGAAAAACGTGCACGTTTGAGCGTGGTGCCGGAAACACCGCGCAGTTCAGATGTCCCGGTAGAACCGCACCGTTACGTCCGTTAAATTGGAGTTCTCGCTATGAATGTCGCTGTGATTACCATGCA
856	Bovine_Rep 528-577	GTTCCGGTGGAACCGGCGCCGCTTCGTCCGCTGAATTGGTCA TCTCGTTATGAGTGCCGTTGCGATTACCATGTCAAATTTGACAGTGTTACTGGCGAGTGCGACGAATGCGAGTACTTAAACCGCGGAAAAAATGGTTGTATCTTT
857	Bovine_Rep 552-601	GCGAAATTCGACAGTGTAAC TGGGAATGTGACGAGTGCGAGTATCTGAATCGCGGTAAAAATGGTTGCATTTTTCATAACGC GACCCATTGTCAAATCTGCCATGCTGTACCGCCGTGGGAGA AAGAAAACGTATCTGATTTTAAC

SEQ ID NO:	Name	Sequence
858	R.pusillus_rep 0-49	ATGAGCTATTACGGTATCGTAGTTCGTATACCGTGGGACGTT ATCTATCAGTTACCGCAGGTTGCTGACAGTGTCTGATTCAA CATGAAACGGCACAGATATTTACTCCGGATGACTCAGATCT GGATATTTATGAAATAAATAAC
859	R.pusillus_rep 24-73	GTCTTGATTACGATGAAACCGCACAGATATTACGCCGGA CGACTCTGATCTGGACATTTATGAGATTAACAATGTGGAAT GGTCAATGGCACAGGAAATGCATGAACATTTTATCAATAAA TGGATTGAGATTACCAAGCATGAG
860	R.pusillus_rep 48-97	AACGTGGAGTGGAGCATGGCACAAGAGATGCATGAACATTT TATTAATAAATGGATTGAAATCACGAAACATGAAGCCGTAA AGTATTTTCGCCCACTTGAAAAGGGCAAAGAGTTTTTCCAT ATTCATTACGTCATTGAGATGACC
861	R.pusillus_rep 72-121	GAAGCTGTGAAGTATTTTGCGCAGTTAGAGAAAGGGAAAGA ATTTTTCCATATTCATTACGTTATTGAAATGACCCGTATGAA GTCTATGTGTTTAGGCCGCTACCTGAACGTAATCGAAGGGC ATGTTATCCGCGAGACGTTCCGA
862	R.pusillus_rep 96-145	ACAGGTATGAAGTCAATGTGCCTGGGACGCTATCTGAACGT CATTGAGGGGCATGTGATTCCGCGAGACGTTCCGGAATTACC ATCATAAGATTGATAACTTTATCCAGATTGATAAGACCCGC ACCAACGGACCGAACCGTCAGTAC
863	R.pusillus_rep 120-169	GGTATTTACCATCATAAGATTGATAACTTTATCCAGATAGAC AAAACACGTACAAACGGACCGAATCGTCAGTATGATGATGA TTTCATTTAGCTTATCTGATTCCGAAACGCCAACC GGAACT GCAATGGGCATGGACAACGATA
864	R.pusillus_rep 144-193	TACGATGACGATTTTATTTTAGCGTACCTGATCCCGAAGCGT CAGCCGAGCTGCAATGGGCATGGACAACAATTGATAAATT CGCTCGCGCCGCCCTGAATATTGCGGAACGTGCCGCTCTGG CCGAAGAATTTAGTTAGGACTT
865	R.pusillus_rep 168-217	ATAGATAAGTTTGTCTCGCGCCGCGCTGAACATTGCTGAACG CGCGCGCTTAGCTGAAGAGTTCCAACCTGGGCCTTGCTGCTCG TCGTGAAGAAGCGCGCTTGGAGCGCATCAGTAACAATAATG GTAACCCGAAAATTTGTGGCAAA
866	R.pusillus_rep 192-241	CTGGCTGCCCCCGCTGAAGAAGCGCGTTTGGAAACGCATTAG CAATAACAATGGGAATCCGAAGATTTGTGGCAAGAGCAGCC GTCGCTATATGGAACCTGGTGAACCTGGTTAGTTGAGAAAGGC GTGACCAGCGAGCGCGACTGGATT
867	R.pusillus_rep 216-265	AAATCTTCACGCCGCTATATGGAATTGGTCAATTGGTTGGTC GAAAAGGGCGTCACGTCTGAGCGCGATTGGATAAAGGAGG ATCAGGAATCTTATTTATCATATAATGCGACGGGCTCTTCTC GCGGCCAGATTAAAGCCGCCTTA
868	R.pusillus_rep 240-289	ATTAAGGAGGACCAGGAAAGTTACCTTTCTTACAACGCAAC CGGTTCAAGCCGTGGTCAGATCAAAGCGGCTTTAGAGAACG CGTGTCGTATTATGTCTACCGTAAAGAAGGCTAGTGACTATC TGTTGGGCACAGAATTTCCGGAA
869	R.pusillus_rep 264-313	CTTGAAAATGCATGTCGTATTATGAGTACCGTAAAAAAGC CAGCGATTATTTAGTCGGGACCGAATTTCCGGAAGATATCG AAAAAAATCGCGTTTACCGCATCTTCCAGATGAATGGGTAT GACCCGGCTTACGCGGGTTCAATC
870	R.pusillus_rep 288-337	GAAGATATTGAGAAAAACCGTGTTTATCGCATCTTCAAAAT GAATGGCTACGATCCGGCGTATGCGGGCTCAATTTTCTGG GATGGTGCCGTCGTACGTTTGAAAGCGCAACACTATATGG CTGTTCCGACCGGCCACAACCGGT

SEQ ID NO:	Name	Sequence
871	R.pusillus_rep 3 12-361	ATCTTTCTGGGTTGGTGTCTGTCGCCAATTTGGGAAACGCAAT ACTATCTGGCTTTTGGTCCGGCTACAACTGGTAAACTAAT ATTGCGGAAGCAGTGGCTCATGCCGTGCCGTTCTACGGCTGT GTGAATTGGACGAACGAAAAC
872	R.pusillus_rep 3 36-385	GGCAAACTAACATTGCGGAAGCCGTAGCGCATGCCGTTCC GTTTTATGGGTGCGTCAATTGGACCAACGAGAATTTCCCGTT CAATGACTGTGTCGATAAGATGATTATTTGGTGGGAAGAGG GCAAGATGACTGCAAAGATTGTA
873	R.pusillus_rep 3 60-409	AACTTTCCGTTTAAATGATTGTGTAGATAAAATGATAATATGG TGGGAAGAGGGCAAAATGACGGCGAAAATAGTGGAGAGTG CTAAGGCGATACTGGGTGGTAGTACCGTCCGCGTTGACCAG AAATGTAAATCAAGCTGCCAGATT
874	R.pusillus_rep 3 84-433	GTCGAGAGTGC AAAAGGCGATACTGGGTGGCTCAACGGTGGC TGTGGATCAGAAATGTAAGAGCTCATGTCAAATAGAACAGA CACCGGTCATAGTCACTTCTAATACGAACATGTGCGCAGTA ATCGACGGAAACAGTACTACTTTT
875	R.pusillus_rep 4 08-457	ATCGAACAGACGCCGGTCATAGTCACATCAAATACCAATAT GTGTGCTGTTCATCGATGGCAACAGTACCACGTTCTGAACATC AACAGCCGTTAGAAGACCGCATGTTCAAGTTTGAGCTGACG ACCCGCTTACAGTCTGACTTTGGG
876	R.pusillus_rep 4 32-481	TTTGAACATCAGCAACCGCTTGAGGATCGTATGTTCAAATTC GAGTTAACCACTCGTCTTCAGAGTGATTTTGGAAAGATTAGC AAGGCCGAAATAAAAAGAATTTTATGATGGGCAGACGTAAA CCGTGTGGAAGTGAAGCATGAA
877	R.pusillus_rep 4 56-505	GGCAAAATTTCAAAGCCGAGATAAAAAGAATTTCTGGCTTG GGCAGATGTAAATCGTGTGTAAGTTAAACATGAATTTCCGCG TTCAGCGTGTTCACCCATGTGATGATGAAACGTCCGGCCC CGGCCTGGGAAGAGCCGACCGAA
878	R.pusillus_rep 4 80-529	GAGTTTCGTGTCCAGCGTGTGTACACGCATGTGATGATGAA ACGTCCGGCCCCGGCATGGGAAGAGCCGACAGAGGGAATA AACACAGCCAAGAAACTGAAAACGGAATCAGTGCCCGCAG TACCGAGTGAGGGAGAAGAGGATTTT
879	R.pusillus_rep 5 04-553	GAAGGCATTAATACAGCCAAAAAACTGAAAACTGAGAGTGT GGCCGCTGTACCGTCTGAAGGTGAGGAAGACTTCGGTCAAC GCTATGTTAACC GTTGACCAACCATATGAATTTAACC GTTA TGCGCTTTCCGTGCAAATTTTGT
880	R.pusillus_rep 5 28-577	TTTGGCCAGCGTTATGTGAATCGTGCACCAATCATATGAAC CTGACGGTTATGCGTTTCCCGTGTAATTTCTGCGCGAAAATG AATCAGACCGAAGACATCTGCTTCACACATGGCGCGAAGTC ATGTGAAATCTGCTTTCCGACA
881	R.pusillus_rep 5 52-601	TGCGCTAAGATGAATCAGACCGAAGACATTTGTTTACACA TGGAGCGAAGTCATGTGAGATTTGTTTCCCGACCAACAACG TCGTAAAACCTTAGTCCGGTAAAGATACAGTACGAAGAAAAA AAGGAACAGATTGTTGAGGCTCCG
882	R.pusillus_rep 5 76-625	ACAAATAATGTTGTGAAATTAAGTCCGGTAAAAATTCATA TGAAGAAAAAAGAAACAAATAGTCGAGGCGCCGAAAGAA CAAATTCTTCTTTGCGAAAAAATGGCCGATGTGGAAGAGGA AATTAATAAAAAAATACAGGAAGAG
883	R.pusillus_rep 6 00-649	CCGAAAGAACAGATTCTGCTGTGCGAGAAGATGGCGGATGT TGAGGAAGAAATAAAAAAAAAAATACAGGAAGAACGTGAC TTCGTTGAACAGTATGGCGACCGTTGTAATATTTGCAAGATG CGTGTTGGTTTAAATCCGAAATGT

SEQ ID NO:	Name	Sequence
884	Rhinolophus_ca p 0-49	ATGATTTCGTGTAGTCATGAGTTTTGTCTGATTACCCGCCGGAT TGGTTAAAAGAAAGTGGCGGGTGGTTTGAAGGAGTTTATCGA CCTGAAACCGGGAGCCCCGAAGCCGAAAGCTAACCAGCAG AAACAAGATCAACGCGGCTTAGTG
885	Rhinolophus_ca p 24-73	GAGTTTATCGACCTGAAACCGGGCGCGCCGAAGCCGAAAGC GAATCAGCAGAAACAGGATCAACGCGGCTGGTATTACCGG GTTACAAATATCTGGGCCCGTTTAAACGGTCTGGACAAAGGT CAACCGGTGAATAAAGCTGATGAA
886	Rhinolophus_ca p 48-97	GTGCTGCCGGGTTATAAATATCTGGGACCGTTCAACGGTTTA GACAAAGGTCAGCCGGTTAATAAGGCTGACGAAGTAGCGCG CGAGCATGACATTGAATATGATAAACTTTTGAAGAGGGCG ATAATCCGTACGTGAAATACAAC
887	Rhinolophus_ca p 72-121	GAGGTTGCACGTGAACATGATATAGAATACGATAAGCTGCT GAAAGAAGGTGACAATCCGTATGTTAAATACAACCATGCCG ATCAGGAGTTTCAAGAGAAGTTAGAAGGAGACGAGTCTTTT GGGGGTAACCTGGGGCGCGCTGTG
888	Rhinolophus_ca p 96-145	AATCATGCCGACCAGGAGTTCCAGGAAAACTGGAAGGGG ACGAATCTTTTGGGGGAAATTTAGGTCGTGCAGTCTTTCAGG CTAAGAAAGCGTTTATTAGAACCGTTTGGCTTGTGAGAGGAA ACTCCGCCGCGTAAACGTCCGGCG
889	Rhinolophus_ca p 120-169	GTTTTTCAGGCGAAAAAGCGCCTTTTAGAACCGTTTGGTCTG TCAGAGGAGACGCCGCCGCGCAAAACGTCCGGCCAGTGAAA ACAACCAAAGCGATGTACCGGCGAAACGTCGTTTATCCTG GACCCGGAGGATAATGGTGCGGCT
890	Rhinolophus_ca p 144-193	GCAAGTGAGAATAATCAAAGTGACGTCCCGGCAAAACGCCG CCTTATCTTAGATCCGGAAGATAATGGGGCAGCAGAGGGGG AGCCGATAGAACAGCAGCAACCGGCCAACGACATGGCAAG CGCAGAAATGGCCGAGGTGGCGGT
891	Rhinolophus_ca p 168-217	GCAGAGGGAGAACCGATCGAACAGCAGCAGCCGGCAAATG ACATGGCAAGCGCGGAAATGGCTGCAGGCGGTGGTGGTCCG GTTGGTGACGACGCACAAGGTGCCGACGGCGTCGGTAGCGC ATCAGGAAACTGGCATTGTGATAGC
892	Rhinolophus_ca p 192-241	GGGGGTCCGGTCCGAGATGATGCTCAGGGCGCAGACGGTGT CGGAAGCGCGAGTGGTAACTGGCATTGTGATTCTATATGGA TGGGGGATCGTGTGATCACGAAGTCTACGCGTACATGGAGC CTGCCGACATATAATAACCATTTG
893	Rhinolophus_ca p 216-265	AGCATCTGGATGGGAGACCGTGTAAATTACGAAGAGCACCCG CACATGGAGCCTGCCGACTTATAATAACCATCTGTACAAAC AAATCAATAGCAATACCACAGATGCGAAAGAAACCTATTTT GGTTACTCAACGCCGTGGGGTTAC
894	Rhinolophus_ca p 240-289	CTTTATAAACAAATCAATTCAAATACCACCGACGCCAAGGA AACTTACTTCGGTTATTCTACTCCGTGGGGCTATTTTGATTTT AACCGTTTTTCATTGCCATTCTCACCGCGCGATTGGCAGCGT TTGATTAACAACCATTTGGGGG
895	Rhinolophus_ca p 264-313	TACTTCGATTTTAAATCGTTTTTCATTGCCATTTTCAGTCCGCG ACTGGCAGCGTTTAAATCAATAACCATTTGGGGTATGCGTCCG AAACGCCTGAATTTCAAACGTGTTAATATCCAGGTGAAAGA GGTAACCAACCAATGATGGGACT
896	Rhinolophus_ca p 288-337	GGTATGCGTCCGAAACGCCTGAATTTTAAGCTGTTCAACATA CAGGTGAAGGAGGTTACCACTAACGATGGTACGAAAACCTAT TGCGAACAATTTAACTTCACTGTTTCAGGTATTCGCCGACAG TGAATACCAGCTTCCGTATGTG

SEQ ID NO:	Name	Sequence
897	Rhinolophus_ca p 312-361	ACGAAAACCATTTGCTAATAATTTAACGAGTACGGTGCAAGT GTTTGCCGATAGTGAATACCAATTGCCGTACGTTCTTGCCAA TGCTCATGAGGGCTGCTTTCCGCCGTTTCCGGCGGATGTGTT CATGCTTCCGCAGTATGGTTAT
898	Rhinolophus_ca p 336-385	GTCTGGGTAATGCTCATGAAGGCTGCTTCCCGCCGTTCCCG GCGGATGTTTTATGCTGCCGCAGTACGGATATCTGACTTTA AATTCAAACGATAACAAAGCAATGCCGCAGAGTAGTTTCTA TTGCTTGGAGTATTTCCCGAGT
899	Rhinolophus_ca p 360-409	TATCTGACTCTTAACTCAAATGACAACAAAGCAATGCCGCA GAGCAGCTTCTATTGCTTGAATACTTCCCGAGCCAGATGCT GCGTACGGGCAATAATTTCACTTTTCAGCTATGAATTTGAATC TGTTCCGTTTCTATCTATGTTT
900	Rhinolophus_ca p 384-433	AGCCAGATGTTACGCACAGGTAATAACTTTACGTTTAGCTAT GAATTTGAATCTGTTCCGTTCCATAGCATGTTTCATGCATAAT CAAAGCCTGGATCGTTTGATGAACCCGCTTATAGATCAATAT CTGTGGTATCTTCATTCACACC
901	Rhinolophus_ca p 408-457	TTTATGCATAACCAGAGTTTGGATCGCTTAATGAATCCGTTA ATCGACCAGTACCTTTGGTACCTGCATTCTACGAACAGCCTT TCACTGAATTTTAAGAAGGTTAAACGTGATCATTTGTATAAA TATTATCGCAATTGGGTCCCG
902	Rhinolophus_ca p 432-481	ACGAACTCACTTTCTCTGAACTTCAAAAAGGTGAAACGCGA TCATCTTTATAAGTACTATCGCAACTGGGTTCCGGGGCCGGG TCAACGTCGCCAACAGTGGTCAGAATCTGGAGGTGCAAATA AACAACTGACTGACCTGTGGCCG
903	Rhinolophus_ca p 456-505	CCGGGGCCGGGTCAGCGTCGCCAACAGTGGAGTGAGAGTGG TGGTGCAAACAAGCAGTTAACGGATTTGTGGCCGTATAATA ATAAGTACAATCTTATGGGCCGCTACAGTAGTCTTGCGCCG GGTATGCCGCAAGCCGCGGCCGAT
904	Rhinolophus_ca p 480-529	CCGTATAACAATAAATAAATCTGATGGGGCGCTACAGCTC TTTGGCGCCGGGATGCCGCAAGCTGCCGCGGACGGGTTTA TTACAGCCGATGGGCAGTTAATTTTCAGTAACGTGCTTCAAG AAAGCGAAGAGGCGTCAGGTGGT
905	Rhinolophus_ca p 504-553	GATGGTTTTATTACCGCCGATGGACAGCTGATTTTTTCAAAC GTTCTGCAAGAAAGCGAAGAAGCCTCTGGAGGGAAGCCGA GTCCGAATCTTCTGATCACCAACGAAAGTGAGGTGCGCCCG ACCAATCCGGCCATCAATGCCCGG
906	Rhinolophus_ca p 528-577	GGCAAGCCGAGTCCGAATCTGCTGATTACGAACGAGTCAGA AGTACGCCCCGACAAACCCGCGGATAAACGCTCCGTGGGGCG ATGTGGCCTTAAACCAGCAGACCAGCACAGTCACCCCGTCA GTTGCGGAGGACAATGAAGCTCAT
907	Rhinolophus_ca p 552-601	CCGTGGGGCGATGTGGCTCTGAATCAGCAGACCAGTACCGT TACACCGAGTGTCGCGGAAGACAATGAGGCGCATATTTTTC CGGGAATGGTGTGGCAGGATCGTGATATATACCTGCAGGGT CCGATATGGGCTAAAATTCCGGAT
908	Rhinolophus_ca p 576-625	CATATTTTCCGGGGATGGTATGGCAAGACCGTGACATATAT CTGCAAGGTCCGATTTGGGCTAAAATCCCGGATACTGATGG GAGCTTCCATCCGTCTCCGCTGATGGGGGGCTTTGGTCTGAA ACATCCGCCGCCGAGATCTTG
909	Rhinolophus_ca p 600-649	GATACGGATGGATCATTTTCATCCGAGTCCGTTAATGGGCGG CTTTGGACTGAAGCATCCGCCGCCGAGATCTTAATAAAAA ACACACCGGTACCGAGCGACCCGCCGTTAGAAATTTAACGGC AAAAAAATTCAAAGTTTTATTACA

SEQ ID NO:	Name	Sequence
910	Rhinolophus_c p 624-673	CTGATTAAAAACACGCCGGTTCCGAGTGATCCGCCGCTGGA ATTTAATGGCAAGAAAATTCAATCTTTTATTACTCAATATAG TACTGGTCAGGTAACAGTGGAGATCGAATGGGAATTGAAAA AAGAACATTCAAAACGCTGGAAT
911	Rhinolophus_c p 648-697	ACGCAATATAGCACCGGGCAGGTAAACCGTTGAAATTGAATG GGAATTGAAAAAAGAACATAGCAAACGTTGGAACCCGGAA ATTCAATATACCTCTAACTTTGATAATACAGATCGCGTCCAG TTTAGCGTAAATGGTGCAGGGAAC
912	168_SDM_R_A _For	GCAGCCTGCagcaAAAAAGATTGAATTTTGGTCAGACTG
913	168_SDM_R_A _Rev	TGGCCCGCCTTTCCGGTT
914	170_SDM_R_A _For	TGCAAGAAAagcaTTGAATTTTGGTCAGACTGGAGACGCAG
915	170_SDM_R_A _Rev	GGCTGCTGGCCCGCCTTT
916	171_SDM_L_A _For	AAGAAAAAGagcaAATTTTGGTCAGACTGGAGACGCAGACTC AGTCCCAGACC
917	171_SDM_L_A _Rev	GCAGGCTGCTGGCCCGCC
918	172_SDM_N_A _For	AAAAAGATTGgcaTTTGGTCAGACTGGAGACGCAGACTCAG
919	172_SDM_N_A _Rev	CTTGCAGGCTGCTGGCCC
920	173_SDM_F_A _For	AAGATTGAATgcaGGTCAGACTGGAGACG
921	173_SDM_F_A _Rev	TTTCTTGCAGGCTGCTGG
922	174_SDM_G_A _for	ATTGAATTTTgcaCAGACTGGAGACG
923	174_SDM_G_A _Rev	CTTTTTCTTGCAGGCTGC
924	175_SDM_Q_A _For	GAATTTTGGTgcaACTGGAGACGCAGAC
925	175_SDM_Q_A _Rev	AATCTTTTTCTTGCAGGC
926	176_SDM_T_A _For	TTTTGGTCAGgcaGGAGACGCAG
927	176_SDM_T_A _Rev	TTCAATCTTTTCTTGCAGGC
928	177_SDM_G_A _For	TGGTCAGACTgcaGACGCAGACT
929	177_SDM_G_A _Rev	AAATTCAATCTTTTCTTGCAGGCTG
930	178_SDM_D_A _For	TCAGACTGGAgcaGCAGACTCAG
931	178_SDM_D_A _Rev	CCAAAATTCAATCTTTTCTTG
932	179_SDM_A_R _For	GACTGGAGACcggGACTCAGTCC
933	179_SDM_A_R _Rev	TGACCAAAATTCAATCTTTTTC

SEQ ID NO:	Name	Sequence
934	180_SDM_D_A _For	TGGAGACGCagcaTCAGTCCCAG
935	180_SDM_D_A _Rev	GTCTGACCAAAATTCAATCTTTTTC
936	181_SDM_S_A _For	AGACGCAGACgcaGTCCCAGACC
937	181_SDM_S_A _Rev	CCAGTCTGACCAAAATTCAATCTTTTCTTG
938	182_SDM_V_A _For	CGCAGACTCagcaCCAGACCCTC
939	182_SDM_V_A _Rev	TCTCCAGTCTGACCAAAATTC
940	183_SDM_P_A _For	AGACTCAGTCgcaGACCCTCAAC
941	183_SDM_P_A _Rev	GCGTCTCCAGTCTGACCA
942	184_SDM_D_A _For	CTCAGTCCCagcaCCTCAACCAATC
943	184_SDM_D_A _Rev	TCTGCGTCTCCAGTCTGA
944	185_SDM_P_A _For	AGTCCCAGACgcaCAACCAATCG
945	185_SDM_P_A _Rev	GAGTCTGCGTCTCCAGTC
946	186_SDM_Q_A _for	CCCAGACCCTgcaCCAATCGGAG
947	186_SDM_Q_A _Rev	ACTGAGTCTGCGTCTCCA
948	187_SDM_P_A _For	AGACCCTCAAgcaATCGGAGAAC
949	187_SDM_P_A _Rev	GGGACTGAGTCTGCGTCT
950	188_SDM_I_A _For	CCCTCAACCagcaGGAGAACCTCCCG
951	188_SDM_I_A _Rev	TCTGGGACTGAGTCTGCG
952	189_SDM_G_A _For	TCAACCAATCgcaGAACCTCCCG
953	189_SDM_G_A _Rev	GGGTCTGGGACTGAGTCT
954	190_SDM_E_A _For	ACCAATCGGAgcaCCTCCCGCAG
955	190_SDM_E_A _Rev	TGAGGGTCTGGGACTGAGTC
956	191_SDM_P_A _For	AATCGGAGAAgcaCCCGCAGCCC
957	191_SDM_P_A _Rev	GGTTGAGGGTCTGGGACTG
958	192_SDM_P_A _For	CGGAGAACCTgcaGCAGCCCCCT
959	192_SDM_P_A _Rev	ATTGGTTGAGGGTCTGGGACTG

SEQ ID NO:	Name	Sequence
960	193_SDM_A_R _For	AGAACCTCCCcggGCCCCCTCAG
961	193_SDM_A_R _Rev	CCGATTGGTTGAGGGTCT
962	194_SDM_A_R _For	ACCTCCCGCAcggCCCTCAGGTG
963	194_SDM_A_R _Rev	TCTCCGATTGGTTGAGGG
964	195_SDM_P_A _For	TCCCGCAGCCgcaTCAGGTGTGG
965	195_SDM_P_A _Rev	GGTTCTCCGATTGGTTGAGGGTC
966	196_SDM_S_A _For	CGCAGCCCCCgcaGGTGTGGGAT
967	196_SDM_S_A _Rev	GGAGGTTCTCCGATTGGTTGAGGGTC
968	197_SDM_G_A _For	AGCCCCCTCAgcaGTGGGATCTC
969	197_SDM_G_A _Rev	GCGGGAGGTTCTCCGATT
970	198_SDM_V_A _For	CCCCTCAGGTgcaGGATCTCTTACAATGGC
971	198_SDM_V_A _Rev	GCTGCGGGAGGTTCTCCG
972	199_SDM_G_A _For	CTCAGGTGTGgcaTCTCTTACAATGGCTG
973	199_SDM_G_A _Rev	GGGGCTGCGGGAGGTTCT
974	200_SDM_S_A _For	AGGTGTGGGAgcaCTTACAATGGCTGCAGG
975	200_SDM_S_A _Rev	GAGGGGGCTGCGGGAGGT
976	201_SDM_L_A _For	TGTGGGATCTgcaACAATGGCTGCAGGCCG
977	201_SDM_L_A _Rev	CCTGAGGGGGCTGCGGGA
978	202_SDM_T_A _For	GGGATCTCTTgcaATGGCTGCAGG
979	202_SDM_T_A _Rev	ACACCTGAGGGGGCTGCG
980	203_SDM_M_A _For	ATCTCTTACAgcaGCTGCAGGCGGTGGCG
981	203_SDM_M_A _Rev	CCCACACCTGAGGGGGCT
982	204_SDM_A_R _For	TCTTACAATGcggGCAGGCGGTGGC
983	204_SDM_A_R _Rev	GATCCCACACCTGAGGGG
984	205_SDM_A_R _For	TACAATGGCTcggGGCGGTGGCG
985	205_SDM_A_R _Rev	AGAGATCCCACACCTGAG

SEQ ID NO:	Name	Sequence
986	206_SDM_G_A _For	AATGGCTGCAGcaGGTGGCGCAC
987	206_SDM_G_A _Rev	GTAAGAGATCCCACACCTG
988	207_SDM_G_A _For	GGCTGCAGGCgcaGGCGCACCAA
989	207_SDM_G_A _Rev	ATTGTAAGAGATCCCACACCTGAGG
990	208_SDM_G_A _For	TGCAGGCGGTgcaGCACCAATGG
991	208_SDM_G_A _Rev	GCCATTGTAAGAGATCCCAC
992	209_SDM_A_R _For	AGGCGGTGGCcggaCCAATGGCAG
993	209_SDM_A_R _Rev	GCAGCCATTGTAAGAGATC
994	210_SDM_P_A _For	CGGTGGCGCAGcaATGGCAGACA
995	210_SDM_P_A _Rev	CCTGCAGCCATTGTAAGAGATCCCAC
996	211_SDM_M_ A_For	TGGCGCACCAgcaGCAGACAATAACGAG
997	211_SDM_M_ A_Rev	CCGCCTGCAGCCATTGTA
998	212_SDM_A_R _For	CGCACCAATGcggaGACAATAACGAGGGCGC
999	212_SDM_A_R _Rev	CCACCGCCTGCAGCCATT
1000	213_SDM_D_A _For	ACCAATGGCAGcaAATAACGAGGGCGCCGACG
1001	213_SDM_D_A _Rev	GCGCCACCGCCTGCAGCC
1002	214_SDM_N_A _For	AATGGCAGACgcaAACGAGGGCGCCGACGG
1003	214_SDM_N_A _Rev	GGTGCGCCACCGCCTGCA
1004	215_SDM_N_A _For	GGCAGACAATgcaGAGGGCGCCGACGG
1005	215_SDM_N_A _Rev	ATTGGTGCGCCACCGCCT
1006	216_SDM_E_A _For	AGACAATAACgcaGGCGCCGACGGAGTG
1007	216_SDM_E_A _Rev	GCCATTGGTGCGCCACCG
1008	217_SDM_G_A _For	CAATAACGAGgcaGCCGACGGAGTGGG
1009	217_SDM_G_A _Rev	TCTGCCATTGGTGCGCCA
1010	WT AAV-DJ	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACT CTCTCTGAAGGAATAAGACAGTGGTGAAGCTCAAACCTGG CCCACCACCACAAAGCCCGCAGAGCGGCATAAGGACGAC AGcaGGGGTCTTGTGCTTCTGGGTACAAGTACCTCGGACCC

SEQ ID NO:	Name	Sequence
		TTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCAG ACGCCGCGGCCCTCGAGCACGACAAAAGCCTACGACCGGCAG CTCGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGC CGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTT TTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAAAG AGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCTAA GACGGCTCCTGGAAAAGAAGAGGCCTGTAGAGCACTCTCCTG TGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGGCCAG CAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGA CGCAGACTCAGTCCCAGACCCTCAACCAATCGGAGAACCICC CGCAGCCCCCTCAGGTGTGGGATCTTTACAATGGCTGCAG GCGGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGA CGGAGTGGGTAATTCCTCGGGAATTTGGCATTGCGATTCCA CATGGATGGGCGACAGAGTCATCACCACCAGCACCCGAACC TGGGCCCTGCCACCTACAACAACCACCTTACAAGCAAAT CTCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCT ACTTCGGCTACAGCACCCCTGGGGGTATTTTGACTTTAACA GATTCCACTGCCACTTTTACCACGTGACTGGCAGCGACTCA TCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTC AAGCTCTTCAACATCCAGGTCAAGGAGGTCACGCAGAATGA AGGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCC AGGTGTTTACGGACTCGGAGTACCAGCTGCCGTACGTTCTCG GCTCTGCCCAACCAGGGCTGCCTGCCTCCGTTCCCGCGGACG TGTTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACG GTAGTCAGGCCGTGGGACGCTCCTCCTTCTACTGCCTGGAAT ACTTTCCTTCGCAGATGCTGAGAACCGGCAACAACTTCCAGT TTACTTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACG CCCACAGCCAGAGCTTGGACCGGCTGATGAATCCTCTGATT GACCAGTACCTGTACTACTTGTCTCGGACTCAAAACAACAGG AGGCACGACAAATACGCAGACTCTGGGCTTCAGCCAAGGTG GGCCTAATAACAATGGCCAATCAGGCAAAGAACTGGCTGCCA GGACCCTGTTACCGCCAGCAGCGAGTATCAAAGACATCTGC GGATAACAACAACAGTGAATACTCGTGGACTGGAGCTACCA AGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGC CCGGCCATGGCAAGCCACAAGGACGATGAAGAAAAAGTTTTT TCCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGCTCAG AGAAAACAAATGTGGACATTGAAAAGGTCATGATTACAGAC GAAGAGGAAATCAGGACAACCAATCCCGTGGCTACGGAGC AGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGA CAAGCAGCTACCGCAGATGTCAACACACAAGGCGTTCTTCC AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGC CCATCTGGGCAAAGATTCCACACACGGACGGACATTTTCAC CCCTCTCCCCCTCATGGGTGGATTTCGGACTTAAACACCCTCCG CCTCAGATCCTGATCAAGAACACGCCTGTACCTGCGGATCCT CCGACCACCTTCAACCAGTCAAAGCTGAACTCTTTCATCACC CAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGTGGGA GCTGCAGAAGGAAAAACAGCAAGCGCTGGAACCCCGAGATC CAGTACACCTCCAATACTACAAATCTACAAGTGTGGACTTT GCTGTTAATACAGAAGGCGTGTACTCTGAACCCCGCCCATTT GGCACCCGTTACCTACCCGTAATCTGTAA
1011	WT AAV-DJ	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPKPAERHKDDSD RGLVLPKYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQL DSGDNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQAKKRL

SEQ ID NO:	Name	Sequence
		LEPLGLVEEAAKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPAR KRLNFGQTGDADSVDPQPIGEPPAAPSGVGSLTMAAGGGAP MADNNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDNRFHCHFS PRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGKTIANN LTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLE LNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHS SYAHSQSLDRLMNPLIDQYLYLSRTQTTGGTTNTQTLGFSQG GPNTMANQAKNWLPGPCYRQQRVSKTSADNNNSEYSWTGAT KYHLNGRDSL VNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEK TNVDIEKVMITDEEEIRTTPVATEQYGSVSTNLQRGNRQAAT ADVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPL MGGFGLKHPPPQILIKNTPVPADPPTTFNQSKLNSFITQYSTGQV SVEIEWELQKENS KRWNPEIQYTSNYYKSTSVDFAVNTEGVYS EPRPIGTRYLTRNL

CLAIMS

1. A composition comprising at least one modified adeno-associated viral (AAV) capsid protein, wherein the composition is resistant to neutralisation or is not neutralised by human neutralising antibodies, wherein the at least one modified adeno-associated viral (AAV) capsid protein is modified at any one or more of residues 24 to 47, 48 to 97, 72 to 121, 120 to 167 and 168 to 217 of an adeno-associated viral (AAV) VP1 capsid protein or an ortholog thereof.
2. The composition of claim 1, wherein the at least one modified adeno-associated viral (AAV) capsid protein is modified at any one or more of residues selected from the group consisting of residues 24 to 93.
3. The composition of claim 2, wherein the at least one modified adeno-associated viral (AAV) capsid protein is modified at any one or more of residues selected from the group consisting of residues 24 to 73 and 48 to 93.
4. The composition of any one of the preceding claims, wherein the at least one modified adeno-associated viral (AAV) capsid protein comprises at least one, at least two, at least 3 mutations or more.
5. The composition of any one of the preceding claims, wherein the mutation results in the modified adeno-associated viral (AAV) capsid protein being epitope masked.
6. The composition of any of the preceding claims, wherein the mutation is selected from the group consisting of a "gca" mutation (alanine), a "cgg" mutation (arginine), a "tct" mutation (serine), and a "gau" or "gac" mutation (aspartic acid).
7. The composition of claim 6, wherein the at least one mutation is present at any one or more of the residues selected from the group consisting of A70, R168, K169, R170, L171, N172, F173, G174, Q175, T176, G177, D178, A179, D180, S181, V182, P183, D184, P185, Q186, P187, I188, G189, E190, P191A, P192, P195, A193, A194, P195, S196, G197, V198, G199, S200, L201, T202, M203, A204, A205, G206, G207, G208, A209, P210, M211, A212, D213, N214, N215, E216, G217, N215, A70, and combinations thereof.
8. The composition of any one of claims 6 to 7, wherein the at least one mutation is selected from the group consisting of A70R, R168A, K169R, R170A, L171A, N172A, F173A, G174A, Q175A, T176A, G177A, D178A, A179R, D180A, S181A, V182A, P183A, D184A, P185A, Q186A,

P187A, I188A, G189A, E190A, P191A, P192A, P195D, A193R, A194R, P195A, S196A, G197A, V198A, G199A, S200A, L201A, T202A, M203A, A204R, A205R, AAV-DJ_G206A, G207A, G208A, A209R, P210A, M211A, A212R, D213A, N214A, N215A, E216A, G217A, N215S, A70R, and combinations thereof.

9. The composition of any one of claims 6 to 8, wherein the at least one “gca” mutation is present at any one or more of the residues selected from the group consisting of R168, R170, L171A, N172, F173, G174, Q175, T176, G177, D178, D180, S181, V182, P183, D184, P185, Q186A, P187, I188, G189, E190, P191, P192, P195, S196, G197, V198, G199, S200, L201, T202, M203, G206, G207, G208, P210, M211, D213A, N214, N215, E216, G217, and combinations thereof.
10. The composition of any of the preceding claims, wherein the at least one modified adeno-associated viral (AAV) capsid protein is selected from the group consisting of AAV-DJ_R168A, AAV-DJ_K169R, AAV-DJ_R170A, AAV-DJ_L171A, AAV-DJ_N172A, AAV-DJ_F173A, AAV-DJ_G174A, AAV-DJ_Q175A, AAV-DJ_T176A, AAV-DJ_G177A, AAV-DJ_D178A, AAV-DJ_A179R, AAV-DJ_D180A, AAV-DJ_S181A, AAV-DJ_V182A, AAV-DJ_P183A, AAV-DJ_D184A, AAV-DJ_P185A, AAV-DJ_Q186A, AAV-DJ_P187A, AAV-DJ_I188A, AAV-DJ_G189A, AAV-DJ_E190A, AAV-DJ_P191A, AAV-DJ_P192A, AAV-DJ_P195D, AAV-DJ_A193R, AAV-DJ_A194R, AAV-DJ_P195A, AAV-DJ_S196A, AAV-DJ_G197A, AAV-DJ_V198A, AAV-DJ_G199A, AAV-DJ_S200A, AAV-DJ_L201A, AAV-DJ_T202A, AAV-DJ_M203A, AAV-DJ_A204R, AAV-DJ_A205R, AAV-DJ_G206A, AAV-DJ_G207A, AAV-DJ_G208A, AAV-DJ_A209R, AAV-DJ_P210A, AAV-DJ_M211A, AAV-DJ_A212R, AAV-DJ_D213A, AAV-DJ_N214A, AAV-DJ_N215A, AAV-DJ_E216A, AAV-DJ_G217A, AAV-DJ_N215S, AAV2_D213A, AAV9_D213A, AAV-DJ_A70R, and AAV-DJ_A70R_D213A.
11. The composition of any one of the preceding claims, wherein the at least one adeno-associated viral (AAV) capsid protein comprises or is selected from the group consisting of SEQ ID Nos 30 to 57 and 61 to 62, or is encoded by a nucleic acid sequence selected from the group consisting of SEQ ID Nos 1 to 29 and 58 to 60.
12. A nucleic acid sequence encoding the composition of any one of claims 1 to 11, or encoding the one or more modified adeno-associated viral (AAV) capsid proteins according to any one of claims 1 to 11.
13. A vector comprising the nucleic acid sequence of claim 12.
14. A host cell comprising the vector of claim 13 or the nucleic acid sequence of claim 12.

15. An adeno-associated virus particle comprising the AAV capsid proteins according to any one of claims 1 to 11.
16. The composition according to any one of claims 1 to 11, the nucleic acid of claim 12, the vector of claim 13, the host cell of claim 14, or the adeno-associated virus particle of claim 15, for use in gene therapy.
17. A method of identifying an adeno-associated viral (AAV) capsid protein or peptide which is resistant to neutralisation or is not neutralised by human neutralising antibodies, the method comprising
 - a. contacting the adeno-associated viral capsid protein or peptide with sera known to contain adeno-associated virus neutralising antibodies, thereby allowing the neutralising antibodies to bind to an epitope comprised within the adeno-associated viral capsid protein or peptide;
 - b. removing the neutralising antibody-bound epitope from the adeno-associated viral capsid protein or peptide; and
 - c. identifying the adeno-associated viral capsid protein or peptide that did not bind to the neutralising antibodies.
18. The method of claim 17, wherein the adeno-associated viral (AAV) capsid protein or peptide is selected from the group consisting of AAV-DJ, AAV1, AAV2, AAV3, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12 AAV13, or an ortholog thereof.
19. A method of preventing an immune response to an engineered adeno-associated virus, the method comprising administering to a subject an engineered adeno-associated virus comprising at least one modified adeno-associated viral (AAV) capsid protein according to claims 1 to 11.