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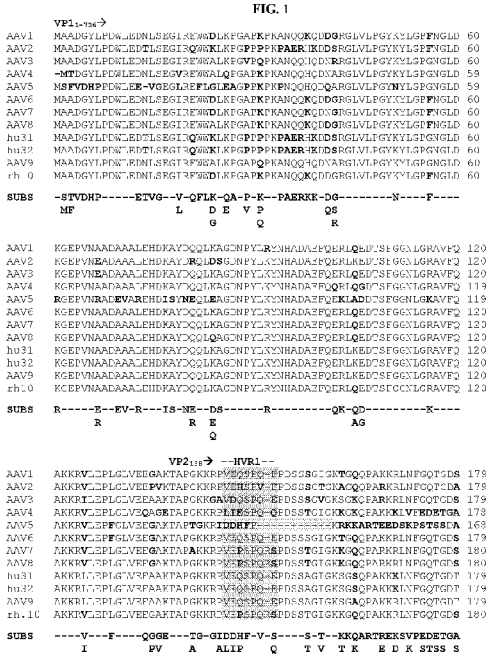
(54) Title: RECOMBINANT ADENO-ASSOCIATED VIRUSES AND USES THEREOF

(57) Abstract: The present invention relates to recombinant adeno-associated viruses (rAAVs) having capsid proteins engineered to include amino acid sequences that confer and/or enhance desired properties. In particular, the invention provides engineered capsid proteins comprising peptide insertions from heterologous proteins inserted within or near variable region IV (VR-IV) of the virus capsid, such that the insertion is surface exposed on the AAV particle. The invention also provides capsid proteins that direct rAAVs to target tissues, in particular, capsid proteins comprising peptides that are inserted into surface-exposed variable regions using a method for replacing a stop codon in the capsid gene with such peptide insert. The invention provides such methods for making the rAAV vectors into vector libraries and selecting the rAAV vectors having peptide inserts that target the rAAV to particular tissues of interest, and thus deliver therapeutics for treating disorders.

FIG. 1



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RECOMBINANT ADENO-ASSOCIATED VIRUSES AND USES THEREOF

SEQUENCE LISTING

[0001] The Sequence Listing submitted herewith as an XML file named 38013_0030P1_SL.xml, created on August 24, 2023, and having a size of 530,415 bytes is hereby incorporated by reference pursuant to 37 C.F.R. §§ 1.831-1.835.

1. FIELD OF THE INVENTION

[0002] The present invention relates to recombinant adeno-associated viruses (rAAVs) having capsid proteins engineered to include amino acid sequences that confer and/or enhance desired properties when incorporated into an rAAV capsid. In particular, the invention provides engineered capsid proteins comprising peptide insertions inserted within or near variable region IV (VR-IV) of the virus capsid, such that the insertion is surface exposed on the AAV particle. The invention also provides capsid proteins that direct rAAVs to target tissues, in particular, capsid proteins derived from rAAV libraries, and provides such libraries constructed to reduce the parental vector production and thus overrepresentation of the parental capsid in the library and comprising random peptides inserted into surface-exposed variable regions to target rAAVs to and/or improve transduction of tissues of interest, including the muscle tissue, and deliver therapeutics for treating muscle disorders.

2. BACKGROUND

[0003] The use of recombinant adeno-associated viruses (AAV) as gene delivery vectors is a promising avenue for the treatment of many patients with unmet needs and/or rare disease. Dozens of naturally occurring AAV capsids have been reported, and mining the natural diversity of AAV sequences in primate tissues has identified over a hundred variants, distributed in clades. AAVs belong to the parvovirus family and are single-stranded DNA viruses with relatively small genomes and simple genetic components. Our current understanding of these capsids, their utility and function has allowed for efforts to further hone the efficiency and effectiveness of carrying therapeutic genome DNA, such as directing tissue tropism to deliver such DNA into target cells, while reducing the tropism to tissues where vector transduction and/or expression of transgene is undesirable, in order to safely ameliorate serious diseases.

[0004] Due to low pathogenicity and the promise of long-term, targeted gene expression, recombinant AAVs (rAAVs) have been used as gene transfer vectors, in which therapeutic sequences are packaged into capsids. Such vectors have been used to deliver a variety of therapeutic genes, thus many gene therapy products are currently in clinical development. Recombinant AAVs, such as AAV9, have demonstrated desirable muscle and neurotropic properties and clinical trials using recombinant AAV9 for treatment of muscle diseases, such as dystrophinopathies, are underway. However, attempts to identify rAAV capsids with desirable properties in human subjects are limited by the methods that select for them.

[0005] There remains a need for rAAV vectors with enhanced tropism to particular tissues and properties for use, *e.g.*, in high transduction to muscles to delivery therapies in treating disorders such as dystrophinopathies. There also is a need for improved methods for identifying such rAAV vectors with enhanced tissue-specific targeting and/or enhanced tissue-specific transduction to deliver therapies using lower dosing than is currently available.

3. SUMMARY OF THE INVENTION

[0006] Provided are recombinant adeno-associated viruses (rAAVs) having capsid proteins engineered to include amino acid sequences that confer and/or enhance desired properties such as tissue targeting, transduction or expression of the rAAV genome. In particular, provided are engineered capsid proteins comprising peptide insertions, derived from peptide libraries, inserted within or near variable region IV (VR-IV) of the virus capsid, or, in certain embodiments, within or near variable region VIII (VR-VIII), such that the peptide insertion is surface exposed on the AAV particle when the engineered capsid protein is incorporated into an rAAV particle. In embodiments, the peptide is 4 to 7 amino acids of one of the peptides having an amino acid sequence of SEQ ID NO: 1-138 (Tables 4, 5, 14, 15 or 16). In embodiments, the insertion is immediately after an amino acid residue corresponding to one of the amino acids 451 to 461 of the AAV9 capsid protein (SEQ ID NO: 151 and as numbered, *e.g.*, in **FIG. 1**), including after the amino acid 454 (*i.e.*, between amino acid 454 and 455) of the AAV9 capsid or in the AAV9.AAA (e.g., SEQ ID NO: 158) capsid protein; or in a capsid protein of a different AAV type after a residue that corresponds to the amino acid 454 of AAV9, see alignment in **FIG. 1** or for AAV types not included in **FIG. 1**, a similar amino acid sequence alignment of the AAV9 capsid protein sequence (SEQ ID NO: 151), such as 451-461 of AAV9 is the same as AAVhu.32 capsid protein sequence (SEQ ID NO: 148) as aligned in **FIG. 1**; and the AAV capsid protein as would be well known in the art). . The capsid protein may be an

AAV9 capsid protein but may also be any AAV capsid protein, such as AAV type 1 (AAV1), serotype 2 (AAV2), serotype 3 (AAV3), serotype 4 (AAV4), serotype 5 (AAV5), serotype 6 (AAV6), serotype 7 (AAV7), serotype 8 (AAV8), serotype rh8 (AAVrh8), serotype 9 (AAV9), serotype hu.31 (AAVhu.31), serotype hu.32 (AAVhu.32), serotype rh10 (AAVrh10), serotype rh20 (AAVrh20), serotype hu.37 (AVVhu.37), serotype rh39 (AAVrh39), and serotype rh74 (AAVrh74), or a variant AAV9 capsid protein AAV9.AAA (496NNN/AAA498 amino acid substitutions), (see, *e.g.*, alignments presented in **FIG. 1**) or may be a capsid protein which has 90%, 95% or 99% amino acid sequence identity to one of the foregoing capsid proteins. Thus, provided is an engineered capsid protein comprising a peptide insertion from a heterologous protein (i.e., not an AAV capsid protein) inserted immediately after or near an amino acid corresponding to the amino acid residue at position 454 of AAV9, as numbered in **FIG. 1**.

[0007] Also provided are engineered capsid proteins that direct rAAVs to target tissues, in particular, capsid proteins comprising peptides (derived from peptide libraries) or a peptide that promotes tissue targeting and/or cellular uptake and/or expression of the rAAV genome, that are inserted into surface-exposed variable regions and that target rAAVs to muscle tissue (skeletal muscle and/or heart), including to the central nervous system, and neurons within the CNS, and to retinal tissue, and deliver therapeutics for treating neurological and ocular disorders. These peptides, including 4, 5, 6, or all 7 contiguous amino acids of one of the peptides in Tables 4, 5, 14, 15, or 16 (SEQ ID Nos: 1-138) are advantageously inserted into the amino acid sequence of the capsid protein such that, when the capsid protein is incorporated into the AAV particle, the inserted peptide is surface exposed. These peptides are inserted immediately after one of the amino acid residues of, or after one of the amino acids corresponding to the amino acid, 585-593 of AAV9 capsid (SEQ ID NO: 151) or AAV9.AAA capsid (SEQ ID NO: 158, *e.g.* see **FIG. 1** for alignment), or immediately after one of the amino acid residues of, or after one of the amino acids corresponding to 451-461 of the AAV9 capsid or AAV9.AAA capsid and amino acids corresponding to any one of positions 451-461 of the AAV9 capsid (SEQ ID NO: 151, see, *e.g.* **FIG. 1** for alignment) or AAV9.AAA capsid. Exemplary modified capsid sequences are provided in Table 17, including capsid proteins having amino acid sequence of one of SEQ ID Nos: 159 to 266 (AAV9.AAA parental capsid) and 268 to 375 (AAVhu.32.AAA parental capsid). In other embodiments, a 4, 5, 6, or 7 amino acid portion of a peptide having an amino acid sequence of SEQ ID NO; 113, 114 or 115 is inserted immediately after position 577 or 578 of AAV5 (SEQ ID NO: 143). In embodiments,

provided are capsid proteins and capsid incorporating capsid proteins having an amino acid sequence of SEQ ID NO; 376, 377 or 378 (AAV5 parental capsid).

[0008] Provided are engineered capsid proteins comprising peptides that target specific tissues, including, when incorporated into an rAAV vector as a capsid to promote or increase cellular uptake and/or integration of an rAAV genome and/or expression of a transgene within the rAAV genome wherein the peptides are inserted into surface-exposed variable regions of the capsid protein. In certain embodiments, the peptides target and/or promote transduction or genome integration in cells of muscle, for example, at least 4 contiguous amino acids or at least 5, 6, or 7 contiguous amino acids of any of the peptides in Tables 4, 5, 14, 15 or 16, and capsids containing one of these peptides, for example, immediately after one of the positions 451-461, including after position 454, of AAV9, AAV9.AAA, AAVhu.32, or AAVhu.32.AAA, preferentially target the rAAV with the capsid to muscle tissue, and, in embodiments detargeting the liver. In embodiments, the capsid having the peptide insert targets and transduces neurons within the CNS, including relative to the transduction of astrocytes in the CNS. In other embodiments, the inserted peptide is at least 4 contiguous amino acids, and in addition the capsid is engineered to have one or more amino acid substitutions which may improve tropism, transduction or reduce immune neutralizing activity. Such amino acid modifications include amino acid substitutions of the NNN (asparagines) at 496 to 498 with AAA (alanines) in the AAV9 capsid. Other parental capsids having the peptide insertion may also have substitutions of the NNN (asparagines) at 498 to 500 with AAA (alanines) in the AAV8 capsid or of the NNN (asparagines) at 497 to 499 with AAA (alanines) in the AAVhu.32 capsid or corresponding substitutions in other AAV type capsids. Still other parental capsids having the peptide insertion may also have substitutions of S263F/S269T/A273T in AAV9, and corresponding substitutions in other AAV type capsids, W530R or Q474A in AAV9, and corresponding substitutions in other AAV type capsids, and/or A269S in AAV8, and corresponding substitutions in other AAV type capsids.

[0009] Also provided are engineered capsid proteins that promote transduction of the rAAV in one or more tissues, including one or more cell types, upon systemic, intravenous, intraperitoneal, or intramuscular administration, wherein the capsid proteins comprise a peptide of Tables 4, 5, 14, 15 or 16 (SEQ ID Nos: 1 to 138) that is inserted into a surface-exposed variable region (VR) of the capsid, *e.g.* VR-I, VR-IV or VR-VIII, or after the first amino acid of VP2, *e.g.*, immediately after residue 138 of the AAV9 capsid (amino acid sequence of SEQ ID NO: 151) or immediately after the corresponding residue of another AAV capsid, or

alternatively is engineered with one or more of the amino acid substitutions described herein, and transduction of the AAV having the engineered capsid in the at least one tissue (such as muscle (skeletal and/or heart, retina, or CNS, including CNS neurons) is increased upon said administration compared (for example, 1 fold, 2 fold, 5 fold, 10 fold or 20 fold greater) to the transduction of the AAV having the corresponding unengineered capsid (parental capsid) or a reference capsid such as AAV9, AAV9.AAA, AAVhu.32 or AAVhu.32.AAA. Such capsids may also exhibit reduced transduction of one or more tissues, including liver, heart or astrocytes upon administration compared (for example, 1 fold, 2 fold, 5 fold, 10 fold or 20 fold greater) to the transduction of the AAV in tissues such as muscle, retina or CNS or having the corresponding unengineered capsid (parental capsid) or a reference capsid such as AAV9, AAV9.AAA, AAVhu.32 or AAVhu.32.AAA In certain embodiments, transduction is measured by detection of transgene, such as DNA, RNA transcript or expressed protein in the cell, *e.g.* reporter transgenes may be utilized and measured such as GFP fluorescence.

[0010] In certain embodiments, provided are rAAVs incorporating the engineered capsids described herein, including rAAVs with genomes comprising a transgene of therapeutic interest. Plasmids and cells for production of a pool (stock) of plasmids for the production of the rAAVs are described herein. Packaging cells and methods for the production of the rAAVs comprising the engineered capsids are also provided herein. Method of treatment by delivery of, and pharmaceutical compositions comprising, the engineered rAAVs described herein are provided. Also provided are methods of manufacturing the rAAVs with the engineered capsids described herein.

[0011] Also provided are methods of making the capsid libraries having the peptide inserts. In embodiments, the method comprises providing a starting plasmid that contains a gene expression cassette encoding a capsid gene, wherein a stop codon is placed at a target insertion site within the capsid gene, randomizing a repertoire of nucleic acids encoding randomized peptides to produce a peptide library; creating individual plasmids based on the starting plasmid 1) each having a nucleic acid encoding a random peptide from the peptide library inserted at the target insertion site of the capsid gene thus replacing the stop codon, and 2) each encoding a barcode for identification of the capsid gene having the insert placed before the 5'- or after the 3'-end of the capsid gene; collecting the individual plasmids to form a population or collection of plasmids encoding the capsids with peptide inserts and transfecting with the collection of plasmids with plasmids encoding a recombinant rAAV genome containing a transgene, including one that is detectable, and necessary genes to produce a collection of

rAAV vectors encapsidating the rAAV genome containing the transgene, wherein the rAAV vectors have capsids with the encoded capsid protein containing a library peptide insert. In embodiments, the parental AAV is AAV9, AAV9.AAA, AAVhu.32, AAVhu.32.AAA, or AAV5 or any other suitable AAV serotype, for example, as in Table 3. The insertion site may be in VR-IV, including immediately after one of amino acids 451-461 of AAV9 or corresponding to one of those residues or in VR-VIII, including immediately after amino acid 588 of AAV9 or corresponding to that position in a different AAV capsid type (see FIG. 1 for alignment).

[0012] The library of modified capsids is harvested from these cells. In embodiments, the rAAV library population produced has high levels of capsids having the peptide inserts, including 85%, 90%, 95% or 98%, 99% or even 100%.

[0013] The invention is illustrated by way of examples *infra* describing the construction of engineered rAAV9 capsids having peptide inserts designed from rAAV libraries enabling the detection of desirable properties such as tissue targeting.

3.1. Embodiments

1. A recombinant adeno-associated virus (rAAV) capsid protein comprising a peptide insertion of at least 4 and up to 7 contiguous amino acids, said peptide insertion being immediately after an amino acid residue corresponding to one of amino acids 451 to 461 of AAV9 capsid protein of FIG. 1, wherein said peptide insertion has an amino acid sequence of one of SEQ ID NOs: 1-138,

   and wherein said capsid protein is a wild-type capsid protein or a variant capsid protein having up to three amino acid substitutions, and

   wherein an rAAV vector prepared from the capsid protein comprising the peptide insertion has enhanced tropism to a target tissue compared to an rAAV vector prepared from a capsid protein without the peptide insertion or a reference capsid protein.

2. The rAAV capsid protein of embodiment 1, wherein said capsid protein is from at least one AAV type selected from AAV type 1 (AAV1), serotype 2 (AAV2), serotype 3 (AAV3), serotype 4 (AAV4), serotype 5 (AAV5), serotype 6 (AAV6), serotype 7 (AAV7), serotype 8 (AAV8), serotype rh8 (AAVrh8), serotype 9 (AAV9), serotype hu.31 (AAVhu.31), serotype hu.32 (AAVhu.32), serotype rh10 (AAVrh10), serotype

rh20 (AAVrh20), serotype hu.37 (AVVhu.37), serotype rh39 (AAVrh39), and serotype rh74 (AAVrh74), or said variant capsid protein is AAV9.AAA or AAVhu.32.AAA or a capsid protein that has 90%, 95%, or 99% sequence identity thereto.

3. The rAAV capsid protein of embodiment 1 or 2, wherein said peptide insertion occurs immediately after one of the amino acid residues within:

(a) 450-459 of AAV1 capsid amino acid sequence (SEQ ID NO: 139);
(b) 449-458 of AAV2 capsid amino acid sequence (SEQ ID NO: 140);
(c) 449-459 of AAV3 capsid amino acid sequence (SEQ ID NO: 141);
(d) 443-453 of AAV4 capsid amino acid sequence (SEQ ID NO: 142);
(e) 442-445 of AAV5 capsid amino acid sequence (SEQ ID NO: 143);
(f) 450-459 of AAV6 capsid amino acid sequence (SEQ ID NO: 144);
(g) 451-461 of AAV7 capsid amino acid sequence (SEQ ID NO: 145);
(h) 451-461 of AAV8 capsid amino acid sequence (SEQ ID NO: 146);
(i) 451-461 of AAV9 capsid amino acid sequence (SEQ ID NO: 151);
(j) 451-461 of AAVhu.32 capsid amino acid sequence (SEQ ID NO: 148);
(k) 452-461 of AAVrh10 capsid amino acid sequence (SEQ ID NO: 152);
(l) 452-461 of AAVrh20 capsid amino acid sequence (SEQ ID NO: 155);
(m) 452-461 of AAVhu.37 capsid amino acid sequence (SEQ ID NO: 153);
(n) 452-461 of AAVrh39 capsid amino acid sequence (SEQ ID NO: 150);
(o) 452-461 of AAVrh74 capsid amino acid sequence (SEQ ID NO: 156 or SEQ ID NO: 157); or
(p) 452-461 of AAV9.AAA capsid amino acid sequence (SEQ ID NO: 158)

as depicted in FIG 1.

4. The rAAV capsid protein of embodiment 3, wherein said peptide insertion occurs after an amino acid residue corresponding to one of amino acids I451, N452, G453, S454, G455, Q456, N457, Q458, Q459, T460, or L461 of the AAV9 capsid or variant AAV9.AAA capsid.

5. The rAAV capsid protein of embodiment 4, wherein said peptide insertion occurs after an amino acid residue corresponding to amino acid S454 of the AAV9 capsid protein, the AAV.32 capsid protein, variant AAV9.AAA capsid protein, or variant AAVhu.32.AAA capsid protein.

6. The rAAV capsid protein of any one of embodiments 1-5 wherein the peptide is 7 amino acids.

7. The rAAV capsid protein of any one of embodiments 1-6 wherein the reference capsid protein is AAV9, AAV9.AAA, AAVhu32, or AAVhu32.AAA.

8. The rAAV capsid protein of any one of embodiments 1 through 7, wherein said peptide insertion comprises an amino acid sequence of at least 4 and up to 7 contiguous amino acids of SEQ ID NO: 135, SEQ ID NO: 136, SEQ ID NO: 137 or SEQ ID NO: 138, where SEQ ID NO: 135 is X_1-Q-V-X_2-X_3-X_4-X_5, wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is any amino acid and X_5 is S, G, V or A, where SEQ ID NO: 136 is X_1-Q-V-X_2-X_3-X_4-X_5, wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is any amino acid and X_5 is S or A, where SEQ ID NO: 137 is X_1-Q-V-X_2-X_3-X_4-X_5, wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is T, S, V, Y, A or P and X_5 is S, G, V or A, or where SEQ ID NO: 138 is X_1-Q-V-X_2-X_3-X_4-X_5, wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is T, S, V, Y, A or P and X_5 is S or A.

9. The rAAV capsid protein of embodiment 8, wherein the peptide insertion has an amino acid sequence of VQVGRAA (SEQ ID NO: 5), VQVGRTS (SEQ ID NO: 8), AQVGRAS (SEQ ID NO: 24), VQVGRVS (SEQ ID NO: 36), VQVGRSS (SEQ ID NO: 44), VQVGRYS (SEQ ID NO: 130), VQVGRAS (SEQ ID NO: 131), VQVGRPS (SEQ ID NO: 132), VQVVRPS (SEQ ID NO: 133) or VQVGHAS (SEQ ID NO: 134).

10. The rAAV capsid protein of embodiment 8 or 9 which has an amino acid sequence of SEQ ID No. 263, 264, 265 or 266.

11. The rAAV capsid protein of any one of embodiments 1-7, wherein said peptide insertion comprises an amino acid sequence of at least 4 and up to 7 contiguous amino acids of SGTVIRS (SEQ ID NO: 1), TRQYVPG (SEQ ID NO: 4), VQVGRTS (SEQ ID NO: 8), RGAVQKV (SEQ ID NO: 13), GQVHQAR (SEQ ID NO: 32), TSGGQIR (SEQ ID NO: 38), HMGHSGK (SEQ ID NO: 88), MRAVSQL (SEQ ID NO: 109), PRQYVPG (SEQ ID NO: 110), RSSSGR (SEQ ID NO: 111), VVKSTKS (SEQ ID NO: 112), RHVSASD (SEQ ID NO: 113), VRSDRDQ (SEQ ID NO: 114), or TVVTSIN (SEQ ID NO: 115).

12. The rAAV capsid protein of embodiment 11 wherein said peptide insertion is SGTVIRS (SEQ ID NO: 1), TRQYVPG (SEQ ID NO: 4), VQVGRTS (SEQ ID NO: 8), RGAVQKV (SEQ ID NO: 13), GQVHQAR (SEQ ID NO: 32), TSGGQIR (SEQ ID NO: 38), HMGHSGK (SEQ ID NO: 88), MRAVSQL (SEQ ID NO: 109), PRQYVPG (SEQ ID NO: 110), RSSSGR (SEQ ID NO: 111), VVKSTKS (SEQ ID NO: 112), RHVSASD (SEQ ID NO: 113), VRSDRDQ (SEQ ID NO: 114), or TVVTSIN (SEQ ID NO: 115).

13. The rAAV capsid protein of any one of embodiments 1 through 7, wherein said peptide insertion comprises an amino acid sequence of at least 4 and up to 7 contiguous amino acids of AQVGRAS (SEQ ID NO: 24), SVTSVRV (SEQ ID NO: 37), SIAKNSA (SEQ ID NO: 76), DGRRIGV (SEQ ID NO: 116), TSGERRG (SEQ ID NO: 117), PSSVQHR (SEQ ID NO: 118), SSSVQHR (SEQ ID NO: 119), SGMQERR (SEQ ID NO: 120), LERGNLE (SEQ ID NO: 121), YRDVRQT (SEQ ID NO: 122), PSAVQHR (SEQ ID NO: 123), YVGGRAV (SEQ ID NO: 124), IGSRGVA (SEQ ID NO: 125), SDVSRPR (SEQ ID NO: 126), GSVRQAA (SEQ ID NO: 127), QSPHTSQ (SEQ ID NO: 128), or ASQAYHG (SEQ ID NO: 128).

14. The rAAV capsid protein of embodiment 13, wherein said peptide insertion is AQVGRAS (SEQ ID NO: 24), SVTSVRV (SEQ ID NO: 37), SIAKNSA (SEQ ID NO: 76), DGRRIGV (SEQ ID NO: 116), TSGERRG (SEQ ID NO: 117), PSSVQHR (SEQ ID NO: 118), SSSVQHR (SEQ ID NO: 119), SGMQERR (SEQ ID NO: 120), LERGNLE (SEQ ID NO: 121), YRDVRQT (SEQ ID NO: 122), PSAVQHR (SEQ ID NO: 123), YVGGRAV (SEQ ID NO: 124), IGSRGVA (SEQ ID NO: 125), SDVSRPR (SEQ ID NO: 126), GSVRQAA (SEQ ID NO: 127), QSPHTSQ (SEQ ID NO: 128), or ASQAYHG (SEQ ID NO: 128).

15. The rAAV capsid protein of embodiment 14, wherein said peptide insertion is AQVGRAS (SEQ ID NO: 24), PSSVQHR (SEQ ID NO: 118), YVGGRAV (SEQ ID NO: 124), IGSRGVA (SEQ ID NO: 125) or GSVRQAA (SEQ ID NO: 127).

16. The rAAV capsid protein of embodiment 14, wherein said peptide insertion is DGRRIGV (SEQ ID NO: 116), SSSVQHR (SEQ ID NO: 119), YRDVRQT (SEQ ID NO: 122) or PSAVQHR (SEQ ID NO: 123).

17. The rAAV capsid protein of embodiment 1, having the amino acid sequence of any one of the amino acid sequences of SEQ ID NO: 159-266 and 268-375.

18. The rAAV capsid protein of any one of the preceding embodiments, wherein said target tissue with enhanced tropism is skeletal muscle or heart muscle.

19. The rAAV capsid protein of embodiment 18, wherein an rAAV vector prepared from the capsid protein exhibits an at least 2 fold, 5 fold, 10 fold, 15 fold, 20 fold, or 25 fold greater transduction of skeletal muscle and/or heart muscle than an rAAV vector prepared from the capsid protein without the peptide insert or the reference capsid protein.

20. The rAAV capsid protein of any one of the preceding embodiments wherein the target tissue is CNS neurons.

21. The rAAV capsid protein of embodiment 20 wherein an rAAV vector prepared from the capsid protein has an at least 2 fold, 5 fold, 10 fold, 15 fold, 20 fold, or 25 fold greater transduction of CNS neurons than an rAAV vector prepared from the capsid protein without the peptide insert or the reference capsid protein.

22. The rAAV capsid protein of any one of the preceding embodiments wherein an rAAV vector prepared from the capsid protein has reduced transduction of liver, heart or astrocytes than an rAAV vector prepared from the capsid protein without the peptide insert or the reference capsid protein.

23. The rAAV capsid protein of embodiment 22 wherein the rAAV vector prepared from the capsid protein has an at least 2 fold, 5 fold, 10 fold, 15 fold, 20 fold, 25 fold or 40 fold lower transduction of liver than an rAAV vector prepared from the capsid protein without the peptide insert or the reference capsid protein.

24. The rAAV capsid protein of any one of embodiments 19, 21, 22, or 23 wherein the reference capsid protein is AAV9 capsid or AAVhu.32 capsid.

25. A nucleic acid comprising a nucleotide sequence encoding the rAAV capsid protein of any one of the preceding embodiments or embodiments 42 to 48, or encoding an amino acid sequence sharing at least 80% identity therewith.

26. The nucleic acid of embodiment 25 which encodes the rAAV capsid protein of any one of the preceding embodiments.

27. A packaging cell capable of expressing the nucleic acid of embodiment 25 or 26 to produce AAV vectors comprising the capsid protein encoded by said nucleotide sequence.

28. A rAAV vector comprising the capsid protein of any one of embodiments 1-24 or embodiments 42 to 48.

29. The rAAV vector of embodiment 28, further comprising a rAAV genome comprising a transgene flanked by AAV ITR sequences.

30. A pharmaceutical composition comprising the rAAV vector of embodiment 28 or 29 and a pharmaceutically acceptable carrier.

31. A method of delivering a transgene to a cell, said method comprising contacting said cell with the rAAV vector of embodiment 28 or 29; or the rAAV vector of embodiment 28 or 29 for use in delivering a transgene to a cell, wherein said cell is contacted with the vector.

32. A method of delivering a transgene to a target tissue of a subject in need thereof, said method comprising administering to said subject the rAAV vector of embodiment 28 or 29; or the rAAV vector of embodiment 28 or 29 for use in delivering a transgene to a target tissue of a subject in need thereof, wherein the vector is administered to said subject.

33. The method, or rAAV vector for use, according to embodiment 32, wherein said rAAV vector is administered systemically, intravenously, intrathecally, intra-nasally, intra-peritoneally, intravitreally, via lumbar puncture or via the cisterna magna.

34. The method, or rAAV vector for use, according to embodiment 32 or embodiment 33, wherein said target tissue is muscle, retina or CNS.

35. A method of making a recombinant AAV (rAAV) vector library comprising

(i) producing a starting plasmid have a gene expression cassette comprising a nucleic acid sequence encoding an AAV capsid protein, wherein a stop codon is placed at a target insertion site within the nucleic acid sequence encoding the AAV capsid protein;

(ii) providing a population of nucleic acids which encode a repertoire of peptides to produce a peptide library;

(iii) creating individual plasmids based on the starting plasmid 1) each comprising the nucleic acid encoding the AAV capsid with a nucleic acid encoding a random peptide from the peptide library inserted at the target insertion site of the nucleic acid encoding the capsid protein thus replacing the stop codon, and 2) each plasmid further containing a nucleic acid encoding a barcode for identification of the nucleic acid encoding the capsid and peptide insert placed before the 5'- or after the 3'-end of the nucleic acid encoding the capsid ;

(iv) collecting the individual plasmids;

(v) transfecting a population of cells with the collection of individual plasmids and one or more plasmids carrying an rAAV genome comprising a transgene and necessary genes;

(vi) culturing the population of transfected cells under appropriate conditions to produce a collection of rAAV vectors each comprising the AAV capsid having the peptide insert encapsidating the rAAV genome comprising the transgene; and

(vii) harvesting the rAAV vector library.

36. The method of embodiment 35, wherein the capsid gene encodes an AAV1 capsid protein (SEQ ID NO: 139), an AAV4 capsid protein (SEQ ID NO: 142), an AAV5 capsid protein (SEQ ID NO: 143), an AAV8 capsid protein (SEQ ID NO: 146), an AAV9 capsid protein (SEQ ID NO: 151), an AAV9.AAA capsid protein (SEQ ID No: 158), AAVhu.32 (SEQ ID NO: 148), AAVhu.32.AAA (SEQ ID NO. 267), an AAV3B capsid protein (SEQ ID NO: 154) or an AAVhu37 capsid protein (SEQ ID NO: 153).

37. The method of any one of embodiments 34 to 36, wherein the target insertion site is at or after an amino acid residue within VR-4 or VR-8 of the capsid protein

38. The method of embodiment 37, wherein after the target insertion site is after an amino acid corresponding to S454 of AAV9 (SEQ ID NO: 151).

39. The method of any one of embodiments 34 to 38 wherein the peptide is a 7 amino acid peptide.

40. An rAAV vector library made by the method of any one of embodiments 34 to 39.

41. An rAAV vector library of embodiment 40 wherein at least 80%, 85%, 90%, 95%, 98%, 99% or 100% of the rAAV vectors in the library have a capsid with a peptide insert.

42. A recombinant adeno-associated virus (rAAV) capsid protein comprising a peptide insertion of at least 4 and up to 7 contiguous amino acids selected from the group consisting of SEQ ID NOs: 1-138, wherein said peptide insertion is surface exposed when said capsid protein is packaged as an AAV particle, and

wherein said capsid protein is a wild-type capsid protein or a variant capsid protein having up to three amino acid substitutions, and

wherein an rAAV vector prepared from the capsid protein comprising the peptide insertion provides enhanced tropism to a target tissue compared to an rAAV vector prepared from a capsid protein without the peptide insertion or a reference capsid protein.

43. The rAAV capsid protein of embodiment 42, wherein said capsid protein is serotype 5 (AAV5) (SEQ ID NO: 143) or a capsid protein that has 90%, 95%, or 99% sequence identity thereto.

44. The rAAV capsid protein of embodiment 42 or 43, wherein said peptide insertion occurs immediately after one of amino acid residues 574 to 584 of the AAV5 capsid protein.

45. The rAAV capsid protein of any one of embodiments 42 to 44, wherein said peptide insertion occurs immediately after amino acid residue 578 of the AAV capsid protein.

46. The rAAV capsid protein of any one of embodiments 42 to 45, wherein said peptide insertion is RHVSASD (SEQ ID NO: 113), VRSDRDQ ((SEQ ID NO: 114) or TVVTSIN (SEQ ID NO: 115).

47. The rAAV capsid protein of any one of embodiments 42 to 46 wherein the reference capsid protein is AAV5, AAV9, AAV9.AAA, AAVhu32, or AAVhu32.AAA.

48. The rAAV capsid protein of any one of embodiments 42 to 47 which has an amino acid sequence of SEQ ID No. 376, 377 or 378.

4. BRIEF DESCRIPTION OF THE FIGURES

[0014] **FIG. 1** depicts alignment of AAVs 1-9, hu31, hu32, and rh10 capsid sequences highlighting the VR-IV insertion site for these capsids (see VR4 corresponding to amino acids 451 to 461 of the AAV9 capsid protein and VR8 corresponding to amino acids 585 to 593 of the AAV9 capsid protein). A Clustal Multiple Sequence Alignment of AAV capsids was performed and illustrates that amino acid substitutions (shown in bold in the bottom rows) can be made to AAV9, AAVhu32 or other capsids by "recruiting" amino acid residues from the corresponding position of other aligned AAV capsids. Sequences shown in gray are hypervariable regions (HVR). The amino acid sequences of the AAV capsids are assigned SEQ ID NOs as follows: AAV1 is SEQ ID NO: 139; AAV2 is SEQ ID NO: 140; AAV3 is SEQ ID NO: 141; AAV4 is SEQ ID NO: 142; AAV5 is SEQ ID NO: 143; AAV6 is SEQ ID NO: 144; AAV7 is SEQ ID NO: 145; AAV8 is SEQ ID NO: 146; AAV9 is SEQ ID NO: 151; AAVrh10 is SEQ ID NO: 152; hu31 is SEQ ID NO: 147; and hu32 is SEQ ID NO: 148.

[0015] **FIG. 2** illustrates a protein model of variable region four and eight of the adeno-associated virus type 9 (AAV9 VR-IV and AAV9 VR-VIII, respectively).

[0016] **FIG. 3** depicts a representative genome construct of the capsid gene for use in construction of rAAV libraries having from 5' to 3': 5'-inverted terminal repeat (ITR), CMV enhancer-promoter, Rep intron, the AAV Cap gene of interest, polyA sequence, and 3'-ITR. The illustration depicts insertion of a random peptide library in the place of a stop codon (see arrow) that was inserted into the Cap gene variable region before construction of the library (to reduce expression of wildtype sequence in the library).

[0017] **FIG. 4** demonstrates the PCR amplicon obtained from libraries A1 to G1 used for NGS analysis of library diversity.

[0018] **FIGs. 5A-5B** show graphed results of the %wildtype and %stop codon sequences by NGS analysis of plasmid and vector libraries. **FIG. 5A** depicts a library having higher parental vector levels following vector production (vector %wt), compared to the percent parental plasmid (plasmid %wt) in the initial plasmid preparation of the library. **FIG. 5B** depicts NGS analysis of a library in which a stop codon was inserted into the template plasmid before plasmid library construction. The results indicate a reduction in stop parental sequence in the vector library (vector %stop) compared to the initial plasmid library(plasmid %stop).

[0019] **FIGs. 6A-6B.** Liquid chromatography-mass spectrometry (LC-MS) of VP3 proteins following generation of an AAV5 vector library with or without stop codon in template.

[0020] **FIG. 7** depicts the peptides analyzed by NGS in various tissues with various shading representing enrichment score. SEQ ID NOs: 1 – 24 (top to bottom) are listed on the left side of the density plot.

[0021] **FIGs. 8A-8C** depicts the relative abundance (RA), represented as fold change, for certain rAAV vectors with peptide insertions (24 = peptide 24 = SEQ ID NO: 24, and so on), relative to the control parental vector, AAV9.AAA. Comparisons of RA are made in heart (FIG. 8A), skeletal muscle (FIG. 8B), and liver (FIG. 8C) tissue.

[0022] **FIGs. 9A-9B** depicts the nRAAFI in NHP for certain rAAV vectors with peptide insertions (NVG01 to NVG14) compared to AAV9, AAVhu32, and AAV5 in skeletal muscle (**A**) and heart (**B**).

[0023] **FIGs. 10A-10B** are bar graphs depicting the mRNA/DNA in NHP of certain rAAV vectors with peptide insertions (NVG01 to NVG14) compared to AAV9, AAVhu32, and AAV5 in skeletal muscle (**A**) and heart (**B**).

[0024] **FIGs. 11A-11B** are bar graphs depicting the nRAAFI of mRNA (**A**) and DNA (**B**) in liver of NHP injected with pooled AAV with peptide insertions (NVG01 to NVG14).

[0025] **FIGs. 12A-C** are bar graphs showing the relative abundance (RA) of mRNA in skeletal muscle (**A**) liver (**B**) or the ratio of mRNA in muscle/liver (**C**) in individual NHP (numbered 1001, 1002, 1003, 4001, and 4003) injected with either AAV9 or AAV9.AAA.NVG07 (SEQ ID NO: 8).

[0026] **FIGs. 13A-B** are bar graphs showing the RNA (TdTom/TBP) or DNA (TdTom GC/ diploid genome) of CB57Bl6 mice injected with 1E14 GC/kg IV dose of AAV (AAVhu.32, AAV9.AAA.NVG07, or AAVhu.32.AAA.NVG09) expressing the CAG.TdTomato transgene at three weeks. RNA and DNA were measured in the heart, gastrocnemius, quadricep, bicep, tibialis anterior (TA), brain, liver and diaphragm.

5. DETAILED DESCRIPTION

[0027] Provided are recombinant adeno-associated viruses (rAAVs) having capsid proteins engineered to include amino acid sequences that confer and/or enhance desired properties, such as tissue targeting, transduction and integration of the rAAV genome. In particular, provided are engineered capsid proteins comprising peptide insertions of 4 to 7 contiguous amino acids, from random peptide libraries, inserted within or near variable region IV (VR-IV) or VR-VIII of the virus capsid, such that the peptide insertion is surface exposed when the capsid protein is packaged as an AAV particle. Also provided are recombinant capsid proteins, and libraries of the individual rAAVs comprising them, that have inserted peptides that target specific tissues and/or promote rAAV cellular uptake, transduction and/or transgene expression, for example, see Table 17.

5.1. Definitions

[0028] The term "AAV" or "adeno-associated virus" refers to a Dependoparvovirus within the Parvoviridae genus of viruses. The AAV can be an AAV derived from a naturally occurring "wild-type" virus, an AAV derived from a rAAV genome packaged into a capsid comprising capsid proteins encoded by a naturally occurring cap gene and/or from a rAAV genome packaged into a capsid comprising capsid proteins encoded by a non-naturally occurring capsid cap gene. An example of the latter includes a rAAV having a capsid protein comprising a peptide insertion into the amino acid sequence of the naturally-occurring capsid.

[0029] The term "rAAV" refers to a "recombinant AAV." In some embodiments, a recombinant AAV has an AAV genome in which part or all of the rep and cap genes have been replaced with heterologous sequences.

[0030] The term "rep-cap helper plasmid" refers to a plasmid that provides the viral rep and cap gene function and aids the production of AAVs from rAAV genomes lacking functional rep and/or the cap gene sequences.

[0031] The term "cap gene" refers to the nucleic acid sequences that encode capsid proteins that form or help form the capsid coat of the virus. For AAV, the capsid protein may be VP1, VP2, or VP3.

[0032] The term "rep gene" refers to the nucleic acid sequences that encode the non-structural protein needed for replication and production of virus.

[0033] The terms "nucleic acids" and "nucleotide sequences" include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), combinations of DNA and RNA

molecules or hybrid DNA/RNA molecules, and analogs of DNA or RNA molecules. Such analogs can be generated using, for example, nucleotide analogs, which include, but are not limited to, inosine or tritylated bases. Such analogs can also comprise DNA or RNA molecules comprising modified backbones that lend beneficial attributes to the molecules such as, for example, nuclease resistance or an increased ability to cross cellular membranes. The nucleic acids or nucleotide sequences can be single-stranded, double-stranded, may contain both single-stranded and double-stranded portions, and may contain triple-stranded portions, but preferably is double-stranded DNA.

[0034] As used herein, the terms "subject", "host", and "patient" are used interchangeably. As used herein, a subject is a mammal such as a non-primate (*e.g.*, cows, pigs, horses, cats, dogs, rats etc.) or a primate (*e.g.*, monkey and human), or, in certain embodiments, a human.

[0035] "Library" or "libraries" generally refer to a repertoire of capsid genes (each unique and usually placed recombinantly into a vehicle, such as in a plasmid) or rAAV vectors produced from the unique capsids.

[0036] As used herein, the term "conservative amino acid substitution" means substitutions made in accordance with Tables A and B.

Table A Amino Acid Substitutions

Original Residue	**Non-limiting Exemplary Conservative Substitutions**
Ala	Ser
Arg	Gly; Gln; Lys
Asn	Gln; His
Asp	Glu
Cys	Ser
Gln	Asn; Lys
Glu	Asp
Gly	Ala
His	Asn; Gln
Ile	Leu; Val
Leu	Ile; Val
Lys	Arg; Gln
Met	Leu; Ile
Phe	Met; Leu; Tyr

Original Residue	Non-limiting Exemplary Conservative Substitutions
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

Table B: Amino Acid Abbreviations

Amino Acid	Abbreviations
Alanine	Ala (A)
Allosoleucine	AIle
Arginine	Arg (R)
Asparagine	Asn (N)
Aspartic Acid	Asp (D)
Cysteine	Cys (C)
Glutamic Acid	Glu (E)
Glutamine	Gln (Q)
Glycine	Gly (G)
Histidine	His (H)
Isolelucine	Ile (I)
Leucine	Leu (L)
Lysine	Lys (K)
Phenylalanine	Phe (F)
Praline	Pro (P)
Pyroglutamic Acid	PGlu (U)
Serine	Ser (S)
Threonine	Thr (T)
Tyrosine	Tyr (Y)
Tryptophan	Trp (W)
Valine	Val (V)

[0037] It is understood that one way to define the variants and derivatives of the disclosed capsid proteins herein is to define them in terms of homology/identity to specific known sequences. Specifically disclosed are variants of capsids herein disclosed which have at least, 70% or at least 75% or at least 80% or at least 85% or at least 90% or at least 91% or at least 92% or at least 93% or at least 94% or at least 95% or at least 96% or at least 97% or at least 98% or at least 99% identity to the capsid sequences specifically recited herein. Those of skill in the art readily understand how to determine the identity of two proteins. Variants of capsids described herein may have 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15 or 20 amino acid substitutions, including conservative amino acid substitutions. Variants of the 4 to 7 amino acid peptides described herein include peptides having 1, 2, or 3 amino acid substitutions, including conservative amino acid substitutions.

[0038] The term "therapeutic agent" refers to any agent which can be used in treating, managing, or ameliorating symptoms associated with a disease or disorder, where the disease or disorder is associated with a function to be provided by a transgene. As used herein, a "therapeutically effective amount" refers to the amount of agent, (*e.g.*, an amount of product expressed by the transgene) that provides at least one therapeutic benefit in the treatment or management of the target disease or disorder, when administered to a subject suffering therefrom. Further, a therapeutically effective amount with respect to an agent of the invention means that amount of agent alone, or when in combination with other therapies, that provides at least one therapeutic benefit in the treatment or management of the disease or disorder.

[0039] As used herein, the term "prophylactic agent" refers to any agent which can be used in the prevention, delay, or slowing down of the progression of a disease or disorder, where the disease or disorder is associated with a function to be provided by a transgene. As used herein, a "prophylactically effective amount" refers to the amount of the prophylactic agent (*e.g.*, an amount of product expressed by the transgene) that provides at least one prophylactic benefit in the prevention or delay of the target disease or disorder, when administered to a subject predisposed thereto. A prophylactically effective amount also may refer to the amount of agent sufficient to prevent or delay the occurrence of the target disease or disorder; or slow the progression of the target disease or disorder; the amount sufficient to delay or minimize the onset of the target disease or disorder; or the amount sufficient to prevent or delay the recurrence or spread thereof. A prophylactically effective amount also may refer to the amount of agent sufficient to prevent or delay the exacerbation of symptoms of a target disease or disorder. Further, a prophylactically effective amount with respect to a prophylactic agent of

the invention means that amount of prophylactic agent alone, or when in combination with other agents, that provides at least one prophylactic benefit in the prevention or delay of the disease or disorder.

[0040] A prophylactic agent of the invention can be administered to a subject "pre-disposed" to a target disease or disorder. A subject that is "pre-disposed" to a disease or disorder is one that shows symptoms associated with the development of the disease or disorder, or that has a genetic makeup, environmental exposure, or other risk factor for such a disease or disorder, but where the symptoms are not yet at the level to be diagnosed as the disease or disorder. For example, a patient with a family history of a disease associated with a missing gene (to be provided by a transgene) may qualify as one predisposed thereto.

5.2. Recombinant AAV Capsids and Vectors

[0041] One aspect relates to capsid protein libraries and the recombinant adeno-associated virus (rAAV) vectors thereof, the capsid proteins within the library engineered to comprise a peptide insertion from a random peptide library, wherein the peptide is not an AAV protein or peptide fragment thereof, where the peptide insertion is surface exposed when packaged as an AAV particle. In some embodiments, the peptide insertion occurs within (i.e., between two amino acids without deleting any capsid amino acids) variable region IV (VR-IV) of an AAV9 capsid or AAV9.AAA capsid, or a corresponding region for another type AAV capsid (see alignment in **FIG. 1**). In some embodiments, the peptide insertion occurs within (*i.e.*, between two amino acids without deleting any capsid amino acids) variable region VIII (VR-VIII) of an AAV9 capsid or AAV9.AAA, or a corresponding region of a capsid for another AAV type (see alignment in **FIG. 1**). In some embodiments, the peptide insertion is from a heterologous protein or domain (that is not an AAV capsid protein or domain), which directs the rAAV particles to target tissues and/or promote rAAV uptake, transduction and/or transgene expression. Also provided are nucleic acids encoding the engineered capsid proteins and variants thereof, packaging cells for expressing the nucleic acids to produce rAAV vectors, rAAV vectors further comprising a transgene, and pharmaceutical compositions of the rAAV vectors, as well as methods of using the rAAV vectors to deliver the transgene to a target cell type or target tissue of a subject in need thereof.

[0042] In the various embodiments, the target tissue may be muscle tissue, such as skeletal muscle or heart muscle, neural tissue, bone, kidney, the eye/retina, or endothelial tissue, and the capsid with the peptide insertion specifically recognizes and/or binds to and/or homes to

that tissue, or for example, one or more specific cell types, such as within the target tissue, or cellular matrix thereof. In particular, peptides that can target rAAVs to muscle tissue, including skeletal muscle and heart, can be useful for delivering therapeutics for treating muscle disorders. In embodiments, rAAV capsids containing the engineered capsid protein with the peptide insert have increased uptake, transduction, and/or transgene expression than the parental capsid or a reference capsid, including AAV9, AAV9.AAA, AAVhu.32, AAVhu.32.AAA or AAV5. The engineered capsids may further have reduced transduction in tissues such as liver, heart, or astrocytes or other tissues relative to the targeted tissue or relative to transduction with the parental capsid or a reference capsid, including AAV9, AAV9.AAA, AAVhu.32, AAVhu.32.AAA or AAV5.

[0043] In various embodiments, the target tissue may be neural tissue, and particularly neurons in the brain. In embodiments, the peptide insertions target rAAVs preferentially to neurons over astrocytes compared to rAAVs that do not have the peptide insertion.

[0044] In embodiments either the parental capsid and/or the peptide insert detarget the rAAV vector prepared from the engineered capsid protein from one or more tissue types, including liver.

5.2.1 rAAV Vectors with Peptide Insertions

[0045] A peptide insertion described as inserted "at" a given site refers to insertion immediately after, that is having a peptide bond to the carboxy group of, the residue normally found at that site in the wild type virus. For example, insertion at S454 in AAV9 means that the peptide insertion appears between S454 and the consecutive amino acid (G455) in the AAV9 wildtype capsid protein sequence (SEQ ID NO: 151). In embodiments, there is no deletion of amino acid residues at or near (within 5, 10, 15 residues or within the structural loop that is the site of the insertion) the point of insertion.

[0046] In embodiments, the capsid protein is an AAV9 capsid protein (SEQ ID NO: 151, or a capsid protein having an amino acid sequence that is 90%, 95%, or 99% identical to SEQ ID NO: 151) or an AAV9.AAA capsid protein and the insertion occurs immediately after at least one of the amino acid residues 451 to 461. In embodiments, the peptide insertion occurs immediately after amino acid I451, N452, G453, S454, G455, Q456, N457, Q458, Q459, T460, or L461 of the AAV9 capsid (amino acid sequence SEQ ID NO: 151). In certain embodiments, the peptide is inserted between residues S454 and G455 of AAV9 capsid protein or between the residues corresponding to S454 and G455 of an AAV capsid protein other than an AAV9

capsid protein (amino acid sequence SEQ ID NO: 151). In embodiments, the capsid protein is an AAV9.AAA capsid protein and the insertion occurs immediately after at least one of the amino acid residues 451 to 461. In embodiments, the peptide insertion occurs immediately after amino acid I451, N452, G453, S454, G455, Q456, N457, Q458, Q459, T460, or L461 of the AAV9.AAA capsid (amino acid sequence SEQ ID NO: 123). In certain embodiments, the peptide is inserted between residues S454 and G455 of AAV9.AAA capsid protein or between the residues corresponding to S454 and G455 of an AAV.AAA capsid protein other than an AAV9 capsid protein (amino acid sequence SEQ ID NO: 123).

[0047] In embodiments, the capsid protein is an hu.32 capsid protein (SEQ ID NO: 148, or a capsid protein having an amino acid sequence that is 90%, 95%, or 99% identical to SEQ ID NO: 148) or an AAVhu.32.AAA capsid protein and the insertion occurs immediately after at least one of the amino acid residues 451 to 461. In embodiments, the peptide insertion occurs immediately after amino acid I451, N452, G453, S454, G455, Q456, N457, Q458, Q459, T460, or L461 of the AAVhu.32 capsid (amino acid sequence SEQ ID NO: 148). In certain embodiments, the peptide is inserted between residues S454 and G455 of AAVhu.32 capsid protein. In embodiments, the capsid protein is an AAVhu.32.AAA capsid protein and the insertion occurs immediately after at least one of the amino acid residues 451 to 461. In embodiments, the peptide insertion occurs immediately after amino acid I451, N452, G453, S454, G455, Q456, N457, Q458, Q459, T460, or L461 of the AAVhu.32.AAA capsid (amino acid sequence SEQ ID NO: 148). In certain embodiments, the peptide is inserted between residues S454 and G455 of AAVhu.32.AAA capsid protein.

[0048] In embodiments, the capsid protein is an AAV5 capsid protein (SEQ ID NO: 143, or a capsid protein having an amino acid sequence that is 90%, 95%, or 99% identical to SEQ ID NO: 143) and the insertion occurs immediately after at least one of the amino acid residues 442 to 447. In embodiments, the peptide insertion occurs immediately after amino acid N442, N443, T444, G445, G446, V447 of the AAV5 capsid (amino acid sequence SEQ ID NO: 143). In embodiments, the peptide is inserted after a residue within VR8 of the AAV5 capsid protein In embodiments, the peptide is inserted after residue 578 of AAV5 capsid protein.

[0049] In other embodiments, the capsid protein is from at least one AAV type selected from AAV serotype 1 (AAV1), serotype 2 (AAV2), serotype 3 (AAV3), serotype 4 (AAV4), serotype 5 (AAV5), serotype 6 (AAV6), serotype 7 (AAV7), serotype 8 (AAV8), serotype rh8 (AAVrh8), serotype 9e (AAV9e), serotype rh10 (AAVrh10), serotype rh20 (AAVrh20), serotype rh39 (AAVrh39), serotype hu.37 (AAVhu.37), and serotype rh74 (AAVrh74, versions

1 and 2) (see **FIG. 1**) or a capsid that is at least 90%, 95% or 99% identical in amino acid sequence to the amino acid sequence of the VP1, VP2, or VP3 of the foregoing capsid proteins, and the insertion occurs immediately after an amino acid residue corresponding to at least one of the amino acid residues 451 to 461 of AAV9. The alignments of these different AAV serotypes, as shown in **FIG. 1**, indicates "corresponding" amino acid residues in the different capsid amino acid sequences such that a "corresponding" amino acid residue is lined up at the same position in the alignment as the residue in the reference sequence. In some embodiments, the peptide insertion occurs immediately after one of the amino acid residues within: 450-459 of AAV1 capsid (SEQ ID NO: 139); 449-458 of AAV2 capsid (SEQ ID NO: 140); 449-459 of AAV3 capsid (SEQ ID NO: 141); 443-453 of AAV4 capsid (SEQ ID NO: 142); 442-445 of AAV5 capsid (SEQ ID NO: 143); 450-459 of AAV6 capsid (SEQ ID NO: 144); 451-461 of AAV7 capsid (SEQ ID NO: 145); 451-461 of AAV8 capsid (SEQ ID NO: 146); 451-461 of AAV9 capsid (SEQ ID NO: 151); 451-461 of AAVhu.32 capsid (SEQ ID NO: 148); 452-461 of AAVrh10 capsid (SEQ ID NO: 152); 452-461 of AAVrh20 capsid (SEQ ID NO: 155); 452-461 of AAVhu.37 (SEQ ID NO: 149); 452-461 of AAVrh74 (SEQ ID NO: 156 or SEQ ID NO: 157); or 452-461 of AAVrh39 (SEQ ID NO: 150), in the sequences depicted in **FIG. 1**. In certain embodiments, the rAAV capsid protein comprises a peptide insertion immediately after (*i.e.*, C-terminal to) amino acid 588 of AAV9 capsid protein (having the amino acid sequence of SEQ ID NO: 151 and see **FIG. 1**) or AAV9.AAA (having SEQ ID NO: 158), where said peptide insertion is surface exposed when the capsid protein is packaged as an AAV particle. In other embodiments, the rAAV capsid protein has a peptide insertion that is not immediately after amino acid 588 of AAV9 or AAV9.AAA, or corresponding to amino acid 588 of AAV9.

[0050] Also provided are AAV vectors comprising the engineered capsids. In some embodiments, the AAV vectors are non-replicating and do not include the nucleotide sequences encoding the rep or cap proteins (these are supplied by the packaging cells in the manufacture of the rAAV vectors). In some embodiments, AAV-based vectors comprise components from one or more serotypes of AAV. In some embodiments, AAV based vectors provided herein comprise capsid components from one or more of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, AAV13, AAV14, AAV15, AAV16, AAV.rh8, AAV.rh10, AAV.rh20, AAV.rh39, AAV.Rh74, AAV.RHM4-1, AAV.hu37, AAV.Anc80, AAV.Anc80L65, AAV.7m8, AAV.PHP.B, AAV.PHP.eB, AAV2.5, AAV2tYF, AAV3B, AAV.LK03, AAV.HSC1, AAV.HSC2, AAV.HSC3, AAV.HSC4, AAV.HSC5, AAV.HSC6, AAV.HSC7, AAV.HSC8, AAV.HSC9, AAV.HSC10, AAV.HSC11,

AAV.HSC12, AAV.HSC13, AAV.HSC14, AAV.HSC15, or AAV.HSC16 or other rAAV particles, or combinations of two or more thereof. In some embodiments, AAV based vectors provided herein comprise components from one or more of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, AAV13, AAV14, AAV15, AAV16, AAV.rh8, AAV.rh10, AAV.rh20, AAV.rh39, AAV.Rh74, AAV.RHM4-1, AAV.hu37, AAV.Anc80, AAV.Anc80L65, AAV.7m8, AAV.PHP.B, AAV.PHP.eB, AAV2.5, AAV2tYF, AAV3B, AAV.LK03, AAV.HSC1, AAV.HSC2, AAV.HSC3, AAV.HSC4, AAV.HSC5, AAV.HSC6, AAV.HSC7, AAV.HSC8, AAV.HSC9, AAV.HSC10, AAV.HSC11, AAV.HSC12, AAV.HSC13, AAV.HSC14, AAV.HSC15, or AAV.HSC16 or other rAAV particles, or combinations of two or more serotypes. In some embodiments, rAAV particles comprise a capsid protein at least 80% or more identical, *e.g.*, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, etc., i.e. up to 100% identical, to *e.g.*, VP1, VP2 and/or VP3 sequence of an AAV capsid serotype selected from AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, AAV13, AAV14, AAV15, AAV16, AAV.rh8, AAV.rh10, AAV.rh20, AAV.rh39, AAV.Rh74, AAV.RHM4-1, AAV.hu37, AAV.Anc80, rAAV.Anc80L65, AAV.7m8, AAV.PHP.B, AAV.PHP.eB, AAV2.5, AAV2tYF, AAV3B, AAV.LK03, AAV.HSC1, AAV.HSC2, AAV.HSC3, AAV.HSC4, AAV.HSC5, AAV.HSC6, AAV.HSC7, AAV.HSC8, AAV.HSC9, AAV.HSC10, AAV.HSC11, AAV.HSC12, AAV.HSC13, AAV.HSC14, AAV.HSC15, or AAV.HSC16, or a derivative, modification, or pseudotype thereof. These engineered AAV vectors may comprise a genome comprising a transgene encoding a therapeutic protein.

[0051] In embodiments, the recombinant AAV for use in compositions and methods herein is Anc80 or Anc80L65 (see, *e.g.*, Zinn *et al.*, 2015, *Cell Rep.* 12(6): 1056-1068, which is incorporated by reference in its entirety). In embodiments, the recombinant AAV for use in compositions and methods herein is AAV.7m8 (including variants thereof) (see, *e.g.*, US 9,193,956; US 9,458,517; US 9,587,282; US 2016/0376323, and WO 2018/075798, each of which is incorporated herein by reference in its entirety). In embodiments, the AAV for use in compositions and methods herein is any AAV disclosed in US 9,585,971, such as AAV-PHP.B. In embodiments, the AAV for use in compositions and methods herein is an AAV2/Rec2 or AAV2/Rec3 vector, which has hybrid capsid sequences derived from AAV8 and serotypes cy5, rh20 or rh39 (see, *e.g.*, Issa *et al.*, 2013, PLoS One 8(4): e60361, which is incorporated by reference herein for these vectors). In embodiments, the AAV for use in compositions and

methods herein is an AAV disclosed in any of the following, each of which is incorporated herein by reference in its entirety: US 7,282,199; US 7,906,111; US 8,524,446; US 8,999,678; US 8,628,966; US 8,927,514; US 8,734,809; US9,284,357; US 9,409,953; US 9,169,299; US 9,193,956; US 9,458,517; US 9,587,282; US 2015/0374803; US 2015/0126588; US 2017/0067908; US 2013/0224836; US 2016/0215024; US 2017/0051257; PCT/US2015/034799; and PCT/EP2015/053335. In some embodiments, rAAV particles have a capsid protein at least 80% or more identical, *e.g.*, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, etc., i.e. up to 100% identical, to the VP1, VP2 and/or VP3 sequence of an AAV capsid disclosed in any of the following patents and patent applications, each of which is incorporated herein by reference in its entirety: United States Patent Nos. 7,282,199; 7,906,111; 8,524,446; 8,999,678; 8,628,966; 8,927,514; 8,734,809; US 9,284,357; 9,409,953; 9,169,299; 9,193,956; 9,458,517; and 9,587,282; US patent application publication nos. 2015/0374803; 2015/0126588; 2017/0067908; 2013/0224836; 2016/0215024; 2017/0051257; and International Patent Application Nos. PCT/US2015/034799; PCT/EP2015/053335.

[0052] In some embodiments, rAAV particles comprise any AAV capsid disclosed in United States Patent No. 9,840,719 and WO 2015/013313, such as AAV.Rh74 and RHM4-1, each of which is incorporated herein by reference in its entirety. In some embodiments, rAAV particles comprise any AAV capsid disclosed in WO 2014/172669, such as AAV rh.74, which is incorporated herein by reference in its entirety. In some embodiments, rAAV particles comprise the capsid of AAV2/5, as described in Georgiadis *et al.,* 2016, Gene Therapy 23: 857-862 and Georgiadis *et al.,* 2018, Gene Therapy 25: 450, each of which is incorporated by reference in its entirety. In some embodiments, rAAV particles comprise any AAV capsid disclosed in WO 2017/070491, such as AAV2tYF, which is incorporated herein by reference in its entirety. In some embodiments, rAAV particles comprise the capsids of AAVLK03 or AAV3B, as described in Puzzo *et al.,* 2017, Sci. Transl. Med. 29(9): 418, which is incorporated by reference in its entirety. In some embodiments, rAAV particles comprise any AAV capsid disclosed in US Pat Nos. 8,628,966; US 8,927,514; US 9,923,120 and WO 2016/049230, such as HSC1, HSC2, HSC3, HSC4, HSC5, HSC6, HSC7, HSC8, HSC9, HSC10, HSC11, HSC12, HSC13, HSC14, HSC15, or HSC16, each of which is incorporated by reference in its entirety.

[0053] In some embodiments, rAAV particles have a capsid protein disclosed in Intl. Appl. Publ. No. WO 2003/052051 (see, *e.g.*, SEQ ID NO: 2 of ′051 publication), WO 2005/033321 (see, *e.g.*, SEQ ID NOs: 123 and 88 of ′321 publication), WO 03/042397 (see, *e.g.*, SEQ ID

NOs: 2, 81, 85, and 97 of ′397 publication), WO 2006/068888 (see, *e.g.*, SEQ ID NOs: 1 and 3-6 of ′888 publication), WO 2006/110689, (see, *e.g.*, SEQ ID NOs: 5-38 of ′689 publication) WO2009/104964 (see, *e.g.*, SEQ ID NOs: 1-5, 7, 9, 20, 22, 24 and 31 of ′964 publication), WO 2010/127097 (see, *e.g.*, SEQ ID NOs: 5-38 of ′097 publication), and WO 2015/191508 (see, *e.g.*, SEQ ID NOs: 80-294 of ′508 publication), and U.S. Appl. Publ. No. 20150023924 (see, *e.g.*, SEQ ID NOs: 1, 5-10 of ′924 publication), the contents of each of which is herein incorporated by reference in its entirety. In some embodiments, rAAV particles have a capsid protein at least 80% or more identical, *e.g.*, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, etc., i.e. up to 100% identical, to the VP1, VP2 and/or VP3 sequence of an AAV capsid disclosed in Intl. Appl. Publ. No. WO 2003/052051 (see, *e.g.*, SEQ ID NO: 2 of ′051 publication), WO 2005/033321 (see, *e.g.*, SEQ ID NOs: 123 and 88 of ′321 publication), WO 03/042397 (see, *e.g.*, SEQ ID NOs: 2, 81, 85, and 97 of ′397 publication), WO 2006/068888 (see, *e.g.*, SEQ ID NOs: 1 and 3-6 of ′888 publication), WO 2006/110689 (see, *e.g.*, SEQ ID NOs: 5-38 of ′689 publication) WO2009/104964 (see, *e.g.*, SEQ ID NOs: 1-5, 7, 9, 20, 22, 24 and 31 of 964 publication), W0 2010/127097 (see, *e.g.*, SEQ ID NOs: 5-38 of ′097 publication), and WO 2015/191508 (see, *e.g.*, SEQ ID NOs: 80-294 of ′508 publication), and U.S. Appl. Publ. No. 20150023924 (see, *e.g.*, SEQ ID NOs: 1, 5-10 of ′924 publication).

[0054] In additional embodiments, rAAV particles comprise a pseudotyped AAV capsid. In some embodiments, the pseudotyped AAV capsids are rAAV2/8 or rAAV2/9 pseudotyped AAV capsids. Methods for producing and using pseudotyped rAAV particles are known in the art (see, *e.g.*, Duan *et al.*, J. Virol., 75:7662-7671 (2001); Halbert *et al.*, J. Virol., 74:1524-1532 (2000); Zolotukhin *et al.*, Methods 28:158-167 (2002); and Auricchio *et al.*, Hum. Molec. Genet. 10:3075-3081, (2001).

[0055] In certain embodiments, a single-stranded AAV (ssAAV) may be used. In certain embodiments, a self-complementary vector, *e.g.*, scAAV, may be used (*see, e.g.*, Wu, 2007, *Human Gene Therapy*, 18(2):171-82; McCarty *et al*, 2001, *Gene Therapy*, 8(16):1248-1254; US 6,596,535; US 7,125,717; and US 7,456,683, each of which is incorporated herein by reference in its entirety).

[0056] Generally, the peptide insertion is sequence of contiguous amino acids from a heterologous protein or domain thereof. The peptide to be inserted typically is long enough to retain a particular biological function, characteristic, or feature of the protein or domain from which it is derived. The peptide to be inserted typically is short enough to allow the capsid

protein to form a coat, similarly or substantially similarly to the native capsid protein without the insertion. In preferred embodiments, the peptide insertion is from about 4 to about 30 amino acid residues in length, about 4 to about 20, about 4 to about 15, about 5 to about 10, or about 7 amino acids in length. The peptide sequences for insertion are at least 4 amino acids in length and may be 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 amino acids in length. In some embodiments, the peptide sequences are 16, 17, 18, 19, or 20 amino acids in length. In embodiments, the peptide is no more than 7 amino acids, 10 amino acids or 12 amino acids in length.

[0057] A "peptide insertion from a heterologous protein" in an AAV capsid protein refers to an amino acid sequence that has been introduced into the capsid protein and that is not native to the AAV serotype capsid into which it is inserted.

[0058] As used herein, the terms "homing" and "targeting" are used interchangeably. These peptides may also or alternatively promote rAAV cell uptake, transduction and/or genome integration in cells of the target tissue.

[0059] Examples of peptides for use as peptide insertions at any of the AAV capsid sites described herein are presented in **Tables 4, 5, 14, 15 and 16** below in the Examples (including the peptides having amino acid sequences of SEQ ID Nos 1-138), and include at least 4 amino acid contiguous portions thereof, or 7 amino acid contiguous portions thereof (and includes variants having 1, 2 or 3 amino acid substitutions, including conservative amino acid substitutions) and have the functional attribute of the peptide being inserted alters the properties of the capsid, particularly its tropism. In certain embodiments, the recombinant AAV capsids and AAV vectors are engineered to include a peptide, or at least 4, 5, 6, or 7 amino acid contiguous portion thereof, from any of **Tables 4, 5, 14, 15 and 16** below (including peptides of amino acid sequences of SEQ ID Nos 1-138), inserted into the AAV capsid sequence in such a way that the peptide insertion is displayed. In other embodiments, the peptides are inserted after an amino acid residue at positions 138, 262-273, 451-461, or 585-593 of the amino acid sequence of the AAV9 capsid (SEQ ID NO: 151) or of the AAV9.AAA capsid (SEQ ID NO: 158) a position corresponding thereto in any other AAV serotype (*see* **FIG. 1** for capsid sequence alignments).

[0060] In another aspect, provided are heterologous peptide insertion libraries. A heterologous peptide insertion library refers to a collection of rAAV vectors that carry the same random peptide insertion at the same insertion site in the virus capsid to make the particular library, *e.g.*, at a position within a given variable region of the capsid. Generally, the capsid proteins used comprise AAV genomes that contain modified rep and cap sequences to prevent

the replication of the virus under conditions in which it could normally replicate (co-infection of a mammalian cell along with a helper virus such as adenovirus). The members of the peptide insertion libraries may then be assayed for functional display of the peptide on the rAAV surface, tissue targeting and/or gene transduction. Enhanced properties or desirable properties may be assessed upon comparison with the parental capsid from which the insertion library was made.

[0061] Provided are peptide insertion libraries and methods of making these libraries. An exemplary method of producing a capsid library with peptide inserts is described herein in Example 2 and such libraries are screened herein. In such libraries, the nucleic acid encoding the parental capsid has a stop codon at the target insertion site for the population of nucleic acids encoding the peptides such that a capsid protein will only be expressed if the peptide insert is present, otherwise, translation will terminate prematurely. Production of the populations of rAAVs from the expression constructs results in an rAAV population with a high percentage of capsids with peptide inserts (including 80%, 85%, 90%, 95%, 98%, 99% or even 100%) (see, for example, FIGs 5A, 5B, 6A, and 6B).

[0062] Also provided are methods of making the capsid libraries having the variable peptide inserts. In embodiments, the method comprises (1) providing a starting plasmid that contains a gene expression cassette comprising a nucleic acid sequence encoding an AAV capsid, wherein a stop codon is placed at the target insertion site within the capsid gene, (2) providing a repertoire of nucleic acids encoding randomized peptides to produce a peptide library; (3) creating individual plasmids based on the starting plasmid a) each having a nucleic acid encoding a random peptide from the peptide library inserted at the target insertion site of the capsid gene thus replacing the stop codon, and b) each encoding a barcode for identification of the capsid gene having the insert placed before the 5'- or after the 3'-end of the capsid gene; (4) collecting the individual plasmids to form a population or collection of plasmids encoding the capsids with peptide inserts and transfecting cells with the collection of plasmids and with plasmids encoding a recombinant rAAV genome containing a transgene, including one that is detectable, and constructs having the necessary genes to produce, under appropriate conditions, a collection of rAAV vectors encapsidating the rAAV genome containing the transgene, wherein the rAAV vectors have capsids with the encoded capsid protein containing a library peptide insert. In embodiments, the parental AAV is AAV9, AAV9.AAA, AAVhu.32, AAVhu.32.AAA, or AAV5 or any other suitable AAV serotype. The insertion site may be in VR-IV, including immediately after one of amino acids 451-461 of AAV9 or corresponding to

one of those residues or in VR-VIII, including immediately after amino acid 588 of AAV9 or corresponding to that position in a different AAV capsid type (see FIG. 1 for alignment). The peptides may be 4, 5, 6, or 7 amino acids in length.

[0063] In embodiments, the rep gene is on a separate expression plasmid from the plasmid encoding the cap gene with the inserts.

[0064] The library of modified capsids is harvested from these cells. In embodiments, the rAAV library population produced has high levels of capsids having the peptide inserts, including 85%, 90%, 95% or 98%, 99% or even 100%.

5.2.2 Capsids containing Muscle-Homing and other Targeting Peptides

[0065] The present inventors also have surprisingly discovered peptides that inserted into rAAV vectors "re-target" or enhance targeting properties of such AAV vectors to specific tissues, organs, or cells; in particular, providing peptides that cause rAAV vectors to target muscle tissue and/or other target tissues of interest, such as retinal tissue, or to cross the blood-brain barrier and target neural tissue of the CNS. This can provide enhanced transport of rAAV particles encapsidating a transgene for optimizing distribution of the vector upon administration to the body. Such peptides, and modified vectors, are described below.

[0066] Another aspect of the present invention relates to capsid proteins selected from the random peptide insertion libraries comprising peptide insertions selected to confer or enhance muscle-homing properties, or "muscle tropism", including homing to muscle tissue, muscle cells or muscle cell matrix. Also included are capsids and rAAV vectors having capsids comprising these peptide-containing capsid proteins. In other aspects, the peptides may target other tissues, such as, retinal, CNS, including preferentially neurons within the CNS and may also detarget tissues such as liver, heart or astrocytes.

[0067] In certain embodiments, the peptide insertion consists of 4 to 7 contiguous amino acids (that is, 4, 5, 6, or 7 contiguous amino acids) of a peptide sequence of **Tables 4, 5, 14, 15 and 16** (SEQ ID Nos 1-138). The peptides disclosed herein were identified by screening libraries of peptides inserted in AAV capsids, which are screened for properties such as tropism for muscle tissue (skeletal and/or heart), retinal tissue, CNS neuronal tissue and other tissues, for example, through mouse and NHP biodistribution studies as described in the examples. In embodiments, the capsids having the peptide insertions have increased tropism for a target tissue, including muscle, retinal tissue, CNS, including neuronal tissue, relative to the parental capsid (that is having the capsid protein without the peptide insert) or a reference capsid, such

as AAV9, AAV9.AAA, AAVhu.32, or AAVhu.32.AAA. The capsids with the peptide inserts may also distribute to liver tissue at levels less than target tissues such as muscle, retina, CNS or other target tissue and/or less than a reference capsid, such as AAV9 or AAVhu.32.

[0068] In embodiments, the peptides that may be inserted into capsid proteins include those listed in tables 4, 5, 14, 15, and 16 and include peptides having amino acid sequences of 4, 5, 6, or 7 contiguous amino acids of one of the amino acid sequences of SEQ ID Nos: 1-134. In embodiments, the peptide is a 4, 5, 6, or 7 contiguous amino acid sequence of one of SGTVIRS (SEQ ID NO: 1), TRQYVPG (SEQ ID NO: 4), VQVGRTS (SEQ ID NO: 8), RGAVQKV (SEQ ID NO: 13), GQVHQAR (SEQ ID NO: 32), TSGGQIR (SEQ ID NO: 38), HMGHSGK (SEQ ID NO: 88), MRAVSQL (SEQ ID NO: 109), PRQYVPG (SEQ ID NO: 110), RSSSGR (SEQ ID NO: 111), VVKSTKS (SEQ ID NO: 112), RHVSASD (SEQ ID NO: 113), VRSDRDQ (SEQ ID NO: 114), or TVVTSIN (SEQ ID NO: 115). In embodiments, the peptide is inserted in VR-IV (including immediately after one of amino acids 451-461 or 454 of AAV9, AAV9.AAA, AAVhu.32, AAVhu.32.AAA).

[0069] In embodiments, the peptide is a 4, 5, 6, or 7 contiguous amino acid sequence of one of AQVGRAS (SEQ ID NO: 24), SVTSVRV (SEQ ID NO: 37), SIAKNSA (SEQ ID NO: 76), DGRRIGV (SEQ ID NO: 116), TSGERRG (SEQ ID NO: 117), PSSVQHR (SEQ ID NO: 118), SSSVQHR (SEQ ID NO: 119), SGMQERR (SEQ ID NO: 120), LERGNLE (SEQ ID NO: 121), YRDVRQT (SEQ ID NO: 122), PSAVQHR (SEQ ID NO: 123), YVGGRAV (SEQ ID NO: 124), IGSRGVA (SEQ ID NO: 125), SDVSRPR (SEQ ID NO: 126), GSVRQAA (SEQ ID NO: 127), QSPHTSQ (SEQ ID NO: 128), or ASQAYHG (SEQ ID NO: 128). In embodiments, the peptide is inserted in VR-IV (including immediately after one of amino acids 451-461 or 454 of AAV9, AAV9.AAA, AAVhu.32, AAVhu.32.AAA).

[0070] In embodiments, provided are capsids having an amino acid sequence of SEQ ID NO 159-266 or 268-375 (see Table 17).

[0071] In other embodiments, the peptide is a variant of one of the amino acid sequences of SEQ ID Nos 1 to 134 which has 1, 2 or 3 amino acid substitutions, including conservative amino acid substitutions, while the peptide, when inserted into a capsid protein, retains its biological activity.

[0072] The inventors have also identified certain consensus sequences of peptides that when inserted into a capsid protein (for example in VR-IV of AAV9, AAV9.AAA, AAVhu.32, or AAVhu.32.AAA) exhibit increased muscle tropism, including AAV uptake, transduction, and/or transgene expression, relative to the parental capsid or a reference capsid such as AAV9,

AAVhu.32, AAV9.AAA,or AAVhu.32.AAA. The peptides analyzed include the peptides of SEQ ID NOs: 5, 8, 24, 36, 44, 130, 131, 132, 133 or 134 (see Table 15, *supra*) all of which exhibited significant increase in muscle tropism compared to AAV9.AAA capsids. Accordingly, provided are capsids with peptide inserts, where the peptide is a 4, 5, 6, or 7 contiguous amino acid sequence of SEQ ID NO: 135, which is X_1-Q-V-X_2-X_3-X_4-X_5, wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is any amino acid and X_5 is S, G, V or A. In embodiments, provided are capsids with peptide inserts, where the peptide is a 4, 5, 6, or 7 contiguous amino acid sequence of SEQ ID NO: 136 is X_1-Q-V-X_2-X_3-X_4-X_5, wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is any amino acid and X_5 is S or A. In embodiments, provided are capsids with peptide inserts, where the peptide is a 4, 5, 6, or 7 contiguous amino acid sequence of SEQ ID NO: 137 is X_1-Q-V-X_2-X_3-X_4-X_5, wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is T, S, V, Y, A or P and X_5 is S, G, V or A. And, in embodiments, provided are capsids with peptide inserts, where the peptide is a 4, 5, 6, or 7 contiguous amino acid sequence of SEQ ID NO: 138 is X_1-Q-V-X_2-X_3-X_4-X_5, wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is T, S, V, Y, A or P and X_5 is S or A. In embodiments, the peptide is a 4, 5, 6, or 7 contiguous amino acid sequence of one of SEQ ID NOs: 5, 8, 24, 36, 44, 130, 131, 132, 133 or 134. In embodiments, the peptide is inserted in region VR-IV (immediately after one of positions 451-461, including immediately after 454 of or corresponding to AAV9) of one of capsids of AAV9, AAV9.AAA, AAVhu.32, or AAVhu.32.AAA. In embodiments, the capsid has an amino acid sequence of SEQ ID No. 263-266 (see Table 17).

[0073] As detailed herein, the peptides may be inserted into wild type or variant capsid protein amino acid sequences at positions such that the peptide is surface displayed when the capsid protein is incorporated into an AAV capsid, for example, at sites that allow surface exposure of the peptide, such as within variable surface-exposed loops, and, in more examples, sites described herein corresponding to VR-I, VR-IV, or VR-VIII, or may be inserted after the first amino acid of VP2, *e.g.* after amino acid 137 (AAV4, AAV4-4, and AAV5) or at amino acid 138 (AAV1, AAV2, AAV3, AAV3-3, AAV6, AAV7, AAV8, AAV9, AAV9e, rh.10, rh.20, rh.39, rh.74v1, rh.74v2, AAVhu.32 and hu.37) (FIG. 1). In embodiments, the capsid protein is an AAV9 capsid protein or an AAV9.AAA capsid protein (or a capsid protein with 90%, 95% or 99% amino acid sequence identity to AAV9 or AAV9.AAA) and the peptide insertion occurs immediately after at least one of (or corresponding to) the amino acid residues 451 to 461 of the AAV9 capsid. In embodiments, the capsid protein is an AAVhu.32 capsid protein or an AAVhu.32.AAA capsid protein (or a capsid protein with 90%, 95% or 99% amino

acid sequence identity to AAVhu.32 or AAVhu.32.AAA) and the peptide insertion occurs immediately after at least one of (or corresponding to) the amino acid residues 451 to 461 of the AAVhu.32 capsid. In other embodiments, the capsid protein is from at least one AAV type selected from AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAVrh8, AAV9, AAV9e, AAVrh10, AAVrh20, AAVhu.31, AAVhu.32, AAVhu.37, AAVrh39, and AAVrh74 (versions 1 and 2) (see, for example, **FIG. 1**) or a capsid protein that has 90%, 95% or 99% amino acid identity to the capsid protein of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAVrh8, AAV9, AAV9e, AAVrh10, AAVrh20, AAVhu.31, AAVhu.32, AAVhu.37, AAVrh39, and AAVrh74 (versions 1 and 2). In embodiments, the peptide insertion occurs immediately after an amino acid residue corresponding to at least one of the amino acid residues 451 to 461 of AAV9 (SEQ ID NO: 151) or, alternatively, 588 of AAV9. In embodiments, the peptide insertion occurs immediately after an amino acid residue corresponding to 578 of AAV5 (SEQ ID NO: 143). The alignments of different AAV serotypes, as shown in **FIG. 1**, indicates corresponding amino acid residues in the different amino acid sequences.

[0074] In embodiments, the capsid protein having the peptide insert is one of the capsid proteins in Table 17, with amino acid sequence SEQ ID Nos: 159 to 266 and 268-375. In embodiments, the capsid protein is 90%, 95% or 99% identical to SEQ ID Nos: 159 to 266 and 268-375, except that it is identical with respect to the peptide insert and retains its biological activity.

[0075] In certain embodiments, the peptide is inserted within VR-VIII of AAV5 (SEQ ID NO: 143), immediately after one of amino acids 574 – 584 (or to 582), including immediately after position 578 (see FIG. 1 for alignment). The peptides include any of peptides having an amino acid sequence of SEQ ID Nos: 1-134, and may include one of peptides having an amino acid sequence SEQ ID NO: 113, 114 or 115. In embodiments, the capsid has the amino acid sequence of SEQ ID NO: 376, 377 or 378.

[0076] In embodiments, the capsids with peptide inserts as described herein have increased tropism for target tissues, such as muscle, retina, CNS and other target tissue relative to the parental capsid, i.e., containing the capsid protein that is identical except that it does not have the peptide insert, or a reference capsid, which may include AAV9, AAV9.AAA, AAVhu.32, or AAVhu.32.AAA, or other capsid of interest that does not contain the peptide insert. In embodiments, the engineered capsid may have reduced tropism or is detargeted for tissues such as liver, including relative to target tissues, including muscle, retina, CNS or others, and/or

relative to the parental capsid or a reference capsid, which may include AAV9, AAV9.AAA, AAVhu.32, or AAVhu.32.AAA. In embodiments, the reference capsid does not contain the 496NNN/AAA498 amino acid substitution—for example if the parental capsid is AAV9.AAA, then the liver tropism/detargeting may be relative to AAV9 without the peptide insert.

[0077] For example, as described in the Examples herein, the tissue tropism may be assessed by introducing an rAAV vector having the engineered capsid and a genome with a detectable transgene into a test animal, such as a mouse or NHP, for example by systemic, intravenous, intramuscular, intrathecal, subcutaneous, ocular, or other administration, at an appropriate dosage (for example 1E12, 1E13 or 1E14 vg/kg) and then after an appropriate period of time harvesting the tissues of the animal and assessing the presence of the vector genome, mRNA transcribed from the genome, the ratio of the mRNA to the vector DNA, transgene protein product or activity, including relative to the parental or reference capsid.

[0078] Accordingly, provided are capsids as described herein which, when administered (for example, IV, IM, subcutaneous administration) to an animal, including a mouse or NHP, exhibit at least 2-fold, 5-fold, 10-fold, 15 fold, 20-fold, or 25 fold, or greater tropism for muscle, including skeletal or heart, or other tissue such as retina or CNS tissue relative to a parental capsid or reference, such as AAV9, AAV9.AAA, AAVhu.32, or AAVhu.32.AAV, as measured by vector genome DNA, transgene mRNA, the ratio of mRNA to vector genome DNA, transgene protein product, including protein product activity. In embodiments, the capsid preferentially transduces neurons over astrocytes or other CNS tissue in the CNS of the animal. In embodiments, provided also are capsids as described herein which when administered (for example, IV, IM, subcutaneous administration) to an animal, including a mouse or NHP, exhibit at least 2-fold, 5-fold, 10-fold, 15 fold, 20-fold, 25 fold, 40-fold or 50-fold, less tropism for liver, either relative to a target tissue such as muscle (skeletal and/or heart), retina or CNS (including the ratio of target tissue to liver) and/or relative to a parental capsid or reference, such as AAV9, AAV9.AAA, AAVhu.32, or AAVhu.32.AAV, as measured by amount of vector genome DNA, transgene mRNA, the ratio of mRNA to vector genome DNA, transgene protein product, including protein product activity.

5.2.3 Additional AAV Capsid Insertion Sites

[0079] The following summarizes insertion sites for the peptides described herein, including the peptides in **Tables 4, 5, 14, 15 and 16** set forth hereinbelow (see also, **FIG. 1**):

AAV1: 138; 262-272; 450-459; 595-593; and in an embodiment, between 453-454 (SEQ ID NO: 139).

AAV2: 138; 262-272; 449-458; 584-592; and in an embodiment, between 452-453 (SEQ ID NO: 140).

AAV3: 138; 262-272; 449-459; 585-593; and in an embodiment, between 452-453 (SEQ ID NO: 141).

AAV4: 137; 256-262; 443-453; 583-591; and in an embodiment, between 446-447 (SEQ ID NO: 142).

AAV5: 137; 252-262; 442-445; 574-582; and in an embodiment, between 445-446 (SEQ ID NO: 143).

AAV6: 138; 262-272; 450-459; 585-593; and in an embodiment, between 452-453 (SEQ ID NO: 144).

AAV7: 138; 263-273; 451-461; 586-594; and in an embodiment, between 453-454 (SEQ ID NO: 145).

AAV8: 138; 263-274; 451-461; 587-595; and in an embodiment, between 453-454 (SEQ ID NO: 146).

AAV9: 138; 262-273; 452-461; 585-593; and in an embodiment, between 454-455 (SEQ ID NO: 151).

AAV9.AAA: 138; 262-273; 452-461; 585-593; and in an embodiment, between 454-455 (SEQ ID NO: 158).

AAVrh10: 138; 263-274; 452-461; 587-595; and in an embodiment, between 454-455 (SEQ ID NO: 152).

AAVrh20: 138; 263-274; 452-461; 587-595; and in an embodiment, between 454-455 (SEQ ID NO: 155).

AAVrh74: 138; 263-274; 452-461; 587-595; and in an embodiment, between 454-455 (SEQ ID NO: 156 or SEQ ID NO: 157).

AAVhu.32: 138; 262-273; 452-461; 585-593; and in an embodiment, between 454-455 (SEQ ID NO: 148).

AAVhu.37: 138; 263-274; 452-461; 587-595; and in an embodiment, between 454-455 (SEQ ID NO: 153)

[0080] In embodiments, the peptide insertion occurs between amino acid residues 588-589 of the AAV9 capsid, or between corresponding residues of another AAV type capsid as determined by an amino acid sequence alignment (for example, as in **FIG. 1**). In embodiments, the peptide insertion occurs immediately after amino acid residue I451 to L461, S268 and Q588 of the AAV9 capsid sequence, or immediately after corresponding residues of another AAV capsid sequence (**FIG. 1**).

[0081] In some embodiments, the capsid is chosen and/or further modified to reduce recognition of the AAV particles by the subject's immune system, such as avoiding pre-existing antibodies in the subject. In some embodiments. In some embodiments, the capsid is chosen and/or further modified to enhance desired tropism/targeting.

5.2.4 Generation of Modified capsids

[0082] In some embodiments, AAV capsids were modified by introducing selected single to multiple amino acid substitutions which increase effective gene delivery to the CNS, detarget the liver, and/or reduce immune responses of neutralizing antibodies, prior to making the rAAV library with random peptide insertions.

[0083] Some modifications to the parental rAAV vector (capsid protein) prior to making the rAAV libraries may be effective for gene delivery to the CNS when intravenously administered rAAV vectors requires crossing the blood brain barrier. Key clusters of residues on the AAVrh.10 capsid that enabled transport across the brain vasculature and widespread neuronal transduction in mice have recently been reported. Specifically, AAVrh.10-derived amino acids N262, G263, T264, S265, G267, S268, T269, and T273 were identified as key residues that promote crossing the BBB (Albright et al, 2018, Mapping the Structural Determinants Required for AAVrh.10 Transport across the Blood-Brain Barrier). Amino acid substitutions in capsids, such as AAV8 and AAV9 capsids that promote rAAV crossing of the blood brain barrier, transduction, detargeting of the liver and/or reduction in immune responses have been identified.

[0084] In some embodiments, provided are capsids having one or more amino acid substitutions that further promote transduction and/or tissue tropism of the rAAV having the modified capsid. In embodiments, provided are capsids having a single mutation at amino acid 269 of the AAV8 capsid replacing alanine with serine (A269S) (see **FIG. 1**) and amino acid substitutions at corresponding positions in other AAV types. In some embodiments, provided are capsids having multiple substitutions at amino acids 263, 269, and 273 of the AAV9 capsid

resulting in the following substitutions: S263G, S269T, and A273T see **FIG. 1**) or substitutions corresponding to these positions in other AAV types.

[0085] Exposure to the AAV capsid can generate an immune response of neutralizing antibodies. One approach to overcome this response is to map the AAV-specific neutralizing epitopes and rationally design an AAV capsid able to evade neutralization. A monoclonal antibody, specific for intact AAV9 capsids, with high neutralizing titer has recently been described (Giles et al, 2018, Mapping an Adeno-associated Virus 9-Specific Neutralizing Epitope To Develop Next-Generation Gene Delivery Vectors). The epitope was mapped to the 3-fold axis of symmetry on the capsid, specifically to residues 496-NNN-498 and 588-QAQAQT-592 of, *e.g.,* AAV9, SEQ ID NO: 151. Capsid mutagenesis demonstrated that single amino acid substitution within this epitope markedly reduced binding and neutralization. In addition, in vivo studies showed that mutations in the epitope conferred a "liver-detargeting" phenotype to the mutant vectors, suggesting that the same residues are also responsible for AAV9 tropism. Liver detargeting has also been associated with substitution of amino acid 503 replacing tryptophan with arginine. Presence of the W503R mutation in the AAV9 capsid was associated with low glycan binding avidity (Shen *et al*, 2012, Glycan Binding Avidity Determines the Systemic Fate of Adeno-Associated Virus Type 9).

[0086] In some embodiments, provided are capsids which were further modified by substituting asparagines at amino acid positions 498, 499, and 500 (such as AAV8.AAA) or 496, 497, and 498 (herein referred to as AAV9.AAA, SEQ ID NO: 158) with alanines. In some embodiments, the AAVrh10 capsid can also be modified by substituting three asparagines at amino acid positions 498, 499, and 500 to alanines (AAVrh10.AAA).). In some embodiments, the AAVhu32 capsid can also be modified by substituting three asparagines at amino acid positions 496, 497, and 498 to alanines (herein referred to as AAVhu.32.AAA, SEQ ID NO: 148).

[0087] In some embodiments, provided are capsids having three asparagines at amino acid positions 496, 497, and 498 of the AAV9 capsid replaced with alanines and also tryptophan at amino acid 503 of the AAV9 capsid with arginine or capsids with substitutions corresponding to these positions in other AAV types. In some embodiments, provided are capsids having glutamine at amino acid position 474 of the AAV9 capsid substituted with alanine or capsids with substitutions corresponding to this position in other AAV types.

[0088] In some embodiments, the rAAVs described herein increase tissue-specific (such as, but not limited to, muscle) cell transduction in a subject (a human, non-human-primate, or

mouse subject) or in cell culture, compared to the rAAV not comprising the peptide insertion. In some embodiments, the increase in tissue specific cell transduction is at least 2, 10, 20, 30, 40, 50, 60, 70, 80, 90, or 100 fold more than that without the peptide insertion. For example, in some embodiments, there is a 50-80 fold increase in tissue specific cell transduction compared to transduction with the same AAV type without a peptide insert. The increase in transduction may be assessed using methods described in the Examples herein and known in the art.

5.3. Methods of Making rAAV Molecules

[0089] Another aspect of the present invention involves making molecules disclosed herein. In some embodiments, a molecule according to the invention is made by providing a nucleotide comprising the nucleic acid sequence encoding any of the capsid protein molecules herein; and using a packaging cell system to prepare corresponding rAAV particles with capsid coats made up of the capsid protein. In some embodiments, the nucleic acid sequence encodes a sequence having at least 60%, 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 99.9%, identity to the sequence of a capsid protein molecule described herein, and retains (or substantially retains) biological function of the capsid protein and the inserted peptide from a heterologous protein or domain thereof. In some embodiments, the nucleic acid encodes a sequence having at least 60%, 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 99.9%, identity to the sequence of the AAV9 capsid protein (SEQ ID NO: 151 and see **FIG. 1**), while retaining (or substantially retaining) biological function of the AAV9 capsid protein and the inserted peptide.

[0090] The capsid protein, coat, and rAAV particles may be produced by techniques known in the art. In some embodiments, the viral genome comprises at least one inverted terminal repeat to allow packaging into a vector. In some embodiments, the viral genome further comprises a cap gene and/or a rep gene for expression and splicing of the cap gene. In other embodiments, the cap and rep genes are provided by a packaging cell and not present in the viral genome.

[0091] In some embodiments, the nucleic acid encoding the engineered capsid protein is cloned into an AAV Rep-Cap helper plasmid in place of the existing capsid gene. When introduced together into host cells, this plasmid helps package an rAAV genome into the engineered capsid protein as the capsid coat. Packaging cells can be any cell type possessing

the genes necessary to promote AAV genome replication, capsid assembly, and packaging. Nonlimiting examples include 293 cells or derivatives thereof, HELA cells, or insect cells.

[0092] Standard techniques can be used for recombinant DNA, oligonucleotide synthesis, and tissue culture and transformation (*e.g.*, electroporation, lipofection). Enzymatic reactions and purification techniques can be performed according to manufacturer's specifications or as commonly accomplished in the art or as described herein. The foregoing techniques and procedures can be generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the present specification. See, e.g., Sambrook et al., Molecular Cloning: A Laboratory Manual (2d ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989)), which is incorporated herein by reference for any purpose. Unless specific definitions are provided, the nomenclatures utilized in connection with, and the laboratory procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well-known and commonly used in the art. Standard techniques can be used for chemical syntheses, chemical analyses, pharmaceutical preparation, formulation, and delivery, and treatment of patients. Nucleic acid sequences of AAV-based viral vectors, and methods of making recombinant AAV and AAV capsids, are taught, *e.g.*, in US 7,282,199; US 7,790,449; US 8,318,480; US 8,962,332; and PCT/EP2014/076466, each of which is incorporated herein by reference in its entirety.

[0093] In some embodiments, the rAAVs provide transgene delivery vectors that can be used in therapeutic and prophylactic applications, as discussed in more detail below. In some embodiments, the rAAV vector also includes regulatory control elements known to one skilled in the art to influence the expression of the RNA and/or protein products encoded by nucleic acids (transgenes) within target cells of the subject. Regulatory control elements and may be tissue-specific, that is, active (or substantially more active or significantly more active) only in the target cell/tissue. In specific embodiments, the AAV vector comprises a regulatory sequence, such as a promoter, operably linked to the transgene that allows for expression in target tissues. The promoter may be a constitutive promoter, for example, the CB7 promoter. Additional promoters include: cytomegalovirus (CMV) promoter, Rous sarcoma virus (RSV) promoter, MMT promoter, EF-1 alpha promoter, UB6 promoter, chicken beta-actin promoter, CAG promoter, RPE65 promoter, opsin promoter, the TBG (Thyroxine-binding Globulin) promoter, the APOA2 promoter, SERPINA1 (hAAT) promoter, or MIR122 promoter. In some

embodiments, particularly where it may be desirable to turn off transgene expression, an inducible promoter is used, *e.g.*, hypoxia-inducible or rapamycin-inducible promoter.

[0094] Provided in embodiments are AAV9 vectors comprising a viral genome comprising an expression cassette for expression of the transgene, under the control of regulatory elements, and flanked by ITRs and an engineered viral capsid as described herein or is at least 95%, 96%, 97%, 98%, 99% or 99.9% identical to the amino acid sequence of the AAV9 capsid protein (see **FIG. 1**), while retaining the biological function of the engineered AAV9 capsid. In certain embodiments, the encoded AAV9 capsid has the sequence of wild type AAV9, with the peptide insertion as described herein, with, in addition, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 amino acid substitutions with respect to the wild type AAV sequence and retains biological function of the AAV9 capsid. Also provided are engineered AAV vectors other than AAV9 vectors, such as engineered AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV9e, AAVrh10, AAVrh20, AAVhu.37, AAVrh39, or AAVrh74 vectors, with the peptide insert as described herein and 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 amino acid substitutions relative to the wild type or unengineered sequence for that AAV type and that retains its biological function.

[0095] The recombinant adenovirus can be a first-generation vector, with an E1 deletion, with or without an E3 deletion, and with the expression cassette inserted into either deleted region. The recombinant adenovirus can be a second-generation vector, which contains full or partial deletions of the E2 and E4 regions. A helper-dependent adenovirus retains only the adenovirus inverted terminal repeats and the packaging signal (phi). The transgene generally is inserted between the packaging signal and the 3'ITR, with or without stuffer sequences to keep the genome close to wild-type size of approximately 36 kb. An exemplary protocol for production of adenoviral vectors may be found in Alba *et al.*, 2005, "Gutless adenovirus: last generation adenovirus for gene therapy," *Gene Therapy* 12:S18-S27, which is incorporated by reference herein in its entirety

[0096] The rAAV vector for delivering the transgene to target tissues, cells, or organs, has a tropism for that particular target tissue, cell, or organ. Tissue-specific promoters may also be used. The construct further can include expression control elements that enhance expression of the transgene driven by the vector (*e.g.*, introns such as the chicken β-actin intron, minute virus of mice (MVM) intron, human factor IX intron (*e.g.*, FIX truncated intron 1), β-globin splice donor/immunoglobulin heavy chain spice acceptor intron, adenovirus splice donor

/immunoglobulin splice acceptor intron, SV40 late splice donor /splice acceptor (19S/16S) intron, and hybrid adenovirus splice donor/IgG splice acceptor intron and polyA signals such as the rabbit β-globin polyA signal, human growth hormone (hGH) polyA signal, SV40 late polyA signal, synthetic polyA (SPA) signal, and bovine growth hormone (bGH) polyA signal. *See, e.g.*, Powell and Rivera-Soto, 2015, *Discov. Med.*, 19(102):49-57.

[0097] In certain embodiments, nucleic acids sequences disclosed herein may be codon-optimized, for example, via any codon-optimization technique known to one of skill in the art (*see, e.g.*, review by Quax et al., 2015, Mol Cell 59:149-161).

[0098] In a specific embodiment, the constructs described herein comprise the following components: (1) AAV9 inverted terminal repeats that flank the expression cassette; (2) control elements, which include a) the CB7 promoter, comprising the CMV enhancer/chicken β-actin promoter, b) a chicken β-actin intron and c) a rabbit β-globin poly A signal; and (3) transgene providing (*e.g.*, coding for) a nucleic acid or protein product of interest. In a specific embodiment, the constructs described herein comprise the following components: (1) AAV9 inverted terminal repeats that flank the expression cassette; (2) control elements, which include a) a hypoxia-inducible promoter, b) a chicken β-actin intron and c) a rabbit β-globin poly A signal; and (3) transgene providing (*e.g.*, coding for) a nucleic acid or protein product of interest.

[0099] The viral vectors provided herein may be manufactured using host cells, *e.g.*, mammalian host cells, including host cells from humans, monkeys, mice, rats, rabbits, or hamsters. Nonlimiting examples include: A549, WEHI, 10T1/2, BHK, MDCK, COS1, COS7, BSC 1, BSC 40, BMT 10, VERO, W138, HeLa, 293, Saos, C2C12, L, HT1080, HepG2, primary fibroblast, hepatocyte, and myoblast cells. Typically, the host cells are stably transformed with the sequences encoding the transgene and associated elements (*i.e.*, the vector genome), and genetic components for producing viruses in the host cells, such as the replication and capsid genes (*e.g.*, the rep and cap genes of AAV). For a method of producing recombinant AAV vectors with AAV8 capsids, see Section IV of the Detailed Description of U.S. Patent No. 7,282,199 B2, which is incorporated herein by reference in its entirety. Genome copy titers of said vectors may be determined, for example, by TAQMAN® analysis. Virions may be recovered, for example, by $CsCl_2$ sedimentation. Alternatively, baculovirus expression systems in insect cells may be used to produce AAV vectors. For a review, see Aponte-Ubillus *et al.*, 2018, *Appl. Microbiol. Biotechnol.* 102:1045-1054, which is incorporated by reference herein in its entirety for manufacturing techniques.

[00100] In vitro assays, *e.g.*, cell culture assays, can be used to measure transgene expression from a vector described herein, thus indicating, *e.g.*, potency of the vector. For example, the PER.C6® Cell Line (Lonza), a cell line derived from human embryonic retinal cells, or retinal pigment epithelial cells, *e.g.*, the retinal pigment epithelial cell line hTERT RPE-1 (available from ATCC®), can be used to assess transgene expression. Alternatively, cell lines derived from liver or other cell types may be used, for example, but not limited, to HuH-7, HEK293, fibrosarcoma HT-1080, HKB-11, and CAP cells. Once expressed, characteristics of the expressed product (*i.e.*, transgene product) can be determined, including determination of the glycosylation and tyrosine sulfation patterns, using assays known in the art.

5.4. Therapeutic and Prophylactic Uses

[00101] Another aspect relates to therapies which involve administering a transgene via a rAAV vector according to the invention to a subject in need thereof, for delaying, preventing, treating, and/or managing a disease or disorder, and/or ameliorating one or more symptoms associated therewith. A subject in need thereof includes a subject suffering from the disease or disorder, or a subject pre-disposed thereto, *e.g.*, a subject at risk of developing or having a recurrence of the disease or disorder. Generally, a rAAV carrying a particular transgene will find use with respect to a given disease or disorder in a subject where the subject's native gene, corresponding to the transgene, is defective in providing the correct gene product, or correct amounts of the gene product. The transgene then can provide a copy of a gene that is defective in the subject.

[00102] Generally, the transgene comprises cDNA that restores protein function to a subject having a genetic mutation(s) in the corresponding native gene. In some embodiments, the cDNA comprises associated RNA for performing genomic engineering, such as genome editing via homologous recombination. In some embodiments, the transgene encodes a therapeutic RNA, such as a shRNA, artificial miRNA, or element that influences splicing.

[00103] **Tables 1A-1B** below provides an exemplary list of transgenes that may be used in any of the rAAV vectors described herein, in particular, to treat or prevent muscle-related disease.

Table 1A

Disease	Transgene
Spinal Muscular Atrophy (SMA)	SMN

Disease	Transgene
Duchenne Muscular Dystrophy	Mini- / Microdystrophin Gene
Limb Girdle Muscular Dystrophy Type 2C|Gamma-sarcoglycanopathy	human-alpha-sarcoglycan
Limb Girdle Muscular Dystrophy Type 2C|Gamma-sarcoglycanopathy	gamma-sarcoglycan
Becker Muscular Dystrophy and Sporadic Inclusion Body Myositis	huFollistatin344
Duchenne Muscular Dystrophy	GALGT2
Limb-Girdle Muscular Dystrophy, Type 2E	hSGCB

Table 1B

ANTIGENS	TRANSGENE/ANTIBODIES	INDICATIONS
Repulsive guidance molecule-A	elezanumab	multiple sclerosis
Complement Component 5	ravulizumab	Myasthenia Gravis
Connective tissue growth factor (CTGF)	pamrevlumab	fibrotic diseases, e.g. diabetic nephropathy, liver fibrosis, idiopathic pulmonary fibrosis
Integrin beta 7	etrolizumab	ulcerative colitis, Crohn's disease
Sclerostin	romosozumab (EVENITY®)	Osteoporosis, abnormal bone loss or weakness
Interleukin receptor 6 (IL6R) or Interleukin 6 (IL6)	Satralizumab Sarilumab Tocilizumab siltuximab, clazakizumab sirukumab olokizumab gerilimzumab	Adverse immune responses (e.g. cytokine storm, CAR-T therapy)
Immunoglobin E (IgE)	omolizumab	Asthma, COPD, eosinophilic asthma, chronic idiopathic urticaria
Thymic stromal lymphopoietin (TSLP)	tezelipumab	Asthma, COPD
Interleukin 5 (IL5)	benralizumab	Asthma, COPD

ANTIGENS		TRANSGENE/ANTIBODIES	INDICATIONS
Interleukin 5 receptor (IL5R)		reslizumab	Asthma, COPD, eosinophilic asthma
Interleukin 13 (IL13)		tralokinumab	Atopic dermatitis
Interleukin 31 recptor alpha (IL31RA)		nemolizumab	Atopic dermatitis
IL17A		Ixekizumab secukinumab	Plaque psoriasis, psoriatic arthritis, ankylosing sponylitis
Interleukins or interleukin receptors	*IL-17A*	ixekizumab (TALTZ®) secukinumab (COSENTYX®)	Plaque psoriasis, psoriatic arthritis, ankylosing sponylitis
	IL-5	mepolizumab (NUCALA®)	Asthma
	IL-12/IL-23	ustekinumab (STELARA®)	Psoriasis & Crohn's disease
	IL-4R	dupilumab	Atopic dermatitis
Integrin		vedolizumab (ENTYVIO®)	Ulcerative colitis & Crohn's disease
		Natalizumab (anti-integrin alpha 4)	Multiple sclerosis & Crohn's disease
Cardiovascular Targets	*PCSK9*	alirocumab (PRALUENT®) evolucomab (REPATHA®)	HeFH & HoFH
	ANGPTL3	evinacumab	HoFH & severe forms of dyslipidema
	Proinflammatory/ proatherogenic phospholipids	E06-scFv	Cardiovascular diseases such as atherosclerosis
RANKL		denosumab (XGEVA® and PROLIA®)	Osteoporosis, increasing bone mass in breast and prostate cancer patients, &

ANTIGENS		TRANSGENE/ANTIBODIES	INDICATIONS
			preventing skeletal-related events due to bone metastasis
PD-1, or PD-L1 or PD-L2		nivolumab (OPDIVO®) pembrolizumab (KEYTRUDA®)	Metastatic melanoma, lymphoma, non-small cell lung carcinoma
BLyS (B-lymphocyte stimulator, also known as B-cell activating factor (BAFF))		belimumab (BENLYSTA®)	Systemic lupus erythromatosis
TNF-alpha		adalimumab (HUMIRA®) and infliximab (REMICADE®)	Rheumatoid arthritis, psoriatic arthritis, askylosing spondylitis, Crohn's disease, plaque psoriasis, ulcerative colitis
Plasma Protein targets	*C5, C5a*	eculizumab (SOLIRIS®)	Paroxysmal nocturnal hemoglobinuria, atypical hemolytic uremic syndrome, complement-mediated thrombotic microangiopathy
	Plasma kallikrein	lanadelumab	Hereditary angioedema (HAE)

[00104] For example, a rAAV vector comprising a transgene encoding a microdystrophin finds use treating/preventing/managing Duchenne Muscular Dystrophy. The microdystrophin may be, for example, a microdystrophin found in WO 2021/108755. In other embodiments, the microdystrophin has an amino acid sequence of SEQ ID NO: 133 (human MD1 (R4-R23/ΔCT), SEQ ID NO: 134 (microdystrophin), SEQ ID NO: 135 (Dys3978), SEQ ID NO: 136 (MD3) or SEQ ID NO: 137 (MD4) as described in WO 2023/004331. In other embodiments, the microdystrophin is SEQ ID NO: 7 of WO 2017/181015 A1. Generally, the rAAV vector is administered systemically. For example, the rAAV vector may be provided by intravenous, intramuscular, intra-nasal, and/or intra-peritoneal administration.

[00105] In aspects, the rAAVs of the present invention find use in delivery to target tissues, or target cell types, including cell matrix associated with the target cell types, associated with the disorder or disease to be treated/prevented. A disease or disorder associated with a particular tissue or cell type is one that largely affects the particular tissue or cell type, in comparison to other tissue of cell types of the body, or one where the effects or symptoms of the disorder appear in the particular tissue or cell type. Methods of delivering a transgene to a target tissue of a subject in need thereof involve administering to the subject tan rAAV where the peptide insertion is a homing peptide. In the case of dystrophinopathies, for example, a rAAV vector comprising a peptide insertion that directs the rAAV to muscle tissue can be used, in particular, where the peptide insertion facilitates the rAAV in transducing muscle cells with high efficiency, including satellite cells, yet results in lower transduction of liver cells.

[00106] For a disease or disorder associated with muscle, rAAV vectors can be selected from the libraries herein that comprise a peptide insertion that directs muscle transduction, relative to the parental rAAV vector without a peptide insertion.

[00107] The rAAV vectors of the invention also can facilitate delivery, in particular, targeted delivery, of oligonucleotides, drugs, imaging agents, inorganic nanoparticles, liposomes, antibodies to target cells or tissues. The rAAV vectors also can facilitate delivery, in particular, targeted delivery, of non-coding DNA, RNA, or oligonucleotides to target tissues.

[00108] The agents may be provided as pharmaceutically acceptable compositions as known in the art and/or as described herein. Also, the rAAV molecule of the invention may be administered alone or in combination with other prophylactic and/or therapeutic agents.

[00109] The dosage amounts and frequencies of administration provided herein are encompassed by the terms therapeutically effective and prophylactically effective. The dosage and frequency will typically vary according to factors specific for each patient depending on the specific therapeutic or prophylactic agents administered, the severity and type of disease, the route of administration, as well as age, body weight, response, and the past medical history of the patient, and should be decided according to the judgment of the practitioner and each patient's circumstances. Suitable regimens can be selected by one skilled in the art by considering such factors and by following, for example, dosages reported in the literature and recommended in the Physician 's Desk Reference (56th ed., 2002). Prophylactic and/or therapeutic agents can be administered repeatedly. Several aspects of the procedure may vary such as the temporal regimen of administering the prophylactic or therapeutic agents, and whether such agents are administered separately or as an admixture.

[00110] The amount of an agent of the invention that will be effective can be determined by standard clinical techniques. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems. For any agent used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC_{50} (*i.e.*, the concentration of the test compound that achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

[00111] Prophylactic and/or therapeutic agents, as well as combinations thereof, can be tested in suitable animal model systems prior to use in humans. Such animal model systems include, but are not limited to, rats, mice, chicken, cows, monkeys, pigs, dogs, rabbits, *etc.* Any animal system well-known in the art may be used. Such model systems are widely used and well known to the skilled artisan. In some embodiments, animal model systems for a CNS condition are used that are based on rats, mice, or other small mammal other than a primate.

[00112] Once the prophylactic and/or therapeutic agents of the invention have been tested in an animal model, they can be tested in clinical trials to establish their efficacy. Establishing clinical trials will be done in accordance with common methodologies known to one skilled in the art, and the optimal dosages and routes of administration as well as toxicity profiles of agents of the invention can be established. For example, a clinical trial can be designed to test a rAAV molecule of the invention for efficacy and toxicity in human patients.

[00113] Toxicity and efficacy of the prophylactic and/or therapeutic agents of the instant invention can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD_{50}/ED_{50}. Prophylactic and/or therapeutic agents that exhibit large therapeutic indices are preferred. While prophylactic and/or therapeutic agents that exhibit toxic side effects may be used, care should be taken to design a delivery system that targets such agents to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

[00114] A rAAV molecule of the invention generally will be administered for a time and in an amount effective for obtain a desired therapeutic and/or prophylactic benefit. The data

obtained from the cell culture assays and animal studies can be used in formulating a range and/or schedule for dosage of the prophylactic and/or therapeutic agents for use in humans. The dosage of such agents lies within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized.

[00115] A therapeutically effective dosage of an rAAV vector for patients is generally from about 0.1 ml to about 100 ml of solution containing concentrations of from about $1x10^9$ to about $1x10^{16}$ genomes rAAV vector, or about $1x10^{10}$ to about $1x10^{15}$, about $1x10^{12}$ to about $1x10^{16}$, or about $1x10^{14}$ to about $1x10^{16}$ AAV genomes. Levels of expression of the transgene can be monitored to determine/adjust dosage amounts, frequency, scheduling, and the like.

[00116] Treatment of a subject with a therapeutically or prophylactically effective amount of the agents of the invention can include a single treatment or can include a series of treatments. For example, pharmaceutical compositions comprising an agent of the invention may be administered once a day, twice a day, or three times a day. In some embodiments, the agent may be administered once a day, every other day, once a week, twice a week, once every two weeks, once a month, once every six weeks, once every two months, twice a year, or once per year. It will also be appreciated that the effective dosage of certain agents, *e.g.*, the effective dosage of agents comprising a dual antigen-binding molecule of the invention, may increase or decrease over the course of treatment.

[00117] In some embodiments, ongoing treatment is indicated, *e.g.*, on a long-term basis, such as in the ongoing treatment and/or management of chronic diseases or disorders. For example, in embodiments, an agent of the invention is administered over a period of time, *e.g.*, for at least 6 months, at least one year, at least two years, at least five years, at least ten years, at least fifteen years, at least twenty years, or for the rest of the lifetime of a subject in need thereof.

[00118] The rAAV molecules of the invention may be administered alone or in combination with other prophylactic and/or therapeutic agents. Each prophylactic or therapeutic agent may be administered at the same time or sequentially in any order at different points in time; however, if not administered at the same time, they should be administered sufficiently close in time so as to provide the desired therapeutic or prophylactic effect. Each therapeutic agent can be administered separately, in any appropriate form and by any suitable route.

[00119] In various embodiments, the different prophylactic and/or therapeutic agents are administered less than 1 hour apart, at about 1 hour apart, at about 1 hour to about 2 hours apart, at about 2 hours to about 3 hours apart, at about 3 hours to about 4 hours apart, at about

4 hours to about 5 hours apart, at about 5 hours to about 6 hours apart, at about 6 hours to about 7 hours apart, at about 7 hours to about 8 hours apart, at about 8 hours to about 9 hours apart, at about 9 hours to about 10 hours apart, at about 10 hours to about 11 hours apart, at about 11 hours to about 12 hours apart, no more than 24 hours apart, or no more than 48 hours apart. In certain embodiments, two or more agents are administered within the same patient visit.

[00120] Methods of administering agents of the invention include, but are not limited to, parenteral administration (*e.g.*, intradermal, intramuscular, intraperitoneal, intravenous, and subcutaneous, including infusion or bolus injection), epidural, and by absorption through epithelial or mucocutaneous or mucosal linings (*e.g.*, intranasal, oral mucosa, rectal, and intestinal mucosa, *etc.*). In embodiments, such as where the transgene is intended to be expressed in the CNS, the vector is administered via lumbar puncture or via cisterna magna.

[00121] In certain embodiments, the agents of the invention are administered intravenously and may be administered together with other biologically active agents.

[00122] In another specific embodiment, agents of the invention may be delivered in a sustained release formulation, *e.g.*, where the formulations provide extended release and thus extended half-life of the administered agent. Controlled release systems suitable for use include, without limitation, diffusion-controlled, solvent-controlled, and chemically-controlled systems. Diffusion controlled systems include, for example reservoir devices, in which the molecules of the invention are enclosed within a device such that release of the molecules is controlled by permeation through a diffusion barrier. Common reservoir devices include, for example, membranes, capsules, microcapsules, liposomes, and hollow fibers. Monolithic (matrix) device are a second type of diffusion controlled system, wherein the dual antigen-binding molecules are dispersed or dissolved in an rate-controlling matrix (*e.g.*, a polymer matrix). Agents of the invention can be homogeneously dispersed throughout a rate-controlling matrix and the rate of release is controlled by diffusion through the matrix. Polymers suitable for use in the monolithic matrix device include naturally occurring polymers, synthetic polymers and synthetically modified natural polymers, as well as polymer derivatives.

[00123] Any technique known to one of skill in the art can be used to produce sustained release formulations comprising one or more agents described herein. See, *e.g.* U.S. Pat. No. 4,526,938; PCT publication WO 91/05548; PCT publication WO 96/20698; Ning et al., "Intratumoral Radioimmunotheraphy of a Human Colon Cancer Xenograft Using a Sustained-Release Gel," *Radiotherapy & Oncology*, 39:179 189, 1996; Song et al., "Antibody Mediated Lung Targeting of Long-Circulating Emulsions," PDA *Journal of Pharmaceutical Science &*

Technology, 50:372 397, 1995; Cleek et al., "Biodegradable Polymeric Carriers for a bFGF Antibody for Cardiovascular Application," *Pro. Intl. Symp. Control. Rel. Bioact. Mater.*, 24:853 854, 1997; and Lam et al., "Microencapsulation of Recombinant Humanized Monoclonal Antibody for Local Delivery," *Proc. Int'l. Symp. Control Rel. Bioact. Mater.*, 24:759 760, 1997, each of which is incorporated herein by reference in its entirety. In one embodiment, a pump may be used in a controlled release system (see Langer, *supra*; Sefton, *CRC Crit. Ref. Biomed. Eng.*, 14:20, 1987; Buchwald et al., *Surgery*, 88:507, 1980; and Saudek et al., *N. Engl. J. Med.*, 321:574, 1989). In another embodiment, polymeric materials can be used to achieve controlled release of agents comprising dual antigen-binding molecule, or antigen-binding fragments thereof (see *e.g.*, Medical Applications of Controlled Release, Langer and Wise (eds.), CRC Pres., Boca Raton, Fla. (1974); Controlled Drug Bioavailability, Drug Product Design and Performance, Smolen and Ball (eds.), Wiley, N.Y. (1984); Ranger and Peppas, J., *Macromol. Sci. Rev. Macromol. Chem.*, 23:61, 1983; see also Levy et al., *Science*, 228:190, 1985; During et al., *Ann. Neurol.*, 25:351, 1989; Howard et al., J. *Neurosurg.*, 7 1:105, 1989); U.S. Pat. No. 5,679,377; U.S. Pat. No. 5,916,597; U.S. Pat. No. 5,912,015; U.S. Pat. No. 5,989,463; U.S. Pat. No. 5,128,326; PCT Publication No. WO 99/15154; and PCT Publication No. WO 99/20253). In yet another embodiment, a controlled release system can be placed in proximity of the therapeutic target (*e.g.*, an affected joint), thus requiring only a fraction of the systemic dose (see, *e.g.*, Goodson, in Medical Applications of Controlled Release, supra, vol. 2, pp. 115 138 (1984)). Other controlled release systems are discussed in the review by Langer, *Science*, 249:1527 1533, 1990.

[00124] In addition, rAAVs can be used for *in vivo* delivery of transgenes for scientific studies such as optogenetics, gene knock-down with miRNAs, recombinase delivery for conditional gene deletion, gene editing with CRISPRs, and the like.

5.5. Pharmaceutical Compositions and Kits

[00125] The invention further provides a pharmaceutical composition comprising a pharmaceutically acceptable carrier and an agent of the invention, said agent comprising a rAAV molecule of the invention. In some embodiments, the pharmaceutical composition comprises rAAV combined with a pharmaceutically acceptable carrier for administration to a subject. In one embodiment, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly in humans.

The term "carrier" refers to a diluent, adjuvant (*e.g.*, Freund's complete and incomplete adjuvant), excipient, or vehicle with which the agent is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable, or synthetic origin, including, *e.g.*, peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a common carrier when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. Additional examples of pharmaceutically acceptable carriers, excipients, and stabilizers include, but are not limited to, buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight polypeptides; proteins, such as serum albumin and gelatin; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™ as known in the art. The pharmaceutical composition of the present invention can also include a lubricant, a wetting agent, a sweetener, a flavoring agent, an emulsifier, a suspending agent, and a preservative, in addition to the above ingredients. These compositions can take the form of solutions, suspensions, emulsion, tablets, pills, capsules, powders, sustained-release formulations and the like.

[00126] In certain embodiments of the invention, pharmaceutical compositions are provided for use in accordance with the methods of the invention, said pharmaceutical compositions comprising a therapeutically and/or prophylactically effective amount of an agent of the invention along with a pharmaceutically acceptable carrier.

[00127] In certain embodiments, the agent of the invention is substantially purified (*i.e.*, substantially free from substances that limit its effect or produce undesired side-effects). In a specific embodiment, the host or subject is an animal, *e.g.*, a mammal such as non-primate (*e.g.*, cows, pigs, horses, cats, dogs, rats etc.) and a primate (*e.g.*, monkey such as, a cynomolgus monkey and a human). In a certain embodiment, the host is a human.

[00128] The invention provides further kits that can be used in the above methods. In one embodiment, a kit comprises one or more agents of the invention, *e.g.*, in one or more

containers. In another embodiment, a kit further comprises one or more other prophylactic or therapeutic agents useful for the treatment of a condition, in one or more containers.

[00129] The invention also provides agents of the invention packaged in a hermetically sealed container such as an ampoule or sachette indicating the quantity of the agent or active agent. In one embodiment, the agent is supplied as a dry sterilized lyophilized powder or water free concentrate in a hermetically sealed container and can be reconstituted, *e.g.*, with water or saline, to the appropriate concentration for administration to a subject. Typically, the agent is supplied as a dry sterile lyophilized powder in a hermetically sealed container at a unit dosage of at least 5 mg, more often at least 10 mg, at least 15 mg, at least 25 mg, at least 35 mg, at least 45 mg, at least 50 mg, or at least 75 mg. The lyophilized agent should be stored at between 2 and 8°C in its original container and the agent should be administered within 12 hours, usually within 6 hours, within 5 hours, within 3 hours, or within 1 hour after being reconstituted. In an alternative embodiment, an agent of the invention is supplied in liquid form in a hermetically sealed container indicating the quantity and concentration of agent or active agent. Typically, the liquid form of the agent is supplied in a hermetically sealed container at least 1 mg/ml, at least 2.5 mg/ml, at least 5 mg/ml, at least 8 mg/ml, at least 10 mg/ml, at least 15 mg/kg, or at least 25 mg/ml.

[00130] The compositions of the invention include bulk drug compositions useful in the manufacture of pharmaceutical compositions (*e.g.*, impure or non-sterile compositions) as well as pharmaceutical compositions (i.e., compositions that are suitable for administration to a subject or patient). Bulk drug compositions can be used in the preparation of unit dosage forms, *e.g.*, comprising a prophylactically or therapeutically effective amount of an agent disclosed herein or a combination of those agents and a pharmaceutically acceptable carrier.

[00131] The invention further provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the agents of the invention. Additionally, one or more other prophylactic or therapeutic agents useful for the treatment of the target disease or disorder can also be included in the pharmaceutical pack or kit. The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use, or sale for human administration.

[00132] Generally, the ingredients of compositions of the invention are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water-free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of agent or active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

6. EXAMPLES

[00133] The following examples report an method of making rAAV libraries containing numerous rAAV capsids having surface-exposed peptides inserted at designated insertion sites of the capsid. The recombinantly engineered capsids are screened to identify candidates for particularly properties, such as tissue tropism. The invention is illustrated by way of examples, describing the construction of rAAV capsids engineered to contain 7-mer peptides (or 4-, 5-, 6-mer peptides), wherein the method is designed to remove bias of the parental capsid formation during manufacture, thereby artificially increasing its abundance and therefore representation in the library. Several libraries of peptide insertion mutants were constructed and the pooled mutants were screened for viable capsid assembly, titer, and biodistribution. The top candidates were then further evaluated for use to re-target rAAV vectors to tissues of interest. Further examples, demonstrate the increased transduction and tissue tropism for certain of the modified AAV capsids described herein.

6.1. Example 1 – Insertion sites of AAV9 capsid or capsids having corresponding sites for insertion

[00134] **FIGs. 1 and 2** depict analysis of variable region four of the adeno-associated virus type 9 (AAV9 VR-IV) by amino acid sequence comparison to other AAVs VR-IV (**FIG. 1**) and protein model (**FIG. 2**). As seen, AAV9 VR-IV is exposed on the surface at the tip or outer surface of the 3-fold spike. AAV9 VR-VIII is also exposed on the surface. Further analysis has indicated that there are polar interactions between VR-IV and VR-V and that the sequence and structure of VR-IV is variable amongst AAV serotypes, and further that there is potential for interrupting a commonly-targeted neutralizing antibody epitope and thus, reducing

immunogenicity of the modified capsid. (See PCT International Publication No. WO2020206189A1, which is hereby incorporated by reference in its entirety.)

6.2. Example 2 – Construction of rAAV libraries

[00135] For generation of rAAV libraries, a custom Rep-only trans-plasmid was created in which the Cap sequence was removed. A custom cis-plasmid was created in which the CMV enhancer-promoter and Rep intron precedes the AAV Cap gene of interest, followed by the RBG polyA. A stop codon was inserted into the Cap gene variable region where the peptide library would be later inserted to reduce expression of wildtype (or parental) sequence in the library and provide capsids capable of "intelligent, guided adaptation" (Novel AAV Vector Intelligent Guided Adaptation Through Evolution = NAVIGATE.)

[00136] AAV peptide insertion libraries were created by synthesis of a DNA fragment incorporating a randomized 21 nucleotide sequence synthesized using column-based Trimer-19 oligos (Genscript). The library fragment was cloned into the desired AAV variable region in the library cis-plasmid, such that the stop codon inserted in the parental capsid of interest would be removed. Following transformation of E. coli, library size was quantified by dilution plate colony counts. Library size generally exceeded 10^7 variants. Next-generation sequencing of the libraries was used to characterize library diversity and the wildtype fraction. A plasmid maxiprep was used to generate 0.5-1 mg of library *cis*-plasmid.

[00137] To produce the library vector, a custom triple transfection of suspension-adapted HEK293 cells (NAVXCell™, REGENXBIO Inc.) was used in which the library cis-plasmid was limited to 100-copies per viable cell (typically ~3,000) to reduce the likelihood of variant cross-packaging and capsid mosaicism. A 20L- or 8L- scale transfection was used to generate libraries. Three days post-transfection, cells were harvested, lysed, clarified, PEG-precipitated, and purified using Iodixanol-gradient ultracentrifugation.

[00138] Vector titer was quantified using digital PCR with polyA primers/probe. Library variant diversity and parental/wildtype fraction following AAV packaging was characterized by next-generation sequencing (NGS) and LC-MS of the VP3 protein. Several libraries were made starting from different parental capsids, and evaluation indicated a high level of diversity in each capsid library. See, *e.g.* **Table 2**.

[00139] Each library was produced at 20L scale, as described above, by the vector core group at REGENXBIO Inc. Library diversity and titer measurements determined that diversity ranged from 1E7-1E8 in such production lots having final BDS titer ranging from 1E12-1E13 (Table

2). Using deep NGS techniques (NovaSeq™, Illumina) to understand the input variant distribution, NGS testing obtained approximately 300 million reads per library.

[00140] Table 2

Lane	Library	BDS Titer (GC/mL)	Library diversity
A1	AAV8.VR4	3.51E+13	4.32E+07
B1	AAV8.VR8	8.15E+13	1.15E+07
C1	AAV9.VR4	1.50E+13	1.02E+07
D1	AAV9.VR8	4.55E+12	1.45E+07
E1	AAV4.VR4	4.25E12	2.26E+07
F1	AAV3B.VR4	2.84E+12	2.70E+08
G1	AAV5.VR8	3.97E+13	1.36E+07

[00141] NGS analysis of initial vector libraries had high parental vector levels (**FIG. 5A**), as indicated by the larger representation of parental vector following production, compared to the percent parental plasmid in the initial preparation of the library. However, the stop codon inserted into the template plasmid prevented wildtype (parental) vector production from carryover template present in the production culture after library cloning. The drop-in vector stop codon abundance levels indicate selection against cross-packaging (**FIG. 5B**).

[00142] Parental fraction following AAV packaging was further characterized by LC-MS of the VP3 protein. Following generation of an AAV5 vector library with no stop codon in template, the parental (AAV5) VP3 theoretical wildtype mass is 59,551.64 Da and AAV5 VP3 with peptide insertion is 59,951 to 60,855 Da. **FIG. 6A** and **FIG. 6B** illustrate (by LC-MS analysis of VP3 proteins in each version of the library) that the addition of stop codon (**FIG. 6B**) significantly reduces the packaging of parental vector.

6.3. Example 3 – Evaluation and selection of capsids from various libraries

[00143] Samples of vector libraries that were made according to the above methods are listed in **Table 3** and were dosed accordingly to non-human primates (NHPs; Cynomolgous macaques) of approximately 2-3 years at study start date. As such, three NHPs per study were dosed at 9.3e10 to 2.9e13 GC/kg by different routes of administration under ketamine sedation, as indicated in **Table 3**.

[00144] Table 3

Library #	Round 1 Library	Insertion Loop	ROA	Dose
1	AAV5	VR8	IV	2.9E13 GC/kg
2	AAV4	VR4		9.30E10 GC/kg
3	AAV8	VR4		9.7E12 GC/kg
			SCS	2.11E12 GC/eye
4	AAV8	VR8	IV	1.8E13 GC/kg
			SCS	9.8E11 GC/eye
5	AAV9.NNN	VR4	IV	1.0E13 GC/kg
6	AAV9.NNN	VR8		2.2E12 GC/kg
7	AAV3B	VR4		6.7E11 GC/kg
			IVT	1.42E11 GC/eye
8	AAV1	VR4	ICV	
9	AAVhu37	VR4		

[00145] Blood was collected immediately prior to dosing, and serum collected and processed. Twenty-one (21) days following dosing, animals were euthanized and blood and target tissues were collected. Tissues were examined, weighed, and then placed into RNAse/DNase-free cryovials and flash frozen in liquid nitrogen. Based on the size of the specified tissue/region, up to five samples of approximately 50-100 mg per sample were collected from each location. Tissue samples were collected using aseptic technique and RNAse-free instruments and workspaces, with care taken to ensure no cross contamination between tissues. Tissues were flash frozen in liquid nitrogen and then maintained on dry ice prior to storage at -70 to -90 °C. DNA and RNA was extracted from all tissues by standard techniques and next generation sequencing (NGS) and quantitative PCR (mRNA transcript expression) was performed, respectively. A custom bioinformatics platform was employed utilizing open-source software packages and R-scripts to analyze cDNA counts and RNA-seq data. For example,

merge_counts.R was utilized to merge peptide counts from all samples into a single dataframe, based on methods well-known in the art and available on github.com. Analysis of the vector repertoire in multiple tissues revealed that 1795 peptides in the AAV9.AAA.VR4 library were detected in one or more muscle tissue samples. The pool of top hits from this library were further evaluated in a similar NHP study.

6.4. Example 4 – Evaluation and selection of capsids transducing muscle from an AAV9.AAA library

[00146] The 496NNN498 -> AAA mutation in AAV9 (SEQ ID NO: 151) provides greater than 100-fold reduced liver transduction. The AAV9.AAA parental capsid was used as a starting template for producing a vector library having random peptide insertions after amino acid residue S454, to generate a AAV9.AAA.VR4 vector library, using the methods described in the Example hereinabove.

[00147] Following the analysis of a vector repertoire containing a diverse set of peptides having tropism for one or more muscle tissue samples in the first round of animal testing, a pool from AAV9.AAA.VR4 was further analyzed by dosing NHPs at 1.52e13 GC/kg. The bioinformatics tools were used to determine vector performance ranking based on readouts such as relative abundance (RA), ES counts, etc. (e.g. using Dunnett's multiple comparison test p-values) to determine an enrichment score. A representative list of 134 hits (peptides) and 4 consensus sequences emerged, as in **Tables 4, 5, 14, 15 and 16** for example, based on selection in muscle, compared to the parental spiked-in vector control (AAV9.AAA). Top 24 hits (peptides) analyzed by NGS in various tissues are represented in **FIG. 7**.

[00148] Table 4

SEQ ID NO:	Peptide sequence
1	**SGTVIRS**
2	**GRPAP**
3	**KDQKIGP**
4	**TRQYVPG**
5	**VQVGRAA**
6	**FTQSRGG**
7	**SRSDRPA**
8	**VQVGRTS**
9	**SSGSQKF**
10	**SGTVLRS**
11	**SHTKSAT**

SEQ ID NO:	Peptide sequence
12	**DQARVRI**
13	**RGAVQKV**
14	**VGRDSRS**
15	**SRSDRQF**
16	**VTRSQIM**
17	**QVGARHP**
18	**GRAAASL**
19	**PSGVPIR**
20	**MSYNQAT**
21	**ITGGVRV**
22	**SRSDRQV**
23	**TSGVPIR**
24	**AQVGRAS**
25	**VKASHHS**
26	**SHTKTVT**
27	**GSVQTVR**
28	DTRIRSM
29	SRTKTAT
30	QVGARQS
31	PSGQRLH
32	GQVHQAR
33	TSGVQIR
34	SIAKTSS
35	SRADRHV
36	VQVGRVS
37	SVTSVRV
38	TSGGQIR
39	SHIKTAT
40	SHIKTST
41	GNIKYGS
42	SRSDRHV
43	TSGAPIR
44	VQVGRSS
45	MKYRGTD
46	HFAGKSV
47	IKYRGTD
48	SIAKHSS
49	SHTRTAT
50	SGTGIRA
51	SIAKHGA
52	GRAAATL
53	SGTVLRA
54	ASAKHAA

SEQ ID NO:	Peptide sequence
55	AHTKTAT
56	VKASHAS
57	SNTKHAT
58	VPVGRAS
59	SISKHSA
60	QKGRNPD
61	QSAVRHP
62	VQGGRAS
63	VKNSSGTF
64	HFTHQSK
65	DKRGVIV
66	HMGQSGK
67	GQVHQSR
68	SHTKPAT
69	KDSGGYR
70	RRVSNVD
71	ARVTASI
72	GNIKSGS
73	DKRGVIG
74	SIAKTAA
75	QSVGRYS
76	SIAKNSA
77	VSGAVRVT
78	PSSKARQ
79	MARPQSI
80	TVRGREQ
81	SHTRTST
82	HMGQYGK
83	TVATSKI
84	RAVTLGV
85	FHTKTAT
86	QQAQR
87	SIARHSA
88	HMGHSGK
89	ATRGVIG
90	SKTFAAS
91	VVAGAMR
92	SSGAQKF
93	EMTSRHV
94	RRVSTVD
95	ITGEVRG
96	IQGVHSK
97	SPARA

SEQ ID NO:	Peptide sequence
98	AGEGP
99	AGPGA
100	RQARR
101	GNIQSRS
102	IIHNQAK
103	PKNVKTT
104	DMNSRHV
105	ENRGIIG
106	YTKTSSV
107	LVNQQKS
108	PSSKDRH

[00149] Skeletal muscle and heart tissue data was compared to liver as in **FIG. 8A-C**, represented as fold change RA relative to the control parental vector. Vector comprising capsid having peptide 01 (SEQ ID NO: 1) exhibited 32-fold increase in relative abundance (mRNA expression) in skeletal muscle and 16-fold in heart. Peptide 24 (SEQ ID NO: 24) insertion resulted in vector that exhibited 55-fold in heart and 12-fold in skeletal muscle. Whereas vectors having insertion of peptide 29 (SEQ ID NO: 29) or peptide 30 (SEQ ID NO: 29) showed increased levels in liver 173-fold and 103-fold, respectively, relative to the parental capsid.

[00150] Following the analysis of a vector repertoire in the second round of animal testing, a third pool (see Table 5) of AAV9.AAA.VR4 capsids as well as capsids from the AAV5.VR8 library (including peptides SEQ ID NO: 118, SEQ ID NO: 119 and SEQ ID NO: 120 in AAV5) was further analyzed in NHP. All study animals were screened for the presence of AAV2, AAV8 and AAV9 neutralizing antibodies in serum by in vitro neutralizing antibody assay (Precision for Medicine) and only animals with titers below a defined threshold were enrolled in the study. Pre-dose blood collections were taken (following ketamine sedation) and placed into serum separator tubes. After a minimum 15 minutes at ambient temperature, blood was centrifuged (2500 x *g* for 10 minutes) and serum harvested.

Table 5 – Peptides analyzed in Round 3

Designation	SEQ ID NO:	Sequence	AAV Capsid
NVG01	SEQ ID NO: 32	GQVHQAR	AAV9.AAA.VR4
NVG02	SEQ ID NO: 38	TSGGQIR	AAV9.AAA.VR4
NVG03	SEQ ID NO: 109	MRAVSQL	AAV9.AAA.VR4
NVG04	SEQ ID NO: 4	TRQYVPG	AAV9.AAA.VR4
NVG05	SEQ ID NO: 88	HMGHSGK	AAV9.AAA.VR4
NVG06	SEQ ID NO: 1	SGTVIRS	AAV9.AAA.VR4
NVG07	SEQ ID NO: 8	VQVGRTS	AAV9.AAA.VR4

Designation	SEQ ID NO:	Sequence	AAV Capsid
NVG08	SEQ ID NO: 13	RGAVQKV	AAV9.AAA.VR4
NVG09	SEQ ID NO: 110	PRQYVPG	AAV9.AAA.VR4
NVG10	SEQ ID NO: 111	RSSSGR	AAV9.AAA.VR4
NVG11	SEQ ID NO: 112	VVKSTKS	AAV9.AAA.VR4
NVG12	SEQ ID NO: 113	RHVSASD	AAV5.(578)VR8
NVG13	SEQ ID NO: 114	VRSDRDQ	AAV5.(578)VR8
NVG14	SEQ ID NO: 115	TVVTSIN	AAV5.(578)VR8

[00151] Test article (pooled capsids) were administered IV (2e13 GC/kg) to each of 3 animals. Test article were administered by IV bolus under ketamine sedation (ketamine hydrochloride (HCl) delivered by intramuscular (IM) injection) followed by a flush of at least 5 mL saline. Following 21 days, animals were anesthetized with ketamine HCl delivered by IM injection. Blood was collected and placed into serum separator tubes. After a minimum 15 minutes at ambient temperature, blood was centrifuged (2500 x *g* for 10 minutes) and serum harvested. Collected tissues were examined, weighed, and then placed into RNAse/DNase-free cryovials. Based on the size of the specified tissue/region, up to five samples of approximately 50-100 mg per sample were collected from each location. Tissue samples were collected using aseptic technique and RNAse-free instruments and workspaces. Tissues were flash frozen in liquid nitrogen and then maintained on dry ice prior to storage at -70 to -90 °C.

[00152] DNA (Kingfisher DNA) and mRNA (Dynabeads mRNA direct) were extracted from the tissues and the vector barcode sequences were amplified by PCR and then detected by NGS on the Illumina Miseq. Units of "nRAAFI", normalized relative abundance adjusted for input, were calculated. Essentially, the relative abundance of each barcode was divided by the input relative abundance and then normalized to a sum of one in each sample to identify the nRAAFI for each barcoded transgene.

[00153] **FIG. 9** shows that AAV9.AAA.NVG07 mediated a 2-fold increase in mRNA expression in skeletal muscle (**FIG. 9A**) and heart (**FIG. 9B**) compared with AAV9. **FIG. 10** shows that AAV9.AAA.NVG07 provided a 10 fold greater ratio of mRNA/DNA in heart (**FIG. 10A**) and skeletal muscle (**FIG. 10B**) compared with AAV9. **FIG. 11** shows the levels of transgene mRNA (**A**) compared to DNA (**B**) in liver. AAV9.AAA.NVG07 is greater than 7 fold liver de-targeted in mRNA compared to AAV9. Several capsids with peptide insertions (from the AAV9.AAA.VR4 or AAV5.VR8 vector library) displayed a favorable biodistribution with respect to muscle vs. liver transduction, some capsids even displaying lower heart transduction which may be desirable for certain transgenes.

[00154] The data from the present NHP study for NVG07 mRNA distribution in skeletal muscle and liver was selected and combined with the NVG07 data from animals 4001 and 4003 from the study described in Example 6, below, that tested the same capsids. AAV9 data values were also taken from these NHP studies and were normalized to 1 to show the fold difference of NVG07 compared to AAV9. **FIG. 12A** (Skeletal muscle) and **FIG. 12B** (liver). The ratio of muscle mRNA to liver mRNA was also calculated for each animal. As shown in **FIG. 12C**, the NVG07 transduction of muscle tissue over liver tissue is approx. 8 to 18 times better than AAV9.

6.5. Example 5: Assessment of Selected Capsids *in vitro* and *in vivo*

[00155] AAV capsid sequences modified by peptide insertions with or without additional substitutions are further evaluated in an *in vitro* assay, as well as for *in vivo* bio-distribution in test animals using next generation sequencing (NGS) and quantitative PCR.

[00156] Studies are performed where selected vectors from the library are produced by method described in these Examples, or by standard methods of triple transfection utilizing Rep/cap *trans* plasmid (containing the engineered capsid gene sequence), *cis plasmid* encoding a transgene, and helper gene plasmid. The engineered vectors of interest are injected individually into test animals, *e.g.* NHPs, mice or rats, and DNA and RNA determinations from extracted tissues are compared to the parental vectors. Quantitative PCR (qPCR) can be done on a QuantStudio 5 (Life Technologies, Inc.) or any standard method such as ddPCR, using primer-probe combinations specific for the transgene.

[00157] From the studies where individual vectors are injected into test animals for characterization, formalin fixed brains may be, *e.g.* sectioned at 40μm thickness on a vibrating blade microtome (VT1000S, Leica) and the floating sections probed with antibodies against transgene (or viewed for fluorescence if fluorescent transgene) to look at the cellular distribution of the delivered vectors.

[00158] C57Bl6 mice (n=5 per test article group) were administered AAV.hu32, AAV9.AAA.VQVGRTS (NVG07) or AAVhu.32.AAA.VQVGRTS capsids carrying a CAG.TdTomato transgene, 1E14 GC/kg IV (tail vein) administration per animal. Following 3 weeks, animals were sacrificed and heart, gastrocnemius, quadriceps, bicep, brain, liver and diaphragm tissues were collected.

[00159] TdTomato genome (cDNA) and transcripts (mRNA) were detected by digital PCR and plotted against a reference gene, TATA-box Binding protein (TBP). Results show that AAV9.AAA.VQVGRTS (NVG07) had lower expression in the liver. **FIGs. 13 A-B**.

[00160] C57Bl6 mice (n=4 per administration group) were administered AAV9 capsids carrying a CAG.TdTomato transgene, 1E13 or 1E14 GC/kg IV administration per animal. Following 3 weeks, animals were sacrificed and brain, liver, bicep and gastrocnemius tissues were collected.

[00161] Separately, C57Bl6 mice (n=5 per administration group) were administered NVG07 capsids carrying a CAG.TdTomato transgene, 1E13 or 1E14 GC/kg IV administration per animal. Following 3 weeks, animals were sacrificed and brain, liver, tibialis anterior (TA) quadricep, bicep and gastrocnemius tissues were collected.

[00162] Brain slices from cortex, hippocampus and striatum tissues from both studies (AAV9 and NVG07) were also prepared for fluorescence imaging (tdTomato/DAPI). AAV9.AAA.NVG07 redirects tropism from astrocytes to neurons in the brain of the mouse (data not shown).

[00163] TdTomato genome (cDNA) and transcripts (mRNA) were detected by digital PCR and plotted against a reference gene, TATA-box Binding protein (TBP). Results are shown in Tables 6-13.

Table 6 - AAV9 / 1E13 / RNA - tdTom transcripts/TBP

Brain	0.036890311	0.111015937	0.086795623	0.199962374	0.284954529
Liver	Not done (Nd)	Nd	Nd	Nd	Nd
Bicep	0.434204944	0.692850013	0.576478591	1.572121792	1.280973036
Gas	0.681902249	0.671394813	0.254783067	2.665095667	0.33763115

Table 7 - AAV9 / 1E13 / DNA- tdTom/diploid cell

Brain	0.013450943	0.011279439	0.021593898	0.038522416	0.018567217
Liver	Nd	Nd	Nd	Nd	Nd
Bicep	0.058739945	0.095610192	0.101944179	0.549394202	0.107221812
Gas	0.077698166	0.048297601	0.03348689	0.073418602	0.085699073

Table 8 - AAV9 / 1E14 / RNA - tdTom transcripts/TBP

Brain	1.178050241	1.217263137	0.895701935	2.134230949	1.218719168
Liver	Nd	Nd	Nd	Nd	Nd
Bicep	15.35463383	2.358943003	10.23422082	60.35947847	29.1243009
Gas	40.62668523	18.44852392	5.587096873	60.87078632	10.39744051

Table 9 - AAV9 / 1E14 / DNA- tdTom/Diploid cell

BRAIN	0.278629609	0.431457095	0.228405767	0.333674887	0.220072005
LIVER	240.8114	328.9249	220.2679	125.229	226.3849
BICEP	1.08169672	0.743156382	0.676354039	0.912752148	1.058356597
GAS	0.394223444	2.054787079	0.932967195	0.606069664	1.117394992

Table 10 - NVG07 / 1E13 / RNA- tdTom Transcripts/TBP

BRAIN	0.00375462	0.028063924	0.020756832	0.032251626	0.01364307
LIVER	3.047034456	8.11774917	2.214509582	5.013711529	1.927788473
TA	0.078822571	0.126637776	0.367988038	0.696732748	0.053506641
QUAD	0.144743958	0.18249131	0.834414732	0.760439126	0.124937345
BICEP	0.028115576	0.131026526	0.174242523	0.152152957	0.056497243
GAS	0.101910779	0.727130082	1.050164729	0.382196398	0.173578122

Table 11 - NVG07 / 1E13 / DNA - tdTom/Diploid cell

BRAIN	0.000488948	0.002704717	0.002265579	0.003374586	0.000431437
LIVER	0.047667814	0.217529774	0.148715088	0.251105783	0.069879203
T.A.	0.003982067	0.010817625	0.012242956	0.027075116	0.006865514
QUAD	0.004530628	0.006238941	0.058679912	0.051015036	0.010696398
BICEP	0.00332028	0.014682863	0.019468111	0.050395935	0.005424901
GAS	0.003626522	0.011423566	0.014696037	0.028799631	0.005488395

Table 12 - NVG07 / 1E14 / RNA- tdTom Transcripts/TBP

BRAIN	1.509950773	0.415176657	0.287061103	0.574066385	*0.02201578**
LIVER	5.921066892	9.549919727	2.540978226	5.791713751	*1.694483204**
TA	5.29366453	11.09910504	14.08705972	16.80101394	*0.058042404**
QUAD	34.15055202	16.94971485	6.788304343	22.18649393	*0.099859085**
BICEP	3.004314619	10.03525839	6.499347379	20.83190632	*0.040049364**
GAS	13.10956254	26.67521715	23.65668044	59.21139309	*0.066293391**

Table 13 - NVG07 / 1E14 / DNA - tdTom/Diploid cell

BRAIN	0.022000771	0.022543271	0.011689717	0.049770374	*0.000542091**
LIVER	5.935441167	11.24125919	0.718609553	6.158077504	*0.055109823**
T.A.	0.19740364	0.162904378	0.278037585	0.285422593	*0.010024539**
QUAD	0.233550486	0.198675241	1.27587749	0.523329496	*0.004910094**
BICEP	0.128187391	0.196211218	0.234569107	0.611000095	*0.005177627**
GAS	0.103334772	0.159689351	0.158928168	0.277316254	*0.006636086**

[00164] At the high dose (1E14 GC/kg) of single-vector administered to mice in this study, NVG07 yielded 40-fold lower genome DNA than AAV9 in liver, yet had essentially equivalent, or slightly lower DNA and RNA, observed than AAV9 in skeletal muscle RNA. Lower liver expression of certain AAV gene therapy transgenes is desirable. Currently, several challenges for AAV therapeutics include potential adverse effects to liver function and immune responses for the patient. For a more systemic distribution such as for a muscle disease,

approved AAV therapeutics are administered intravenously in high doses, typically greater than 1 x 10^{13} (1E13) genome copies per kilogram of body weight of the patient (vector genomes (vg) = genome copies (GC)), e.g. delandistrogene moxeparvovec administered at 1.33E14 vector genomes (vg)/kg of body weight. An AAV therapeutic having less distribution to the liver, where liver transduction is not warranted or may be the cause of adverse reactions, would prove beneficial to patients, especially if other properties of the AAV therapy convey the intended efficacy. Based on the finding that NVG07 exhibited higher observable neuronal expression (by fluorescent imaging) than AAV9, which transduced mostly astrocytes, the NVG07 capsid also provides an advantage for neuromuscular diseases where neuronal expression of an AAV-delivered transgene would be warranted.

6.6. Example 6 – Evaluation and selection of capsids from a library

[00165] Another round of peptides were selected from the B4 pool and administered to NHP as described above.

Table 14.

Capsid Name (peptide SEQ ID NO)	Diaphragm (mRNA)		GAS (mRNA)		Quad (mRNA)		TA (mRNA)		Bicep (mRNA)	
	NHP 4001	NHP 4003	NHP 4001	NHP 4003	NHP 4001	NHP 4003	NHP 4001	NHP 4003	NHP 4001	NHP 4003
AAV5	0.020035	0	0.0000142	0	0.0000796	0	0.001013	0	0.001892	0.002466
AAV9.AAA	0	0.014883	0.002098	0.015461	0.001959	0.00104	0.027122	0.032811	0.007654	0.010425
AAV10	0	0.007773	0.000175	0.008254	0	0.002042	0	0.005185	0	0.000915
AAV11	0	0	0.0000292	0	0.0000256	0	0.001255	0	0	0
AAV12	0.004601	0	0.005313	0	0.003358	0	0	0	0.003805	0
AAV13	0	0	0.00000578	0	0	0	0	0	0	0
AAV8	0	0.009535	0.002891	0.010214	0.0000676	0.011017	0	0	0	0.009527
AAV9	0.092047	0.047408	0.036513	0.041086	0.043732	0.06434	0.115277	0.077566	0.126715	0.081175
AAV9.AAA.NVG07 (SEQ ID NO: 8)	0.073887	0.02668	0.036421	0.017508	0.033896	0.019427	0.028239	0.015125	0.063989	0.015024
AAV9.455.DGRRIGV (SEQ ID NO: 116)	0	0.012639	0.062059	0.060865	0.056926	0.008295	0	0	0.030957	0.042943
AAV9.455.TSGERRG (SEQ ID NO: 117)	0.018763	0.02622	0.026409	0.017124	0.035988	0.015875	0.012235	0.026689	0.015389	0.017502
AAV9.455.PSSVQHR (SEQ ID NO: 118)	0.072458	0.063784	0.082454	0.031916	0.099667	0.041616	0.048056	0.0507	0.055866	0.02608
AAV9.455.SSSVQHR (SEQ ID NO: 119)	0.010228	0.032451	0.037711	0.022562	0.041583	0.029147	0.025958	0.027321	0.026488	0.019774
AAV9.455.SGMQERR (SEQ ID NO: 120)	0.006042	0.030419	0.027733	0.016933	0.029535	0.00861	0.005449	0.010547	0.004598	0.004968
AAV9.455.SIAKNSA (SEQ ID NO: 76)	0	0.00745	0.006203	0.028216	0.004649	0.011929	0.008024	0.026454	0.004576	0.018454
AAV9.455.LERGNLE	0	0.003682	0.001149	0.005734	0.001289	0.011628	0.004441	0.014179	0.006002	0.00535

Capsid Name (peptide SEQ ID NO)	Diaphragm (mRNA)		GAS (mRNA)		Quad (mRNA)		TA (mRNA)		Bicep (mRNA)	
(SEQ ID NO: 121)										
AAV9.455.YRDVRQT (SEQ ID NO: 122)	0	0.047833	0.011339	0.048707	0.002079	0.021824	0.000879	0.038864	0.000976	0.028987
AAV9.455.PSAVQHR (SEQ ID NO: 123)	0.026604	0.029804	0.0506	0.027253	0.05717	0.021541	0.007626	0.027586	0.037618	0.009481
AAV9.455.AQVGRAS (SEQ ID NO: 24)	0.088632	0.046325	0.038686	0.031259	0.049969	0.038609	0.093481	0.024328	0.055467	0.044654
AAV9.455.SVTSVRV (SEQ ID NO: 37)	0.017695	0.032461	0.027767	0.028252	0.022977	0.029828	0.015916	0.024275	0.009741	0.034885
AAV9.455.YVGGRAV (SEQ ID NO: 124)	0.047559	0.08009	0.091561	0.056149	0.114782	0.062423	0.089687	0.057371	0.063298	0.061322
AAV9.455.MKYRGTD (SEQ ID NO: 45)	0.020127	0.013741	0.028148	0.01385	0.035928	0.019683	0.029912	0.021126	0.034469	0.014141
AAV9.455.HMGQYGK (SEQ ID NO: 82)	0	0.034439	0.014707	0.017065	0.003132	0.028222	0	0.029524	0	0.033974
AAV9.455.IGSRGVA (SEQ ID NO: 125)	0.025609	0.041979	0.04564	0.055189	0.053971	0.04909	0.063916	0.035789	0.04762	0.054291
AAV9.455.SDVSRPR (SEQ ID NO: 126)	0.020171	0.01173	0.088732	0.012306	0.099453	0.003151	0.026286	0.003998	0.033182	0.00384
AAV9.455.GSVRQAA (SEQ ID NO: 127)	0.009634	0.079906	0.035125	0.073909	0.022702	0.067478	0.033772	0.094574	0.006611	0.082951
AAV9.455.QSPHTSQ (SEQ ID NO: 128)	0.035755	0.025078	0.006733	0.019373	0.006917	0.035874	0.012861	0.02567	0.016607	0.017489
AAV9.455.ASQAYHG (SEQ ID NO: 129)	0	0.024187	0.003581	0.058372	0.000812	0.054513	0	0.02941	0	0.043668

0 = Not Detected

[00166] In the B4 study of pooled vectors, several vectors having peptide inserts (e.g. DGRRIGV, YVGGRAV, PSSVQHR, IGSRGVA, GSVRQAA, SDVSRPR, AQVGRAS) exhibited higher mRNA expression in skeletal muscle tissues (such as gastrocnemius) than AAV9.

6.7. Example 7 – Evaluation of a Consensus Sequence

[00167] Highly similar sequences and motifs were found amongst the peptides that transduced muscle efficiently while de-targeting the liver in the AAV9.AAA capsid library.

[00168] The "Fold-difference" value in the chart represents the fold-difference in muscle tropism for the capsid with the peptide compared to its parental. As indicated in Table 15, AAV9.AAA capsids comprising these peptides which have similar amino acid motifs convey greater than 2-fold up to 27-fold greater transduction in muscle compared to an AAV9.AAA capsid.

Table 15:

Sequence	Input Counts	Number Samples	Mean	CV	Fold-difference
VQVGRTS (SEQ ID NO: 8)	180	7	11.52	1.43	26.84
VQVGRSS (SEQ ID NO: 44)	199	6	3.16	1.56	7.37
VQVGRVS (SEQ ID NO: 36)	254	5	4.32	1.50	10.07
VQVGRYS (SEQ ID NO: 130)	93	2	1.12	2.56	2.61
VQVGRAS (SEQ ID NO: 131)	172	1	1.03	3.32	2.39
VQVGRPS (SEQ ID NO: 132)	81	1	0.99	3.32	2.30
AQVGRAS (SEQ ID NO: 24)	171	8	7.47	1.65	17.4
VQVGRAA (SEQ ID NO: 5)	86	4	11.79	2.10	27.47
VQVVRPS (SEQ ID NO: 133)	63	3	6.90	2.37	16.09
VQVGHAS (SEQ ID NO: 134)	152	3	1.27	2.92	2.96
NO INSERT	2103	5	0.43	1.35	1.00

[00169] The concensus sequence SEQ ID NO: 135 is X_1-Q-V-X_2-X_3-X_4-X_5, wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is any amino acid and X_5 is S, G, V or A. The concensus sequence SEQ ID NO: 136 is X_1-Q-V-X_2-X_3-X_4-X_5, wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is any amino acid and X_5 is S or A. The concensus sequence SEQ ID NO: 137 is X_1-Q-V-X_2-X_3-X_4-X_5, wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is T, S, V, Y, A or P and X_5 is S, G, V or A. The concensus sequence SEQ ID NO: 138 is X_1-Q-V-X_2-X_3-X_4-X_5, wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is T, S, V, Y, A or P and X_5 is S or A.

Table 16: Consensus Peptide Sequences

SEQ ID NO:	Consensus Peptide Sequences	X_1	X_2	X_3	X_4	X_5
135	X_1-Q-V-X_2-X_3-X_4-X_5	V or A	S, G, V or A	R or H	Any Amino Acid	S, G, V or A
136	X_1-Q-V-X_2-X_3-X_4-X_5	V or A	S, G, V or A	R or H	Any Amino Acid	S or A
137	X_1-Q-V-X_2-X_3-X_4-X_5	V or A	S, G, V or A	R or H	T, S, V, Y, A or P	S, G, V or A
138	X_1-Q-V-X_2-X_3-X_4-X_5	V or A	S, G, V or A	R or H	T, S, V, Y, A or P	S or A

6.7.1.1 Conclusions

[00170] AAV capsid modifications performed by random peptide insertions in surface exposed loop of VR-IV were able to produce sufficient library titers in the production system described herein for analysis of transduction properties in NHP tissues. The method provided for reducing carryover parental plasmid following cloning of the random insertions and was

shown to reduce overrepresentation of the parental vector in the library biodistribution and transduction studies.

[00171] Intravenous administration of AAV9.AAA.VR4 to NHPs resulted in a number of higher relative abundance engineered vectors in muscle suitable for use as a gene therapy vector carrying a gene of interest to treat a muscle disorder.

Table 17. Capsid Amino Acid Sequences

Capsid Name	Insert/ modification	Amino Acid Sequence
AAV1	n/a	MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPV NAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG LVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQPLGEPPATP AAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQI SSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVT TNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQAVGR SSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSGS AQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINP GTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNVMITDEEEIKATNPVATERFGTVAVNFQ SSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIK NTPVPANPPAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTV DNNGLYTEPRPIGTRYLTRPL (SEQ ID NO: 139)
AAV2	n/a	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPFNGLDKGEPV NEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG LVEEPVKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPARKRLNFGQTGDADSVPDPQPLGQPPAAP SGLGTNTMATGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNHLYKQI SSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTQ NDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNGSQAVGRS SFYCLEYFPSQMLRTGNNFTFSYTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTNTPSGTT TQSRLQFSQAGASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSLVNPG PAMASHKDDEEKFFPQSGVLIFGKQGSEKTNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQR GNRQAATADVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKN TPVPANPSTTFSAAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVD TNGVYSEPRPIGTRYLTR (SEQ ID NO: 140)
AAV3	n/a	MAADGYLPDWLEDNLSEGIREWWALKPGVPQPKANQQHQDNRRGLVLPGYKYLGPGNGLDKGEPV NEADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRILEPLG LVEEAAKTAPGKKGAVDQSPQEPDSSSGVGKSGKQPARKRLNFGQTGDSESVPDPQPLGEPPAAP TSLGSNTMASGGGAPMADNNEGADGVGNSSGNWHCDSQWLGDRVITTSTRTWALPTYNNHLYKQI SSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKKLSFKLFNIQVRGVTQ NDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNGSQAVGRS SFYCLEYFPSQMLRTGNNFQFSYTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQGTTSGT TNQSRLLFSQAGPQSMSLQARNWLPGPCYRQQRLSKTANDNNNSNFPWTAASKYHLNGRDSLVNP GPAMASHKDDEEKFFPMHGNLIFGKEGTTASNAELDNVMITDEEEIRTTNPVATEQYGTVANNLQ SSNTAPTTGTVNHQGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQIMIK NTPVPANPPTTFSPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTV DTNGVYSEPRPIGTRYLTRNL (SEQ ID NO: 141)
AAV4	n/a	MTDGYLPDWLEDNLSEGVREWWALQPGAPKPKANQQHQDNARGLVLPGYKYLGPGNGLDKGEPVN AADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQQRLQGDTSFGGNLGRAVFQAKKRVLEPLGL VEQAGETAPGKKRPLIESPQQPDSSTGIGKKGKQPAKKKLVFEDETGAGDGPPEGSTSGAMSDDS EMRAAAGGAAVEGGQGADGVGNASGDWHCDSTWSEGHVTTTSTRTWVLPTYNNHLYKRLGESLQS NTYNGFSTPWGYFDFNRFHCHFSPRDWQRLINNNWGMRPKAMRVKIFNIQVKEVTTSNGETTVAN NLTSTVQIFADSSYELPYVMDAGQEGSLPPFPNDVFMVPQYGYCGLVTGNTSQQQTDRNAFYCLE YFPSQMLRTGNNFEITYSFEKVPFHSMYAHSQSLDRLMNPLIDQYLWGLQSTTTGTTLNAGTATT NFTKLRPTNFSNFKKNWLPGPSIKQQGFSKTANQNYKIPATGSDSLIKYETHSTLDGRWSALTPG PPMATAGPADSKFSNSQLIFAGPKQNGNTATVPGTLIFTSEEELAATNATDTDMWGNLPGGDQSN SNLPTVDRLTALGAVPGMVWQNRDIYYQGPIWAKIPHTDGHFHPSPLIGGFGLKHPPPQIFIKNT PVPANPATTFSSTPVNSFITQYSTGQVSVQIDWEIQKERSKRWNPEVQFTSNYGQQNSLLWAPDA AGKYTEPRAIGTRYLTHHL (SEQ ID NO: 142)
AAV5	n/a	MSFVDHPPDWLEEVGEGLREFLGLEAGPPKPKPNQQHQDQARGLVLPGYNYLGPGNGLDRGEPVN RADEVAREHDISYNEQLEAGDNPYLKYNHADAEFQEKLADDTSFGGNLGKAVFQAKKRVLEPFGL VEEGAKTAPTGKRIDDHFPKRKKARTEEDSKPSTSSDAEAGPSGSQQLQIPAQPASSLGADTMSA

Capsid Name	Insert/ modification	Amino Acid Sequence
		GGGGPLGDNNQGADGVGNASGDWHCDSTWMGDRVVTKSTRTWVLPSYNNHQYREIKSGSVDGSNA NAYFGYSTPWGYFDFNRFHSHWSPRDWQRLINNYWGFRPRSLRVKIFNIQVKEVTVQDSTTTIAN NLTSTVQVFTDDDYQLPYVVGNGTEGCLPAFPPQVFTLPQYGYATLNRDNTENPTERSSFFCLEY FPSKMLRTGNNFEFTYNFEEVPFHSSFAPSQNLFKLANPLVDQYLYRFVSTNNTGGVQFNKNLAG RYANTYKNWFPGPMGRTQGWNLGSGVNRASVSAFATTNRMELEGASYQVPPQPNGMTNNLQGSNT YALENTMIFNSQPANPGTTATYLEGNMLITSESETQPVNRVAYNVGGQMATNNQSSTTAPATGTY NLQEIVPGSVWMERDVYLQGPIWAKIPETGAHFHPSPAMGGFGLKHPPPMMLIKNTPVPGNITSF SDVPVSSFITQYSTGQVTVEMEWELKKENSKRWNPEIQYTNNYNDPQFVDFAPDSTGEYRTTRPI GTRYLTRPL (SEQ ID NO: 143)
AAV6	n/a	MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPV NAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPFG LVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQPLGEPPATP AAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQI SSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVT TNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQAVGR SSFYCLEYFPSQMLRTGNNFTFSYTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSGS AQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINP GTAMASHKDDKDKFFPMSGVMIFGKESAGASNTALDNVMITDEEEIKATNPVATERFGTVAVNLQ SSSTDPATGDVHVMGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIK NTPVPANPPAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTV DNNGLYTEPRPIGTRYLTRPL (SEQ ID NO: 144)
AAV7	n/a	MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDNGRGLVLPGYKYLGPFNGLDKGEPV NAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG LVEEGAKTAPAKKRPVEPSPQRSPDSSTGIGKKGQQPARKRLNFGQTGDSESVPDPQPLGEPPAA PSSVGSGTVAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQ ISSETAGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKKLRFKLFNIQVKEV TTNDGVTTIANNLTSTIQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQSVG RSSFYCLEYFPSQMLRTGNNFEFSYSFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQSNPG GTAGNRELQFYQGGPSTMAEQAKNWLPGPCFRQQRVSKTLDQNNNSNFAWTGATKYHLNGRNSLV NPGVAMATHKDDEDRFFPSSGVLIFGKTGATNKTTLENVLMTNEEEIRPTNPVATEEYGIVSSNL QAANTAAQTQVVNNQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPQILI KNTPVPANPPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNFEKQTGVDFA VDSQGVYSEPRPIGTRYLTRNL (SEQ ID NO: 145)
AAV8	n/a	MAADGYLPDWLEDNLSEGIREWWALKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPV NAADAAALEHDKAYDQQLQAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG LVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPARKRLNFGQTGDSESVPDPQPLGEPPAA PSGVGPNTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQ ISNGTSGGATNDNTYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLSFKLFNIQVKE VTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQAV GRSSFYCLEYFPSQMLRTGNNFQFTYTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQTTG GTANTQTLGFSQGGPNTMANQAKNWLPGPCYRQQRVSTTTGQNNNSNFAWTAGTKYHLNGRNSLA NPGIAMATHKDDEERFFPSNGILIFGKQNAARDNADYSDVMLTSEEEIKTTNPVATEEYGIVADN LQQQNTAPQIGTVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPQIL IKNTPVPADPPTTFNQSKLNSFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSTSVDF AVNTEGVYSEPRPIGTRYLTRNL (SEQ ID NO: 146)
AAVhu31	n/a	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPGNGLDKGEPV NAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRLLEPLG LVEEAAKTAPGKKRPVEQSPQEPDSSAGIGKSGSQPAKKKLNFGQTGDTESVPDPQPIGEPPAAP SGVGSLTMASGGGAPVADNNEGADGVGSSSGNWHCDSQWLGDRVITTSTRTWALPTYNNHLYKQI SNSTSGGSSNDNAYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEV TDNNGVKTIANNLTSTVQVFTDSDYQLPYVLGSAHEGCLPPFPADVFMIPQYGYLTLNDGSQAVG RSSFYCLEYFPSQMLRTGNNFQFSYEFENVPFHSSYAHSQSLDRLMNPLIDQYLYYLSKTINGSG QNQQTLKFSVAGPSNMAVQGRNYIPGPSYRQQRVSTTVTQNNNSEFAWPGASSWALNGRNSLMNP GPAMASHKEGEDRFFPLSGSLIFGKQGTGRDNVDADKVMITNEEEIKTTNPVATESYGQVATNHQ SAQAQAQTGWVQNQGILPGMVWQDRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGMKHPPPQILIK NTPVPADPPTAFNKDKLNSFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSNNVEFAV STEGVYSEPRPIGTRYLTRNL (SEQ ID NO: 147)
AAVhu32	n/a	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPGNGLDKGEPV NAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRLLEPLG LVEEAAKTAPGKKRPVEQSPQEPDSSAGIGKSGSQPAKKKLNFGQTGDTESVPDPGQPIGEPPAA PSGVGSLTMASGGGAPVADNNEGADGVGSSSGNWHCDSQWLGDRVITTSTRTWALPTYNNHLYKQ ISNSTSGGSSNDNAYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKE VTDNNGVKTIANNLTSTVQVFTDSDYQLPYVLGSAHEGCLPPFPADVFMIPQYGYLTLNDGSQAV GRSSFYCLEYFPSQMLRTGNNFQFSYEFENVPFHSSYAHSQSLDRLMNPLIDQYLYYLSKTINGS

Capsid Name	Insert/ modification	Amino Acid Sequence
		GQNQQTLKFSVAGPSNMAVQGRNYIPGPSYRQQRVSTTVTQNNNSEFAWPGASSWALNGRNSLMN PGPAMASHKEGEDRFFPLSGSLIFGKQGTGRDNVDADKVMITNEEEIKTTNPVATESYGQVATNH QSAQAQAQTGWVQNQGILPGMVWQDRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGMKHPPPQILI KNTPVPADPPTAFNKDKLNSFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSNNVEFA VNTEGVYSEPRPIGTRYLTRNL(SEQ ID NO: 148)
AAVrh39		MAADGYLPDWLEDNLSEGIREWWALKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPV NAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG LVEEAAKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPAKKRLNFGQTGDSESVPDPQPIGEPPAG PSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQ ISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLSFKLFNIQVKE VTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQAV GRSSFYCLEYFPSQMLRTGNNFEFSYTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTG GTQGTQQLLFSQAGPANMSAQAKNWLPGPCYRQQRVSTTLSQNNNSNFAWTGATKYHLNGRDSLV NPGVAMATHKDDEERFFPSSGVLMFGKQGAGRDNVDYSSVMLTSEEEIKTTNPVATEQYGVVADN LQQTNTGPIVGNVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPQIL IKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSTNVDF AVNTEGTYSEPRPIGTRYLTRNL (SEQ ID NO: 150)
AAV9	n/a	MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDNARGLVLPGYKYLGPGNGLDKGEPV NAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRLLEPLG LVEEAAKTAPGKKRPVEQSPQEPDSSAGIGKSGAQPAKKRLNFGQTGDTESVPDPQPIGEPPAAP SGVGSLTMASGGGAPVADNNEGADGVGSSSGNWHCDSQWLGDRVITTSTRTWALPTYNNHLYKQI SNSTSGGSSNDNAYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEV TDNNGVKTIANNLTSTVQVFTDSDYQLPYVLGSAHEGCLPPFPADVFMIPQYGYLTLNDGSQAVG RSSFYCLEYFPSQMLRTGNNFQFSYEFENVPFHSSYAHSQSLDRLMNPLIDQYLYYLSKTINGSG QNQQTLKFSVAGPSNMAVQGRNYIPGPSYRQQRVSTTVTQNNNSEFAWPGASSWALNGRNSLMNP GPAMASHKEGEDRFFPLSGSLIFGKQGTGRDNVDADKVMITNEEEIKTTNPVATESYGQVATNHQ SAQAQAQTGWVQNQGILPGMVWQDRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGMKHPPPQILIK NTPVPADPPTAFNKDKLNSFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSNNVEFAV NTEGVYSEPRPIGTRYLTRNL(SEQ ID NO: 151)
AAVrh10	n/a	MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPV NAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFCGNLGRAVFQAKKRVLEPLG LVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPAKKRLNFGQTGDSESVPDPQPIGEPPAG PSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQ ISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKE VTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQAV GRSSFYCLEYFPSQMLRTGNNFEFSYQFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTG GTAGTQQLLFSQAGPNNMSAQAKNWLPGPCYRQQRVSTTLSQNNNSNFAWTGATKYHLNGRDSLV NPGVAMATHKDDEERFFPSSGVLMFGKQGAGKDNVDYSSVMLTSEEEIKTTNPVATEQYGVVADN LQQQNAAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPQIL IKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSTNVDF AVNTDGTYSEPRPIGTRYLTRNL (SEQ ID NO: 152)
AAVhu37	n/a	MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPV NAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG LVEEAAKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPAKKRLNFGQTGDSESVPDPQPIGEPPAG PSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQ ISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLSFKLFNIQVKE VTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQAV GRSSFYCLEYFPSQMLRTGNNFEFSYTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTG GTQGTQQLLFSQAGPANMSAQAKNWLPGPCYRQQRVSTTLSQNNNSNFAWTGATKYHLNGRDSLV NPGVAMATHKDDEERFFPSSGVLMFGKQGAGRDNVDYSSVMLTSEEEIKTTNPVATEQYGVVADN LQQTNTGPIVGNVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPQIL IKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSTNVDF AVNTEGTYSEPRPIGTRYLTRNL (SEQ ID NO: 153)
AAV3B	n/a	MAADGYLPDWLEDNLSEGIREWWALKPGVPQPKANQQHQDNRRGLVLPGYKYLGPGNGLDKGEPV NEADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRILEPLG LVEEAAKTAPGKKRPVDQSPQEPDSSSGVGKSGKQPARKRLNFGQTGDSESVPDPQPLGEPPAAP TSLGSNTMASGGGAPMADNNEGADGVGNSSGNWHCDSQWLGDRVITTSTRTWALPTYNNHLYKQI SSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKKLSFKLFNIQVKEVTQ NDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNGSQAVGRS SFYCLEYFPSQMLRTGNNFQFSYTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQGTTSGT TNQSRLLFSQAGPQSMSLQARNWLPGPCYRQQRLSKTANDNNNSNFPWTAASKYHLNGRDSLVNP GPAMASHKDDEEKFFPMHGNLIFGKEGTTASNAELDNVMITDEEEIRTTNPVATEQYGTVANNLQ SSNTAPTTRTVNDQGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQIMIK NTPVPANPPTTFSPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTV

Capsid Name	Insert/ modification	Amino Acid Sequence
		DTNGVYSEPRPIGTRYLTRNL(SEQ ID NO: 154)
AAVrh.20	n/a	MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPV NAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG LVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKTGQQPAKKRLNFGQTGDSESVPDPQPIGEPPAG PSGLGSGTMAAGGAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQ ISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKE VTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQAV GRSSFYCLEYFPSQMLRTGNNFEFSYQFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTG GTAGTQQLLFSQAGPNNMSAQAKNWLPGPCYRQQRVSTTLSQNNNSNFAWTGATKYHLNGRDSLV NPGVAMATHKDDEERFFPSSGVLMFGKQGAGKDNVDYSSVMLTSEEEIKTTNPVATEQYGVVADN LQQQNAAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPQIL IKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSTNVDF AVNTEGTYSEPRPIGTRYLTRNL (SEQ ID NO: 155)
AAVrh.74 version 1	n/a	MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDNGRGLVLPGYKYLGPFNGLDKGEPV NAADAAALEHDKAYDQQLQAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG LVESPVKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPAKKRLNFGQTGDSESVPDPQPIGEPPAG PSGLGSGTMAAGGAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQ ISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKE VTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQAV GRSSFYCLEYFPSQMLRTGNNFEFSYNFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTG GTAGTQQLLFSQAGPNNMSAQAKNWLPGPCYRQQRVSTTLSQNNNSNFAWTGATKYHLNGRDSLV NPGVAMATHKDDEERFFPSSGVLMFGKQGAGKDNVDYSSVMLTSEEEIKTTNPVATEQYGVVADN LQQQNAAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPQIL IKNTPVPADPPTTFTKAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSTNVDF AVNTEGTYSEPRPIGTRYLTRNL (SEQ ID NO: 156)
AAVrh.74 version 2	n/a	MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDNGRGLVLPGYKYLGPFNGLDKGEPV NAADAAALEHDKAYDQQLQAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG LVESPVKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPAKKRLNFGQTGDSESVPDPQPIGEPPAG PSGLGSGTMAAGGAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQ ISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKE VTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQAV GRSSFYCLEYFPSQMLRTGNNFEFSYNFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTG GTAGTQQLLFSQAGPNNMSAQAKNWLPGPCYRQQRVSTTLSQNNNSNFAWTGATKYHLNGRDSLV NPGVAMATHKDDEERFFPSSGVLMFGKQGAGKDNVDYSSVMLTSEEEIKTTNPVATEQYGVVADN LQQQNAAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPQIL IKNTPVPADPPTTFNQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSTNVDF AVNTEGTYSEPRPIGTRYLTRNL (SEQ ID NO: 157)

Capsid Name	Insert/ modification	Amino Acid Sequence
AAV9.AAA	496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSGQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 158)
AAV9.AAA.VR4-peptide 1	SGTVIRS (SEQ ID NO: 1) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SGTVIRS** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 159)
AAV9.AAA.VR4-peptide 2	GRPAP (SEQ ID NO: 2) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**GRPAP** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 160)
AAV9.AAA.VR4-peptide 3	KDQKIGP (SEQ ID NO: 3) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**KDQKIGP** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 161)
AAV9.AAA.VR4-peptide 4	TRQYVPG (SEQ ID NO: 4) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**TRQYVPG** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF

Capsid Name	Insert/ modification	Amino Acid Sequence
		AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 162)
AAV9.AAA.VR4-peptide 5	VQVGRAA (SEQ ID NO: 5) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**VQVGRAA** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 163)
AAV9.AAA.VR4-peptide 6	FTQSRGG (SEQ ID NO: 6) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**FTQSRGG** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 164)
AAV9.AAA.VR4-peptide 7	SRSDRPA (SEQ ID NO: 7) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SRSDRPA** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 165)
AAV9.AAA.VR4-peptide 8	VQVGRTS (SEQ ID NO: 8) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**VQVGRTS** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 166)
AAV9.AAA.VR4-peptide 9	SSGSQKF (SEQ ID NO: 9) and 496NNN498 substitution	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SSGSQKF** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT

Capsid Name	Insert/ modification	Amino Acid Sequence
	to AAA	GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 167)
AAV9.AAA.VR4-peptide 10	SGTVLRS (SEQ ID NO: 10) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SGTVLRS** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 168)
AAV9.AAA.VR4-peptide 11	SHTKSAT (SEQ ID NO: 11) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SHTKSAT** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 169)
AAV9.AAA.VR4-peptide 12	DQARVRI (SEQ ID NO: 12) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**DQARVRI** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 170)
AAV9.AAA.VR4-peptide 13	RGAVQKV (SEQ ID NO: 13) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**RGAVQKV** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 171)
AAV9.AAA.VR4-peptide 14	VGRDSRS (SEQ ID NO: 14)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**VGRDSRS** GQNQQTLKF SVAGPSNMAV

Capsid Name	Insert/ modification	Amino Acid Sequence
	and 496NNN498 substitution to AAA	QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 172)
AAV9.AAA.VR4-peptide 15	SRSDRQF (SEQ ID NO: 15) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SRSDRQF** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 173)
AAV9.AAA.VR4-peptide 16	VTRSQIM (SEQ ID NO: 16) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**VTRSQIM** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 174)
AAV9.AAA.VR4-peptide 17	QVGARHP (SEQ ID NO: 17) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**QVGARHP** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 175)
AAV9.AAA.VR4-peptide 18	GRAAASL (SEQ ID NO: 18) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**GRAAASL** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 176)
AAV9.AAA.VR4	PSGVPIR (SEQ ID NO: 19)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI

Capsid Name	Insert/ modification	Amino Acid Sequence
-peptide 19	and 496NNN498 substitution to AAA	TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**PSGVPIR** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 177)
AAV9.AAA.VR4-peptide 20	MSYNQAT (SEQ ID NO: 20) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**MSYNQAT** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 178)
AAV9.AAA.VR4-peptide 21	ITGGVRV (SEQ ID NO: 21) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**ITGGVRV** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 179)
AAV9.AAA.VR4-peptide 22	SRSDRQV (SEQ ID NO: 22) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SRSDRQV** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 180)
AAV9.AAA.VR4-peptide 23	TSGVPIR (SEQ ID NO: 23) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**TSGVPIR** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 181)
AAV9.AAA.VR4	AQVGRAS	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE

Capsid Name	Insert/ modification	Amino Acid Sequence
-peptide 24	(SEQ ID NO: 24) and 496NNN498 substitution to AAA	SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**AQVGRAS** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 182)
AAV9.AAA.VR4 -peptide 25	VKASHHS (SEQ ID NO: 25) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**VKASHHS** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 183)
AAV9.AAA.VR4 -peptide 26	SHTKTVT (SEQ ID NO: 26) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SHTKTVT** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 184)
AAV9.AAA.VR4 -peptide 27	GSVQTVR (SEQ ID NO: 27) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**GSVQTVR** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 185)
AAV9.AAA.VR4 -peptide 28	DTRIRSM (SEQ ID NO: 28) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**DTRIRSM** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 186)

Capsid Name	Insert/ modification	Amino Acid Sequence
AAV9.AAA.VR4-peptide 29	SRTKTAT (SEQ ID NO: 29) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SRTKTAT** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 187)
AAV9.AAA.VR4-peptide 30	QVGARQS (SEQ ID NO: 30) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**QVGARQS** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 188)
AAV9.AAA.VR4-peptide 37	SVTSVRV (SEQ ID NO: 37) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SVTSVRV** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 189)
AAV9.AAA.VR4-peptide 45	MKYRGTD (SEQ ID NO: 45) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**MKYRGTD** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 190)
AAV9.AAA.VR4-peptide 76	SIAKNSA (SEQ ID NO: 76) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SIAKNSA** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF

Capsid Name	Insert/ modification	Amino Acid Sequence
		AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 191)
AAV9.AAA.VR4-peptide 82	HMGQYGK (SEQ ID NO:82) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**HMGQYGK** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 192)
AAV9.AAA.VR4-peptide 109	MRAVSQL (SEQ ID NO: 109) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**MRAVSQL** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 193)
AAV9.AAA.VR4-peptide 110	PRQYVPG (SEQ ID NO: 110) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**PRQYVPG** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 194)
AAV9.AAA.VR4-peptide 111	RSSSGR (SEQ ID NO: 111) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**RSSSGR** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 195)
AAV9.AAA.VR4-peptide 112	VVKSTKS (SEQ ID NO: 112) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**VVKSTKS** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP

Capsid Name	Insert/ modification	Amino Acid Sequence
		VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 196)
AAV9.AAA.VR4-peptide 118	PSSVQHR (SEQ ID NO: 118) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**PSSVQHR** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 197)
AAV9.AAA.VR4-peptide 119	SSSVQHR (SEQ ID NO: 119) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SSSVQHR** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 198)
AAV9.AAA.VR4-peptide 120	SGMQERR (SEQ ID NO: 120) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SGMQERR** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 199)
AAV9.AAA.VR4-peptide 121	LERGNLE (SEQ ID NO: 121) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**LERGNLE** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 200)

Capsid Name	Insert/ modification	Amino Acid Sequence
AAV9.AAA.VR4-peptide 122	YRDQRVT (SEQ ID NO: 122) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**YRDQRVT** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 201)
AAV9.AAA.VR4-peptide 123	PSAVQHR (SEQ ID NO: 123) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**PSAVQHR** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 202)
AAV9.AAA.VR4-peptide 124	YVGGRAV (SEQ ID NO: 124) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**YVGGRAV** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 203)
AAV9.AAA.VR4-peptide 125	IGSRGVA (SEQ ID NO: 125) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**IGSRGVA** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 204)
AAV9.AAA.VR4-peptide 126	SDVSRPR (SEQ ID NO: 126) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SDVSRPR** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF

Capsid Name	Insert/ modification	Amino Acid Sequence
		AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 205)
AAV9.AAA.VR4-peptide 127	GSVRQAA (SEQ ID NO: 127) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**GSVRQAA** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 206)
AAV9.AAA.VR4-peptide 128	QSPHTSQ (SEQ ID NO: 128) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**QSPHTSQ** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 207)
AAV9.AAA.VR4-peptide 129	ASQAYHG (SEQ ID NO: 129) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**ASQAYHG** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 208)
AAV9.AAA.VR4-peptide 135	X_1-Q-V-X_2-X_3-X_4-X_5, (SEQ ID NO: 135) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**X_1QV$X_2$$X_3$$X_4$$X_5$** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 209) wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is any amino acid and X_5 is S, G, V or A

Capsid Name	Insert/ modification	Amino Acid Sequence
AAV9.AAA.VR4-peptide 136	X_1-Q-V-X_2-X_3-X_4-X_5, (SEQ ID NO: 136) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**X_1QV$X_2$$X_3$$X_4$$X_5$** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 210) wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is any amino acid and X_5 is S or A
AAV9.AAA.VR4-peptide 137	X_1-Q-V-X_2-X_3-X_4-X_5, (SEQ ID NO: 137) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**X_1QV$X_2$$X_3$$X_4$$X_5$** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 211) wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is T, S, V, Y, A or P and X_5 is S, G, V or A
AAV9.AAA.VR4-peptide 138	X_1-Q-V-X_2-X_3-X_4-X_5, (SEQ ID NO: 138) and 496NNN498 substitution to AAA	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**X_1QV$X_2$$X_3$$X_4$$X_5$** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQ**AAA**SEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 212) wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is T, S, V, Y, A or P and X_5 is S or A

Capsid Name	Insert/ modification	Amino Acid Sequence
AAV9.V R4-peptide 1	SGTVIRS (SEQ ID NO: 1)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SGTVIRS** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 213)
AAV9.V R4-peptide 2	GRPAP (SEQ ID NO: 2)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**GRPAP** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 214)
AAV9.V R4-peptide 3	KDQKIGP (SEQ ID NO: 3)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**KDQKIGP** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 215)
AAV9.V R4-peptide 4	TRQYVPG (SEQ ID NO: 4)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**TRQYVPG** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 216)
AAV9.V R4-peptide 5	VQVGRAA (SEQ ID NO: 5)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**VQVGRAA** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF

Capsid Name	Insert/ modification	Amino Acid Sequence
		AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 217)
AAV9.V R4-peptide 6	FTQSRGG (SEQ ID NO: 6)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**FTQSRGG** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 218)
AAV9.V R4-peptide 7	SRSDRPA (SEQ ID NO: 7)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SRSDRPA** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 219)
AAV9.V R4-peptide 8	VQVGRTS (SEQ ID NO: 8)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**VQVGRTS** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO:220)
AAV9.V R4-peptide 9	SSGSQKF (SEQ ID NO: 9)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SSGSQKF** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 221)
AAV9.V R4-peptide 10	SGTVLRS (SEQ ID NO: 10)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SGTVLRS** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP

Capsid Name	Insert/ modification	Amino Acid Sequence
		VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 222)
AAV9.VR4-peptide 11	SHTKSAT (SEQ ID NO: 11)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SHTKSAT** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 223)
AAV9.VR4-peptide 12	DQARVRI (SEQ ID NO: 12)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**DQARVRI** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 224)
AAV9.VR4-peptide 13	RGAVQKV (SEQ ID NO: 13)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**RGAVQKV** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 225)
AAV9.VR4-peptide 14	VGRDSRS (SEQ ID NO: 14)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**VGRDSRS** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 226)
AAV9.VR4-peptide 15	SRSDRQF (SEQ ID NO: 15)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SRSDRQF** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT

Capsid Name	Insert/ modification	Amino Acid Sequence
		GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 227)
AAV9.VR4-peptide 16	VTRSQIM (SEQ ID NO: 16)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**VTRSQIM** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 228)
AAV9.VR4-peptide 17	QVGARHP (SEQ ID NO: 17)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**QVGARHP** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 229)
AAV9.VR4-peptide 18	GRAAASL (SEQ ID NO: 18)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**GRAAASL** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 230)
AAV9.VR4-peptide 19	PSGVPIR (SEQ ID NO: 19)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**PSGVPIR** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 231)
AAV9.VR4-peptide 20	MSYNQAT (SEQ ID NO: 20)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**MSYNQAT** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR

Capsid Name	Insert/ modification	Amino Acid Sequence
		FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 232)
AAV9.VR4-peptide 21	ITGGVRV (SEQ ID NO: 21)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**ITGGVRV** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 233)
AAV9.VR4-peptide 22	SRSDRQV (SEQ ID NO: 22)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SRSDRQV** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 234)
AAV9.VR4-peptide 23	TSGVPIR (SEQ ID NO: 23)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**TSGVPIR** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 235)
AAV9.VR4-peptide 24	AQVGRAS (SEQ ID NO: 24)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**AQVGRAS** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 236)
AAV9.VR4-peptide 25	VKASHHS (SEQ ID NO: 25)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**VKASHHS** GQNQQTLKF SVAGPSNMAV

Capsid Name	Insert/ modification	Amino Acid Sequence
		QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 237)
AAV9.VR4-peptide 26	SHTKTVT (SEQ ID NO: 26)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SHTKTVT** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 238)
AAV9.VR4-peptide 27	GSVQTVR (SEQ ID NO: 27)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**GSVQTVR** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 239)
AAV9.VR4-peptide 28	DTRIRSM (SEQ ID NO: 28)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**DTRIRSM** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 240)
AAV9.VR4-peptide 29	SRTKTAT (SEQ ID NO: 29)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SRTKTAT** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 241)
AAV9.VR4-peptide 30	QVGARQS (SEQ ID NO: 30)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV

Capsid Name	Insert/ modification	Amino Acid Sequence
		PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**QVGARQS** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 242)
AAV9.VR4-peptide 37	SVTSVRV (SEQ ID NO: 37)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SVTSVRV** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 243)
AAV9.VR4-peptide 45	MKYRGTD (SEQ ID NO: 45)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**MKYRGTD** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 244)
AAV9.VR4-peptide 76	SIAKNSA (SEQ ID NO: 76)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SIAKNSA** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 245)
AAV9.VR4-peptide 82	HMGQYGK (SEQ ID NO:82)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**HMGQYGK** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 246)
AAV9.VR4-peptide 109	MRAVSQL (SEQ ID NO: 109)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH

Capsid Name	Insert/ modification	Amino Acid Sequence
		EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**MRAVSQL** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 247)
AAV9.VR4-peptide 110	PRQYVPG (SEQ ID NO: 110)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**PRQYVPG** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 248)
AAV9.VR4-peptide 111	RSSSGR (SEQ ID NO: 111)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**RSSSGR** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 249)
AAV9.VR4-peptide 112	VVKSTKS (SEQ ID NO: 112)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**VVKSTKS** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 250)
AAV9.VR4-peptide 118	PSSVQHR (SEQ ID NO: 118)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**PSSVQHR** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 251)

Capsid Name	Insert/ modification	Amino Acid Sequence
AAV9.VR4-peptide 119	SSSVQHR (SEQ ID NO: 119)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SSSVQHR** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 252)
AAV9.VR4-peptide 120	SGMQERR (SEQ ID NO: 120)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SGMQERR** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 253)
AAV9.VR4-peptide 121	LERGNLE (SEQ ID NO: 121)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**LERGNLE** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 254)
AAV9.VR4-peptide 122	YRDQRVT (SEQ ID NO: 122)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**YRDQRVT** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 255)
AAV9.VR4-peptide 123	PSAVQHR (SEQ ID NO: 123)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**PSAVQHR** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF

Capsid Name	Insert/ modification	Amino Acid Sequence
		AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 256)
AAV9.VR4-peptide 124	YVGGRAV (SEQ ID NO: 124)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**YVGGRAV** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 257)
AAV9.VR4-peptide 125	IGSRGVA (SEQ ID NO: 125)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**IGSRGVA** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 258)
AAV9.VR4-peptide 126	SDVSRPR (SEQ ID NO: 126)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**SDVSRPR** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 258)
AAV9.VR4-peptide 127	GSVRQAA (SEQ ID NO: 127)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**GSVRQAA** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 260)
AAV9.VR4-peptide 128	QSPHTSQ (SEQ ID NO: 128)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**QSPHTSQ** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP

Capsid Name	Insert/ modification	Amino Acid Sequence
		VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 261)
AAV9.VR4-peptide 129	ASQAYHG (SEQ ID NO: 129)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**ASQAYHG** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 262)
AAV9.VR4-peptide 135	X_1-Q-V-X_2-X_3-X_4-X_5, (SEQ ID NO: 135)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**X_1QV$X_2$$X_3$$X_4$$X_5$** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 263) wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is any amino acid and X_5 is S, G, V or A
AAV9.VR4-peptide 136	X_1-Q-V-X_2-X_3-X_4-X_5, (SEQ ID NO: 136)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**X_1QV$X_2$$X_3$$X_4$$X_5$** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 264) wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is any amino acid and X_5 is S or A
AAV9.VR4-peptide 137	X_1-Q-V-X_2-X_3-X_4-X_5, (SEQ ID NO: 137)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPICE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**X_1QV$X_2$$X_3$$X_4$$X_5$** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 265) wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is T, S, V, Y, A or P and X_5 is S, G, V or A

Capsid Name	Insert/ modification	Amino Acid Sequence
AAV9.VR4-peptide 138	X_1-Q-V-X_2-X_3-X_4-X_5, (SEQ ID NO: 138)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**X_1QV$X_2$$X_3$$X_4$$X_5$** GQNQQTLKF SVAGPSNMAV QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 266) wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is T, S, V, Y, A or P and X_5 is S or A
AAVhu32.AAA	497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGSGQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 267)
AAVhu32.AAA.VR4-peptide 1	SGTVIRS (SEQ ID NO: 1) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SGTVIRS** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 268)
AAVhu32.AAA.VR4-peptide 2	GRPAP (SEQ ID NO: 2) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**GRPAP** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 269)

Capsid Name	Insert/ modification	Amino Acid Sequence
AAVhu32.AAA.VR4-peptide 3	KDQKIGP (SEQ ID NO: 3) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**KDQKIGP** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 270)
AAVhu32.AAA.VR4-peptide 4	TRQYVPG (SEQ ID NO: 4) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**TRQYVPG** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 271)
AAVhu32.AAA.VR4-peptide 5	VQVGRAA (SEQ ID NO: 5) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**VQVGRAA** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 272)
AAVhu32.AAA.VR4-peptide 6	FTQSRGG (SEQ ID NO: 6) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**FTQSRGG** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 273)
AAVhu32.AAA.VR4-peptide 7	SRSDRPA (SEQ ID NO: 7) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SRSDRPA** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI

Capsid Name	Insert/ modification	Amino Acid Sequence
		KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 274)
AAVhu32.AAA.VR4-peptide 8	VQVGRTS (SEQ ID NO: 8) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**VQVGRTS** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 275)
AAVhu32.AAA.VR4-peptide 9	SSGSQKF (SEQ ID NO: 9) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SSGSQKF** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 276)
AAVhu32.AAA.VR4-peptide 10	SGTVLRS (SEQ ID NO: 10) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SGTVLRS** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 277)
AAVhu32.AAA.VR4-peptide 11	SHTKSAT (SEQ ID NO: 11) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SHTKSAT** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 278)

Capsid Name	Insert/ modification	Amino Acid Sequence
AAVhu32.AAA.VR4-peptide 12	DQARVRI (SEQ ID NO: 12) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**DQARVRI** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 279)
AAVhu32.AAA.VR4-peptide 13	RGAVQKV (SEQ ID NO: 13) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**RGAVQKV** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 280)
AAVhu32.AAA.VR4-peptide 14	VGRDSRS (SEQ ID NO: 14) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**VGRDSRS** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 281)
AAVhu32.AAA.VR4-peptide 15	SRSDRQF (SEQ ID NO: 15) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SRSDRQF** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 282)
AAVhu32.AAA.VR4-peptide 16	VTRSQIM (SEQ ID NO: 16) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**VTRSQIM** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI

Capsid Name	Insert/ modification	Amino Acid Sequence
		KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 283)
AAVhu32.AAA.VR4-peptide 17	QVGARHP (SEQ ID NO: 17) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**QVGARHP** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 284)
AAVhu32.AAA.VR4-peptide 18	GRAAASL (SEQ ID NO: 18) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**GRAAASL** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 285)
AAVhu32.AAA.VR4-peptide 19	PSGVPIR (SEQ ID NO: 19) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**PSGVPIR** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 286)
AAVhu32.AAA.VR4-peptide 20	MSYNQAT (SEQ ID NO: 20) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**MSYNQAT** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 287)

Capsid Name	Insert/ modification	Amino Acid Sequence
AAVhu32.AAA.VR4-peptide 21	ITGGVRV (SEQ ID NO: 21) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**ITGGVRV** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 288)
AAVhu32.AAA.VR4-peptide 22	SRSDRQV (SEQ ID NO: 22) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SRSDRQV** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 289)
AAVhu32.AAA.VR4-peptide 23	TSGVPIR (SEQ ID NO: 23) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**TSGVPIR** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 290)
AAVhu32.AAA.VR4-peptide 24	AQVGRAS (SEQ ID NO: 24) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**AQVGRAS** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 291)
AAVhu32.AAA.VR4-peptide 25	VKASHHS (SEQ ID NO: 25) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**VKASHHS** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI

Capsid Name	Insert/ modification	Amino Acid Sequence
		KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 292)
AAVhu32.AAA.VR4-peptide 26	SHTKTVT (SEQ ID NO: 26) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SHTKTVT** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 293)
AAVhu32.AAA.VR4-peptide 27	GSVQTVR (SEQ ID NO: 27) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**GSVQTVR** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 294)
AAVhu32.AAA.VR4-peptide 28	DTRIRSM (SEQ ID NO: 28) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**DTRIRSM** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 295)
AAVhu32.AAA.VR4-peptide 29	SRTKTAT (SEQ ID NO: 29) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SRTKTAT** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 296)

Capsid Name	Insert/ modification	Amino Acid Sequence
AAVhu32.AAA.VR4-peptide 30	QVGARQS (SEQ ID NO: 30) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGSQVGARQS GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQAAAS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 297)
AAVhu32.AAA.VR4-peptide 37	SVTSVRV (SEQ ID NO: 37) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGSSVTSVRV GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQAAAS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 298)
AAVhu32.AAA.VR4-peptide 45	MKYRGTD (SEQ ID NO: 45) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGSMKYRGTD GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQAAAS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 299)
AAVhu32.AAA.VR4-peptide 76	SIAKNSA (SEQ ID NO: 76) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGSSIAKNSA GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQAAAS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 300)
AAVhu32.AAA.VR4-peptide 82	HMGQYGK (SEQ ID NO:82) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGSHMGQYGK GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQAAAS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI

Capsid Name	Insert/ modification	Amino Acid Sequence
		KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 301)
AAVhu32.AAA.VR4-peptide 109	MRAVSQL (SEQ ID NO: 109) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGSMRAVSQL GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQAAAS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 302)
AAVhu32.AAA.VR4-peptide 110	PRQYVPG (SEQ ID NO: 110) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGSPRQYVPG GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQAAAS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 303)
AAVhu32.AAA.VR4-peptide 111	RSSSGR (SEQ ID NO: 111) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGSRSSSGR GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQAAAS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 304)
AAVhu32.AAA.VR4-peptide 112	VVKSTKS (SEQ ID NO: 112) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGSVVKSTKS GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQAAAS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 305)

Capsid Name	Insert/ modification	Amino Acid Sequence
AAVhu32.AAA.VR4-peptide 118	PSSVQHR (SEQ ID NO: 118) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**PSSVQHR** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 306)
AAVhu32.AAA.VR4-peptide 119	SSSVQHR (SEQ ID NO: 119) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SSSVQHR** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 307)
AAVhu32.AAA.VR4-peptide 120	SGMQERR (SEQ ID NO: 120) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SGMQERR** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 308)
AAVhu32.AAA.VR4-peptide 121	LERGNLE (SEQ ID NO: 121) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**LERGNLE** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 309)
AAVhu32.AAA.VR4-peptide 122	YRDVRQT (SEQ ID NO: 122) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**YRDVRQT** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI

Capsid Name	Insert/ modification	Amino Acid Sequence
		KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 310)
AAVhu32.AAA.VR4-peptide 123	PSAVQHR (SEQ ID NO: 123) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**PSAVQHR** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 311)
AAVhu32.AAA.VR4-peptide 124	YVGGRAV (SEQ ID NO: 124) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**YVGGRAV** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 312)
AAVhu32.AAA.VR4-peptide 125	IGSRGVA (SEQ ID NO: 125) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**IGSRGVA** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 313)
AAVhu32.AAA.VR4-peptide 126	SDVSRPR (SEQ ID NO: 126) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SDVSRPR** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 314)

Capsid Name	Insert/ modification	Amino Acid Sequence
AAVhu32.AAA.VR4-peptide 127	GSVRQAA (SEQ ID NO: 127) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**GSVRQAA** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 315)
AAVhu32.AAA.VR4-peptide 128	QSPHTSQ (SEQ ID NO: 128) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**QSPHTSQ** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 316)
AAVhu32.AAA.VR4-peptide 129	ASQAYHG (SEQ ID NO: 129) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**ASQAYHG** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 317)
AAVhu32.AAA.VR4-peptide 135	X_1-Q-V-X_2-X_3-X_4-X_5, (SEQ ID NO: 135) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**X_1QV$X_2$$X_3$$X_4$$X_5$** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 318) wherein X_1 is V or A, X_2 is G or V or A, X_3 is R or H, X_4 is any amino acid and X_5 is S, G, V or A

Capsid Name	Insert/ modification	Amino Acid Sequence
AAVhu32.AAA.VR4-peptide 136	X_1-Q-V-X_2-X_3-X_4-X_5, (SEQ ID NO: 136) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**X_1QV$X_2$$X_3$$X_4$$X_5$** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 319) wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is any amino acid and X_5 is S or A
AAVhu32.AAA.VR4-peptide 137	X_1-Q-V-X_2-X_3-X_4-X_5, (SEQ ID NO: 137) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**X_1QV$X_2$$X_3$$X_4$$X_5$** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 320) wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is T, S, V, Y, A or P and X_5 is S, G, V or A
AAVhu32.AAA.VR4-peptide 138	X_1-Q-V-X_2-X_3-X_4-X_5, (SEQ ID NO: 138) and 497NNN499 substitution to AAA	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**X_1QV$X_2$$X_3$$X_4$$X_5$** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQ**AAA**S EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 321) wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is T, S, V, Y, A or P and X_5 is S or A
AAVhu32.VR4-peptide 1	SGTVIRS (SEQ ID NO: 1)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SGTVIRS** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 322)

Capsid Name	Insert/ modification	Amino Acid Sequence
AAVhu32.VR4-peptide 2	GRPAP (SEQ ID NO: 2)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**GRPAP** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 323)
AAVhu32.VR4-peptide 3	KDQKIGP (SEQ ID NO: 3)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**KDQKIGP** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 324)
AAVhu32.VR4-peptide 4	TRQYVPG (SEQ ID NO: 4)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**TRQYVPG** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 325)
AAVhu32.VR4-peptide 5	VQVGRAA (SEQ ID NO: 5)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**VQVGRAA** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 326)
AAVhu32.VR4-peptide 6	FTQSRGG (SEQ ID NO: 6)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**FTQSRGG** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI

Capsid Name	Insert/ modification	Amino Acid Sequence
		KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 327)
AAVhu32.VR4-peptide 7	SRSDRPA (SEQ ID NO: 7)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SRSDRPA** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 328)
AAVhu32.VR4-peptide 8	VQVGRTS (SEQ ID NO: 8)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**VQVGRTS** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 329)
AAVhu32.VR4-peptide 9	SSGSQKF (SEQ ID NO: 9)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SSGSQKF** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 330)
AAVhu32.VR4-peptide 10	SGTVLRS (SEQ ID NO: 10)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SGTVLRS** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 331)
AAVhu32.VR4-peptide 11	SHTKSAT (SEQ ID NO: 11)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SHTKSAT** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA

Capsid Name	Insert/ modification	Amino Acid Sequence
		QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 332)
AAVhu32.VR4-peptide 12	DQARVRI (SEQ ID NO: 12)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYV_GSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**DQARVRI** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 333)
AAVhu32.VR4-peptide 13	RGAVQKV (SEQ ID NO: 13)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYV_GSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**RGAVQKV** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 334)
AAVhu32.VR4-peptide 14	VGRDSRS (SEQ ID NO: 14)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYV_GSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**VGRDSRS** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 335)
AAVhu32.VR4-peptide 15	SRSDRQF (SEQ ID NO: 15)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYV_GSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SRSDRQF** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 336)
AAVhu32.VR4-peptide 16	VTRSQIM (SEQ ID NO: 16)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYV_GSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**VTRSQIM** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE

Capsid Name	Insert/ modification	Amino Acid Sequence
		GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 337)
AAVhu32.VR4-peptide17	QVGARHP (SEQ ID NO: 17)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**QVGARHP** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 338)
AAVhu32.VR4-peptide18	GRAAASL (SEQ ID NO: 18)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**GRAAASL** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 339)
AAVhu32.VR4-peptide19	PSGVPIR (SEQ ID NO: 19)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**PSGVPIR** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 340)
AAVhu32.VR4-peptide20	MSYNQAT (SEQ ID NO: 20)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**MSYNQAT** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 341)
AAVhu32.VR4-peptide21	ITGGVRV (SEQ ID NO: 21)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**ITGGVRV** GQNQQ TLKFSVAGPS

Capsid Name	Insert/ modification	Amino Acid Sequence
		NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 342)
AAVhu32.VR4-peptide 22	SRSDRQV (SEQ ID NO: 22)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SRSDRQV** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 343)
AAVhu32.VR4-peptide 23	TSGVPIR (SEQ ID NO: 23)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**TSGVPIR** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 344)
AAVhu32.VR4-peptide 24	AQVGRAS (SEQ ID NO: 24)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**AQVGRAS** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 345)
AAVhu32.VR4-peptide 25	VKASHHS (SEQ ID NO: 25)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**VKASHHS** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 346)
AAVhu32.VR4-peptide 26	SHTKTVT (SEQ ID NO: 26)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN

Capsid Name	Insert/ modification	Amino Acid Sequence
		VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SHTKTVT** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 347)
AAVhu32.VR4-peptide 27	GSVQTVR (SEQ ID NO: 27)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**GSVQTVR** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 348)
AAVhu32.VR4-peptide 28	DTRIRSM (SEQ ID NO: 28)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**DTRIRSM** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 349)
AAVhu32.VR4-peptide 29	SRTKTAT (SEQ ID NO: 29)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SRTKTAT** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 350)
AAVhu32.VR4-peptide 30	QVGARQS (SEQ ID NO: 30)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**QVGARQS** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 351)
AAVhu32.VR4-peptide 37	SVTSVRV (SEQ ID NO: 37)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA

Capsid Name	Insert/ modification	Amino Acid Sequence
		HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SVTSVRV** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 352)
AAVhu32.VR4-peptide 45	MKYRGTD (SEQ ID NO: 45)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**MKYRGTD** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 353)
AAVhu32.VR4-peptide 76	SIAKNSA (SEQ ID NO: 76)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SIAKNSA** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 354)
AAVhu32.VR4-peptide 82	HMGQYGK (SEQ ID NO:82)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**HMGQYGK** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 355)
AAVhu32.VR4-peptide 109	MRAVSQL (SEQ ID NO: 109)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**MRAVSQL** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 356)
AAVhu32.VR4-peptide 110	PRQYVPG (SEQ ID NO: 110)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ

Capsid Name	Insert/ modification	Amino Acid Sequence
		RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYV_GSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**PRQYVPG** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 357)
AAVhu32.VR4-peptide 111	RSSSGR (SEQ ID NO: 111)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYV_GSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**RSSSGR** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 358)
AAVhu32.VR4-peptide 112	VVKSTKS (SEQ ID NO: 112)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYV_GSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**VVKSTKS** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 359)
AAVhu32.VR4-peptide 118	PSSVQHR (SEQ ID NO: 118)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYV_GSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**PSSVQHR** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 360)
AAVhu32.VR4-peptide 119	SSSVQHR (SEQ ID NO: 119)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYV_GSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SSSVQHR** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 361)

Capsid Name	Insert/ modification	Amino Acid Sequence
AAVhu32.VR4-peptide 120	SGMQERR (SEQ ID NO: 120)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SGMQERR** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 362)
AAVhu32.VR4-peptide 121	LERGNLE (SEQ ID NO: 121)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**LERGNLE** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 363)
AAVhu32.VR4-peptide 122	YRDVRQT (SEQ ID NO: 122)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**YRDVRQT** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 364)
AAVhu32.VR4-peptide 123	PSAVQHR (SEQ ID NO: 123)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**PSAVQHR** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 365)
AAVhu32.VR4-peptide 124	YVGGRAV (SEQ ID NO: 124)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**YVGGRAV** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI

Capsid Name	Insert/ modification	Amino Acid Sequence
		KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 366)
AAVhu32.VR4-peptide 125	IGSRGVA (SEQ ID NO: 125)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**IGSRGVA** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 367)
AAVhu32.VR4-peptide 126	SDVSRPR (SEQ ID NO: 126)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**SDVSRPR** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 368)
AAVhu32.VR4-peptide 127	GSVRQAA (SEQ ID NO: 127)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**GSVRQAA** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 369)
AAVhu32.VR4-peptide 128	QSPHTSQ (SEQ ID NO: 128)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**QSPHTSQ** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 370)
AAVhu32.VR4-peptide 129	ASQAYHG (SEQ ID NO: 129)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYVLGSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**ASQAYHG** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA

Capsid Name	Insert/ modification	Amino Acid Sequence
		QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 371)
AAVhu32.VR4-peptide 135	X_1-Q-V-X_2-X_3-X_4-X_5, (SEQ ID NO: 135)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYV_GSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**X_1QV$X_2$$X_3$$X_4$$X_5$** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 372) wherein X_1 is V or A, X_2 is G or V or A, X_3 is R or H, X_4 is any amino acid and X_5 is S, G, V or A
AAVhu32.VR4-peptide 136	X_1-Q-V-X_2-X_3-X_4-X_5, (SEQ ID NO: 136)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYV_GSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**X_1QV$X_2$$X_3$$X_4$$X_5$** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 373) wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is any amino acid and X_5 is S or A
AAVhu32.VR4-peptide 137	X_1-Q-V-X_2-X_3-X_4-X_5, (SEQ ID NO: 137)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYV_GSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**X_1QV$X_2$$X_3$$X_4$$X_5$** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 374) wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is T, S, V, Y, A or P and X_5 is S, G, V or A
AAVhu32.VR4-peptide 138	X_1-Q-V-X_2-X_3-X_4-X_5, (SEQ ID NO: 138)	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPGQPIG EPPAAPSGVG SLTMASGGGA PVADNNEGAD GVGSSSGNWH CDSQWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNSTSGGSS NDNAYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLNFKLFN IQVKEVTDNN GVKTIANNLT STVQVFTDSD YQLPYV_GSA HEGCLPPFPA DVFMIPQYGY LTLNDGSQAV GRSSFYCLEY FPSQMLRTGN NFQFSYEFEN VPFHSSYAHS QSLDRLMNPL IDQYLYYLSK TINGS**X_1QV$X_2$$X_3$$X_4$$X_5$** GQNQQ TLKFSVAGPS NMAVQGRNYI PGPSYRQQRV STTVTQNNNS EFAWPGASSW ALNGRNSLMN PGPAMASHKE GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN NVEFAVNTEG VYSEPRPIGT RYLTRNL(SEQ ID NO: 375)

Capsid Name	Insert/ modification	Amino Acid Sequence
		wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is T, S, V, Y, A or P and X_5 is S or A
AAV5-peptide 113	RHVSASD (SEQ ID NO: 113)	MSFVDHPPDW LEEVGEGLRE FLGLEAGPPK PKPNQQHQDQ ARGLVLPGYN YLGPGNGLDR GEPVNRADEV AREHDISYNE QLEAGDNPYL KYNHADAEFQ EKLADDTSFG GNLGKAVFQA KKRVLEPFGL VEEGAKTAPT GKRIDDHFPK RKKARTEEDS KPSTSSDAEA GPSGSQQLQI PAQPASSLGA DTMSAGGGGP LGDNNQGADG VGNASGDWHC DSTWMGDRVV TKSTRTWVLP SYNNHQYREI KSGSVDGSNA NAYFGYSTPW GYFDFNRFHS HWSPRDWQRL INNYWGFRPR SLRVKIFNIQ VKEVTVQDST TTIANNLTST VQVFTDDDYQ LPYVVGNGTE GCLPAFPPQV FTLPQYGYAT LNRDNTENPT ERSSFFCLEY FPSKMLRTGN NFEFTYNFEE VPFHSSFAPS QNLFKLANPL VDQYLYRFVS TNNTGGVQFN KNLAGRYANT YKNWFPGPMG RTQGWNLGSG VNRASVSAFA TTNRMELEGA SYQVPPQPNG MTNNLQGSNT YALENTMIFN SQPANPGTTA TYLEGNMLIT SESETQPVNR VAYNVGGQMA TNNQSSTT**RHVSASD** AP ATGTYNLQEI VPGSVWMERD VYLQGPIWAK IPETGAHFHP SPAMGGFGLK HPPPMMLIKN TPVPGNITSF SDVPVSSFIT QYSTGQVTVE MEWELKKENS KRWNPEIQYT NNYNDPQFVD FAPDSTGEYR TTRPIGTRYL TRPL(SEQ ID NO: 376)
AAV5-peptide 114	VRSDRDQ (SEQ ID NO: 114)	MSFVDHPPDW LEEVGEGLRE FLGLEAGPPK PKPNQQHQDQ ARGLVLPGYN YLGPGNGLDR GEPVNRADEV AREHDISYNE QLEAGDNPYL KYNHADAEFQ EKLADDTSFG GNLGKAVFQA KKRVLEPFGL VEEGAKTAPT GKRIDDHFPK RKKARTEEDS KPSTSSDAEA GPSGSQQLQI PAQPASSLGA DTMSAGGGGP LGDNNQGADG VGNASGDWHC DSTWMGDRVV TKSTRTWVLP SYNNHQYREI KSGSVDGSNA NAYFGYSTPW GYFDFNRFHS HWSPRDWQRL INNYWGFRPR SLRVKIFNIQ VKEVTVQDST TTIANNLTST VQVFTDDDYQ LPYVVGNGTE GCLPAFPPQV FTLPQYGYAT LNRDNTENPT ERSSFFCLEY FPSKMLRTGN NFEFTYNFEE VPFHSSFAPS QNLFKLANPL VDQYLYRFVS TNNTGGVQFN KNLAGRYANT YKNWFPGPMG RTQGWNLGSG VNRASVSAFA TTNRMELEGA SYQVPPQPNG MTNNLQGSNT YALENTMIFN SQPANPGTTA TYLEGNMLIT SESETQPVNR VAYNVGGQMA TNNQSSTT**VRSDRDQ** AP ATGTYNLQEI VPGSVWMERD VYLQGPIWAK IPETGAHFHP SPAMGGFGLK HPPPMMLIKN TPVPGNITSF SDVPVSSFIT QYSTGQVTVE MEWELKKENS KRWNPEIQYT NNYNDPQFVD FAPDSTGEYR TTRPIGTRYL TRPL(SEQ ID NO: 377)
AAV5-peptide 115	TVVTSIN (SEQ ID NO: 115)	MSFVDHPPDW LEEVGEGLRE FLGLEAGPPK PKPNQQHQDQ ARGLVLPGYN YLGPGNGLDR GEPVNRADEV AREHDISYNE QLEAGDNPYL KYNHADAEFQ EKLADDTSFG GNLGKAVFQA KKRVLEPFGL VEEGAKTAPT GKRIDDHFPK RKKARTEEDS KPSTSSDAEA GPSGSQQLQI PAQPASSLGA DTMSAGGGGP LGDNNQGADG VGNASGDWHC DSTWMGDRVV TKSTRTWVLP SYNNHQYREI KSGSVDGSNA NAYFGYSTPW GYFDFNRFHS HWSPRDWQRL INNYWGFRPR SLRVKIFNIQ VKEVTVQDST TTIANNLTST VQVFTDDDYQ LPYVVGNGTE GCLPAFPPQV FTLPQYGYAT LNRDNTENPT ERSSFFCLEY FPSKMLRTGN NFEFTYNFEE VPFHSSFAPS QNLFKLANPL VDQYLYRFVS TNNTGGVQFN KNLAGRYANT YKNWFPGPMG RTQGWNLGSG VNRASVSAFA TTNRMELEGA SYQVPPQPNG MTNNLQGSNT YALENTMIFN SQPANPGTTA TYLEGNMLIT SESETQPVNR VAYNVGGQMA TNNQSSTT**TVVTSIN** AP ATGTYNLQEI VPGSVWMERD VYLQGPIWAK IPETGAHFHP SPAMGGFGLK HPPPMMLIKN TPVPGNITSF SDVPVSSFIT QYSTGQVTVE MEWELKKENS KRWNPEIQYT NNYNDPQFVD FAPDSTGEYR TTRPIGTRYL TRPL(SEQ ID NO: 378)

7. Equivalents

[00172] Although the invention is described in detail with reference to specific embodiments thereof, it will be understood that variations which are functionally equivalent are within the scope of this invention. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of

the invention described herein. Such equivalents are intended to be encompassed by the following claims.

[00173] All publications, patents and patent applications mentioned in this specification are herein incorporated by reference into the specification to the same extent as if each individual publication, patent or patent application was specifically and individually indicated to be incorporated herein by reference in their entireties.

[00174] The discussion herein provides a better understanding of the nature of the problems confronting the art and should not be construed in any way as an admission as to prior art nor should the citation of any reference herein be construed as an admission that such reference constitutes "prior art" to the instant application.

[00175] All references including patent applications and publications cited herein are incorporated herein by reference in their entirety and for all purposes to the same extent as if each individual publication or patent or patent application was specifically and individually indicated to be incorporated by reference in its entirety for all purposes. Many modifications and variations of this invention can be made without departing from its spirit and scope, as will be apparent to those skilled in the art. The specific embodiments described herein are offered by way of example only, and the invention is to be limited only by the terms of the appended claims, along with the full scope of equivalents to which such claims are entitled.

We claim:

1. A recombinant adeno-associated virus (rAAV) capsid protein comprising a peptide insertion of at least 4 and up to 7 contiguous amino acids, said peptide insertion being immediately after an amino acid residue corresponding to one of amino acids 451 to 461 of AAV9 capsid protein of FIG. 1, wherein said peptide insertion has an amino acid sequence of one of SEQ ID NOs: 1-138,

and wherein said capsid protein is a wild-type capsid protein or a variant capsid protein having up to three amino acid substitutions, and

wherein an rAAV vector prepared from the capsid protein comprising the peptide insertion has enhanced tropism to a target tissue compared to an rAAV vector prepared from a capsid protein without the peptide insertion or a reference capsid protein.

2. The rAAV capsid protein of claim 1, wherein said capsid protein is from at least one AAV type selected from AAV type 1 (AAV1), serotype 2 (AAV2), serotype 3 (AAV3), serotype 4 (AAV4), serotype 5 (AAV5), serotype 6 (AAV6), serotype 7 (AAV7), serotype 8 (AAV8), serotype rh8 (AAVrh8), serotype 9 (AAV9), serotype hu.31 (AAVhu.31), serotype hu.32 (AAVhu.32), serotype rh10 (AAVrh10), serotype rh20 (AAVrh20), serotype hu.37 (AVVhu.37), serotype rh39 (AAVrh39), and serotype rh74 (AAVrh74), or said variant capsid protein is AAV9.AAA or AAVhu.32.AAA or a capsid protein that has 90%, 95%, or 99% sequence identity thereto.

3. The rAAV capsid protein of claim 1 or 2, wherein said peptide insertion occurs immediately after one of the amino acid residues within:

(a) 450-459 of AAV1 capsid amino acid sequence (SEQ ID NO: 139);
(b) 449-458 of AAV2 capsid amino acid sequence (SEQ ID NO: 140);
(c) 449-459 of AAV3 capsid amino acid sequence (SEQ ID NO: 141);
(d) 443-453 of AAV4 capsid amino acid sequence (SEQ ID NO: 142);
(e) 442-445 of AAV5 capsid amino acid sequence (SEQ ID NO: 143);
(f) 450-459 of AAV6 capsid amino acid sequence (SEQ ID NO: 144);
(g) 451-461 of AAV7 capsid amino acid sequence (SEQ ID NO: 145);
(h) 451-461 of AAV8 capsid amino acid sequence (SEQ ID NO: 146);
(i) 451-461 of AAV9 capsid amino acid sequence (SEQ ID NO: 151);

(j) 451-461 of AAVhu.32 capsid amino acid sequence (SEQ ID NO: 148);

(k) 452-461 of AAVrh10 capsid amino acid sequence (SEQ ID NO: 152);

(l) 452-461 of AAVrh20 capsid amino acid sequence (SEQ ID NO: 155);

(m) 452-461 of AAVhu.37 capsid amino acid sequence (SEQ ID NO: 153);

(n) 452-461 of AAVrh39 capsid amino acid sequence (SEQ ID NO: 150);

(o) 452-461 of AAVrh74 capsid amino acid sequence (SEQ ID NO: 156 or SEQ ID NO: 157); or

(p) 452-461 of AAV9.AAA capsid amino acid sequence (SEQ ID NO: 158)

as depicted in FIG 1.

4. The rAAV capsid protein of claim 3, wherein said peptide insertion occurs after an amino acid residue corresponding to one of amino acids I451, N452, G453, S454, G455, Q456, N457, Q458, Q459, T460, or L461 of the AAV9 capsid or variant AAV9.AAA capsid.

5. The rAAV capsid protein of claim 4, wherein said peptide insertion occurs after an amino acid residue corresponding to amino acid S454 of the AAV9 capsid protein, the AAV.32 capsid protein, variant AAV9.AAA capsid protein, or variant AAVhu.32.AAA capsid protein.

6. The rAAV capsid protein of any one of claims 1-5 wherein the peptide is 7 amino acids.

7. The rAAV capsid protein of any one of claims 1-6 wherein the reference capsid protein is AAV9, AAV9.AAA, AAVhu32, or AAVhu32.AAA.

8. The rAAV capsid protein of any one of claims 1 through 7, wherein said peptide insertion comprises an amino acid sequence of at least 4 and up to 7 contiguous amino acids of SEQ ID NO: 135, SEQ ID NO: 136, SEQ ID NO: 137 or SEQ ID NO: 138, where SEQ ID NO: 135 is X_1-Q-V-X_2-X_3-X_4-X_5, wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is any amino acid and X_5 is S, G, V or A, where SEQ ID NO: 136 is X_1-Q-V-X_2-X_3-X_4-X_5, wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is any amino acid and X_5 is S or A, where SEQ ID NO: 137 is X_1-Q-V-X_2-X_3-X_4-X_5, wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is T, S, V, Y, A or P and X_5 is S, G, V or A, or where SEQ ID NO: 138 is X_1-Q-V-X_2-X_3-X_4-X_5, wherein X_1 is V or A, X_2 is S, G, V or A, X_3 is R or H, X_4 is T, S, V, Y, A or P and X_5 is S or A.

9. The rAAV capsid protein of claim 8, wherein the peptide insertion has an amino acid sequence of VQVGRAA (SEQ ID NO: 5), VQVGRTS (SEQ ID NO: 8), AQVGRAS (SEQ ID NO: 24), VQVGRVS (SEQ ID NO: 36), VQVGRSS (SEQ ID NO: 44), VQVGRYS (SEQ ID NO: 130), VQVGRAS (SEQ ID NO: 131), VQVGRPS (SEQ ID NO: 132), VQVVRPS (SEQ ID NO: 133) or VQVGHAS (SEQ ID NO: 134).

10. The rAAV capsid protein of claim 8 or 9 which has an amino acid sequence of SEQ ID No. 263, 264, 265 or 266.

11. The rAAV capsid protein of any one of claims 1-7, wherein said peptide insertion comprises an amino acid sequence of at least 4 and up to 7 contiguous amino acids of SGTVIRS (SEQ ID NO: 1), TRQYVPG (SEQ ID NO: 4), VQVGRTS (SEQ ID NO: 8), RGAVQKV (SEQ ID NO: 13), GQVHQAR (SEQ ID NO: 32), TSGGQIR (SEQ ID NO: 38), HMGHSGK (SEQ ID NO: 88), MRAVSQL (SEQ ID NO: 109), PRQYVPG (SEQ ID NO: 110), RSSSGR (SEQ ID NO: 111), VVKSTKS (SEQ ID NO: 112), RHVSASD (SEQ ID NO: 113), VRSDRDQ (SEQ ID NO: 114), or TVVTSIN (SEQ ID NO: 115).

12. The rAAV capsid protein of claim 11 wherein said peptide insertion is SGTVIRS (SEQ ID NO: 1), TRQYVPG (SEQ ID NO: 4), VQVGRTS (SEQ ID NO: 8), RGAVQKV (SEQ ID NO: 13), GQVHQAR (SEQ ID NO: 32), TSGGQIR (SEQ ID NO: 38), HMGHSGK (SEQ ID NO: 88), MRAVSQL (SEQ ID NO: 109), PRQYVPG (SEQ ID NO: 110), RSSSGR (SEQ ID NO: 111), VVKSTKS (SEQ ID NO: 112), RHVSASD (SEQ ID NO: 113), VRSDRDQ (SEQ ID NO: 114), or TVVTSIN (SEQ ID NO: 115).

13. The rAAV capsid protein of any one of claims 1 through 7, wherein said peptide insertion comprises an amino acid sequence of at least 4 and up to 7 contiguous amino acids of AQVGRAS (SEQ ID NO: 24), SVTSVRV (SEQ ID NO: 37), SIAKNSA (SEQ ID NO: 76), DGRRIGV (SEQ ID NO: 116), TSGERRG (SEQ ID NO: 117), PSSVQHR (SEQ ID NO: 118), SSSVQHR (SEQ ID NO: 119), SGMQERR (SEQ ID NO: 120), LERGNLE (SEQ ID NO: 121), YRDVRQT (SEQ ID NO: 122), PSAVQHR (SEQ ID NO: 123), YVGGRAV (SEQ ID NO: 124), IGSRGVA (SEQ ID NO: 125), SDVSRPR (SEQ ID NO: 126), GSVRQAA (SEQ ID NO: 127), QSPHTSQ (SEQ ID NO: 128), or ASQAYHG (SEQ ID NO: 128).

14. The rAAV capsid protein of claim 13, wherein said peptide insertion is AQVGRAS (SEQ ID NO: 24), SVTSVRV (SEQ ID NO: 37), SIAKNSA (SEQ ID NO: 76), DGRRIGV (SEQ ID NO: 116), TSGERRG (SEQ ID NO: 117), PSSVQHR (SEQ ID NO: 118), SSSVQHR (SEQ ID NO: 119), SGMQERR (SEQ ID NO: 120), LERGNLE (SEQ ID NO: 121), YRDVRQT (SEQ ID NO: 122), PSAVQHR (SEQ ID NO: 123), YVGGRAV (SEQ ID NO: 124), IGSRGVA (SEQ ID NO: 125), SDVSRPR (SEQ ID NO: 126), GSVRQAA (SEQ ID NO: 127), QSPHTSQ (SEQ ID NO: 128), or ASQAYHG (SEQ ID NO: 128).

15. The rAAV capsid protein of claim 14, wherein said peptide insertion is AQVGRAS (SEQ ID NO: 24), PSSVQHR (SEQ ID NO: 118), YVGGRAV (SEQ ID NO: 124), IGSRGVA (SEQ ID NO: 125) or GSVRQAA (SEQ ID NO: 127).

16. The rAAV capsid protein of claim 14, wherein said peptide insertion is DGRRIGV (SEQ ID NO: 116), SSSVQHR (SEQ ID NO: 119), YRDVRQT (SEQ ID NO: 122) or PSAVQHR (SEQ ID NO: 123).

17. The rAAV capsid protein of claim 1, having the amino acid sequence of any one of the amino acid sequences of SEQ ID NO: 159-266 and 268-375.

18. The rAAV capsid protein of any one of the preceding claims, wherein said target tissue with enhanced tropism is skeletal muscle or heart muscle.

19. The rAAV capsid protein of claim 18, wherein an rAAV vector prepared from the capsid protein exhibits an at least 2 fold, 5 fold, 10 fold, 15 fold, 20 fold, or 25 fold greater transduction of skeletal muscle and/or heart muscle than an rAAV vector prepared from the capsid protein without the peptide insert or the reference capsid protein.

20. The rAAV capsid protein of any one of the preceding claims wherein the target tissue is CNS neurons.

21. The rAAV capsid protein of claim 20 wherein an rAAV vector prepared from the capsid protein has an at least 2 fold, 5 fold, 10 fold, 15 fold, 20 fold, or 25 fold greater transduction of CNS neurons than an rAAV vector prepared from the capsid protein without the peptide insert or the reference capsid protein.

22. The rAAV capsid protein of any one of the preceding claims wherein an rAAV vector prepared from the capsid protein has reduced transduction of liver, heart or astrocytes than an rAAV vector prepared from the capsid protein without the peptide insert or the reference capsid protein.

23. The rAAV capsid protein of claim 22 wherein the rAAV vector prepared from the capsid protein has an at least 2 fold, 5 fold, 10 fold, 15 fold, 20 fold, 25 fold or 40 fold lower transduction of liver than an rAAV vector prepared from the capsid protein without the peptide insert or the reference capsid protein.

24. The rAAV capsid protein of any one of claims 19, 21, 22, or 23 wherein the reference capsid protein is AAV9 capsid or AAVhu.32 capsid.

25. A nucleic acid comprising a nucleotide sequence encoding the rAAV capsid protein of any one of the preceding claims, or encoding an amino acid sequence sharing at least 80% identity therewith.

26. The nucleic acid of claim 25 which encodes the rAAV capsid protein of any one of the preceding claims.

27. A packaging cell capable of expressing the nucleic acid of claim 25 or 26 to produce AAV vectors comprising the capsid protein encoded by said nucleotide sequence.

28. A rAAV vector comprising the capsid protein of any one of claims 1-24.

29. The rAAV vector of claim 28, further comprising a rAAV genome comprising a transgene flanked by AAV ITR sequences.

30. A pharmaceutical composition comprising the rAAV vector of claim 28 or 29 and a pharmaceutically acceptable carrier.

31. A method of delivering a transgene to a cell, said method comprising contacting said cell with the rAAV vector of claim 28 or 29; or the rAAV vector of claim 28 or 29 for use in delivering a transgene to a cell, wherein said cell is contacted with the vector.

32. A method of delivering a transgene to a target tissue of a subject in need thereof, said method comprising administering to said subject the rAAV vector of claim 28 or 29; or

the rAAV vector of claim 28 or 29 for use in delivering a transgene to a target tissue of a subject in need thereof, wherein the vector is administered to said subject.

33. The method, or rAAV vector for use, according to claim 32, wherein said rAAV vector is administered systemically, intravenously, intrathecally, intra-nasally, intra-peritoneally, intravitreally, via lumbar puncture or via the cisterna magna.

34. The method, or rAAV vector for use, according to claim 32 or claim 33, wherein said target tissue is muscle, retina or CNS.

35. A method of making a recombinant AAV (rAAV) vector library comprising

(i) producing a starting plasmid have a gene expression cassette comprising a nucleic acid sequence encoding an AAV capsid protein, wherein a stop codon is placed at a target insertion site within the nucleic acid sequence encoding the AAV capsid protein;

(ii) providing a population of nucleic acids which encode a repertoire of peptides to produce a peptide library;

(iii) creating individual plasmids based on the starting plasmid 1) each comprising the nucleic acid encoding the AAV capsid with a nucleic acid encoding a random peptide from the peptide library inserted at the target insertion site of the nucleic acid encoding the capsid protein thus replacing the stop codon, and 2) each plasmid further containing a nucleic acid encoding a barcode for identification of the nucleic acid encoding the capsid and peptide insert placed before the 5'- or after the 3'-end of the nucleic acid encoding the capsid ;

(iv) collecting the individual plasmids;

(v) transfecting a population of cells with the collection of individual plasmids and one or more plasmids carrying an rAAV genome comprising a transgene and necessary genes;

(vi) culturing the population of transfected cells under appropriate conditions to produce a collection of rAAV vectors each comprising the AAV capsid having the peptide insert encapsidating the rAAV genome comprising the transgene; and

(vii) harvesting the rAAV vector library.

36. The method of claim 35, wherein the capsid gene encodes an AAV1 capsid protein (SEQ ID NO: 139), an AAV4 capsid protein (SEQ ID NO: 142), an AAV5 capsid protein (SEQ ID NO: 143), an AAV8 capsid protein (SEQ ID NO: 146), an AAV9 capsid protein (SEQ ID NO: 151), an AAV9.AAA capsid protein (SEQ ID No: 158), AAVhu.32 (SEQ ID NO: 148), AAVhu.32.AAA (SEQ ID NO. 267), an AAV3B capsid protein (SEQ ID NO: 154) or an AAVhu37 capsid protein (SEQ ID NO: 153).

37. The method of any one of claims 34 to 36, wherein the target insertion site is at or after an amino acid residue within VR-4 or VR-8 of the capsid protein

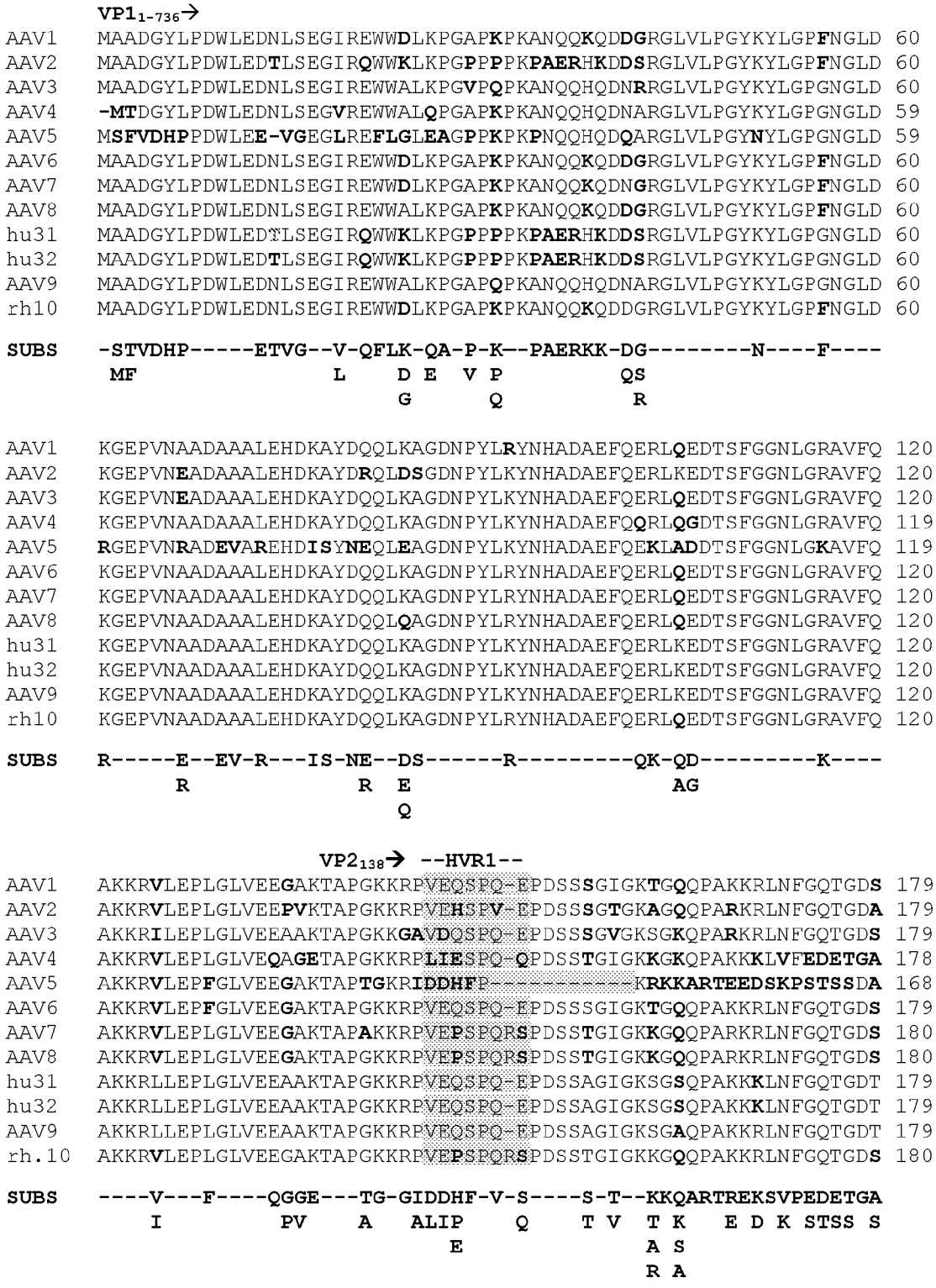
38. The method of claim 37, wherein after the target insertion site is after an amino acid corresponding to S454 of AAV9 (SEQ ID NO: 151).

39. The method of any one of claims 34 to 38 wherein the peptide is a 7 amino acid peptide.

40. An rAAV vector library made by the method of any one of claims 34 to 39.

41. An rAAV vector library of claim 40 wherein at least 80%, 85%, 90%, 95%, 98%, 99% or 100% of the rAAV vectors in the library have a capsid with a peptide insert.

FIG. 1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AAV3 MAADGYLPDWLEDNLSEGIREWWALKPGVPQPKANQQHQDNRRGLVLPGYKYLGPGNGLD 60
AAV4 -MTDGYLPDWLEDNLSEGVREWWALQPGAPKPKANQQHQDNARGLVLPGYKYLGPGNGLD 59
AAV5 MSFVDHPPDWLEE-VGEGLREFLGLEAGPPKPKPNQQHQDQARGLVLPGYNYLGPGNGLD 59
AAV6 MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD 60
AAV7 MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDNGRGLVLPGYKYLGPFNGLD 60
AAV8 MAADGYLPDWLEDNLSEGIREWWALKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD 60
hu31 MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPGNGLD 60
hu32 MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPGNGLD 60
AAV9 MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDNARGLVLPGYKYLGPGNGLD 60
rh10 MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD 60
SUBS -STVDHP-----ETVG--V-QFLK-QA-P-K--PAERKK-DG--------N----F----
MF L D E V P QS
G Q R
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AAV2 KGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQ 120
AAV3 KGEPVNEADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
AAV4 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQQRLQGDTSFGGNLGRAVFQ 119
AAV5 RGEPVNRADEVAREHDISYNEQLEAGDNPYLKYNHADAEFQEKLADDTSFGGNLGKAVFQ 119
AAV6 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
AAV7 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
AAV8 KGEPVNAADAAALEHDKAYDQQLQAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
hu31 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQ 120
hu32 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQ 120
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rh10 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
SUBS R-----E--EV-R---IS-NE--DS------R---------QK-QD---------K----
R R E AG
Q
VP2 138→ --HVR1--
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AAV2 AKKRVLEPLGLVEEPVKTAPGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDA 179
AAV3 AKKRILEPLGLVEEAAKTAPGKKGAVDQSPQ-EPDSSSGVGKSGKQPARKRLNFGQTGDS 179
AAV4 AKKRVLEPLGLVEQAGETAPGKKRPLIESPQ-QPDSSTGIGKKGKQPAKKKLVFEDETGA 178
AAV5 AKKRVLEPFGLVEEGAKTAPTGKRIDDHFP----------KRKKARTEEDSKPSTSSDA 168
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AAV7 AKKRVLEPLGLVEEGAKTAPAKKRPVEPSPQRSPDSSTGIGKKGQQPARKRLNFGQTGDS 180
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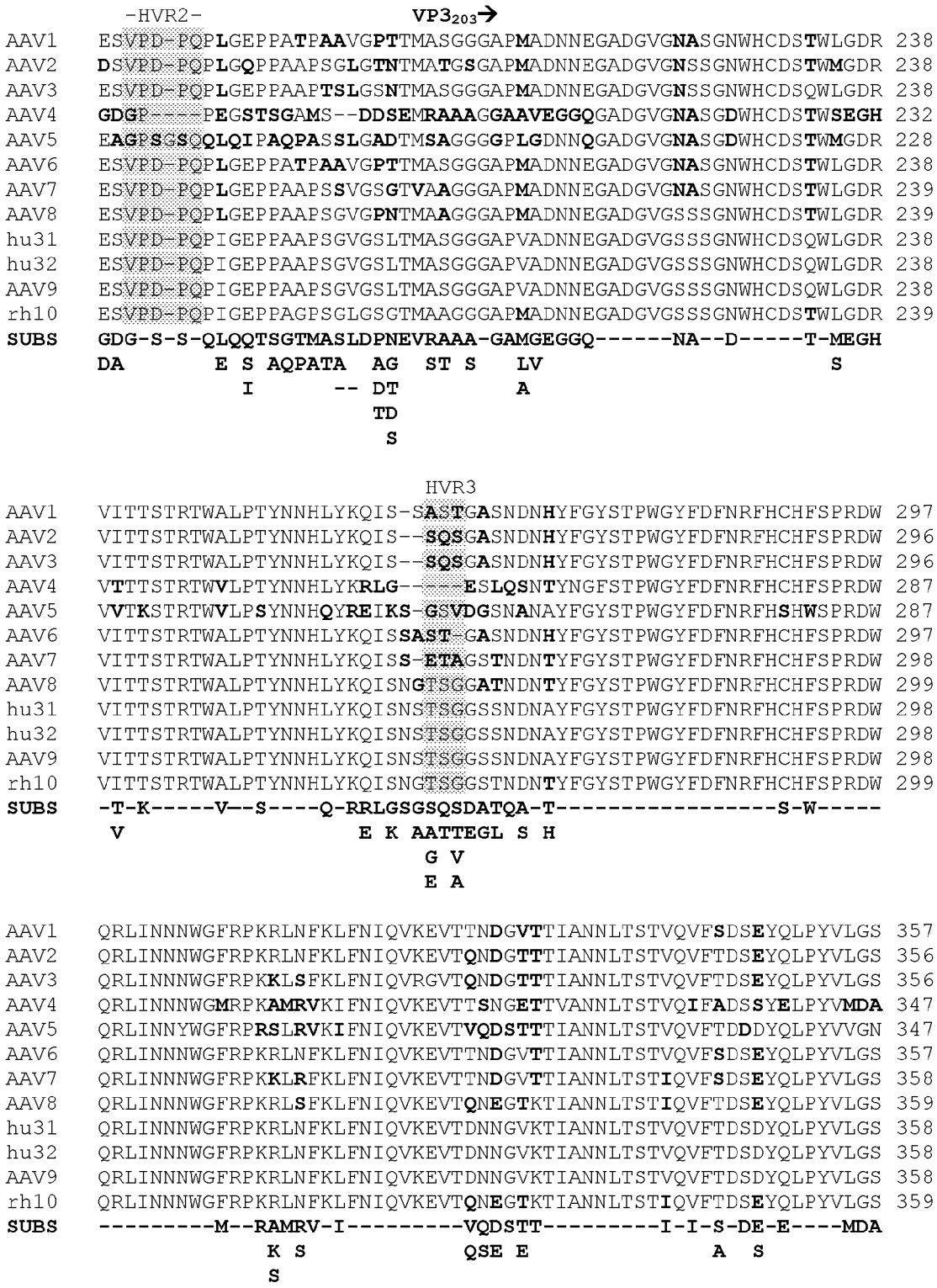
hu31 AKKRLLEPLGLVEEAAKTAPGKKRPVEQSPQ-EPDSSAGIGKSGSQPAKKKLNFGQTGDT 179
hu32 AKKRLLEPLGLVEEAAKTAPGKKRPVEQSPQ-EPDSSAGIGKSGSQPAKKKLNFGQTGDT 179
AAV9 AKKRLLEPLGLVEEAAKTAPGKKRPVEQSPQ-EPDSSAGIGKSGAQPAKKRLNFGQTGDT 179
rh.10 AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPAKKRLNFGQTGDS 180
SUBS ----V---F----QGGE---TG-GIDDHF-V-S----S-T--KKQARTREKSVPEDETGA
I PV A ALIP Q T V T K E D K STSS S
E A S
R A

FIG. 1 (CON'T)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AAV3 ESVPD-PQPLGEPPAAPTSLGSNTMASGGGAPMADNNEGADGVGNSSGNWHCDSQWLGDR 238
AAV4 GDGP-----PEGSTSGAMS--DDSEMRAAAGGAAVEGGQGADGVGNASGDWHCDSTWSEGH 232
AAV5 EAGPSGSQQLQIPAQPASSLGADTMSAGGGGPLGDNNQGADGVGNASGDWHCDSTWMGDR 228
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AAV7 ESVPD-PQPLGEPPAAPSSVGSGTVAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR 239
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hu32 ESVPD-PQPIGEPPAAPSGVGSLTMASGGGAPVADNNEGADGVGSSSGNWHCDSQWLGDR 238
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rh10 ESVPD-PQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR 239
SUBS GDG-S-S-QLQQTSGTMASLDPNEVRAAA-GAMGEGGQ------NA--D-----T-MEGH
DA E S AQPATA AG ST S LV S
I -- DT A
TD
S
HVR3
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AAV3 VITTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDW 296
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AAV9 VITTSTRTWALPTYNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFNRFHCHFSPRDW 298
rh10 VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW 299
SUBS -T-K-----V--S----Q-RRLGSGSQSDATQA-T----------S-W-----
V E K AATTEGL S H
G V
E A
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AAV3 QRLINNNWGFRPKKLSFKLFNIQVRGVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGS 356
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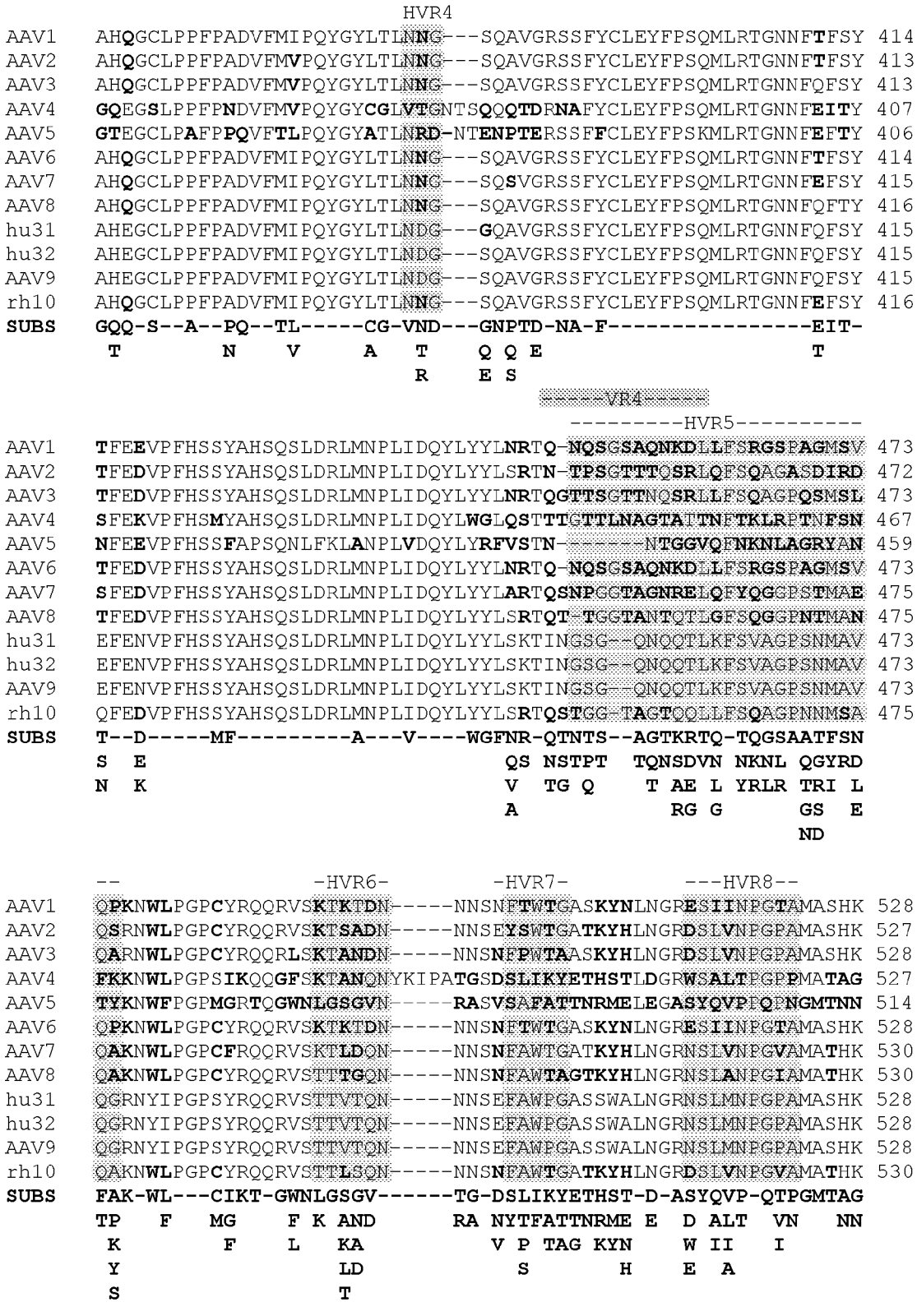
K S QSE E A S
S

FIG. 1 (CON'T)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rh10 AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY 416
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T N V A T Q Q E T
R E S
-----VR4-----
---------HVR5----------
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AAV3 TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQGTTSGTTNQSRLLFSQAGPQSMSL 473
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rh10 QFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTGG-TAGTQQLLFSQAGPNNMSA 475
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S E QS NSTPT TQNSDVN NKNL QGYRD
N K V TG Q T AE L YRLR TRI L
A RG G GS E
ND
-- -HVR6- -HVR7- ---HVR8--
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AAV2 QSRNWLPGPCYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDSLVNPGPAMASHK 527
AAV3 QARNWLPGPCYRQQRLSKTANDN-----NNSNFPWTAASKYHLNGRDSLVNPGPAMASHK 528
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AAV5 TYKNWFPGPMGRTQGWNLGSGVN-----RASVSAFATTNRMELEGASYQVPPQPNGMTNN 514
AAV6 QPKNWLPGPCYRQQRVSKTKTDN-----NNSNFTWTGASKYNLNGRESIINPGTAMASHK 528
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rh10 QAKNWLPGPCYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVNPGVAMATHK 530
SUBS FAK-WL---CIKT-GWNLGSGV------TG-DSLIKYETHST-D-ASYQVP-QTPGMTAG
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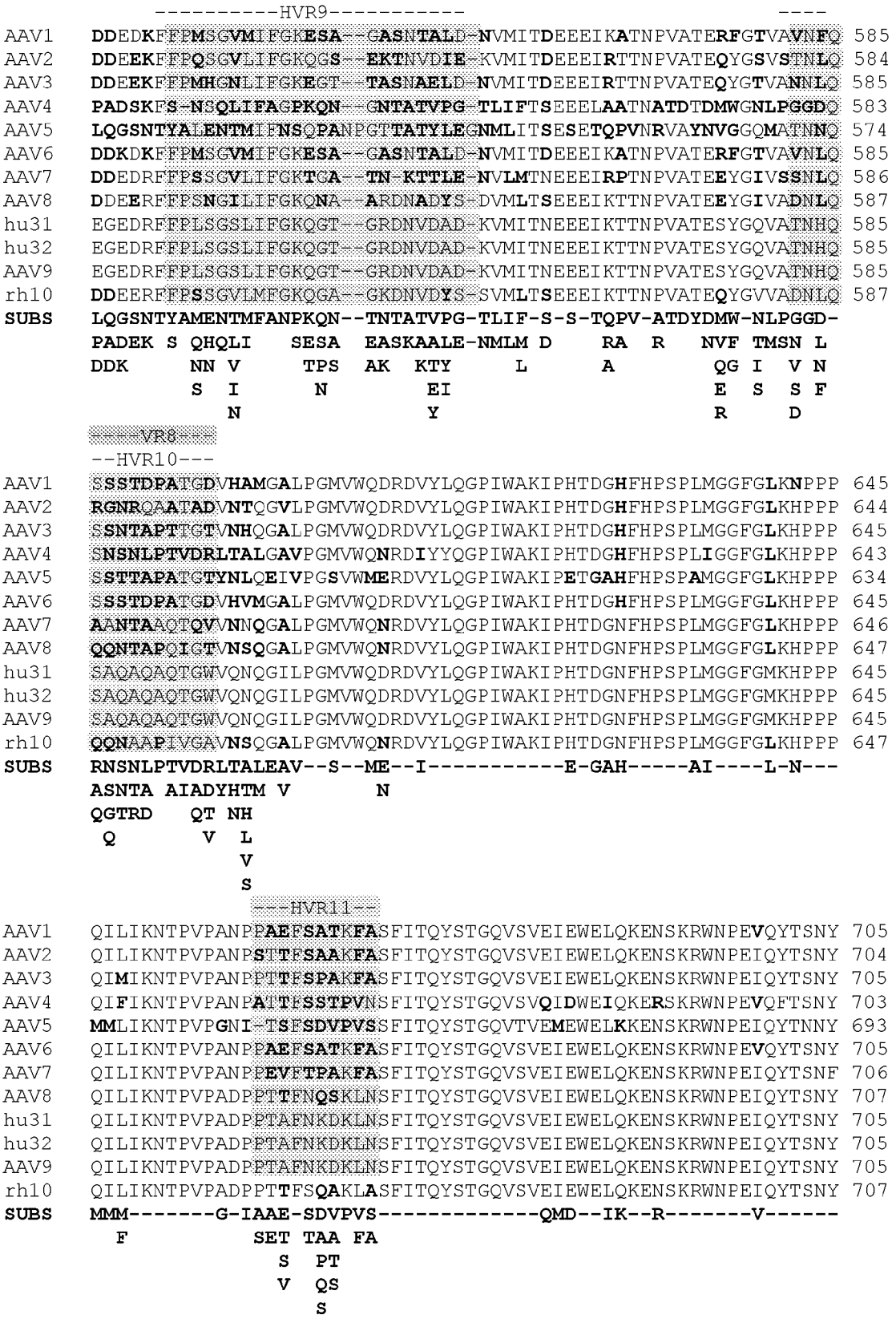
K F L KA V P TAG KYN W II I
Y LD S H E A
S T

FIG. 1 (CON'T)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AAV5 LQGSNTYALENTMIFNSQPANPGTTATYLEGNMLITSESETQPVNRVAYNVGGQMATNNQ 574
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AAV8 DDEERFFPSNGILIFGKQNA--ARDNADYS-DVMLTSEEEIKTTNPVATEEYGIVADNLQ 587
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rh10 DDEERFFPSSGVLMFGKQGA--GKDNVDYS-SVMLTSEEEIKTTNPVATEQYGVVADNLQ 587
SUBS LQGSNTYAMENTMFANPKQN--TNTATVPG-TLIF-S-S-TQPV-ATDYDMW-NLPGGD-
PADEK S QHQLI SESA EASKAALE-NMLM D RA R NVF TMSN L
DDK NN V TPS AK KTY L A QG I V N
S I N EI E S S F
N Y R D
VR8
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AAV2 RGNRQAATADVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPP 644
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hu32 SAQAQAQTGWVQNQGILPGMVWQDRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGMKHPPP 645
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rh10 QQNAAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPP 647
SUBS RNSNLPTVDRLTALEAV--S--ME--I----------E-GAH-----AI----L-N---
ASNTA AIADYHTM V N
QGTRD QT NH
Q V L
V
S
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rh10 QILIKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY 707
SUBS MMM-------G-IAAE-SDVPVS----------QMD--IK--R-------V------
F SET TAA FA
S PT
V QS
S

FIG. 1 (CON'T)

```
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AAV2    NKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL 735 (SEQ ID NO: 140)
AAV3    NKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL 736 (SEQ ID NO: 141)
AAV4    GQQNSLLWAPDAACKYTEPRAIGTRYLTHHL 734 (SEQ ID NO: 142)
AAV5    NDPQFVDFAPDSTGEYRTTRPIGTRYLTRPL 724 (SEQ ID NO: 143)
AAV6    AKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 736 (SEQ ID NO: 144)
AAV7    EKQTGVDFAVDSQGVYSEPRPIGTRYLTRNL 737 (SEQ ID NO: 145)
AAV8    YKSTSVDFAVNTEGVYSEPRPIGTRYLTRNL 738 (SEQ ID NO: 146)
hu31    YKSNNVEFAVSTEGVYSEPRPIGTRYLTRNL 736 (SEQ ID NO: 147)
hu32    YKSNNVEFAVNTEGVYSEPRPIGTRYLTRNL 736 (SEQ ID NO: 148)
AAV9    YKSNNVEFAVNTEGVYSEPRPIGTRYLTRNL 736 (SEQ ID NO: 151)
rh10    YKSTNVDFAVNTDGTYSEPRPIGTRYLTRNL 738 (SEQ ID NO: 152)
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        A  TG      NQ L
        E  A        T
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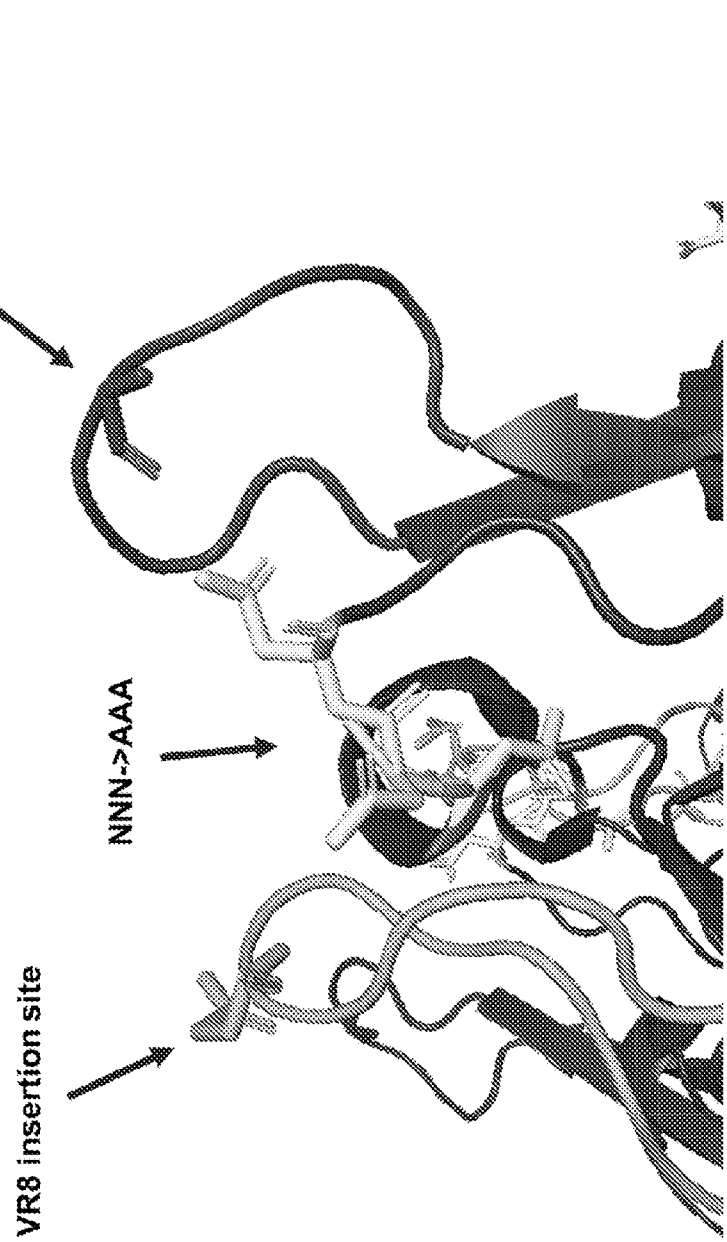


FIG. 2

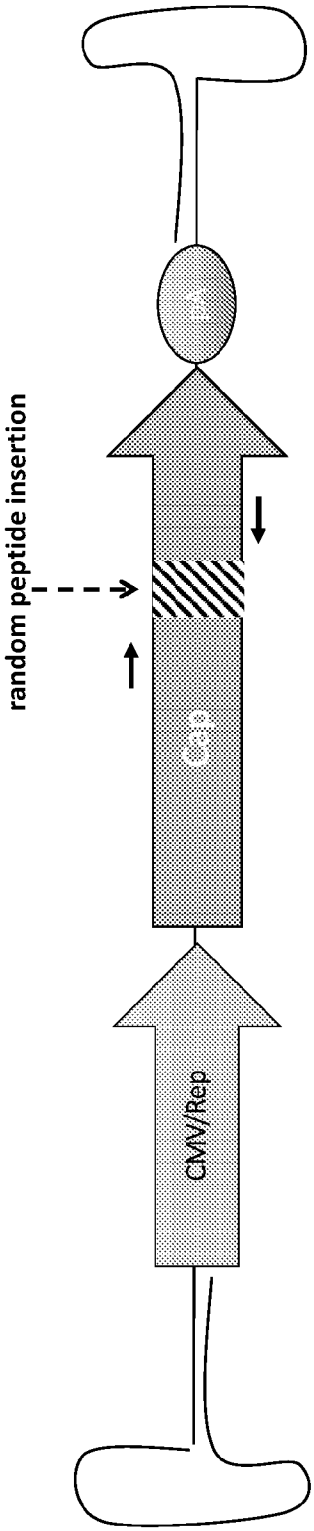


FIG. 3

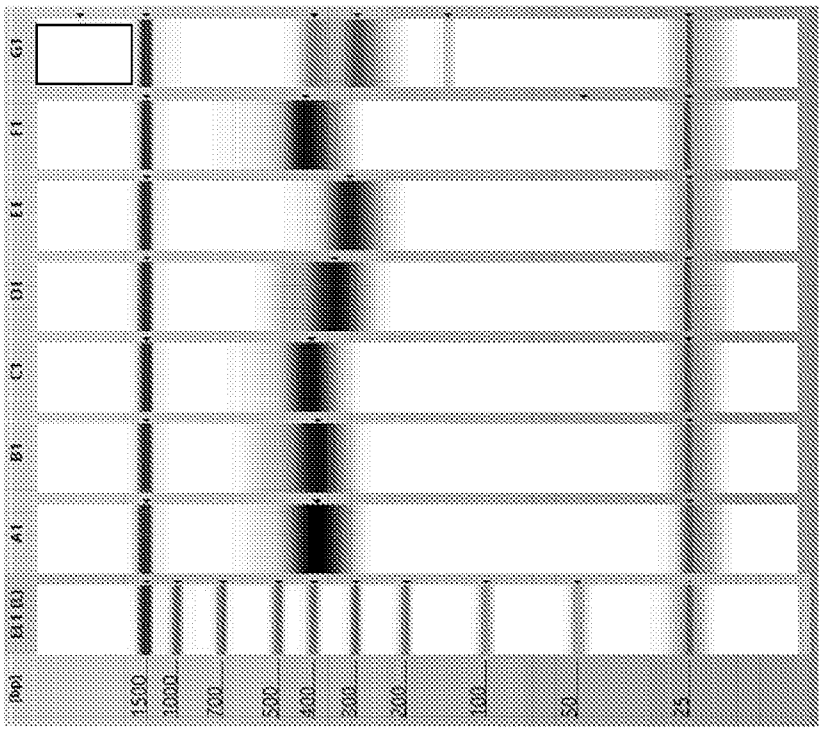
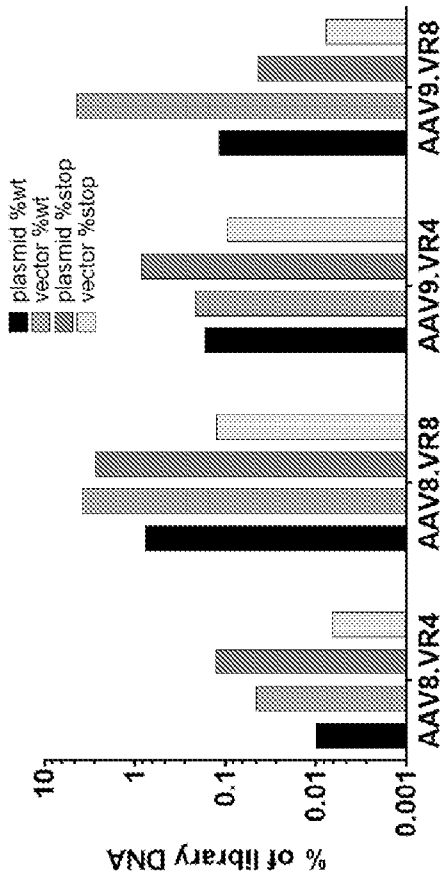
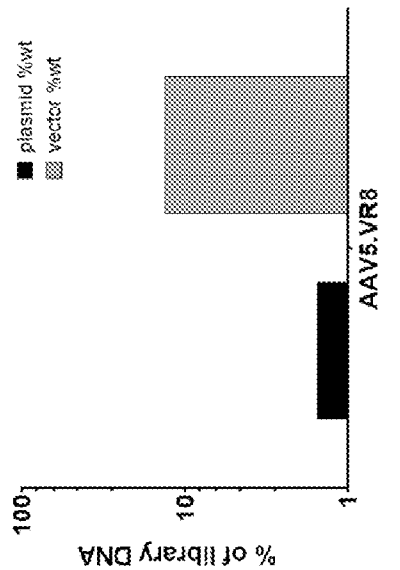


FIG. 4


plasmid %wt
vector %wt
plasmid %stop
vector %stop
% of library DNA
10
1
0.1
0.01
0.001
AAV8.VR4
AAV8.VR8
AAV9.VR4
AAV9.VR8

B


plasmid %wt
vector %wt
% of library DNA
100
10
1
AAV5.VR8

A

FIG. 5

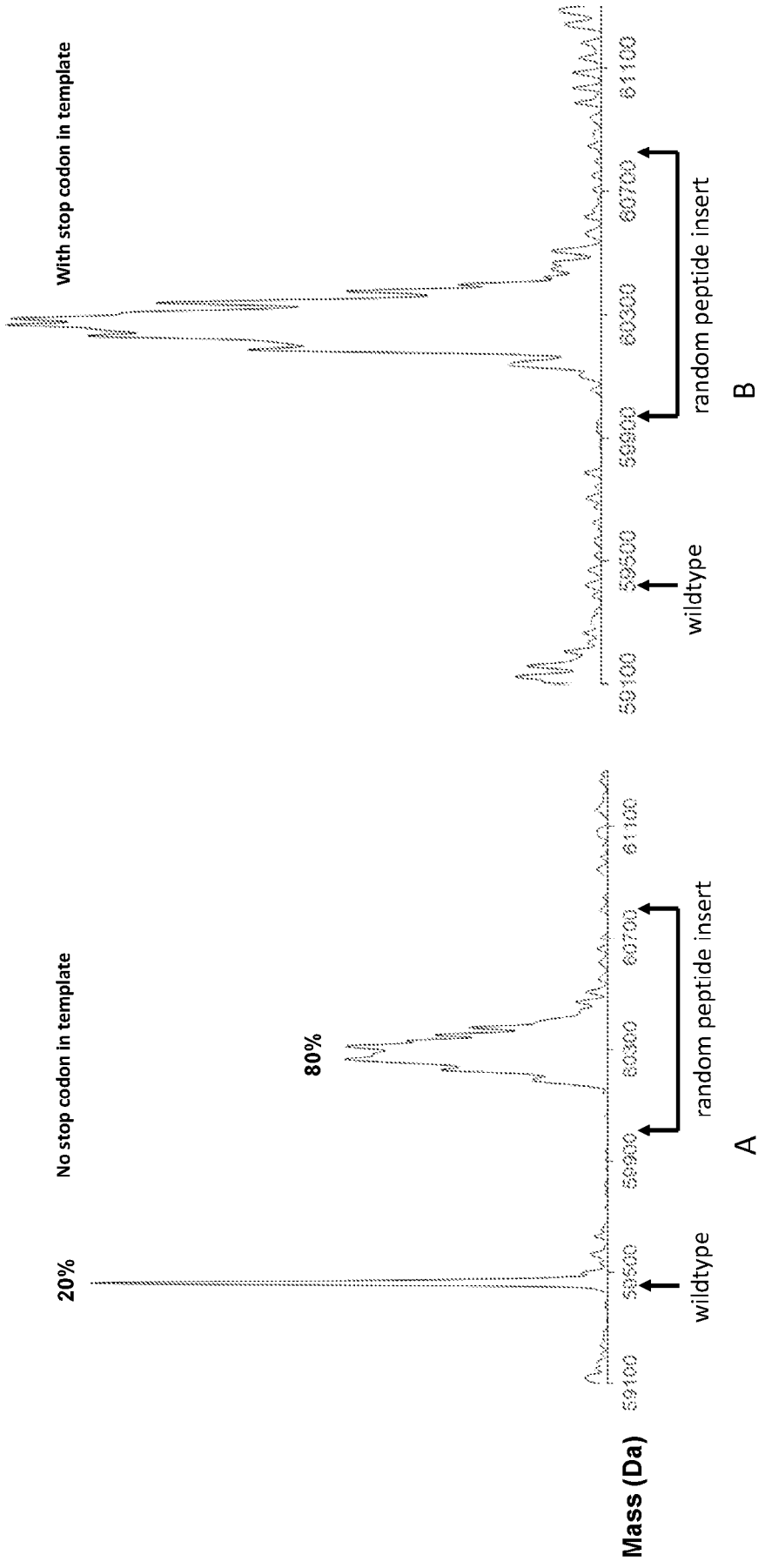
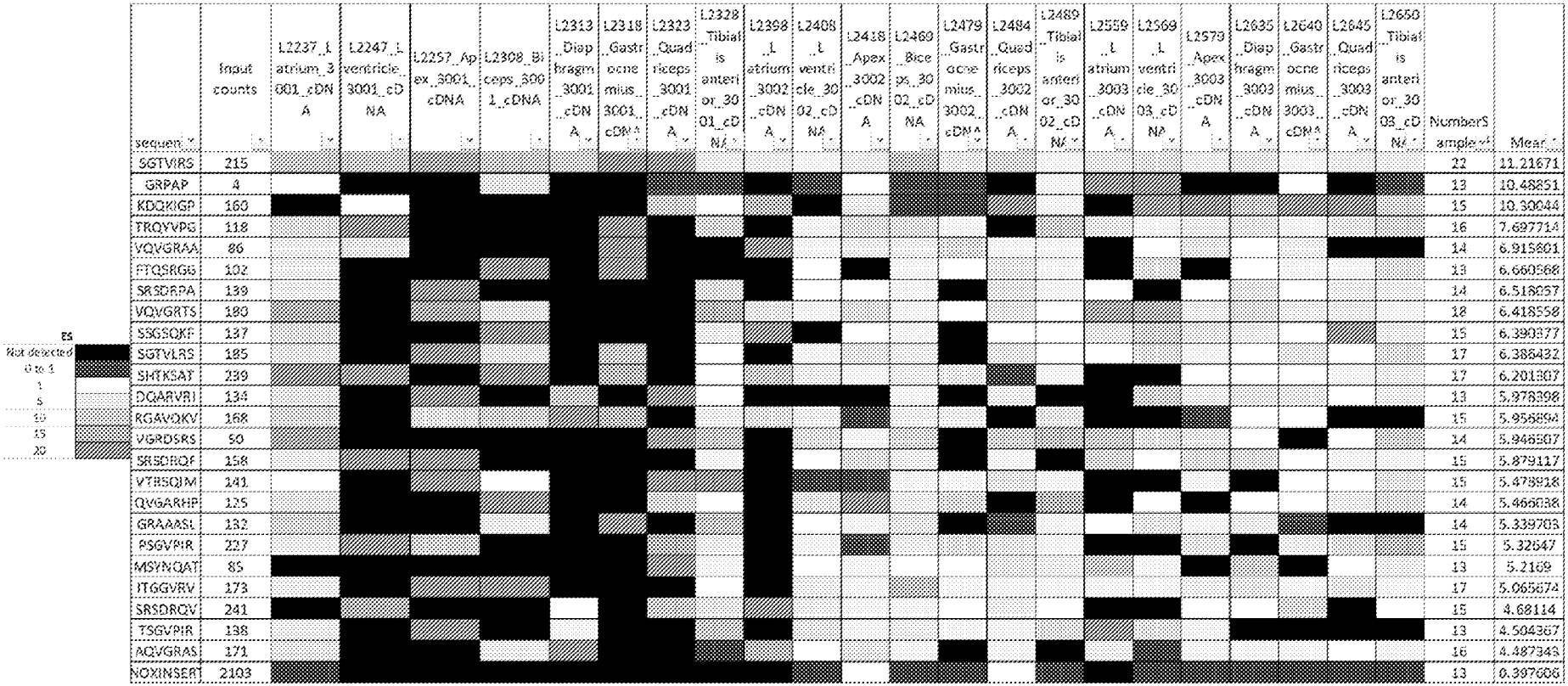

No stop codon in template
20%
80%
wildtype
random peptide insert
A
With stop codon in template
wildtype
random peptide insert
B
Mass (Da)
59100
59600
59900
60300
60700
61100

FIG. 6



sequen	Input counts	L2237_Latrium_3001_cDNA	L2247_Lventricle_3001_cDNA	L2257_Apex_3001_cDNA	L2308_Biceps_3001_cDNA	L2313_Diaphragm_3001_cDNA	L2318_Gastrocnemius_3001_cDNA	L2323_Quadriceps_3001_cDNA	L2328_Tibialis anterior_3001_cDNA	L2398_Latrium_3002_cDNA	L2408_Lventricle_3002_cDNA	L2418_Apex_3002_cDNA	L2469_Biceps_3002_cDNA	L2479_Gastrocnemius_3002_cDNA	L2484_Quadriceps_3002_cDNA	L2489_Tibialis anterior_3002_cDNA	L2559_Latrium_3003_cDNA	L2569_Lventricle_3003_cDNA	L2579_Apex_3003_cDNA	L2635_Diaphragm_3003_cDNA	L2640_Gastrocnemius_3003_cDNA	L2645_Quadriceps_3003_cDNA	L2650_Tibialis anterior_3003_cDNA	NumberSample	Mean
SGTVIRS	215																							22	11.21671
GRPAP	4																							13	10.48851
KDQKIGP	160																							15	10.30044
TRQYVPG	118																							16	7.697714
VQVGRAA	86																							14	6.915601
FTQSRGG	102																							13	6.660568
SRSDRPA	139																							14	6.518057
VQVGRTS	180																							18	6.418558
SSGSQKF	137																							15	6.390377
SGTVLRS	185																							17	6.386432
SHTKSAT	239																							17	6.201307
DQARVRI	134																							13	5.978398
RGAVQKV	168																							15	5.956894
VGRDSRS	50																							14	5.946507
SRSDRQF	158																							15	5.879117
VTRSQIM	141																							15	5.478918
QVGARHP	125																							14	5.466038
GRAAASL	132																							14	5.339703
PSGVPIR	227																							15	5.32647
MSYNQAT	85																							13	5.2169
ITGGVRV	173																							17	5.065674
SRSDRQV	241																							15	4.68114
TSGVPIR	138																							13	4.504367
AQVGRAS	171																							16	4.487343
NOXINSERT	2103																							13	0.397606

FIG. 7

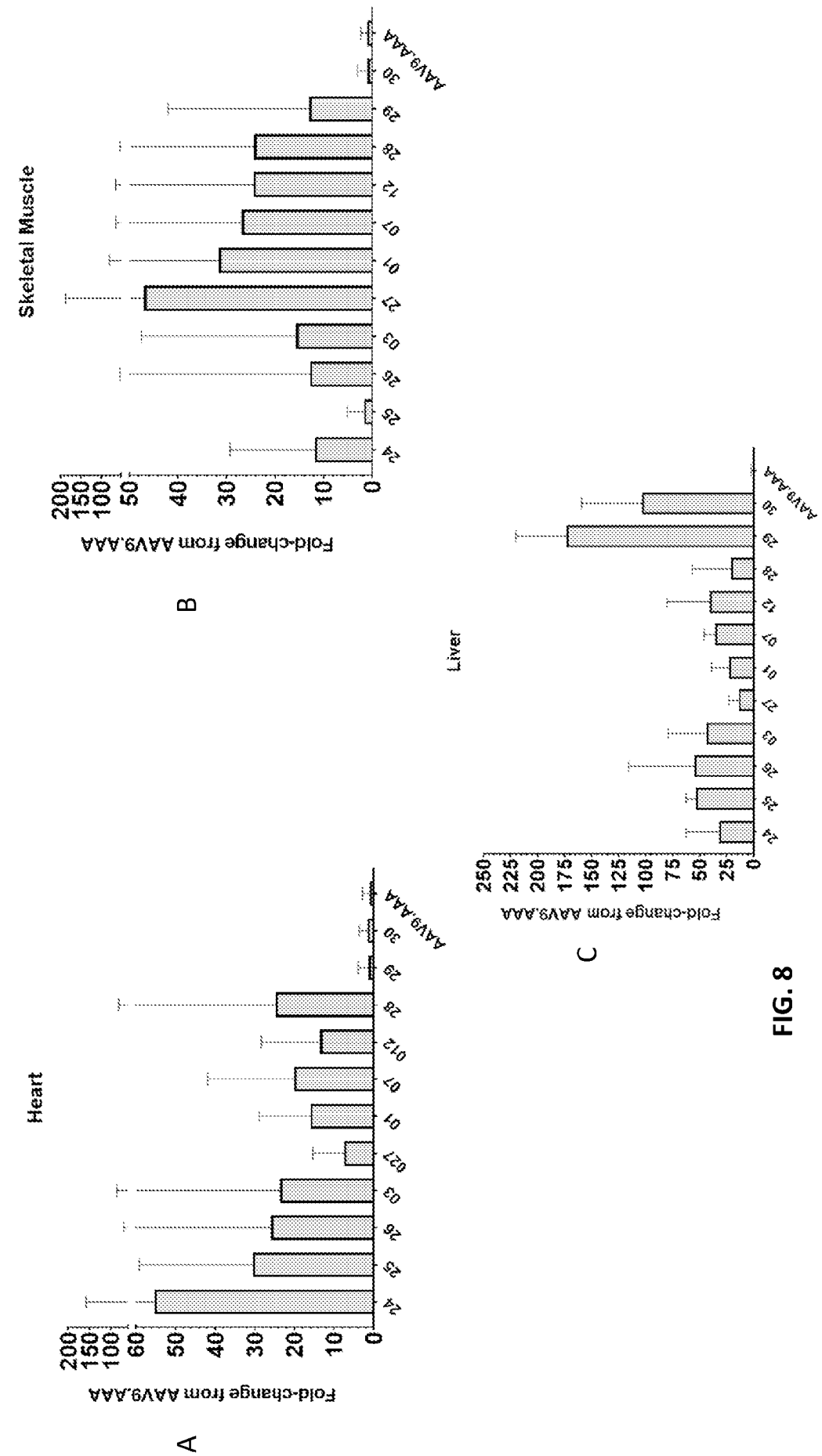
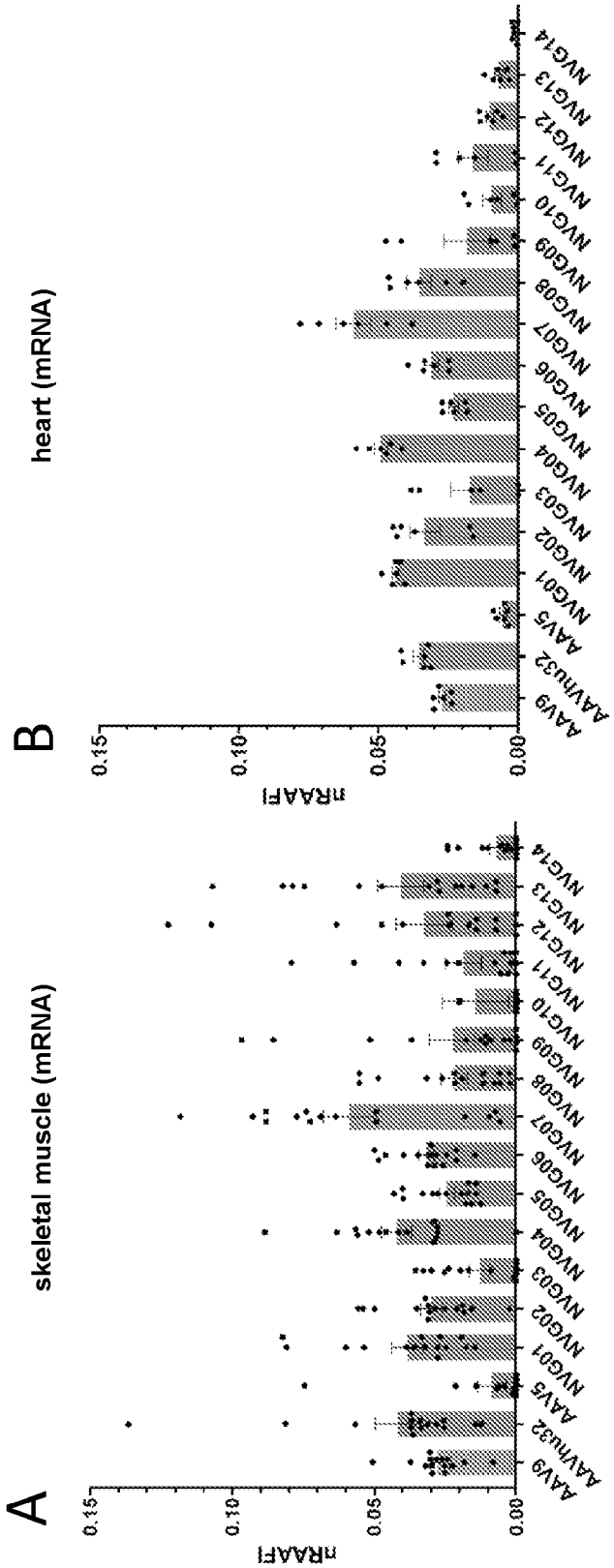
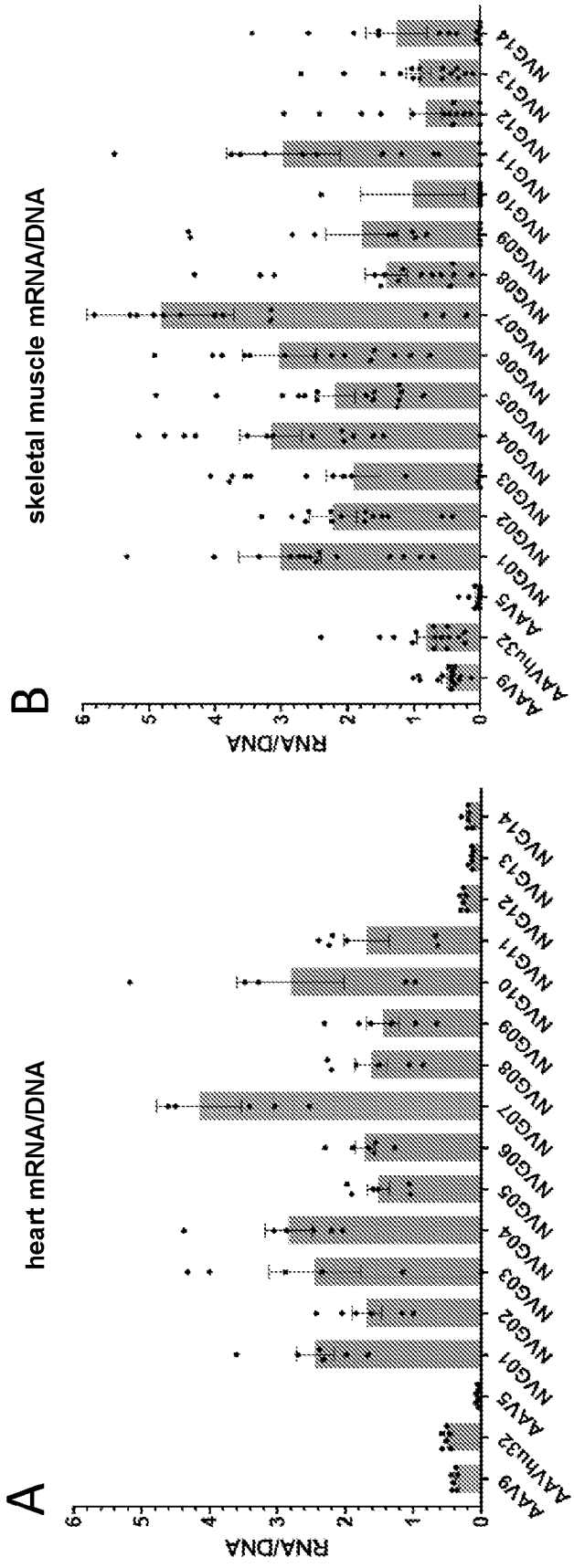

Heart
Fold-change from AAV9.AAA
0
10
20
30
40
50
60
100
150
200
24
25
26
03
027
01
07
012
28
29
30
AAV9.AAA
A
Skeletal Muscle
Fold-change from AAV9.AAA
0
10
20
30
40
50
100
150
200
24
25
26
03
27
01
07
12
28
29
30
AAV9.AAA
B
Liver
Fold-change from AAV9.AAA
0
25
50
75
100
125
150
175
200
225
250
24
25
26
03
27
01
07
12
28
29
30
AAV9.AAA
C

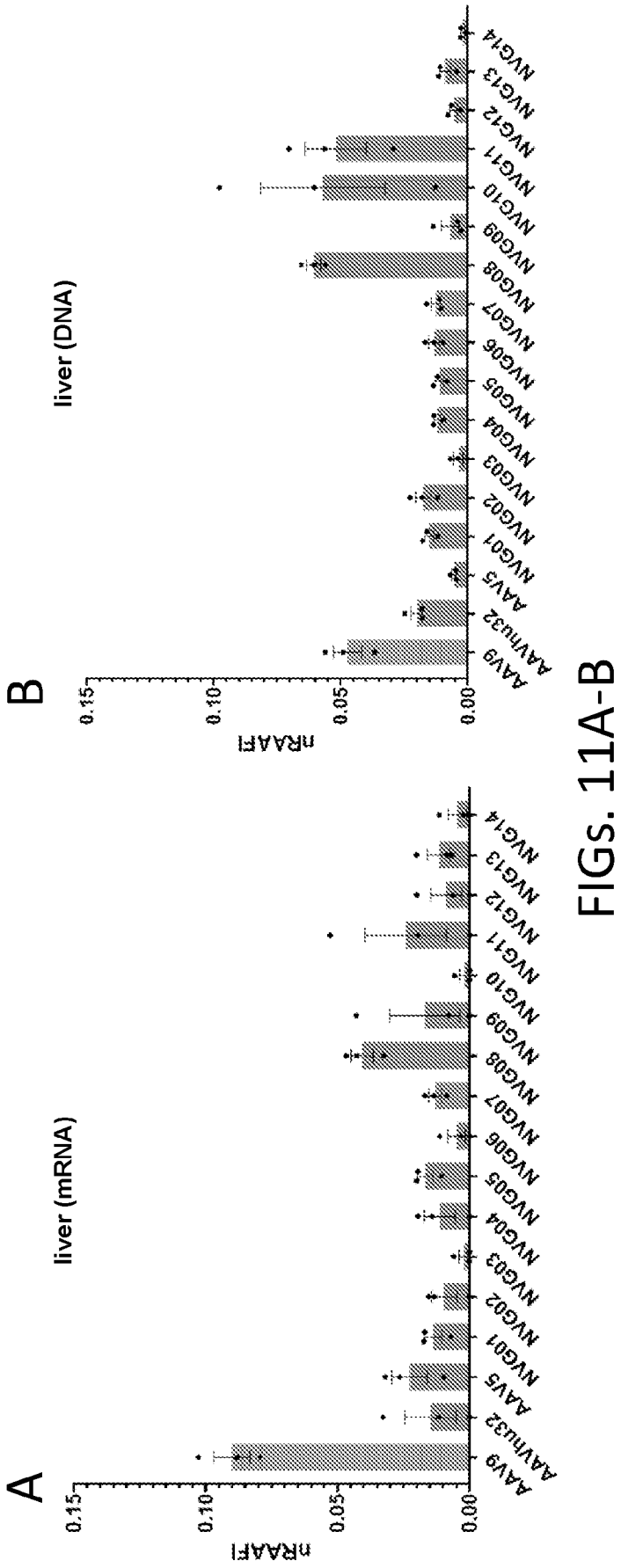
FIG. 8


A
skeletal muscle (mRNA)
nRAAFI
0.15
0.10
0.05
0.00
AAV9
AAVhu32
AAV5
NVG01
NVG02
NVG03
NVG04
NVG05
NVG06
NVG07
NVG08
NVG09
NVG10
NVG11
NVG12
NVG13
NVG14
B
heart (mRNA)
nRAAFI
0.15
0.10
0.05
0.00
AAV9
AAVhu32
AAV5
NVG01
NVG02
NVG03
NVG04
NVG05
NVG06
NVG07
NVG08
NVG09
NVG10
NVG11
NVG12
NVG13
NVG14

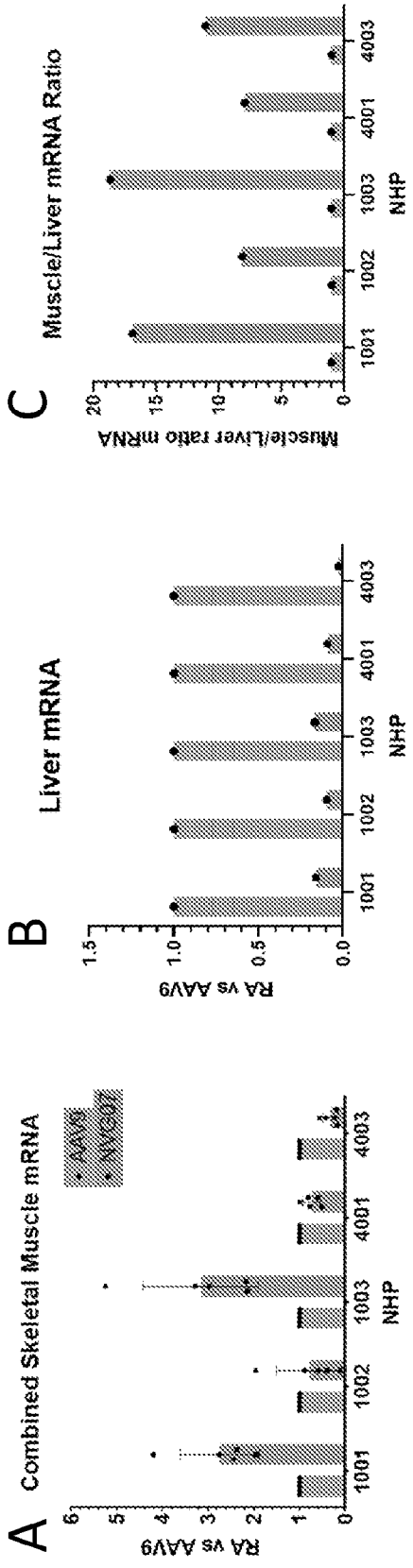
FIGs. 9A-B


A
heart mRNA/DNA
RNA/DNA
0
1
2
3
4
5
6
AAV9
AAVhu32
AAV5
NVG01
NVG02
NVG03
NVG04
NVG05
NVG06
NVG07
NVG08
NVG09
NVG10
NVG11
NVG12
NVG13
NVG14
B
skeletal muscle mRNA/DNA
RNA/DNA
0
1
2
3
4
5
6
AAV9
AAVhu32
AAV5
NVG01
NVG02
NVG03
NVG04
NVG05
NVG06
NVG07
NVG08
NVG09
NVG10
NVG11
NVG12
NVG13
NVG14

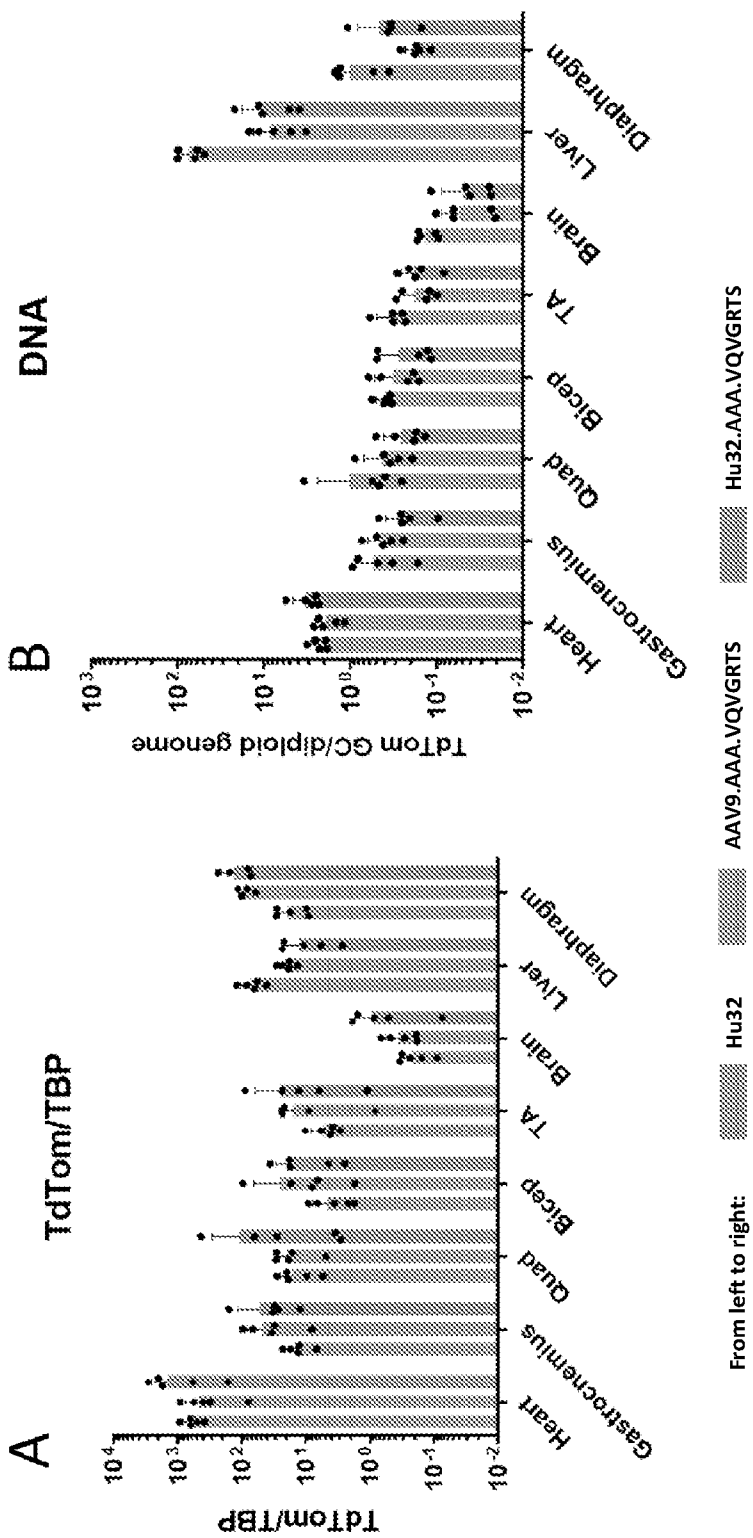
FIGs. 10A-B


A
liver (mRNA)
nRAAFI
0.15
0.10
0.05
0.00
AAV9
AAVhu32
AAV5
NVG01
NVG02
NVG03
NVG04
NVG05
NVG06
NVG07
NVG08
NVG09
NVG10
NVG11
NVG12
NVG13
NVG14
B
liver (DNA)
nRAAFI
0.15
0.10
0.05
0.00
AAV9
AAVhu32
AAV5
NVG01
NVG02
NVG03
NVG04
NVG05
NVG06
NVG07
NVG08
NVG09
NVG10
NVG11
NVG12
NVG13
NVG14

FIGs. 11A-B


A
Combined Skeletal Muscle mRNA
RA vs AAV9
NHP
1001
1002
1003
4001
4003
B
Liver mRNA
RA vs AAV9
NHP
C
Muscle/Liver mRNA Ratio
Muscle/Liver ratio mRNA
NHP

FIGs. 12A-C


A
TdTom/TBP
TdTom/TBP
10^{4}
10^{3}
10^{2}
10^{1}
10^{0}
10^{-1}
10^{-2}
Heart
Gastrocnemius
Quad
Bicep
TA
Brain
Liver
Diaphragm
B
DNA
TdTom GC/diploid genome
10^{3}
10^{2}
10^{1}
10^{0}
10^{-1}
10^{-2}
Heart
Gastrocnemius
Quad
Bicep
TA
Brain
Liver
Diaphragm
From left to right:
Hu32
AAV9.AAA.VQVGRTS
Hu32.AAA.VQVGRTS

FIGs. 13A-B