

10359W001_ST25
SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.
Sabin, Leah
Schoenherr, Christopher
Economides, Aris N
Kyratsous, Christos
Murphy, Andrew J

<120> Tropism-Modified Recombinant Viral Particles And Uses Thereof For
The Targeted Introduction Of Genetic Material Into Human Cells

<130> 009108.359W01/10359W001

<150> 62525708
<151> 2017-06-27

<160> 55

<170> PatentIn version 3.5

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<220>
<223> SpyTag

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Val Asp Thr Leu Ser Gly Leu Ser Ser Glu Gln Gly Gln Ser Gly Asp
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Met Thr Ile Glu Glu Asp Ser Ala Thr His Ile Lys Phe Ser Lys Arg
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Asp Glu Asp Gly Lys Glu Leu Ala Gly Ala Thr Met Glu Leu Arg Asp

35 40 10359wo01_ST25 45

Ser Ser Gly Lys Thr Ile Ser Thr Trp Ile Ser Asp Gly Gln Val Lys
50 55 60

Asp Phe Tyr Leu Tyr Pro Gly Lys Tyr Thr Phe Val Glu Thr Ala Ala
65 70 75 80

Pro Asp Gly Tyr Glu Val Ala Thr Ala Ile Thr Phe Thr Val Asn Glu
85 90 95

Gln Gly Gln Val Thr Val Asn Gly Lys Ala Thr Lys Gly Asp Ala His
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Gly Asp Gly Lys Glu Leu Ala Gly Ala Thr Met Glu Leu Arg Asp Ser
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Ser Gly Lys Thr Ile Ser Thr Trp Ile Ser Asp Gly Gln Val Lys Asp
35 40 45

Phe Tyr Leu Tyr Pro Gly Lys Tyr Thr Phe Val Glu Thr Ala Ala Pro
50 55 60

Asp Gly Tyr Glu Val Ala Thr Ala Ile Thr Phe Thr Val Asn Glu Gln
65 70 75 80

Gly Gln Val Thr Val Asn Gly Lys Ala Thr Lys Gly Gly Ser Gly Gly
85 90 95

Ser Gly Gly Ser Gly Glu Asp Ser Ala Thr His Ile
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Lys Leu Gly Asp Ile Glu Phe Ile Lys Val Asn Lys
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<211> 133

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<223> SnoopCatcher

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Arg Gly Ser His Met Lys Pro Leu Arg Gly Ala Val Phe Ser Leu Gln
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Lys Gln His Pro Asp Tyr Pro Asp Ile Tyr Gly Ala Ile Asp Gln Asn
 35 40 45

Gly Thr Tyr Gln Asn Val Arg Thr Gly Glu Asp Gly Lys Leu Thr Phe
 50 55 60

Lys Asn Leu Ser Asp Gly Lys Tyr Arg Leu Phe Glu Asn Ser Glu Pro
 65 70 75 80

Ala Gly Tyr Lys Pro Val Gln Asn Lys Pro Ile Val Ala Phe Gln Ile
 85 90 95

Val Asn Gly Glu Val Arg Asp Val Thr Ser Ile Val Pro Gln Asp Ile
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Pro Ala Thr Tyr Glu Phe Thr Asn Gly Lys His Tyr Ile Thr Asn Glu
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Pro Ile Pro Pro Lys
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<211> 16

<212> PRT

<213> Artificial Sequence

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<211> 735

<212> PRT

<213> adeno-associated virus 2

<400> 9

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Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

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

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

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

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

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

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

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190

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Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
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 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
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Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
 580 585 590
 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605
 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620
 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640
 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
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 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670
 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685
 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
 690 695 700
 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
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 725 730 735

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 <211> 2208
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pAAV2-CAP R585A R588A (HBM) DNA

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 aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960
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 <212> PRT
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 <223> pAAV2-CAP R585A R588A (HBM) AA

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Lys	Pro	Ala	Glu	Arg	His	Lys	Asp	Asp	Ser	Arg	Gly	Leu	Val	Leu	Pro
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Gly	Tyr	Lys	Tyr	Leu	Gly	Pro	Phe	Asn	Gly	Leu	Asp	Lys	Gly	Glu	Pro
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Val	Asn	Glu	Ala	Asp	Ala	Ala	Ala	Leu	Glu	His	Asp	Lys	Ala	Tyr	Asp
65					70					75					80

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

Asp	Ala	Glu	Phe	Gln	Glu	Arg	Leu	Lys	Glu	Asp	Thr	Ser	Phe	Gly	Gly
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Asn	Leu	Gly	Arg	Ala	Val	Phe	Gln	Ala	Lys	Lys	Arg	Val	Leu	Glu	Pro
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Leu	Gly	Leu	Val	Glu	Glu	Pro	Val	Lys	Thr	Ala	Pro	Gly	Lys	Lys	Arg
	130					135					140				

Pro	Val	Glu	His	Ser	Pro	Val	Glu	Pro	Asp	Ser	Ser	Ser	Gly	Thr	Gly
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Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
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 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
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 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
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 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430

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Leu Met Asn₄₃₅ Pro Leu Ile Asp Gln₄₄₀ Tyr Leu Tyr Tyr Leu₄₄₅ Ser Arg Thr
 Asn Thr₄₅₀ Pro Ser Gly Thr Thr₄₅₅ Thr Gln Ser Arg Leu₄₆₀ Gln Phe Ser Gln
 Ala Gly Ala Ser Asp Ile₄₇₀ Arg Asp Gln Ser Arg₄₇₅ Asn Trp Leu Pro Gly₄₈₀
 Pro Cys Tyr Arg Gln₄₈₅ Gln Arg Val Ser Lys₄₉₀ Thr Ser Ala Asp Asn₄₉₅ Asn
 Asn Ser Glu₅₀₀ Tyr Ser Trp Thr Gly Ala₅₀₅ Thr Lys Tyr His Leu₅₁₀ Asn Gly
 Arg Asp Ser₅₁₅ Leu Val Asn Pro Gly₅₂₀ Pro Ala Met Ala Ser₅₂₅ His Lys Asp
 Asp Glu₅₃₀ Glu Lys Phe Phe Pro₅₃₅ Gln Ser Gly Val Leu₅₄₀ Ile Phe Gly Lys
 Gln Gly Ser Glu Lys Thr₅₅₀ Asn Val Asp Ile Glu₅₅₅ Lys Val Met Ile Thr₅₆₀
 Asp Glu Glu Glu Ile₅₆₅ Arg Thr Thr Asn Pro₅₇₀ Val Ala Thr Glu Gln₅₇₅ Tyr
 Gly Ser Val Ser₅₈₀ Thr Asn Leu Gln Ala₅₈₅ Gly Asn Ala Gln Ala₅₉₀ Ala Thr
 Ala Asp Val₅₉₅ Asn Thr Gln Gly Val₆₀₀ Leu Pro Gly Met Val₆₀₅ Trp Gln Asp
 Arg Asp₆₁₀ Val Tyr Leu Gln Gly₆₁₅ Pro Ile Trp Ala Lys₆₂₀ Ile Pro His Thr
 Asp Gly His Phe His Pro₆₃₀ Ser Pro Leu Met Gly₆₃₅ Gly Phe Gly Leu Lys₆₄₀
 His Pro Pro Pro Gln₆₄₅ Ile Leu Ile Lys Asn₆₅₀ Thr Pro Val Pro Ala₆₅₅ Asn
 Pro Ser Thr Thr₆₆₀ Phe Ser Ala Ala Lys₆₆₅ Phe Ala Ser Phe Ile₆₇₀ Thr Gln
 Tyr Ser Thr₆₇₅ Gly Gln Val Ser Val₆₈₀ Glu Ile Glu Trp Glu₆₈₅ Leu Gln Lys
 Glu Asn₆₉₀ Ser Lys Arg Trp Asn₆₉₅ Pro Glu Ile Gln Tyr₇₀₀ Thr Ser Asn Tyr

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Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
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Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

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<212> DNA
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<220>
<223> pAAV2-CAP N587 SpyTag HBM DNA

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caagcagcta ccgcagatgt caacacacaa ggcgttcttc caggcatggt ctggcaggac 1860
agagatgtgt accttcaggg gcccatctgg gcaaagattc cacacacgga cggacatttt 1920
caccctctc ccctcatggg tggattcgga cttaaacc ctcctccaca gattctcatc 1980
aagaacaccc cggtacctgc gaatccttcg accaccttca gtgcggcaaa gtttgcttcc 2040
ttcatcacac agtactccac gggacaggtc agcgtggaga tcgagtggga gctgcagaag 2100
gaaaacagca aacgctggaa tcccgaatt cagtacactt ccaactacaa caagtctggt 2160
aatgtggact ttactgtgga cactaatggc gtgtattcag agcctcgccc cattggcacc 2220
agatacctga ctcgtaatct gtaa 2244

<210> 13
<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<223> pAAV2-CAP N587 SpyTag HBM AA

<400> 13

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

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

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

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

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

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

Leu Gly 130 Leu Val Glu Glu Pro 135 Val Lys Thr Ala Pro 140 Gly Lys Lys Arg
 Pro 145 Val Glu His Ser Pro 150 Val Glu Pro Asp Ser 155 Ser Ser Gly Thr Gly 160
 Lys Ala Gly Gln Gln 165 Pro Ala Arg Lys Arg 170 Leu Asn Phe Gly Gln 175 Thr
 Gly Asp Ala Asp 180 Ser Val Pro Asp Pro 185 Gln Pro Leu Gly Gln 190 Pro Pro
 Ala Ala Pro 195 Ser Gly Leu Gly Thr 200 Asn Thr Met Ala Thr 205 Gly Ser Gly
 Ala Pro 210 Met Ala Asp Asn Asn 215 Glu Gly Ala Asp Gly 220 Val Gly Asn Ser
 Ser 225 Gly Asn Trp His Cys 230 Asp Ser Thr Trp Met 235 Gly Asp Arg Val Ile 240
 Thr Thr Ser Thr Arg 245 Thr Trp Ala Leu Pro 250 Thr Tyr Asn Asn His 255 Leu
 Tyr Lys Gln Ile 260 Ser Ser Gln Ser Gly 265 Ala Ser Asn Asp Asn 270 His Tyr
 Phe Gly Tyr 275 Ser Thr Pro Trp Gly 280 Tyr Phe Asp Phe Asn 285 Arg Phe His
 Cys His 290 Phe Ser Pro Arg Asp 295 Trp Gln Arg Leu Ile 300 Asn Asn Asn Trp
 Gly 305 Phe Arg Pro Lys Arg 310 Leu Asn Phe Lys Leu 315 Phe Asn Ile Gln Val 320
 Lys Glu Val Thr Gln 325 Asn Asp Gly Thr Thr 330 Thr Ile Ala Asn Asn 335 Leu
 Thr Ser Thr Val 340 Gln Val Phe Thr Asp 345 Ser Glu Tyr Gln Leu 350 Pro Tyr
 Val Leu Gly 355 Ser Ala His Gln Gly 360 Cys Leu Pro Pro Phe 365 Pro Ala Asp
 Val 370 Phe Met Val Pro Gln Tyr 375 Gly Tyr Leu Thr Leu 380 Asn Asn Gly Ser
 Gln 385 Ala Val Gly Arg Ser 390 Ser Phe Tyr Cys Leu 395 Glu Tyr Phe Pro Ser 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Ala Gly Asn Ala His Ile Val Met
 580 585 590
 Val Asp Ala Tyr Lys Pro Thr Lys Gln Ala Ala Thr Ala Asp Val Asn
 595 600 605
 Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr
 610 615 620
 Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe
 625 630 635 640
 His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
 645 650 655
 Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Thr Thr
 660 665 670

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Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
675 680 685

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
690 695 700

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn Lys Ser Val
705 710 715 720

Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg
725 730 735

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
740 745

<210> 14
<211> 2253
<212> DNA
<213> Artificial Sequence

<220>
<223> pAAV2-CAP N587 Linker 1 SpyTag HBM DNA

<400> 14
atggctgccc atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60
cagtgggtga agtcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
cggcagctcg acagcggaga caaccggtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480
aaggcgggccc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctctctg tctgggaact 600
aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcca cagagtcac 720
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaatt 780
tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840
tattttgact tcaacagatt cactgccac ttttcaccac gtgactggca aagactcatc 900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960
aaagaggtca cgcagaatga cggtagcagc acgattgccca ataaccttac cagcacgggt 1020
caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
tgcctcccg cgttcccagc agacgtcttc atggtgccac agtatggata cctcacctg 1140
aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

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cagatgctgc gtaccgga aaactttacc ttcagctaca cttttgagga cgttcctttc 1260
cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320
tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380
cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440
ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500
tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560
ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620
atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggc catgattaca 1680
gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740
accaacctcc aggccggcaa cgcgagcgcc cacatcgtga tggcggacgc ctacaagccg 1800
acgaaggcgc aagcagctac cgcagatgtc aacacacaag gcgttcttcc aggcattggtc 1860
tggcaggaca gagatgtgta ccttcagggg cccatctggg caaagattcc acacacggac 1920
ggacattttc acccctctcc cctcatgggt ggattcggac ttaaaccacc tcctccacag 1980
attctcatca agaaccctcc ggtacctgcg aatccttcga ccaccttcag tgcggcaaag 2040
tttgcttcct tcatcacaca gtactccacg ggacaggcca gcgtggagat cgagtgaggag 2100
ctgcagaagg aaaacagcaa acgctggaat cccgaaattc agtacacttc caactacaac 2160
aagtctgtta atgtggactt tactgtggac actaatggcg tgtattcaga gcctcgcccc 2220
attggcacca gatacctgac tcgtaatctg taa 2253

<210> 15
<211> 750
<212> PRT
<213> Artificial Sequence

<220>
<223> pAAV2-CAP N587 Linker 1 SpyTag HBM AA
<400> 15

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

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

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

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Arg Gln Leu Asp Ser₈₅ Gly Asp Asn Pro Tyr₉₀ Leu Lys Tyr Asn His₉₅ Ala
 Asp Ala Glu Phe₁₀₀ Gln Glu Arg Leu Lys₁₀₅ Glu Asp Thr Ser Phe₁₁₀ Gly Gly
 Asn Leu Gly₁₁₅ Arg Ala Val Phe₁₂₀ Ala Lys Lys Arg Val₁₂₅ Leu Glu Pro
 Leu Gly₁₃₀ Leu Val Glu Glu Pro₁₃₅ Val Lys Thr Ala Pro₁₄₀ Gly Lys Lys Arg
 Pro Val₁₄₅ Glu His Ser Pro₁₅₀ Val Glu Pro Asp Ser₁₅₅ Ser Ser Gly Thr Gly₁₆₀
 Lys Ala Gly Gln Gln₁₆₅ Pro Ala Arg Lys Arg₁₇₀ Leu Asn Phe Gly Gln₁₇₅ Thr
 Gly Asp Ala Asp₁₈₀ Ser Val Pro Asp Pro₁₈₅ Gln Pro Leu Gly Gln₁₉₀ Pro Pro
 Ala Ala Pro₁₉₅ Ser Gly Leu Gly Thr₂₀₀ Asn Thr Met Ala Thr₂₀₅ Gly Ser Gly
 Ala Pro₂₁₀ Met Ala Asp Asn Asn₂₁₅ Glu Gly Ala Asp Gly₂₂₀ Val Gly Asn Ser
 Ser₂₂₅ Gly Asn Trp His Cys₂₃₀ Asp Ser Thr Trp Met₂₃₅ Gly Asp Arg Val Ile₂₄₀
 Thr Thr Ser Thr Arg₂₄₅ Thr Trp Ala Leu Pro₂₅₀ Thr Tyr Asn Asn His₂₅₅ Leu
 Tyr Lys Gln Ile₂₆₀ Ser Ser Gln Ser Gly₂₆₅ Ala Ser Asn Asp Asn₂₇₀ His Tyr
 Phe Gly Tyr₂₇₅ Ser Thr Pro Trp Gly₂₈₀ Tyr Phe Asp Phe Asn₂₈₅ Arg Phe His
 Cys His₂₉₀ Phe Ser Pro Arg Asp₂₉₅ Trp Gln Arg Leu Ile₃₀₀ Asn Asn Asn Trp
 Gly Phe Arg Pro Lys Arg₃₁₀ Leu Asn Phe Lys Leu₃₁₅ Phe Asn Ile Gln Val₃₂₀
 Lys Glu Val Thr Gln₃₂₅ Asn Asp Gly Thr Thr₃₃₀ Thr Ile Ala Asn Asn₃₃₅ Leu
 Thr Ser Thr Val₃₄₀ Gln Val Phe Thr Asp₃₄₅ Ser Glu Tyr Gln Leu₃₅₀ Pro Tyr

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Ala Gly Asn Ala Ser Ala His Ile
 580 585 590

Val Met Val Asp Ala Tyr Lys Pro Thr Lys Ala Gln Ala Ala Thr Ala
 595 600 605

Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp Arg
 610 615 620

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Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
625 630 635 640

Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
645 650 655

Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
660 665 670

Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
675 680 685

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
690 695 700

Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
705 710 715 720

Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
725 730 735

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
740 745 750

<210> 16
<211> 2256
<212> DNA
<213> Artificial Sequence

<220>
<223> pAAV2-CAP N587 Linker 2 SpyTag HBM DNA

<400> 16
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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcgagagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gactctcct gtggagccag actcctcctc gggaaccgga 480
aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctcttg tctgggaact 600
aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcca cagagtcac 720
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaatt 780
tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

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tat	ttttgact	tcaacagatt	ccactgccac	ttttcaccac	gtgactggca	aagactcatc	900
aaca	acaact	ggggattccg	acccaagaga	ctcaacttca	agctctttta	cattcaagtc	960
aaag	agggtca	cgcagaatga	cggtagcagc	acgattgcc	ataaccttac	cagcacggtt	1020
cagg	tgttta	ctgactcgga	gtaccagctc	ccgtacgtcc	tcggctcggc	gcatcaagga	1080
tgc	ctcccgc	cgttcccagc	agacgtcttc	atggtgccac	agtatggata	cctcaccctg	1140
aaca	acggga	gtcaggcagt	aggacgctct	tcattttact	gcctggagta	ctttccttct	1200
caga	tgtctgc	gtaccggaaa	caactttacc	ttcagctaca	cttttgagga	cgttcctttc	1260
cacag	cagct	acgctcacag	ccagagtctg	gaccgtctca	tgaatcctct	catcgaccag	1320
tac	ctgtatt	acttgagcag	aacaaacact	ccaagtggaa	ccaccacgca	gtcaaggctt	1380
cag	ttttctc	aggccggagc	gagtgacatt	cgggaccagt	ctaggaactg	gcttcctgga	1440
cc	ctgttacc	gccagcagcg	agtatcaaag	acatctgcgg	ataacaacaa	cagtgaatac	1500
tc	gtggactg	gagctaccaa	gtaccacctc	aatggcagag	actctctggt	gaatccgggc	1560
cc	ggccatgg	caagccacaa	ggacgatgaa	gaaaagtttt	ttcctcagag	cggggttctc	1620
at	ctttggga	agcaaggctc	agagaaaaca	aatgtggaca	ttgaaaaggt	catgattaca	1680
gac	gaagagg	aaatcaggac	aaccaatccc	gtggctacgg	agcagtatgg	ttctgtatct	1740
acca	acctcc	aggcgggcaa	cggcagcgcc	cacatcgtga	tgggtggacgc	ctacaagccg	1800
ac	gaagggca	gccaagcagc	taccgcagat	gtcaacacac	aaggcgttct	tccaggcatg	1860
gt	ctggcagg	acagagatgt	gtaccttcag	gggcccattct	gggcaaagat	tccacacacg	1920
gac	ggacatt	ttcacccctc	tcccctcatg	ggtggattcg	gacttaaaca	ccctcctcca	1980
caga	ttctca	tcaagaacac	cccgggtacct	gcgaatcctt	cgaccacctt	cagtgcggca	2040
aag	tttgctt	ccttcatcac	acagtactcc	acgggacagg	tcagcgtgga	gatcgagtgg	2100
gag	ctgcaga	aggaaaacag	caaacgctgg	aatccccgaaa	ttcagtacac	ttccaactac	2160
aaca	agtctg	ttaatgtgga	ctttactgtg	gacactaatg	gcgtgtattc	agagcctcgc	2220
ccc	attggca	ccagatacct	gactcgtaat	ctgtaa			2256

<210> 17

<211> 751

<212> PRT

<213> Artificial Sequence

<220>

<223> pAAV2-CAP N587 Linker 2 SpyTag HBM AA

<400> 17

Met	Ala	Ala	Asp	Gly	Tyr	Leu	Pro	Asp	Trp	Leu	Glu	Asp	Thr	Leu	Ser
1				5					10					15	

Glu	Gly	Ile	Arg	Gln	Trp	Trp	Lys	Leu	Lys	Pro	Gly	Pro	Pro	Pro	Pro
			20					25				30			

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Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300

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Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575

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Gly Ser Val Ser Thr Asn Leu Gln Ala Gly Asn Gly Ser Ala His Ile
580 585 590

Val Met Val Asp Ala Tyr Lys Pro Thr Lys Gly Ser Gln Ala Ala Thr
595 600 605

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
610 615 620

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
625 630 635 640

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
645 650 655

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
660 665 670

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
675 680 685

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
690 695 700

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
705 710 715 720

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
725 730 735

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
740 745 750

<210> 18
<211> 2268
<212> DNA
<213> Artificial Sequence

<220>
<223> pAAV2-CAP N587 Linker 4 SpyTag HBM DNA

<400> 18
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cagtgggtgga agctcaaacc tggcccacca ccaccaaagc cgcgagagcg gcataaggac 120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

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aaggcgggcc	agcagcctgc	aagaaaaaga	ttgaattttg	gtcagactgg	agacgcagac	540
tcagtacctg	acccccagcc	tctcggacag	ccaccagcag	ccccctctgg	tctgggaact	600
aatacgatgg	ctacaggcag	tggcgcacca	atggcagaca	ataacgaggg	cgccgacgga	660
gtgggtaatt	cctcgggaaa	ttggcattgc	gattccacat	ggatgggcga	cagagtcatc	720
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gagatcgagt	gggagctgca	gaaggaaaac	agcaaacgct	ggaatcccga	aattcagtac	2160
acttccaact	acaacaagtc	tgtaaatgtg	gactttactg	tggacactaa	tggcgtgtat	2220
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<210> 19
 <211> 755
 <212> PRT
 <213> Artificial Sequence

<220>

<223> pAAV2-CAP N587 Linker 4 SpyTag HBM AA

<400> 19

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20 25 30Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
195 200 205Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225 230 235 240Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Ala Gly Asn Gly Leu Ser Gly Ala
 580 585 590

His Ile Val Met Val Asp Ala Tyr Lys Pro Thr Lys Gly Leu Ser Gly
 595 600 605

Gln Ala Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met
 610 615 620

Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys
 625 630 635 640

Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly
 645 650 655

Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro
 660 665 670

Val Pro Ala Asn Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser
 675 680 685

Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp
 690 695 700

Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr
 705 710 715 720

Thr Ser Asn Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr
 725 730 735

Asn Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr
 740 745 750

Arg Asn Leu
 755

<210> 20
 <211> 2280
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pAAV2-CAP N587 Linker 6 SpyTag HBM DNA

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<400> 20
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caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
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gaaattcagt acacttccaa ctacaacaag tctgttaatg tggactttac tgtggacact 2220
aatggcgtgt attcagagcc tcgccccatt ggcaccagat acctgactcg taatctgtaa 2280

<210> 21
<211> 759
<212> PRT
<213> Artificial Sequence

<220>
<223> pAAV2-CAP N587 Linker 6 SpyTag HBM AA
<400> 21

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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

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

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

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

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

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

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

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190

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Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
435 440 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
450 455 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Ala Gly Asn Gly Leu Ser Gly Ser
 580 585 590
 Gly Ala His Ile Val Met Val Asp Ala Tyr Lys Pro Thr Lys Gly Leu
 595 600 605
 Ser Gly Ser Gly Gln Ala Ala Thr Ala Asp Val Asn Thr Gln Gly Val
 610 615 620
 Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
 625 630 635 640
 Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro
 645 650 655
 Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile
 660 665 670
 Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Thr Thr Phe Ser Ala Ala
 675 680 685
 Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
 690 695 700
 Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
 705 710 715 720
 Glu Ile Gln Tyr Thr Ser Asn Tyr Asn Lys Ser Val Asn Val Asp Phe
 725 730 735

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Thr Val Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
 740 745 750

Arg Tyr Leu Thr Arg Asn Leu
 755

<210> 22
 <211> 2292
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pAAV2-CAP N587 Linker 8 SpyTag HBM DNA

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 aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
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 gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
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 aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660
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 tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840
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 aaagaggtca cgcagaatga cggtagcagc acgattgcc aataaccttac cagcacgggt 1020
 cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
 tgcctcccg cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140
 aacaacggga gtcaggcagt aggacgtctc tcattttact gcctggagta ctttccttct 1200
 cagatgctgc gtaccgga aactttacc ttcagctaca cttttgagga cgttcctttc 1260
 cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320
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 cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440
 ccctgttacc gccagcagc agtatcaaag acatctgcgg ataacaaca cagtgaatac 1500
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tactccacgg gacaggtcag cgtggagatc gagtgggagc tgcagaagga aaacagcaaa 2160
cgctggaatc ccgaaattca gtacacttcc aactacaaca agtctgttaa tgtggacttt 2220
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cgtaatctgt aa 2292

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<210> 23
 <211> 763
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> pAAV2-CAP N587 Linker 8 SpyTag HBM AA
 <400> 23

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

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

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

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

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

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

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Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400

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Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
435 440 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
450 455 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
530 535 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Ala Gly Asn Gly Leu Ser Gly Leu
580 585 590

Ser Gly Ser Ala His Ile Val Met Val Asp Ala Tyr Lys Pro Thr Lys
595 600 605

Gly Leu Ser Gly Leu Ser Gly Ser Gln Ala Ala Thr Ala Asp Val Asn
610 615 620

Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr
625 630 635 640

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe
645 650 655

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
660 665 670

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Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Thr Thr
675 680 685

Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
690 695 700

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
705 710 715 720

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn Lys Ser Val
725 730 735

Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg
740 745 750

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
755 760

<210> 24
<211> 2304
<212> DNA
<213> Artificial Sequence

<220>
<223> pAAV2-CAP N587 Linker 10 SpyTag HBM DNA

<400> 24
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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
cggcagctcg acagcggaga caacccttac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gactctcct gtggagccag actcctcctc gggaaccgga 480
aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggaact 600
aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac 720
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaatt 780
tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840
tattttgact tcaacagatt cactgcccac ttttcaccac gtgactggca aagactcatc 900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttta cattcaagtc 960
aaagaggtca cgcagaatga cggtagcagc acgattgcca ataaccttac cagcacgggt 1020

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caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080
 tgcctcccg cgttcccagc agacgtcttc atgggtccac agtatggata cctcacctg 1140
 aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200
 cagatgctgc gtaccgga aaactttacc ttcagctaca cttttgagga cgttcctttc 1260
 cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320
 tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380
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 ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaaca cagtgaatac 1500
 tcgtggactg gagctacaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560
 ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620
 atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaagg catgattaca 1680
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 gtgatgggtg acgcctacaa gccgacgaag ggcctgagcg gcctgagcgg cctgagcggc 1860
 caagcagcta ccgcagatgt caacacacaa ggcgttcttc caggcatggt ctggcaggac 1920
 agagatgtgt accttcaggg gcccatctgg gcaaagattc cacacacgga cggacatttt 1980
 caccctctc ccctcatggg tggattcgga cttaaacc ctcctccaca gattctcatc 2040
 aagaacacc cggtacctgc gaatccttcg accaccttca gtgcggcaaa gtttgcttcc 2100
 ttcacacac agtactccac gggacaggtc agcgtggaga tcgagtggga gctgcagaag 2160
 gaaaacagca aacgctggaa tcccgaatt cagtacactt ccaactacaa caagtctgtt 2220
 aatgtggact ttactgtgga cactaatggc gtgtattcag agcctcgccc cattggcacc 2280
 agatacctga ctcgtaatct gtaa 2304

<210> 25
 <211> 767
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> pAAV2-CAP N587 Linker 10 SpyTag HBM AA
 <400> 25

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 1 5 10 15
 Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30
 Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45

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Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320

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Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460
 Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Ala Gly Asn Gly Leu Ser Gly Leu
 580 585 590

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Ser Gly Leu Ser Gly Ala His Ile Val Met Val Asp Ala Tyr Lys Pro
595 600 605

Thr Lys Gly Leu Ser Gly Leu Ser Gly Leu Ser Gly Gln Ala Ala Thr
610 615 620

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
625 630 635 640

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
645 650 655

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
660 665 670

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
675 680 685

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
690 695 700

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
705 710 715 720

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
725 730 735

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
740 745 750

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
755 760 765

<210> 26
<211> 2247
<212> DNA
<213> Artificial Sequence

<220>
<223> pAAV2-CAP G453 SpyTag HBM DNA

<400> 26
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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180
aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240
cggcagctcg acagcggaga caaccgtac ctcaagtaca accacgccga cgcggagttt 300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

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tcagtacctg acccccagcc tctcggacag ccaccagcag cccctcttgg tctgggaact	600
aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga	660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcca cagagtcac	720
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaatt	780
tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg	840
tattttgact tcaacagatt cactgcccac ttttcaccac gtgactggca aagactcatc	900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc	960
aaagagggtca cgcagaatga cggtagcagc acgattgcc aataccttac cagcacgggt	1020
cagggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga	1080
tgctcccg cgctccagc agacgtcttc atgggtccac agtatggata cctcacctg	1140
aacaacggga gtcaggcagt aggacgtctc tcattttact gcctggagta ctttccttct	1200
cagatgctgc gtaccgaaa caactttacc ttcagctaca cttttgagga cgctccttc	1260
cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag	1320
tacctgtatt acttgagcag aacaacact ccaagtggag cccacatcgt gatggtggac	1380
gcctacaagc cgacgaagac caccacgcag tcaaggcttc agttttctca ggccggagcg	1440
agtgacattc gggaccagtc taggaactgg ctctctggac cctgttacgc ccagcaggcc	1500
gtatcaaaga catctgcgga taacaacaac agtgaatact cgtggactgg agctaccaag	1560
taccacctca atggcagaga ctctctggtg aatccgggcc cggccatggc aagccacaag	1620
gacgatgaag aagccttttt tcctcagagc ggggttctca tctttgggaa gcaaggctca	1680
gagaaaacaa atgtggacat tgaaaaggtc atgattacag acgaagagga aatcaggaca	1740
accaatcccg tggctacgga gcagtatggt tctgtatcta ccaacctcca ggccggcaac	1800
gccaagcag ctaccgcaga tgtcaacaca caaggcgctc ttccaggcat ggtctggcag	1860
gacagagatg tgtaccttca ggggccatc tgggcaaaga ttccacacac ggacggacat	1920
tttcaccctt ctccctcat ggggtgattc ggacttaaac accctcctcc acagattctc	1980
atcaagaaca ccccggtacc tgcgaatcct tcgaccacct tcagtgcggc aaagtttgct	2040
tccttcatca cacagtactc cacgggacag gtcagcgtgg agatcgagtg ggagctgcag	2100
aaggaaaaca gcaaacgctg gaatcccgaa attcagtaca cttccaacta caacaagtct	2160
gttaatgtgg actttactgt ggacactaat ggcgtgtatt cagagcctcg cccattggc	2220
accagatacc tgactcgtaa tctgtaa	2247

<210> 27
 <211> 748
 <212> PRT
 <213> Artificial Sequence

<220>

<223> pAAV2-CAP G453 SpyTag HBM AA

<400> 27

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
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20 25 30Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
195 200 205Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225 230 235 240Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445
 Asn Thr Pro Ser Gly Ala His Ile Val Met Val Asp Ala Tyr Lys Pro
 450 455 460
 Thr Lys Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln Ala Gly Ala
 465 470 475 480
 Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly Pro Cys Tyr
 485 490 495
 Ala Gln Gln Ala Val Ser Lys Thr Ser Ala Asp Asn Asn Asn Ser Glu
 500 505 510
 Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser
 515 520 525

Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp Glu Glu
530 535 540

Ala Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys Gln Gly Ser
545 550 555 560

Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr Asp Glu Glu
565 570 575

Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Ser Val
580 585 590

Ser Thr Asn Leu Gln Ala Gly Asn Ala Gln Ala Ala Thr Ala Asp Val
595 600 605

Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val
610 615 620

Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His
625 630 635 640

Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro
645 650 655

Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Thr
660 665 670

Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr
675 680 685

Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser
690 695 700

Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn Lys Ser
705 710 715 720

Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser Glu Pro
725 730 735

Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
740 745

<210> 28

<211> 2307

<212> DNA

<213> Artificial Sequence

<220>

<223> pAAV2-CAP G453 Linker10 SpyTag HBM DNA

<400> 28

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cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

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cggcagctcg	acagcggaga	caacccgtac	ctcaagtaca	accacgccga	cgcggagttt	300
caggagcgcc	ttaaagaaga	tacgtctttt	gggggcaacc	tcggacgagc	agtcttccag	360
gcgaaaaaga	gggttcttga	acctctgggc	ctggttgagg	aacctgttaa	gacggctccg	420
ggaaaaaaga	ggccggtaga	gcactctcct	gtggagccag	actcctcctc	gggaaccgga	480
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tcagtacctg	acccccagcc	tctcggacag	ccaccagcag	ccccctctgg	tctgggaact	600
aatacgatgg	ctacaggcag	tggcgcacca	atggcagaca	ataacgaggg	cgccgacgga	660
gtgggtaatt	cctcgggaaa	ttggcattgc	gattccacat	ggatgggcga	cagagtcatc	720
accaccagca	cccgaacctg	ggccctgccc	acctacaaca	accacctcta	caaacaaatt	780
tccagccaat	caggagcctc	gaacgacaat	cactactttg	gctacagcac	cccttggggg	840
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aacaacaact	ggggattccg	acccaagaga	ctcaacttca	agctctttta	cattcaagtc	960
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cagggtgtta	ctgactcgga	gtaccagctc	ccgtacgtcc	tcggctcggc	gcatcaagga	1080
tgcctcccgc	cgttcccagc	agacgtcttc	atgggtgcc	agtatggata	cctcaccttg	1140
aacaacggga	gtcaggcagt	aggacgtctt	tcattttact	gcctggagta	ctttccttct	1200
cagatgctgc	gtaccggaaa	caactttacc	ttcagctaca	cttttgagga	cgttcctttc	1260
cacagcagct	acgtcacag	ccagagtctg	gaccgtctca	tgaatcctct	catcgaccag	1320
tacctgtatt	acttgagcag	aacaaacact	ccaagtggag	gcctgagcgg	cctgagcggc	1380
ctgagcggcg	cccacatcgt	gatggtggac	gcctacaagc	cgacgaaggg	cctgagcggc	1440
ctgagcggcc	tgagcggcac	caccacgcag	tcaaggcttc	agttttctca	ggccggagcg	1500
agtgcattc	gggaccagtc	taggaactgg	cttcctggac	cctgttacgc	ccagcaggcc	1560
gtatcaaaga	catctgcgga	taacaacaac	agtgaatact	cgtggactgg	agctaccaag	1620
taccacctca	atggcagaga	ctctctggtg	aatccgggcc	cggccatggc	aagccacaag	1680
gacgatgaag	aagccttttt	tcctcagagc	ggggttctca	tctttgggaa	gcaaggctca	1740
gagaaaacaa	atgtggacat	tgaaaaggtc	atgattacag	acgaagagga	aatcaggaca	1800
accaatcccc	tggctacgga	gcagtatggt	tctgtatcta	ccaacctcca	ggccggcaac	1860
gccaagcag	ctaccgcaga	tgtcaacaca	caaggcgttc	ttccaggcat	ggtctggcag	1920
gacagagatg	tgtaccttca	ggggcccatc	tgggcaaaga	ttccacacac	ggacggacat	1980
tttcacccct	ctccccctcat	gggtggattc	ggacttaaac	accctcctcc	acagattctc	2040
atcaagaaca	ccccggtacc	tgcgaatcct	tcgaccacct	tcagtgcggc	aaagtttgct	2100
tccttcatca	cacagtactc	cacgggacag	gtcagcgtgg	agatcgagtg	ggagctgcag	2160

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aaggaaaaca gcaaacgctg gaatcccgaa attcagtaca cttccaacta caacaagtct 2220
 gttaatgtgg actttactgt ggacactaat ggcgtgtatt cagagcctcg cccattggc 2280
 accagatacc tgactcgtaa tctgtaa 2307

<210> 29
 <211> 768
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> pAAV2-CAP G453 Linker10 SpyTag HBM AA
 <400> 29

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45

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

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

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

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

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

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

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205

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Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
435 440 445

Asn Thr Pro Ser Gly Gly Leu Ser Gly Leu Ser Gly Leu Ser Gly Ala
450 455 460

His Ile Val Met Val Asp Ala Tyr Lys Pro Thr Lys Gly Leu Ser Gly
465 470 475 480

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Leu Ser Gly Leu Ser₄₈₅ Gly Thr Thr Thr Gln₄₉₀ Ser Arg Leu Gln Phe₄₉₅ Ser
 Gln Ala Gly Ala₅₀₀ Ser Asp Ile Arg Asp₅₀₅ Gln Ser Arg Asn Trp₅₁₀ Leu Pro
 Gly Pro Cys₅₁₅ Tyr Ala Gln Gln Ala₅₂₀ Val Ser Lys Thr Ser₅₂₅ Ala Asp Asn
 Asn Asn₅₃₀ Ser Glu Tyr Ser Trp₅₃₅ Thr Gly Ala Thr Lys₅₄₀ Tyr His Leu Asn
 Gly₅₄₅ Arg Asp Ser Leu Val₅₅₀ Asn Pro Gly Pro Ala₅₅₅ Met Ala Ser His Lys₅₆₀
 Asp Asp Glu Glu Ala₅₆₅ Phe Phe Pro Gln Ser₅₇₀ Gly Val Leu Ile Phe₅₇₅ Gly
 Lys Gln Gly Ser₅₈₀ Glu Lys Thr Asn Val₅₈₅ Asp Ile Glu Lys Val₅₉₀ Met Ile
 Thr Asp Glu₅₉₅ Glu Glu Ile Arg Thr₆₀₀ Thr Asn Pro Val Ala₆₀₅ Thr Glu Gln
 Tyr Gly₆₁₀ Ser Val Ser Thr Asn₆₁₅ Leu Gln Ala Gly Asn₆₂₀ Ala Gln Ala Ala
 Thr₆₂₅ Ala Asp Val Asn Thr₆₃₀ Gln Gly Val Leu Pro₆₃₅ Gly Met Val Trp Gln₆₄₀
 Asp Arg Asp Val₆₄₅ Tyr Leu Gln Gly Pro Ile₆₅₀ Trp Ala Lys Ile Pro₆₅₅ His
 Thr Asp Gly His₆₆₀ Phe His Pro Ser Pro₆₆₅ Leu Met Gly Gly Phe₆₇₀ Gly Leu
 Lys His Pro₆₇₅ Pro Pro Gln Ile Leu₆₈₀ Ile Lys Asn Thr Pro₆₈₅ Val Pro Ala
 Asn Pro₆₉₀ Ser Thr Thr Phe Ser₆₉₅ Ala Ala Lys Phe Ala₇₀₀ Ser Phe Ile Thr
 Gln Tyr Ser Thr Gly Gln₇₁₀ Val Ser Val Glu Ile₇₁₅ Glu Trp Glu Leu Gln₇₂₀
 Lys Glu Asn Ser Lys₇₂₅ Arg Trp Asn Pro Glu₇₃₀ Ile Gln Tyr Thr Ser₇₃₅ Asn
 Tyr Asn Lys Ser₇₄₀ Val Asn Val Asp Phe₇₄₅ Thr Val Asp Thr Asn₇₅₀ Gly Val

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Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
755 760 765

<210> 30
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> pAAV9-CAP wt DNA

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aagggggagc cggtaacgc agcagacgcg gcggccctcg agcagacaa ggcctacgac 240
cagcagctca aggccggaga caaccggtac ctcaagtaca accacgccga cgccgagttc 300
caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggagagc agtcttccag 360
gccaaaaaga ggcttcttga acctcttggg ctggttgagg aagcggctaa gacggctcct 420
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gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380
ctaaaattca gtgtggccgg accagcaac atggctgtcc aggaagaaa ctacatacct 1440
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ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

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 tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160
 tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 31
 <211> 736
 <212> PRT
 <213> adeno-associated virus 9
 <400> 31

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 Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
 20 25 30
 Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
 35 40 45
 Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
 145 150 155 160

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Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
 195 200 205
 Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
 260 265 270
 Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
 340 345 350
 Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
 370 375 380
 Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
 405 410 415
 Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430

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Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
 435 440 445
 Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
 450 455 460
 Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
 465 470 475 480
 Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
 485 490 495
 Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
 500 505 510
 Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
 515 520 525
 Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
 530 535 540
 Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
 545 550 555 560
 Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
 565 570 575
 Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
 580 585 590
 Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
 595 600 605
 Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620
 Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
 625 630 635 640
 Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
 645 650 655
 Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
 660 665 670
 Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 675 680 685
 Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
 690 695 700

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Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

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

<210> 32
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> pAAV9-CAP W503A DNA

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccgcaa cggactcgac 180
aagggggagc cgggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240
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<210> 33
 <211> 736
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> pAAV9-CAP W503A AA

<400> 33

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

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

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

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

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

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

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

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg

130

135

140

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

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
 180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
 195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
 210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
 260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
 325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
 340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
 355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
 370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

Asn Asn Ser Glu Phe Ala Ala Pro Gly Ala Ser Ser Trp Ala Leu Asn
500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
515 520 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln

675

680

685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
 690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
 705 710 715 720

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

<210> 34
 <211> 2250
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pAAV9-CAP A589 SpyTag W503A DNA

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<210> 35

<211> 749

<212> PRT

<213> Artificial Sequence

<220>

<223> pAAV9-CAP A589 SpyTag W503A AA

<400> 35

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
 20 25 30

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

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

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

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
 145 150 155 160
 Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
 195 200 205
 Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
 260 265 270
 Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320
 Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
 340 345 350
 Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp

370

375

380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
 405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
 435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
 450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
 465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
 485 490 495

Asn Asn Ser Glu Phe Ala Ala Pro Gly Ala Ser Ser Trp Ala Leu Asn
 500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
 515 520 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
 530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
 545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
 565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Ala His Ile
 580 585 590

Val Met Val Asp Ala Tyr Lys Pro Thr Lys Gln Ala Gln Thr Gly Trp
 595 600 605

Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp Arg Asp
 610 615 620

Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
 625 630 635 640

Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met Lys His Pro
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645

650

655

Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro
 660 665 670

Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser
 675 680 685

Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
 690 695 700

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys
 705 710 715 720

Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val Tyr Ser Glu
 725 730 735

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 740 745

<210> 36
 <211> 2310
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pAAV9-CAP A589 Linker10 SpyTag W503A DNA

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 aacgctcgag gtcttgtgct tccgggttac aaataccttg gaccggaac cgactcgac 180
 aagggggagc cggtaacgc agcagacgcg gcggccctcg agcacgaca ggcctacgac 240
 cagcagctca aggccggaga caaccgtac ctcaagtaca accacgccga cgccgagttc 300
 caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggagagc agtcttccag 360
 gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420
 ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggattggc 480
 aaatcgggtg cacagccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540
 tcagtcccag acctcaacc aatcggagaa cctcccgcag cccctcagg tgtgggatct 600
 cttacaatgg cttcaggtgg tggcgacca gtggcagaca ataacgaagg tgccgatgga 660
 gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatt 720
 accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaattc 780
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 ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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 gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140
 acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200
 ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260
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 cagaaggaaa acagcaagcg ctggaacccg gagatccagt acacttccaa ctattacaag 2220
 tctaataatg ttgaatttgc tgtaatact gaaggtgtat atagtgaacc ccgccccatt 2280
 ggcaccagat acctgactcg taatctgtaa 2310

<210> 37

<211> 769

<212> PRT

<213> Artificial Sequence

<220>

<223> pAAV9-CAP A589 Linker10 SpyTag W503A AA

<400> 37

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
 20 25 30

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

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Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60
 Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80
 Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
 115 120 125
 Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140
 Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
 145 150 155 160
 Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175
 Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
 180 185 190
 Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
 195 200 205
 Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
 210 215 220
 Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
 260 265 270
 Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320

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Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

Asn Asn Ser Glu Phe Ala Ala Pro Gly Ala Ser Ser Trp Ala Leu Asn
500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
515 520 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gly Leu Ser
580 585 590

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Ser Gly Ser Gly Leu Ser Gly Ala His Ile Val Met Val Asp Ala Tyr
595 600 605

Lys Pro Thr Lys Gly Leu Ser Gly Gly Ser Gly Leu Ser Gly Gln Ala
610 615 620

Gln Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp
625 630 635 640

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
645 650 655

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
660 665 670

Met Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
675 680 685

Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile
690 695 700

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
705 710 715 720

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
725 730 735

Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly
740 745 750

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
755 760 765

Leu

<210> 38
<211> 2310
<212> DNA
<213> Artificial Sequence

<220>
<223> pAAV9-CAP G453 Linker10 SpyTag W503A DNA

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gaccggcaa cggactcgac	180
aaggggggagc cgggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac	240
cagcagctca aggccggaga caaccgtac ctcaagtaca accacgccga cgccgagttc	300

10359w001_ST25						
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gccaaaaaga	ggcttcttga	acctcttggg	ctggttgagg	aagcggctaa	gacggctcct	420
ggaaagaaga	ggcctgtaga	gcagtctcct	caggaaccgg	actcctccgc	gggtattggc	480
aaatcgggtg	cacagcccg	taaaaagaga	ctcaatttcg	gtcagactgg	cgacacagag	540
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tgggggtatt	ttgacttcaa	cagattccac	tgccacttct	caccacgtga	ctggcagcga	900
ctcatcaaca	acaactgggg	attccggcct	aagcgactca	acttcaagct	cttcaacatt	960
caggtcaaag	aggttacgga	caacaatgga	gtcaagacca	tcgccaataa	ccttaccagc	1020
acggtccagg	tcttcacgga	ctcagactat	cagctcccgt	acgtgctcgg	gtcggctcac	1080
gagggctgcc	tcccgccgtt	cccagcggac	gttttcatga	ttcctcagta	cgggtatctg	1140
acgcttaatg	atggaagcca	ggccgtgggt	cgttcgtcct	tttactgcct	ggaatatttc	1200
ccgtcgcaaa	tgctaagaac	gggtaacaac	ttccagttca	gctacgagtt	tgagaacgta	1260
cctttccata	gcagctacgc	tcacagccaa	agcctggacc	gactaatgaa	tccactcatc	1320
gaccaatact	tgtactatct	ctcaaagact	attaacgggtg	gcctgagcag	cggcagcggc	1380
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actggaagag	acaacgtgga	tgcggacaaa	gtcatgataa	ccaacgaaga	agaaattaaa	1800
actactaacc	cggtagcaac	ggagtcctat	ggacaagtgg	ccacaaacca	ccagagtgcc	1860
caagcacagg	cgcagaccgg	ctgggttcaa	aaccaaggaa	tacttccggg	tatggtttgg	1920
caggacagag	atgtgtacct	gcaaggacct	atttgggcca	aaattcctca	cacggacggc	1980
aactttcacc	cttctccgct	gatgggaggg	tttggaatga	agcaccgcgc	tcctcagatc	2040
ctcatcaaaa	acacacctgt	acctgcggat	cctccaacgg	ccttcaacaa	ggacaagctg	2100
aactctttca	tcaccagta	ttctactggc	caagtcagcg	tggagatcga	gtgggagctg	2160
cagaaggaaa	acagcaagcg	ctggaacccg	gagatccagt	acacttccaa	ctattacaag	2220
tctaataatg	ttgaatttgc	tgtaataact	gaaggtgtat	atagtgaacc	ccgccccatt	2280
ggcaccagat	acctgactcg	taatctgtaa				2310

<210> 39
 <211> 769
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> pAAV9-RC G453 Linker10 SpyTag w503A AA

<400> 39

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
 20 25 30

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

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

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

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

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

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

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

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

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
 180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
 195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
 210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
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225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
 260 265 270
 Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285
 Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300
 Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315
 Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
 325 330 335
 Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
 340 345 350
 Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
 355 360 365
 Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
 370 375 380
 Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400
 Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
 405 410 415
 Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430
 Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
 435 440 445
 Lys Thr Ile Asn Gly Gly Leu Ser Ser Gly Ser Gly Leu Ser Gly Ala
 450 455 460
 His Ile Val Met Val Asp Ala Tyr Lys Pro Thr Lys Gly Leu Ser Gly
 465 470 475 480
 Gly Ser Gly Leu Ser Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe
 485 490 495
 Ser Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile

500

505

510

Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln
 515 520 525
 Asn Asn Asn Ser Glu Phe Ala Ala Pro Gly Ala Ser Ser Trp Ala Leu
 530 535 540
 Asn Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His
 545 550 555 560
 Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe
 565 570 575
 Gly Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met
 580 585 590
 Ile Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
 595 600 605
 Ser Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala
 610 615 620
 Gln Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp
 625 630 635 640
 Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
 645 650 655
 His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
 660 665 670
 Met Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
 675 680 685
 Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile
 690 695 700
 Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
 705 710 715 720
 Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
 725 730 735
 Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly
 740 745 750
 Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
 755 760 765

Leu

<210> 40
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4 linker

<400> 40

Gly Leu Ser Gly
 1

<210> 41
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 6 linker

<400> 41

Gly Leu Ser Gly Ser Gly
 1 5

<210> 42
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 8 linker

<400> 42

Gly Leu Ser Gly Leu Ser Gly Ser
 1 5

<210> 43
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 10 linker

<400> 43

Gly Leu Ser Gly Leu Ser Gly Leu Ser Gly
 1 5 10

<210> 44
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 10 linker SEQ ID NO:44

<400> 44

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Gly Leu Ser Gly Gly Ser Gly Leu Ser Gly
1 5 10

<210> 45
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> Human IgG4 heavy chain - linker - SpyCatcher

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tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 180
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg cacgaagacc 240
tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc 300
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ttcctgttcc ccccaaaacc caaggacact ctcatgatct cccggacccc tgagggtcacg 420
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ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagttcaa cagcacgtac 540
cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaacggcaa ggagtacaag 600
tgcaagggtct ccaacaaagg cctcccgtcc tccatcgaga aaaccatctc caaagccaaa 660
gggcagcccc gagagccaca ggtgtacacc ctgcccccat cccaggagga gatgaccaag 720
aaccagggtca gcctgacctg cctgggtcaaa ggcttctacc ccagcgacat cgccgtggag 780
tgaggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 840
gacggctcct tcttcctcta cagcaggctc accgtggaca agagcagggtg gcaggagggg 900
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ctgtatccag gaaagtacac atttgtcgaa accgctgcac cagacggata tgagggtggct 1260
acagctatta cttttacagt gaatgagcaa ggacaggtga ctgttaatgg caaagctact 1320
aaaggagacg ctcatattta a 1341

<210> 46
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> SEQ ID NO:46

<400> 46

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
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 Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
 65 70 75 80
 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
 100 105 110
 Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 115 120 125
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 130 135 140
 Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
 145 150 155 160
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
 165 170 175
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 180 185 190
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
 195 200 205
 Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 210 215 220
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 225 230 235 240
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 245 250 255
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

260

265

270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
 290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 305 310 315 320

Leu Ser Leu Ser Leu Gly Lys Gly Ser Gly Glu Ser Gly Val Asp Thr
 325 330 335

Leu Ser Gly Leu Ser Ser Glu Gln Gly Gln Ser Gly Asp Met Thr Ile
 340 345 350

Glu Glu Asp Ser Ala Thr His Ile Lys Phe Ser Lys Arg Asp Glu Asp
 355 360 365

Gly Lys Glu Leu Ala Gly Ala Thr Met Glu Leu Arg Asp Ser Ser Gly
 370 375 380

Lys Thr Ile Ser Thr Trp Ile Ser Asp Gly Gln Val Lys Asp Phe Tyr
 385 390 395 400

Leu Tyr Pro Gly Lys Tyr Thr Phe Val Glu Thr Ala Ala Pro Asp Gly
 405 410 415

Tyr Glu Val Ala Thr Ala Ile Thr Phe Thr Val Asn Glu Gln Gly Gln
 420 425 430

Val Thr Val Asn Gly Lys Ala Thr Lys Gly Asp Ala His Ile
 435 440 445

<210> 47
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IgG-SpyCatcher Linker DNA

<400> 47
 ggaagcggcg aaagcggc

18

<210> 48
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IgG-SpyCatcher Linker AA

<400> 48

Gly Ser Gly Glu Ser Gly
1 5

<210> 49
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG

<400> 49
gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag 60
agcacagccg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg 120
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 180
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg cacgaagacc 240
tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc 300
aaatatggtc ccccatgccc accctgcccga gcacctgagt tcctgggggg accatcagtc 360
ttcctgttcc ccccaaaacc caaggacact ctcatgatct cccggacccc tgagggtcacg 420
tgcgtgggtg tggacgtgag ccaggaagac cccgaggtcc agttcaactg gtacgtggat 480
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagttcaa cagcacgtac 540
cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaacggcaa ggagtacaag 600
tgcaagggtct ccaacaaagg cctcccgtcc tccatcgaga aaaccatctc caaagccaaa 660
gggcagcccc gagagccaca ggtgtacacc ctgcccccat cccaggagga gatgaccaag 720
aaccagggtca gcctgacctg cctgggtcaaa ggcttctacc ccagcgacat cgccgtggag 780
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 840
gacggctcct tcttcctcta cagcaggctc accgtggaca agagcaggtg gcaggagggg 900
aatgtcttct catgctccgt gatgcatgag gctctgcaca accactacac acagaagtcc 960
ctctccctgt ctctgggtaa aggaagcggc gaaagcggcg tggataccct gtccggactg 1020

<210> 50
<211> 327
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG AA

<400> 50

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
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35

40

45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
 65 70 75 80
 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
 100 105 110
 Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 115 120 125
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 130 135 140
 Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
 145 150 155 160
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
 165 170 175
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 180 185 190
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
 195 200 205
 Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 210 215 220
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 225 230 235 240
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 245 250 255
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 260 265 270
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 275 280 285
 Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
 290 295 300
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser

305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
325

<210> 51
<211> 736
<212> PRT
<213> adeno-associated virus 6
<400> 51

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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

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

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

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

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

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

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

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

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
210 215 220

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Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
 225 230 235 240
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255
 Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
 260 265 270
 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
 275 280 285
 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
 290 295 300
 Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
 305 310 315 320
 Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
 325 330 335
 Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
 340 345 350
 Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
 355 360 365
 Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
 370 375 380
 Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
 385 390 395 400
 Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
 405 410 415
 Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
 420 425 430
 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
 435 440 445
 Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
 450 455 460
 Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
 465 470 475 480
 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
 485 490 495

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Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

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

<210> 52
<211> 2238
<212> DNA
<213> Artificial Sequence

<220>

<223> encodes pAAV2N587Myc

<400> 52

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cagtgggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac	120
gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac	180
aagggagagc cgggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac	240
cggcagctcg acagcggaga caaccctgac ctcaagtaca accacgccga cgcggagttt	300
caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag	360
gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg	420
ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga	480
aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac	540
tcagtacctg acccccagcc tctcggacag ccaccagcag cccctctggt tctgggaact	600
aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga	660
gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcac	720
accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaatt	780
tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg	840
tattttgact tcaacagatt cactgccac ttttcaccac gtgactggca aagactcatc	900
aacaacaact ggggattccg acccaagaga ctcaacttca agctctttta cattcaagtc	960
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cagggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga	1080
tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcacctg	1140
aacaacggga gtcaggcagt aggacgtctt tcattttact gcctggagta ctttccttct	1200
cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc	1260
cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag	1320
tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt	1380
cagttttctc aggccggagc gagtgcatt cgggaccagt ctaggaactg gcttcctgga	1440
ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaaca cagtgaatac	1500
tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc	1560
ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc	1620
atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaagg catgattaca	1680
gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct	1740
accaacctcc agagaggcaa cgaacaaaaa ctcatctcag aagaggatct gagacaagca	1800
gtaccgcag atgtcaacac acaaggcggt cttccaggca tggctctggca ggacagagat	1860
gtgtaccttc aggggcccac ctgggcaaag attccacaca cggacggaca ttttcacccc	1920
tctcccctca tgggtggatt cggacttaaa caccctcctc cacagattct catcaagaac	1980

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accccggtac ctgcgaatcc ttcgaccacc ttcagtgcgg caaagtttgc ttccttcac 2040
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 agcaaacgct ggaatcccgga aattcagtac acttccaact acaacaagtc tgттаатgtg 2160
 gactttactg tggacactaa tggcgtgtat tcagagcctc gccccattgg caccagatac 2220
 ctgactcgta atctgtaa 2238

<210> 53
 <211> 745
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of pAAV2N587 Myc

<400> 53

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45

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

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

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

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

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

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

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190

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Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
435 440 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
450 455 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480
 Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495
 Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510
 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525
 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540
 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560
 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575
 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Glu Gln Lys Leu Ile
 580 585 590
 Ser Glu Glu Asp Leu Arg Gln Ala Ala Thr Ala Asp Val Asn Thr Gln
 595 600 605
 Gly Val Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln
 610 615 620
 Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro
 625 630 635 640
 Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
 645 650 655
 Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Thr Thr Phe Ser
 660 665 670
 Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
 675 680 685
 Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
 690 695 700
 Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn Lys Ser Val Asn Val
 705 710 715 720
 Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg Pro Ile
 725 730 735

Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 740 745

<210> 54
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SpyTag002

<400> 54

Val Pro Thr Ile Val Met Val Asp Ala Tyr Lys Arg Tyr Lys
 1 5 10

<210> 55
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SpyCatcher002

<400> 55

Val Thr Thr Leu Ser Gly Leu Ser Gly Glu Gln Gly Pro Ser Gly Asp
 1 5 10 15

Met Thr Thr Glu Glu Asp Ser Ala Thr His Ile Lys Phe Ser Lys Arg
 20 25 30

Asp Glu Asp Gly Arg Glu Leu Ala Gly Ala Thr Met Glu Leu Arg Asp
 35 40 45

Ser Ser Gly Lys Thr Ile Ser Thr Trp Ile Ser Asp Gly His Val Lys
 50 55 60

Asp Phe Tyr Leu Tyr Pro Gly Lys Tyr Thr Phe Val Glu Thr Ala Ala
 65 70 75 80

Pro Asp Gly Tyr Glu Val Ala Thr Ala Ile Thr Phe Thr Val Asn Glu
 85 90 95

Gln Gly Gln Val Thr Val Asn Gly Glu Ala Thr Lys Gly Asp Ala His
 100 105 110

Thr