

SEQUENCE LISTING

<110> JIANGSU HENGRUI PHARMACEUTICALS CO., LTD.
SHANGHAI SHENGDI PHARMACEUTICAL CO., LTD.

<120> RECOMBINANT ADENO-ASSOCIATED VIRUS HAVING VARIANT CAPSID, AND APPLICATION THEREOF

<130> 722062CPCT

<150> CN 202110594986.X

<151> 2021-05-28

<160> 41

<170> PatentIn version 3.5

<210> 1

<211> 735

<212> PRT

<213> AAV2

<400> 1

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

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

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

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

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

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

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

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670

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

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

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

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

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 <212> PRT
 <213> AAV2.7m8

<400> 2

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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

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 Leu Ala Leu Gly Glu
580 585 590

Thr Thr Arg Pro Ala 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 Ile 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> 3
<211> 745
<212> PRT
<213> Artificial Sequence

<220>
<223> AAV2 seq1

<400> 3

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

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

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	Leu	Ala	Leu	Ala	Glu
			580					585					590		
Thr	Thr	Arg	Pro	Ala	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 Ile 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

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

<220>
<223> AAV2 seq2

<400> 4

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
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
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
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 Leu Ala Leu Gly Asp
580 585 590

Thr Thr Arg Pro Ala 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 Ile 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> 5
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<213> Artificial Sequence

<220>
<223> AAV2 seq3

<400> 5

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

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

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 Leu Ala Leu Gly Glu

580

585

590

Thr Thr Arg Asn Ala 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 Ile 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> 6

<211> 745

<212> PRT

<213> Artificial Sequence

<220>

<223> AAV2 seq4

<400> 6

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

210

215

220

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

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 Leu Ala Lys Ala Asp
580 585 590

Thr Thr Lys Asn Ala 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 Ile 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> 7
<211> 745
<212> PRT
<213> Artificial Sequence

<220>
<223> AAV2 seq5

<400> 7

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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 Leu Ala Lys Asp Asp
580 585 590

Thr Thr Arg Asn Ala 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 Ile 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> 8

<211> 745

<212> PRT

<213> Artificial Sequence

<220>

<223> AAV2 seq6

<400> 8

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
 20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

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

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 Leu Ala Leu Ala Asp
580 585 590

Thr Thr Lys Asn Ala 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 Ile 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> 9
 <211> 746
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AAV9 seq2

<400> 9

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

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro 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
 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 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 Leu Ala Leu Gly
 580 585 590

Asp Thr Thr Arg Pro Ala Ala Gln Ala Gln Thr Gly Trp Val Gln Asn
595 600 605

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

Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His
625 630 635 640

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

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

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

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

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

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

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

<210> 10
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of EGFP

<400> 10

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

```
<210> 11
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> seq1 (without linker)

<400> 11
```

Leu Ala Glu Thr Thr Arg Pro
1 5

```
<210> 12
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> seq2 (without linker)

<400> 12
```

Leu Gly Asp Thr Thr Arg Pro
1 5

```
<210> 13
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> seq3 (without linker)

<400> 13
```

Leu Gly Glu Thr Thr Arg Asn
1 5

```
<210> 14
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> seq4 (without linker)
```

<400> 14

Lys Ala Asp Thr Thr Lys Asn
1 5

<210> 15

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> seq5 (without linker)

<400> 15

Lys Asp Asp Thr Thr Arg Asn
1 5

<210> 16

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> seq6 (without linker)

<400> 16

Leu Ala Asp Thr Thr Lys Asn
1 5

<210> 17

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> seq1

<400> 17

Leu Ala Leu Ala Glu Thr Thr Arg Pro Ala
1 5 10

<210> 18

<211> 10

<212> PRT

<213> Artificial Sequence

<220>
<223> seq2

<400> 18

Leu Ala Leu Gly Asp Thr Thr Arg Pro Ala
1 5 10

<210> 19
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> seq3

<400> 19

Leu Ala Leu Gly Glu Thr Thr Arg Asn Ala
1 5 10

<210> 20
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> seq4

<400> 20

Leu Ala Lys Ala Asp Thr Thr Lys Asn Ala
1 5 10

<210> 21
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> seq5

<400> 21

Leu Ala Lys Asp Asp Thr Thr Arg Asn Ala
1 5 10

<210> 22

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

<220>
<223> seq6

<400> 22

Leu Ala Leu Ala Asp Thr Thr Lys Asn Ala
1 5 10

<210> 23
<211> 745
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of AAV2 seq2 capsid (708V)

<400> 23

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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 Leu Ala Leu Gly Asp
 580 585 590

Thr Thr Arg Pro Ala 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> 24

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

<220>
<223> Amino acid sequence of AAV2 seq3 capsid (708V)

<400> 24

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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
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
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 Leu Ala Leu Gly Glu						
		580		585		590
Thr Thr Arg Asn Ala 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> 25

<211> 745

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of AAV2 seq4 capsid (708V)

<400> 25

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

30

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 Leu Ala Lys Ala Asp
 580 585 590

Thr Thr Lys Asn Ala 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> 26

<211> 745

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of AAV2 seq5 capsid (708V)

<400> 26

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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
Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr		
	565	570
Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Leu Ala Lys Asp Asp		
	580	585
Thr Thr Arg Asn Ala Arg Gln Ala Ala Thr Ala Asp Val Asn Thr Gln		
	595	600
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
Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile		
	645	650
Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Thr Thr Phe Ser		
	660	665
Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val		
	675	680
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> 27
<211> 745
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of AAV2 seq6 capsid (708V)

<400> 27

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

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

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

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

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

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

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

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

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

130		135		140
Pro Val Glu His Ser	Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly			
145	150	155		160
Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr				
	165	170		175
Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro				
	180	185		190
Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly				
	195	200		205
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser				
	210	215		220
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile				
225	230	235		240
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 Leu Ala Leu Ala Asp
580 585 590

Thr Thr Lys Asn Ala 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> 28
<211> 304
<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of CMV enhancer

<400> 28

Cys Gly Thr Thr Ala Cys Ala Thr Ala Ala Cys Thr Thr Ala Cys Gly
1 5 10 15

Gly Thr Ala Ala Ala Thr Gly Gly Cys Cys Cys Gly Cys Cys Thr Gly
20 25 30

Gly Cys Thr Gly Ala Cys Cys Gly Cys Cys Cys Ala Ala Cys Gly Ala
35 40 45

Cys Cys Cys Cys Cys Gly Cys Cys Cys Ala Thr Thr Gly Ala Cys Gly
50 55 60

Thr Cys Ala Ala Thr Ala Ala Thr Gly Ala Cys Gly Thr Ala Thr Gly
65 70 75 80

Thr Thr Cys Cys Cys Ala Thr Ala Gly Thr Ala Ala Cys Gly Cys Cys
85 90 95

Ala Ala Thr Ala Gly Gly Gly Ala Cys Thr Thr Thr Cys Cys Ala Thr
100 105 110

Thr Gly Ala Cys Gly Thr Cys Ala Ala Thr Gly Gly Gly Thr Gly Gly
115 120 125

Ala Gly Thr Ala Thr Thr Thr Ala Cys Gly Gly Thr Ala Ala Ala Cys
130 135 140

Thr Gly Cys Cys Cys Ala Cys Thr Thr Gly Gly Cys Ala Gly Thr Ala
145 150 155 160

Cys Ala Thr Cys Ala Ala Gly Thr Gly Thr Ala Thr Cys Ala Thr Ala
165 170 175

Thr Gly Cys Cys Ala Ala Gly Thr Ala Cys Gly Cys Cys Cys Cys Cys
180 185 190

Thr Ala Thr Thr Gly Ala Cys Gly Thr Cys Ala Ala Thr Gly Ala Cys
 195 200 205

Gly Gly Thr Ala Ala Ala Thr Gly Gly Cys Cys Cys Gly Cys Cys Thr
 210 215 220

Gly Gly Cys Ala Thr Thr Ala Thr Gly Cys Cys Cys Ala Gly Thr Ala
 225 230 235 240

Cys Ala Thr Gly Ala Cys Cys Thr Thr Ala Thr Gly Gly Gly Ala Cys
 245 250 255

Thr Thr Thr Cys Cys Thr Ala Cys Thr Thr Gly Gly Cys Ala Gly Thr
 260 265 270

Ala Cys Ala Thr Cys Thr Ala Cys Gly Thr Ala Thr Thr Ala Gly Thr
 275 280 285

Cys Ala Thr Cys Gly Cys Thr Ala Thr Thr Ala Cys Cys Ala Thr Gly
 290 295 300

<210> 29
 <211> 309
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Sequence of CMV promoter

<400> 29

Thr Gly Cys Thr Gly Ala Thr Gly Cys Gly Gly Thr Thr Thr Thr Gly
 1 5 10 15

Gly Cys Ala Gly Thr Ala Cys Ala Cys Cys Ala Ala Thr Gly Gly Gly
 20 25 30

Cys Gly Thr Gly Gly Ala Thr Ala Gly Cys Gly Gly Thr Thr Thr Gly
 35 40 45

Ala Cys Thr Cys Ala Cys Gly Gly Gly Gly Ala Thr Thr Thr Cys Cys

50

55

60

Ala Ala Gly Thr Cys Thr Cys Cys Ala Cys Cys Cys Ala Thr Thr
65 70 75 80

Gly Ala Cys Gly Thr Cys Ala Ala Thr Gly Gly Gly Ala Gly Thr Thr
85 90 95

Thr Gly Thr Thr Thr Thr Gly Gly Cys Ala Cys Cys Ala Ala Ala Ala
100 105 110

Thr Cys Ala Ala Cys Gly Gly Gly Ala Cys Thr Thr Thr Cys Cys Ala
115 120 125

Ala Ala Ala Thr Gly Thr Cys Gly Thr Ala Ala Thr Ala Ala Cys Cys
130 135 140

Cys Cys Gly Cys Cys Cys Cys Gly Thr Thr Gly Ala Cys Gly Cys Ala
145 150 155 160

Ala Ala Thr Gly Gly Gly Cys Gly Gly Thr Ala Gly Gly Cys Gly Thr
165 170 175

Gly Thr Ala Cys Gly Gly Thr Gly Gly Gly Ala Gly Gly Thr Cys Thr
180 185 190

Ala Thr Ala Thr Ala Ala Gly Cys Ala Gly Ala Gly Cys Thr Cys Gly
195 200 205

Thr Thr Thr Ala Gly Thr Gly Ala Ala Cys Cys Gly Thr Cys Ala Gly
210 215 220

Ala Thr Cys Gly Cys Cys Thr Gly Gly Ala Gly Ala Gly Gly Cys Cys
225 230 235 240

Ala Thr Cys Cys Ala Cys Gly Cys Thr Gly Thr Thr Thr Thr Gly Ala
245 250 255

Cys Cys Thr Cys Cys Ala Thr Ala Gly Thr Gly Gly Ala Cys Ala Cys
260 265 270

Cys Gly Gly Gly Ala Cys Cys Gly Ala Thr Cys Cys Ala Gly Cys Cys
 275 280 285

Thr Cys Cys Gly Cys Gly Thr Cys Thr Cys Ala Gly Gly Gly Gly Ala
 290 295 300

Ala Gly Cys Thr Thr
 305

<210> 30
 <211> 43
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Sequence of 5'UTR

<400> 30

Cys Thr Thr Gly Thr Thr Cys Thr Thr Thr Thr Thr Gly Cys Ala Gly
 1 5 10 15

Ala Ala Gly Cys Thr Cys Ala Gly Ala Ala Thr Ala Ala Ala Cys Gly
 20 25 30

Cys Thr Cys Ala Ala Cys Thr Thr Thr Gly Gly
 35 40

<210> 31
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Kozak Sequence

<400> 31

Gly Cys Cys Ala Cys Cys
 1 5

<210> 32
 <211> 133
 <212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of 3'UTR

<400> 32

Gly Thr Cys Thr Ala Gly Ala Ala Ala Cys Cys Ala Gly Cys Cys Thr
1 5 10 15

Cys Ala Ala Gly Ala Ala Cys Ala Cys Cys Cys Gly Ala Ala Thr Gly
20 25 30

Gly Ala Gly Thr Cys Thr Cys Thr Ala Ala Gly Cys Thr Ala Cys Ala
35 40 45

Thr Ala Ala Thr Ala Cys Cys Ala Ala Cys Thr Thr Ala Cys Ala Cys
50 55 60

Thr Thr Thr Ala Cys Ala Ala Ala Ala Thr Gly Thr Thr Gly Thr Cys
65 70 75 80

Cys Cys Cys Cys Ala Ala Ala Ala Thr Gly Thr Ala Gly Cys Cys Ala
85 90 95

Thr Thr Cys Gly Thr Ala Thr Cys Thr Gly Cys Thr Cys Cys Thr Ala
100 105 110

Ala Thr Ala Ala Ala Ala Ala Gly Ala Ala Ala Gly Thr Thr Thr Cys
115 120 125

Thr Thr Cys Ala Cys
130

<210> 33

<211> 589

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of WPRE

<400> 33

Ala Ala Thr Cys Ala Ala Cys Cys Thr Cys Thr Gly Gly Ala Thr Thr
 1 5 10 15

Ala Cys Ala Ala Ala Ala Thr Thr Thr Gly Thr Gly Ala Ala Ala Gly
 20 25 30

Ala Thr Thr Gly Ala Cys Thr Gly Gly Thr Ala Thr Thr Cys Thr Thr
 35 40 45

Ala Ala Cys Thr Ala Thr Gly Thr Thr Gly Cys Thr Cys Cys Thr Thr
 50 55 60

Thr Thr Ala Cys Gly Cys Thr Ala Thr Gly Thr Gly Gly Ala Thr Ala
 65 70 75 80

Cys Gly Cys Thr Gly Cys Thr Thr Thr Ala Ala Thr Gly Cys Cys Thr
 85 90 95

Thr Thr Gly Thr Ala Thr Cys Ala Thr Gly Cys Thr Ala Thr Thr Gly
 100 105 110

Cys Thr Thr Cys Cys Cys Gly Thr Ala Thr Gly Gly Cys Thr Thr Thr
 115 120 125

Cys Ala Thr Thr Thr Thr Cys Thr Cys Cys Thr Cys Cys Thr Thr Gly
 130 135 140

Thr Ala Thr Ala Ala Ala Thr Cys Cys Thr Gly Gly Thr Thr Gly Cys
 145 150 155 160

Thr Gly Thr Cys Thr Cys Thr Thr Thr Ala Thr Gly Ala Gly Gly Ala
 165 170 175

Gly Thr Thr Gly Thr Gly Gly Cys Cys Cys Gly Thr Thr Gly Thr Cys
 180 185 190

Ala Gly Gly Cys Ala Ala Cys Gly Thr Gly Gly Cys Gly Thr Gly Gly
 195 200 205

Thr Gly Thr Gly Cys Ala Cys Thr Gly Thr Gly Thr Thr Thr Gly Cys

210

215

220

Thr Gly Ala Cys Gly Cys Ala Ala Cys Cys Cys Cys Cys Ala Cys Thr
 225 230 235 240

Gly Gly Thr Thr Gly Gly Gly Gly Cys Ala Thr Thr Gly Cys Cys Ala
 245 250 255

Cys Cys Ala Cys Cys Thr Gly Thr Cys Ala Gly Cys Thr Cys Cys Thr
 260 265 270

Thr Thr Cys Cys Gly Gly Gly Ala Cys Thr Thr Thr Cys Gly Cys Thr
 275 280 285

Thr Thr Cys Cys Cys Cys Cys Thr Cys Cys Cys Thr Ala Thr Thr Gly
 290 295 300

Cys Cys Ala Cys Gly Gly Cys Gly Gly Ala Ala Cys Thr Cys Ala Thr
 305 310 315 320

Cys Gly Cys Cys Gly Cys Cys Thr Gly Cys Cys Thr Thr Gly Cys Cys
 325 330 335

Cys Gly Cys Thr Gly Cys Thr Gly Gly Ala Cys Ala Gly Gly Gly Gly
 340 345 350

Cys Thr Cys Gly Gly Cys Thr Gly Thr Thr Gly Gly Gly Cys Ala Cys
 355 360 365

Thr Gly Ala Cys Ala Ala Thr Thr Cys Cys Gly Thr Gly Gly Thr Gly
 370 375 380

Thr Thr Gly Thr Cys Gly Gly Gly Gly Ala Ala Ala Thr Cys Ala Thr
 385 390 395 400

Cys Gly Thr Cys Cys Thr Thr Thr Cys Cys Thr Thr Gly Gly Cys Thr
 405 410 415

Gly Cys Thr Cys Gly Cys Cys Thr Gly Thr Gly Thr Thr Gly Cys Cys
 420 425 430

Ala Cys Cys Thr Gly Gly Ala Thr Thr Cys Thr Gly Cys Gly Cys Gly
435 440 445

Gly Gly Ala Cys Gly Thr Cys Cys Thr Thr Cys Thr Gly Cys Thr Ala
450 455 460

Cys Gly Thr Cys Cys Cys Thr Thr Cys Gly Gly Cys Cys Cys Thr Cys
465 470 475 480

Ala Ala Thr Cys Cys Ala Gly Cys Gly Gly Ala Cys Cys Thr Thr Cys
485 490 495

Cys Thr Thr Cys Cys Cys Gly Cys Gly Gly Cys Cys Thr Gly Cys Thr
500 505 510

Gly Cys Cys Gly Gly Cys Thr Cys Thr Gly Cys Gly Gly Cys Cys Thr
515 520 525

Cys Thr Thr Cys Cys Gly Cys Gly Thr Cys Thr Thr Cys Gly Cys Cys
530 535 540

Thr Thr Cys Gly Cys Cys Cys Thr Cys Ala Gly Ala Cys Gly Ala Gly
545 550 555 560

Thr Cys Gly Gly Ala Thr Cys Thr Cys Cys Cys Thr Thr Thr Gly Gly
565 570 575

Gly Cys Cys Gly Cys Cys Thr Cys Cys Cys Cys Gly Cys
580 585

<210> 34

<211> 140

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of SV40polyA

<400> 34

Cys Cys Thr Ala Gly Gly Thr Ala Ala Gly Ala Thr Ala Cys Ala Thr

1	5	10	15
Thr Gly Ala Thr Gly Ala Gly Thr Thr Thr Gly Gly Ala Cys Ala Ala	20	25	30
Ala Cys Cys Ala Cys Ala Ala Cys Thr Ala Gly Ala Ala Thr Gly Cys	35	40	45
Ala Gly Thr Gly Ala Ala Ala Ala Ala Ala Thr Gly Cys Thr Thr	50	55	60
Thr Ala Thr Thr Thr Gly Thr Gly Ala Ala Ala Thr Thr Thr Gly Thr	65	70	75
Gly Ala Thr Gly Cys Thr Ala Thr Thr Gly Cys Thr Thr Thr Ala Thr	85	90	95
Thr Thr Gly Thr Ala Ala Cys Cys Ala Thr Thr Ala Thr Ala Ala Gly	100	105	110
Cys Thr Gly Cys Ala Ala Thr Ala Ala Ala Cys Ala Ala Gly Thr Thr	115	120	125
Ala Thr Cys Gly Ala Thr Ala Gly Ala Thr Cys Thr	130	135	140

<210> 35
 <211> 7
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Variant AAV2 capsid protein

 <220>
 <221> VARIANT
 <222> (1)..(1)
 <223> Xaa can be L or K

 <220>
 <221> VARIANT
 <222> (2)..(2)
 <223> Xaa can be G, D or A

<220>
<221> VARIANT
<222> (3)..(3)
<223> Xaa can be D or E

<220>
<221> VARIANT
<222> (6)..(6)
<223> Xaa can be R or K

<220>
<221> VARIANT
<222> (7)..(7)
<223> Xaa can be P or N

<400> 35

Xaa Xaa Xaa Thr Thr Xaa Xaa
1 5

<210> 36
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant AAV2 capsid protein

<220>
<221> VARIANT
<222> (1)..(1)
<223> Xaa can be deleted, or can be A, L, G, S or T

<220>
<221> VARIANT
<222> (2)..(2)
<223> Xaa can be deleted, or can be A, L, G, S or T

<220>
<221> VARIANT
<222> (3)..(3)
<223> Xaa can be L or K

<220>
<221> VARIANT
<222> (4)..(4)
<223> Xaa can be G, D or A

<220>
<221> VARIANT

<222> (5)..(5)
<223> Xaa can be D or E

<220>
<221> VARIANT
<222> (8)..(8)
<223> Xaa can be R or K

<220>
<221> VARIANT
<222> (9)..(9)
<223> Xaa can be P or N

<220>
<221> VARIANT
<222> (10)..(10)
<223> Xaa can be deleted, or can be A, L, G, S or T

<220>
<221> VARIANT
<222> (11)..(11)
<223> Xaa can be deleted, or can be A, L, G, S or T

<400> 36

Xaa Xaa Xaa Xaa Xaa Thr Thr Xaa Xaa Xaa Xaa
1 5 10

<210> 37
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of AAV9 capsid

<400> 37

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

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro 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
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 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

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> 38

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of aflibercept protein

<400> 38

Met Pro Leu Leu Leu Leu Pro Leu Leu Trp Ala Gly Ala Leu Ala
 1 5 10 15

Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu
 20 25 30

Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val
 35 40 45

Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr
 50 55 60

Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe
 65 70 75 80

Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu
 85 90 95

Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg
 100 105 110

Gln Thr Asn Thr Ile Ile Asp Val Val Leu Ser Pro Ser His Gly Ile
 115 120 125

Glu Leu Ser Val Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr
130 135 140

Glu Leu Asn Val Gly Ile Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys
145 150 155 160

His Gln His Lys Lys Leu Val Asn Arg Asp Leu Lys Thr Gln Ser Gly
165 170 175

Ser Glu Met Lys Lys Phe Leu Ser Thr Leu Thr Ile Asp Gly Val Thr
180 185 190

Arg Ser Asp Gln Gly Leu Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met
195 200 205

Thr Lys Lys Asn Ser Thr Phe Val Arg Val His Glu Lys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu

340

345

350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 39

<211> 1347

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence 1 of aflibercept

<400> 39

atgcccctgc tcctgctcct gcccctgctg tgggccggcg ccctggctag cgacaccggc 60

agacccttcg tggagatgta cagcgagatc cccgagatca tccacatgac cgagggcaga 120

gagctggtga tcccctgcag agtgacaagc cccaacatca ccgtgaccct gaaaaaattc 180

cctctggaca ccctgatccc cgacggcaag agaatcatct gggacagcag aaagggttc 240

atcatcagca acgccaccta caaggagatc ggcctgctga cctgcgaggc caccgtgaac 300

ggccacctgt acaagaccaa ctacctgacc cacagacaga ccaacaccat catcgacgtg 360

gtgctgagcc ctagccacgg catcgagctg agcgtgggcg agaagctggt gctgaactgc 420

accgctagaa ccgagctgaa cgtgggcatc gacttcaact gggagtaccc tagcagcaag 480

catcagcaca agaagctggt gaacagagac ctgaagacac agagcggcag cgagatgaag 540

aagttcctga gcaccctgac catcgacggc gtgacaagaa gcgaccaagg cctgtacacc	600
tgcgccgcta gcagcggcct gatgaccaag aagaacagca ctttcgtgag agtgcatgag	660
aaggacaaga cccacacctg cccccctgc cccgctcctg aactgctggg cggccctagc	720
gtgttcctgt tccccccaa gcccaaggac acactcatga tcagcagaac ccccgaggtg	780
acctgcgtgg tcgtggacgt gagccacgag gaccccgagg tgaagttcaa ctggtacgtg	840
gacggcgtgg aggtgcacaa cgccaagacc aagcctagag aggagcagta caacagcacc	900
tacagagtgg tgagcgtgct gaccgtgctg caccaagact ggctgaacgg caaggagtac	960
aagtgcaagg tgagcaacaa ggccctgccc gccccatcg agaagaccat cagcaaggcc	1020
aaggggcagc ctagagagcc ccaagtgtac accctgcccc ctagcagaga cgagctgacc	1080
aagaaccaag tgagcctgac ctgcctggtg aagggttctt accctagcga catcgccgtg	1140
gagtgggaga gcaacgggca gcccgagaac aactacaaga ccaccccccc cgtgctggac	1200
agcgacggca gcttcttctt gtacagcaag ctgaccgtgg acaagagcag atggcagcaa	1260
ggcaacgtgt tcagctgcag cgtgatgcac gaggccctgc acaaccacta cacacagaag	1320
agcctgagcc tgagccccgg caagtga	1347

<210> 40
 <211> 1347
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence 2 of aflibercept

<400> 40	
atgcctctgc tcctgctgct ccctctgctg tgggccggcg ccctggccag cgacacaggc	60
cgcccccttcg tggaaatgta cagcgagatc cctgagatca tccacatgac agagggccgg	120
gaactggtca tcccttgtag agtgacatct ccaaacatca ccgtgaccct gaaaaagtgc	180
cccctggaca cactgatccc tgacggcaaa agaatcatct gggattcccg gaagggttc	240
atcatcagca atgccaccta caaggaaatc ggactgctga cctgtgaagc cacagtgaac	300
ggccacctgt acaagaccaa ctacctgacc cataggcaga ccaataccat catcgatgtg	360
gtgctgtctc cttctcacgg catcgagctc agcgtcggcg agaaactggg gctgaactgc	420

accgccagaa ccgagctgaa cgtgggcatc gacttcaact gggaataccc cagttctaag	480
caccagcaca agaaactggt taatagagat ctgaagaccc aaagcggcag cgagatgaaa	540
aagtttctgt ctacactgac aattgacggt gttaccagaa gcgatcaggg cctgtataca	600
tgcgccgctt ctagcggcct gatgaccaag aagaacagca ctttcgtgcg ggtgcacgag	660
aaggacaaga cccacacctg cccccctgt ccagctcctg aactgctggg aggccctagc	720
gtgttcctgt tccctccaaa gcctaaggac acccttatga ttagcagaac acctgaggtg	780
acctgcgtgg tggtcgacgt gtcccacgag gaccccgagg tgaaatttaa ctggtacgtg	840
gatggcgtgg aagttcacia cgccaagacc aagcccagag aggaacagta caacagcaca	900
tatagagtgg tgtccgtgct gaccgttctg caccaggact ggctgaatgg aaaagagtac	960
aagtgcaagg tgtccaacia ggccctgcct gcccttatcg agaagactat cagcaaggct	1020
aagggccaac ctcgggaacc ccaggtgtac accctgcccc ccagccggga cgagctgaca	1080
aagaaccagg tgtccctgac atgcctggtg aagggatttt accctagcga tatcgccgtg	1140
gaatgggaga gcaacggcca gcctgagaac aactacaaaa cgaccctcc tgtgctggac	1200
tctgatggca gcttcttctt gtacagcaag ctgaccgtgg acaagagcag atggcagcag	1260
ggcaacgtgt tctcatgcag cgtgatgcac gaggccctgc ataataccta caccagaaa	1320
agcctgagcc tgagccctgg caagtga	1347

<210> 41

<211> 1347

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence 3 of aflibercept

<400> 41

atgccactgc tcttgctttt gcccttgctt tgggctggtg cccttgctc agacactgga	60
aggccgttcg tagaaatgta ctccgagatc cctgaaataa tccacatgac ggaggggcca	120
gagttggtga taccatgtcg agttacgagc ccgaatatta cagtaacatt gaagaaattc	180
ccactcgaca ctctcattcc agatggtaag agaattatat gggattcacg aaagggttc	240
attatatcta acgtactta caaagagata ggcttgctca catgcgaggc aactgtcaat	300
ggccacttgt ataaaacaa ttatctcaca cataggcaga ctaatacgat aatagacgtt	360

gtcctttctc cgagccatgg cattgaattg agtgtcggtg agaagctcgt attgaactgc	420
actgctagga ccgagcttaa cgtagggatc gactttaact gggagtaccc atcatcaaag	480
catcagcata aaaagctcgt caaccgggac cttaaagacgc agagtggctc agagatgaag	540
aagttccttt ctacactgac catcgatggt gtaaccagaa gtgaccaggg actctatacc	600
tgtgccgcat cctccggcct tatgacgaag aaaaacagca catttgttcg ggtccacgag	660
aaggacaaga ctcatacgtg tccgccgtgt ccagccccag aattgctcgg ggggccttcc	720
gtgtttctgt tccctccaaa gccaaaggac acgcttatga tttcaaggac tcccgaagtc	780
acctgcgtcg tggttgacgt ttctcatgag gaccagagg tgaaattcaa ctggtacgtg	840
gatggagtag aggtacataa cgccaaaaca aaaccacgag aagagcagta taactcaacg	900
tatcgggtag tttctgtgct tacggttctc caccaagatt ggttgaatgg aaaagagtat	960
aagtgtaaag tctcaaaca agccctgccg gcacccatcg agaagaccat tagcaaagca	1020
aaaggccaac ctagagaacc gcaggtgtac acgttgccac cgtcaaggga tgaacttacg	1080
aagaatcaag tatcactcac atgtttgggt aaaggatttt atcccagcga catcgccgta	1140
gaatgggaga gtaacggcca gcctgaaaat aactataaga cgacaccccc tgttttggat	1200
tctgacgggtt catttttttt gtatagtaaa ctcacagtcg acaagagtcg ctggcaacaa	1260
ggtaatgtat ttagctgtag cgtgatgcat gaagctttgc acaaccacta tacacagaag	1320
tccttgtctc tgtctccggg aaaatga	1347